Introduction, Breeding, Propagation and Deployment of Pacific Northwest Conifers Around the World: 70 years of Progress, Opportunities and Challenges

Virtual International Conference
8-10 November 2021
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RÉSEAU MiDi Milieux & Diversité
Réseau thématique de recherche
en Région Centre Val de Loire

IUFRO

LE STUDIUM
Loire Valley
Institute for Advanced Studies

LIECO
SUCCESSFUL AFFORESTATION

FGC
Forest Genetics Council
of British Columbia

ORGANIZERS

Organizer : The MiDi (Habitats & Diversity [Milieux & Diversité]) network is an interdisciplinary Thematic Research Network in the Centre-Val de Loire Region (France).

Sponsor: International Union of Forest Research Organizations, The MiDi (Habitats & Diversity [Milieux & Diversité])

Host: LE STUDIUM Loire Valley Institute for Advanced Studies

ORGANIZING COMMITTEE

Brian Baltunis (Weyerhaeuser Company, USA)

Keith Jayawickrama (Oregon State University, USA)

Jaroslav Klápste (Scion, New Zealand)

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Philippe Rozenberg (INRAE, France)

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Richard Sniezko (United States Forest Service, USA)

Nick Ukrainetz (British Columbia Minsitry of Forests, Lands, Natural Resources, Rural Development, Canada)

Terrance Ye (Oregon State University, USA)

Virtual International

CONFERENCE

8-10 NOVEMBER 2021

ABSTRACTS

Introduction, Breeding, Propagation and Deployment of Pacific Northwest Conifers Around the World: 70 years of Progress, Opportunities and Challenges

INTRODUCTION

Dear Tree Improvers, Researchers, Seed Orchardists, Foresters, and other Colleagues around the world: We are pleased to offer a most cordial welcome to the first ever virtual meeting of IUFRO Working Group 2.02.05 "Breeding and Genetic Resources of Pacific Northwest Conifers"!

Yes, there has been much disruption since covid-19 made its appearance, but PNW conifer trees have kept growing and providing many benefits in their area of origin and around the world! Breeding programs are entering their third or fourth cycle, high-gain orchard seed is becoming abundant, and the need to respond to changing climates grows ever more pressing. WG 2.02.05 has not met since Forest Genetics 2013 in Whistler, British Columbia, Canada in July 2013. We feel this meeting is overdue.

By means of modern technology, we hope you will join from wherever you are based, learn about and share your recent genetics-related experiences, research and progress with these magnificent tree species!

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POSTERS

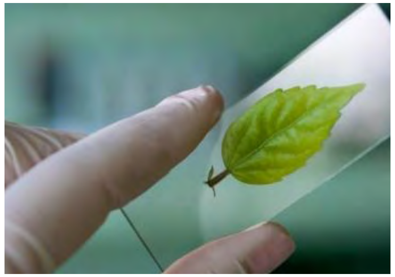
IUFRO

INTERNATIONAL UNION OF FOREST RESEARCH ORGANIZATIONS

Forests.

Forests and trees cover about one third of the world's land base. They grow in different climates and environments and on different soils, and they offer various goods and services. The livelihoods of more than a quarter of the Earth's population depend on forests.

Science.



Scientists worldwide want to know more about forests and trees. They want to understand exactly how they grow, what makes them healthy, and how to use their goods and services sustainably. And they want to help them cope with impacts from an increasing world population and climate change.

People.

People's well-being and prosperity depend on the productivity and robustness of the world's ecosystems and the services they provide. Scientific knowledge and research capacity contribute to ensuring a resilient and diverse natural resource base and support sound decision making.

IUFRO.

IUFRO, the International Union of Forest Research Organizations, offers a global network for voluntary cooperation. The network is open to all individuals and organizations dedicated to forest and forest products research and related disciplines. IUFRO aims to contribute to achieving the Sustainable Development Goals set by the United Nations.

Participate.

IUFRO is a global, non-profit, non-governmental and non-discriminatory organization established in 1892 with headquarters in Vienna, Austria. It unites about 650 member organizations in more than 120 countries representing over 15,000 scientists.

70 meetings are held on average every year. IUFRO World Congresses take place every 4-5 years.

SPONSORS

MiDi

(HABITATS & DIVERSITY [MILIEUX & DIVERSITÉ])

MiDi (Habitats and Diversity) is a interdisciplinary Research Thematic Network, focused on biodiversity and habitats ; and funded by the Centre-Val de Loire Region. The network aims to promote studies in multiple fields of BioGeoSciences and Human and Social Sciences in relation to global changes.
On the basis of the competences present in the Region on habitats and social dynamics, MiDi has defined 3 research axes and 4 object studies :

RESEARCH AXES

The dynamics of natural resources under conditions of global change

Adaptation mechanisms of living organisms to variations in habitats

The technical and social engineering of habitats and biodiversity

OBJECTS

Water

Forest

Soil

City

Our missions

- Research dynamics

To promote meetings and the inter knowledge of laboratories in the Centre Val de Loire Region and abroad with environmental themes and to increase the visibility of academic skills in the Centre Val de Loire Region

- Supporting research projects

To help researchers in the setting up of their project and to contribute to the development of the project

- To engage in training activities

Propose training days for students, young researchers

Our activities

- Scientific events

To organize and support scientific and technical events

Develop interactions between research activities and socio economic activities located in the region; enhance research work and knowledge sharing

- Research projects

Supporting researchers in the preparation of applications for international projects, drafting the "socio economic impact" section, leading thematic groups, helping with international mobility.
Support for regional, national and international projects International mobility of researchers

- Develop the link between research and training through training activities for students and researchers

Workshops for master and doctoral students

LIECO

LIECO GMBH & CO KG

LIECO has been producing high quality containerized forest seedlings since 1985. The family-owned company is holding the market leadership in Austria and Germany. Due to the long production experience and R&D efforts, LIECO is also playing the leading role in terms of technology- and know how in the forest-nursery sector.
In 2019 and 2020 LIECO Group expanded the activities in Germany by acquiring two forest-nurseries (P & P and Lürssen).
The company offers the whole assortement of plants (bareroot and containerized seedlings) and forest service.

Facts:

- 6 production sites in Austria and Germany
- 335 ha production area
- 28 Million seedlings sold in 2020
- 250 employees

FGC

FOREST GENETICS COUNCIL OF BRITISH COLUMBIA

The **Forest Genetics Council of British Columbia** (FGC) is a multistakeholder advisory body whose members are appointed by the Provincial Chief Forester from the provincial and federal governments, forest-sector companies, and universities. FGC's website lists current FGC members. FGC's mission is to enhance the conservation, adaptation, productivity and health of BC's forests so current and future generations continue to enjoy the benefits derived from them. FGC accomplishes its mission by planning and coordinating research and operational activities, and by advising the Ministry on related policies and funding priorities. FGC is supported by three technical advisory comittees: Conservation, Coast and Interior. FGC owns Select Seed Company Ltd., which contributes to FGC's goals by producing and selling improved tree seed for reforestation. Select Seed also provides services to FGC and supports the Ministry's breeding program.

FGC's scope includes BC's 43 native tree species with emphasis on commercial tree species planted on Crown and private forest land. Activities include forest genetics research, conservation, conventional tree breeding, seed production, seed supply management, seed deployment, silviculture, and their related policies and practices.

Guiding Principles

- Encourage equity, diversity, inclusivity and collaboration
- Respect participants' independence.
- Respond to environmental, social, economic, and technological changes.
- Incorporate science, health & safety, operational feasibility, and traditional knowledge into policies and practice.
- Measure, evaluate, and improve activities and performance.

PROGRAMME DAY 1

MONDAY 8 NOVEMBER 2021 (16:00-19:50 CET) (07:00-10:50 PST)

16:00 / 07:00 Welcome Address **Santiago C. González-Martínez**
Organisation notes **Keith Jayawickrama**
Sponsor messages

SESSION 1 : PROVENANCE RESEARCH AND TREE BREEDING

Moderator : Philippe Rozenberg

16:20 / 07:20 **Johan Kroon** - Introduction, tree breeding and use of PNW Conifers in Sweden

16:40 / 07:40 **Aris Jansons** - Performance of lodgepole pine provenances in hemiboreal forests of Europe, Latvia

17:00 / 08:00 **Keith Jayawickrama** -Testing and deployment of coastal redwood in California and Oregon

17:20 / 08:20 **Brian Baltunis** - Weyerhaeuser's Advanced Generation Breeding and Testing of Douglas-fir

POSTER SESSION

Moderator : Silvio Schüler

17:40 / 08:40 **Seppo Ruotsalainen** - Experiences with PNW Conifers in Finland

17:43 / 08:43 **Xiali Guo** - Common-garden experiment reveals clinal trends of bud phenology in black spruce populations from a latitudinal gradient in the boreal forest

17:46 / 08:46 **Georgeta Mihai** - Could Douglas fir be an alternative species in a changing climate? Comparative analysis with local Norway spruce in western Romania

17:49 / 08:49 **Chuanping Yang** - Genetic variation and climate response of radial growth of Larix olgensis at four trails in northeast China

17:52 / 08:52 **Mirko Liesebach** - The German breeding concept on Douglas-fir – current status

17:55 / 08:55 Poster discussion (Chat) & Coffee Break

SESSION 2 : TREE BREEDING

Moderator : Brian Baltunis

18:10 / 09:10 **Domen Finzgar** - Genetic assessment of the Sitka spruce British breeding programme

18:30 / 09:30 **Trevor Doerksen** - Overview of tree breeding programs in the interior of British Columbia, Canada

18:50 / 09:50 **Charlie Cartwright** - Early Results from New Realized Gain Trials with Western Hemlock on the British Columbia Coast

19:10 / 10:10 **Keith Jayawickrama** - Updates on Cooperative Tree Improvement for Coastal Douglas-fir in western Washington, western Oregon, and NW California

19:30 / 10:30 **Milos Ivkovich** - Scaling of Estimated Breeding Values in Australian Pinus radiata Breeding Program

19:50 / 10:50 End

PROGRAMME DAY 2

TUESDAY 9 NOVEMBER 2021 (16:00-19:50 CET) (07:00-10:50 PST)

SESSION 1 : CLIMATE CHANGE - GENECOLOGY

Moderator : Keith Jayawickrama

16:00 / 07:00 **Philippe Rozenberg** - Potential of adaptation to drought in Douglas-fir: twenty years of research efforts

16:20 / 07:20 **Silvio Schüler** - Will climate change result into a new era of introductions of conifers? A case study about needs, opportunities and risks in Austria

16:40 / 07:40 **Marie Vance** - Drought screening in ponderosa pine

17:00 / 08:00 **Joseph Stewart** - Optimizing Assisted Gene Flow for Forests

17:20 / 08:20 **Jeff Debell & Peter Gould** - The PNW Seed Source Project: A low-cost collaborative approach to provide both data and demonstration in support of climate change adaptation decisions

POSTER SESSION

Moderator : Silvio Schüler

17:40 / 08:40 **Richard Sniezko** - Searching for White Pine Blister Rust Resistance in Foxtail Pine (Pinus balfouriana)

17:43 / 08:43 **Keith Jayawickrama** - Diverse PNW Forests for the 21st Century - Developing Secondary Conifers

17:46 / 08:46 **Terrance Ye** - Early Assessment on Realized Genetic Gains from Second-Cycle Western Hemlock Tree Improvement

17:49 / 08:49 **Diāna Jansone** - Growth of Sitka Spruce and Douglas Fir in European hemiboreal forests, Latvia

17:52 / 08:52 **Zihaohan Sang** - Should we plant trees at higher latitudes or at higher elevations to compensate for climate change? An evaluation of frost risks

17:55 / 08:55 Poster discussion (Chat) & Coffee Break

SESSION 2 : FOREST HEALTH - GENECOLOGY

Moderator : Marcela van Loo

18:10 / 09:10 **Magdalena Kacprzyk** - Biotic threats to key Pacific Northwest Species in Western and Central Europe

18:30 / 09:30 **Geoffrey Williams** - A Sentinel Network Information Platform for N. American Woody Flora: Leveraging Established ex situ Plantings of PNW Conifers and Integration with Parallel Efforts

18:50 / 09:50 **Richard Sniezko** - Developing and Using White Pine Blister Rust-Resistant Populations of Pinus monticola, P. albicaulis and P. lambertiana

19:10 / 10:10 **Gregory O'Neill** - Genecology forest health traits in western North American conifers

19:30 / 10:30 **Richard Sniezko** - Port-Oford-cedar (Chamaecyparis lawsoniana) and resistance to Port-Orford-cedar root disease and Stigmina foliage blight

19:50 / 10-50 End

PROGRAMME DAY 3

WEDNESDAY 10 NOVEMBER 2021 (16:00-19:50 CET) (07:00-10:50 PST)

SESSION 1 : SEED AND SEEDLING MANAGEMENT - MOLECULAR GENETICS AND BREEDING

Moderator : Richard Sniezko

16:00 / 07:00 **Dave Kolotelo** - Deployment Bottlenecks: Cone and Seed Processing, Storage and Inventory Management

16:20 / 07:20 **Brian Barber -** Overview of the British Columbia Seed Orchard Program

16:40 / 07:40 **Madlen Walther & Andrea Rupps -** Vegetative propagation of Pseudotsuga menziesii by refined somatic embryogenesis and its application in multilateral field trials

17:00 / 08:00 **Hayley Tumas -** A SNP marks the spot: a high-density linkage map for UK Sitka spruce (Picea sitchensis [Bong.] Carr.)

17:20 / 08:20 **Marcela van Loo -** Douglas-fir: Whole-exome sequencing unravels genomic signals of climatic adaptation

POSTER SESSION

Moderator : Terrance Ye

17:40 / 08:40 **Andrew Bower -** Seed source evaluation trials to evaluate the feasibility of operational assisted migration

17:43 / 08:43 **Andrew Bower** - Establishment of white pine blister rust resistant seed orchards for whitebark pine in the Pacific Northwest

17:46 / 08:46 **Amanda De La Torre -** Differences in growth, heat and drought tolerance among advanced-generation hybrids and coastal Douglas fir families

17:49 / 08:49 **Omnia Gamal El-Dien** - Genomic Selection in western redcedar breeding program in BC: from proof of concept to application

17:52 / 08:52 Poster discussion (Chat) & Coffee Break

SESSION 2 : SEED AND SEEDLING MANAGEMENT - MOLECULAR GENETICS AND BREEDING

Moderator : Nicholas Ukrainetz

18:10 / 09:10 **BUSINESS SESSION - Opportunity to elect new office-bearers**

18:30 / 09:30 **Jia Guo -** Low-density SNP Genotyping in Douglas-fir using Targeted Genotyping-by-sequencing

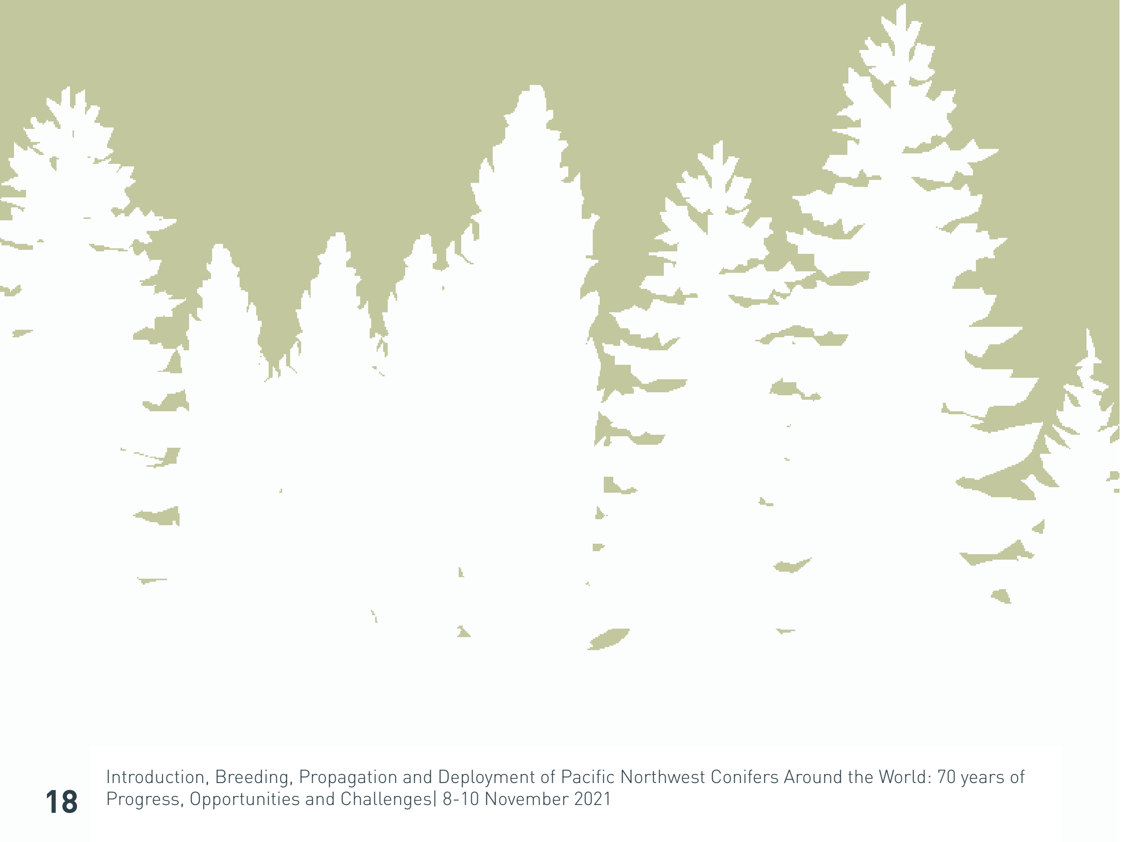
18:50 / 09:50 **Jun-Jun Liu -** Genomics-assisted breeding of western white pine resistance to white pine blister rust

19:10 / 10:10 **Jaroslav Klapste** - Genomics-enabled radiata pine breeding in New Zealand

19:30 / 10:30 **Natalie Graham** - Development of a 36K SNP array for radiata pine

19:50 / 10-50 End

ORAL COMMUNICATIONS



Brian Baltunis

Weyerhaeuser

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Brian Baltunis is a Tree Improvement Manager at Weyerhaeuser Company where he manages a breeding and testing program for Douglas-fir. Brian has a background in quantitative genetics, tree improvement, breeding and testing, vegetative propagation, and clonal forestry. Brian's broad experience in forest genetics research includes experience in private industry, academics, private consulting, and public-sector research organizations. Brian has a Ph.D. in Forest Genetics (minor in Statistics) from University of Florida, M.S. in Forestry (focusing on applied tree improvement) from University of Maine, and a B.S. in Forest Resources Management (minor Plant Biology) from Southern Illinois University in Carbondale.

Weyerhaeuser's Advanced Generation Breeding and Testing of Douglas-fir

This paper will review the history of Weyerhaeuser's Douglas-fir tree improvement program from 1st generation to present with major emphasis on advanced generation breeding and testing of low-elevation Douglas-fir for Weyerhaeuser's ownership in Oregon and Washington, USA. Weyerhaeuser's current advanced generation program is continuous with overlapping generations; and breeding, testing, and selections occur on an annual basis. A major strategic priority is to maintain or enhance productivity, quality, and adaptability of Weyerhaeuser's forests. A wide testing strategy was implemented after results from the Washington Wide Adaptability Study and other 1st generation source movement trials indicated that genotype by environment interaction (GxE) was of little practical importance in breeding coastal Douglas-fir across regions of western Washington and Oregon; it was possible to select coastal Douglas-fir that produce strong, stable growth across this range of environments; movement of improved seed can lead to positive outcomes for plantation productivity; and, strategies of having separate breeding lines of coastal Douglas-fir based on local regions would deliver suboptimal genetic gain (Stonecypher et al. 1996; Dean 2007). A major aim of this advanced generation breeding and testing program is to further explore the extent of GxE across Weyerhaeuser's ownership to guide both breeding and deployment decisions. The importance of retaining progeny trials thru to rotation (trendsetters) is also discussed in relation to age-age genetic correlations and assessing long-term adaptability.

Key words : Weyerhaeuser, Douglas-fir, breeding, testing, GxE

Brian Barber

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Brian obtained his BSF from the University of British Columbia in 1987 and a MA in Environment and Management from Royal Roads University in 2007. He is a member of the Association of BC Forest Professionals and the Canadian Institute of Forestry. Since 2016, Brian has served as CEO, Select Seed Co. Ltd., a not-for-profit company owned by Forest Genetics Council of BC (FGC). Select Seed produces tree seed under contract with companies in BC's southern interior. Brian also supports FGC as Program Manager. Previously, Brian served as Director, Tree Improvement Branch, BC Ministry of Forests. In that role he had oversight for forest genetics research, tree breeding, seed orchards, seed regulations and information systems, and the Tree Seed Centre. He also served as Co-chair, FGC.

Overview of British Columbia's Seed Orchard Programs

British Columbia's (BC) forest genetics program began in the 1950 with Coastal Douglas-fir under the direction of Dr. Alan Orr-Ewing and the Plus Tree Board. Today, over a dozen species are represented in the BC Ministry of Forests' tree breeding programs and in over 100 seed orchards managed by the Ministry and private companies. These orchards produce approx. 70% of seed used to grow the 300 million seedlings planted annually by forest tenure holders and the government in BC.

The Forest Genetics Council of British Columbia (FGC), appointed by the Provincial Chief Forester, guides funding and activities that enhance the conservation, adaptation, health, and productivity of BC's forests. These activities include ex situ seed collections, provenance and progeny testing, seed orchards and tree seed regulations and standards.

In 2018, the Chief Forester introduced new climate-based seed transfer (CBST) standards, which take into consideration recent past and future climate. Seed demand under CBST, coupled with declining allowable annual harvest levels, shifts in reforestation practices (e.g. species selection and planting densities) and the rehabilitation of areas destroyed by wildfires, remain somewhat uncertain. Nonetheless, new second-cycle seed orchards are currently being established to supply seed under CBST.

This presentation will summarize the current opportunities and challenges faced by BC's forest genetic program, with emphasis on tree seed production and use.

Key words: Forest Genetics, Seed Orchards

Charlie Cartwright

Cowichan Lake Research Station

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Started work in forestry in the late 1970s with the Coastal Douglas-fir Forest Genetics Program of the Province of British Columbia. This was followed by a BSc (Hons) in Forest Biology (UBC, 1984) and a MS in Wood Science and Technology at UC Berkeley (1988). From that point forward there were contracts with the Research Branch of the BC Forest Service, followed by joining staff as a science officer (1994). Initial endeavours were in tree improvement of western redcedar and Alaska yellow cedar, then western hemlock and Sitka spruce. As our science staff dwindled our responsibilities expanded so that currently my work includes hemlock, Sitka spruce, the true firs and gene conservation. With whitebark pine gaining endangered status in Canada, action was required, so my tree improvements skills were applied to it as well.

Early Results from New Realized Gain Trials with Western Hemlock on the British Columbia Coast

Co-author : John King

The forest genetics program for western hemlock in British Columbia (BC) began with parent tree selections in the late 1950s, and first progeny trials being established by Tahsis Company in the early 1970s. Further first-generation testing followed, planted by BC Ministry of Forest's Research Branch late in that decade. A co-operative approach with American interests started at that time and developed farther with formation of the Hemlock Tree Improvement Cooperative which put together second- generation trials. These tests went into the ground around the end of the twentieth century. Best families from the advanced generation were contrasted with woods run standards in 3 realized gain trials in BC with others going into the ground in the USA. The Canadian tests have natural regeneration as a treatment since that is a common method of regenerating hemlock ground in the province. Early results (age 5 years) are reported including details of patchiness and regeneration delay.

CLIMATE / GENECOLOGY

Jeff DeBell

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Jeff DeBell is a managing scientist responsible for forest genetics and seed production for the Washington State Department of Natural Resources (WDNR). In that role, his goal is to ensure that the seedlings planted by WDNR will be adapted to future climates as well as future markets. Jeff holds a Ph.D. in Forest Science and Forest Products from Oregon State University.

CLIMATE / GENECOLOGY

Peter Gould

Peter Gould is the forest biometrician at the Washington State Department of Natural Resources were he is involved in managing 2.1 million acres of forest. He earned a PhD in forestry in 2005 from the Pennsylvania State University. His research work has included incorporating genetic gain into forest growth models and predicting forest growth responses to climate change in the Pacific Northwest.

The PNW Seed Source Project: A low-cost collaborative approach to provide both data and demonstration in support of climate change adaptation decisions

Seed source choices for planting in forestry programs will need to be modified in order to adapt to climate change. Better knowledge of the response of species and seed sources across a wide range of environmental conditions is important for making good decisions in the future. While such data is available for some species (e.g. lodgepole pine in British Columbia from the well-known Illingworth trial), there are relatively few datasets for the U.S. Pacific Northwest that are well-suited for this purpose. In addition to generating data that allows us to model effects of seed movement, we believe that it is also valuable to provide demonstration plots where people can observe seed source performance in their own local areas. Tangible examples should increase the comfort level with planting non-local sources and acceptance of the recommendations from modelling of the data. This consideration leads us to design a provenance experiment that serves both data and demonstration goals.

We plan to establish a common set of 23 Douglas-fir seed sources across a large number of small, inexpensive sites in order to create a robust dataset and provide convenient local demonstration areas for many people. This strategy also reduces barriers for others to establish sites for our network, allowing us to sample environments not represented within our land base. Although most sites will likely be on large ownerships managed by foresters, we are trying to keep the installation and measurement protocols simple enough that small landowners can participate as well. This "citizen science" approach can open communication channels that will facilitate technology transfer as results become available. Our design choices reflect the focus on keeping sites simple and inexpensive to achieve a large number of sites. Row plots of each source will be used to improve demonstration value and minimize monumentation costs and identity errors. Rectangular spacing will be used to minimize inter-source competition as the trees grow larger. There will not be internal replication at each site, allowing available trees to be used over more sites. We are planning to limit regular measurements to a short list of easily measured traits. This basic set of data can be supplemented with more detailed measurements if budgets allow, but it is important that the basic measurements be simple and inexpensive so that collaborators will be able to reliably complete the measurements on their sites. We are working on an efficient system to remind collaborators when it is time to measure, allow them to submit the data easily, and provide a results site where everyone can see current results. We are starting small, with enough seedlings growing in the nursery to plant the first five sites. We will continue to grow more seedlings each year, and provide installation "kits" that can be distributed to collaborators who agree to plant and measure sites over time. Although this beginning effort is focused on Douglas-fir, we hope to be able to extend this model to other species as the project becomes more established.

Key words : climate adaptation, seed source, citizen science, demonstration

Trevor Doerksen

BC Ministry of Forests, Lands, Natural Resource Operations and Rural Development

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Trevor is a government tree breeder working on hybrid (white-Engelmann) spruce, Douglas-fir and western larch in the interior of British Columbia, Canada. Current interests/projects include genetic evaluation for growth (using large-scale multienvironment trial analysis), terminal pine weevil and root rot resistance and wood quality traits; economic weights/indices among traits, delineation of breeding groups and breeding program design.

Overview of tree breeding programs in the interior of British Columbia, Canada

In British Columbia, Canada, nearly 300 million conifer seedlings are planted annually, with most planted in the interior of the province which has a continental climate that is characterized by relatively low precipitation and a wide range of temperatures. Nearly all seedlings are grown from seed orchard seed, from genetically evaluated, superior parents (A-class seed). Gaps in A-class seed are filled by wild collections (B-class seed), planned expansion of new & existing breeding programs, establishment of new second-generation orchards and redefining target deployment environments. Breeding objectives for all programs are to increase height (volume) growth for a target environment, maintain wood quality and investigate resistance to (at least) one major pest per species.

The interior (hybrid) spruce (Picea glauca x Picea engelmannii) and lodgepole pine (Pinus contorta) breeding programs, initiated in the 1970's, are the largest and oldest breeding programs with second-cycle testing nearly complete, second-cycle (forward) selections moving into new orchards and third-cycle mating beginning. Special seed orchards with resistance to spruce weevil (Pissodes strobi) and western gall rust (Endocronartium harknessii) have been created and are foreseen for resistance to comandra rust (Cronartium comandrae). The Douglas-fir (Pseudotsuga menziesii var glauca) and western larch (Larix occidentalis) programs, started in the 1980's, have just begun second-cycle testing. The white pine program is continuing first-cycle testing to identify parents resistant to blister rust (Cronartium ribicola). Similarly, a western red cedar (Thuja plicata) program is being established in the interior with expanded first-cycle testing, borrowing heavily from coastal genetic resources. A ponderosa pine (Pinus ponderosa) program is currently being launched, with new interior parent-tree selections from British Columbia and genetic material exchanges from the Pacific Northwestern United States, for planned first-cycle testing.

A new challenge for all programs is the shift from deploying seedlings to target environments using a geographic-based seed transfer (GBST) system, to a climate-based (CBST) system. Historically, breeding populations aligned perfectly with a GBST system, which simplified seed production targets and deployment to those zones. In a CBST framework, deployment zones are projected to future predicted climates for each population, which are different from GBST zones. Breeders are thus required to revisit the delineation of target environments for each breeding population, using a combination of ortet climates, progeny test site climates, transfer functions and leveraging large historical progeny test data to standardize genetic values and define the extent of genotype by environment interaction, or stability of genotypes across environments.

Domen Finzgar

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Born in Ljubljana (Slovenia), 1990. BSc and MSc in Forestry, University of Ljubljana. In pursuit of a PhD at the University of Edinburgh. After studying fungal communities on coarse woody debris in Slovenian virgin forests, I switched to forest genetics. I was a part of the LIFEGENMON team at the Slovenian Forestry Institute for four years, developing a forest genetic monitoring system for European beech and Silver fir on a transect between Germany and Greece. Now, I am in my final year of a PhD project, focusing on the genetic diversity of Sitka spruce in Great Britain.

Genetic assessment of the Sitka spruce British breeding programme

Co-authors : Gustavo Lopez[2], Joan Cottrell[2], Richard Ennos[1]

[1] Institute of Evolutionary Biology, [2]Forest Research

Sitka spruce (*Picea sitchensis* (Bong.) Carr) is a non-native forest tree species with great economic importance for forestry in Great Britain (GB). It is estimated that Sitka plantations contribute to around 51% of all GB woodland area. Every year more than 35 million Sitka trees are being restocked or used for new plantations. About 97% of all Sitka trees planted in GB come from the improved Sitka planting stock. Such stock originates from the home-produced supply from the Sitka spruce British breeding programme (The Programme): either vegetatively propagated material derived from controlled crosses of genetically superior parent clones or seeds sold to the nursery sector from a range of seed orchards based on grafted superior clones.

Since the beginning of The Programme in 1963, no systematic genetic assessment of the whole Programme was ever conducted. Nevertheless, such assessment would be of utmost importance for several reasons:

a) It provides internal quality control for The Programme. For example, labelling mistakes could have been made when grafting superior plus trees inside different clonal archives in different years.

b) It provides internal quality control for tree nurseries to help them improve their standard operational procedures.

c) It identifies the extent of violation of the panmixia assumption inside the tree orchard and detects pollen contaminations.

d) It can be used to measure the loss of genetic gain inside Sitka plantations due to the discrepancies between the management plan and the actual genetic composition of superior full-sib families.

e) It can be used to compare genetic diversity in The Programme with the unimproved FRM from seed stands or Sitka natural populations.

Most importantly, a systematic genetic assessment would help us answer a simple but essential question: Is The Programme meeting our expectations and what could be done better?

Within a 3.5-year PhD project, different sites of The Programme were identified:

a) IUFRO Farigaig provenance trial (natural population proxy); b) natural regeneration from the unimproved Sitka plantation; c) commercial Sitka plantation; d) tree nurseries; e) seed orchard and f) clonal archives.

Throughout the listed stages, more than 1200 DNA samples were collected. Furthermore, different phenological and demographical data were recorded in three growing seasons.
All samples were analysed with the same 12 microsatellite (SSR) markers, allowing direct comparisons of different sample sets. Additionally, a subset of samples was analysed using a Sequenom MassARRAY SNP genotyping platform.

This talk presents the extent of the project after the final growth season and the early results of some of the analyses made so far.

Acknowledgements

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A number of samples were collected with the help of the Davis Expedition Fund. The Sequenom MassARRAY SNP chip was developed by the BBSRC Sitka spruced project and the ConiferBreeding Co-operative.

Key words : Genetic diversity, microsatellites, SNP, seed orchard, full-sib families

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Natalie Graham is a scientist at Scion (New Zealand Forest Research Institute), working in the Forest Genetics and Biotechnology team. She has been with Scion for 12 years, working on a range of projects within the Genomics Selection Partnership, the Healthy Trees, Healthy Future Programme, and more recently the Resilient Forests and Tree Root Microbiome programmes. Her interests lie in finding new ways that we can add value to NZ's forestry industry using molecular and genomic tools, such as using DNA to predict traits such as wood properties or disease resistance.

Development of a 36K SNP array for radiata pine

Co-authors : Emily Telfer[1], Tancred Frickey[1], Gancho Slavov[1], Ahmed Ismael[2,1], Klapste Jaroslav[1], Heidi Dungey[1]

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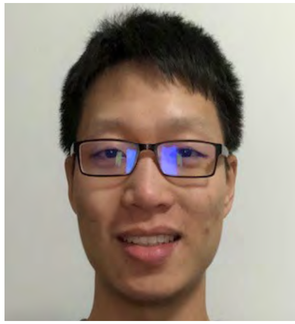
Developing genomic resources have been a key priority in recent years for the New Zealand radiata pine (*Pinus radiata* D.Don) breeding programme and associated research activities. In spite of being one of the world's most domesticated pines, and a commercially important species to New Zealand, the size and complexity of the genome has slowed progress in this regard. However, with increasing interest in applying genomic selection approaches, there has been increased motivation to develop cost effective and reliable high throughput genotyping platforms for this species. Development of an exome capture panel, that leveraged off an existing transcriptomic resource, allowed for the identification and evaluation of over a million single nucleotide polymorphisms (SNPs) in some key populations. Using these markers, we have now developed an Affymetrix Axiom array for 36,285 SNPs, as part of an international Conifer SNP Consortium. This array has been tested on several thousand individuals and is performing well, with sample call rates over 98% and reproducibility of 99.9%. This array represents a step change for breeders and researches in terms of both affordability and reproducibility. We report on the development of this array and some early applications towards better understanding the structure of the New Zealand breeding programme.

Key words : SNP array, breeding, radiata pine



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Jia is a postdoctoral fellow at the Pacific Northwest Tree Improvement Research Cooperative (PNWTIRC). He graduated from the Crop Sciences Department at The University of Illinois in 2017. His research focuses on the field of tree genetics and genomics. He aims to develop pipelines for analyzing genomic data from low-cost genotyping platforms. He also contributes to the development of genetic linkage maps in Douglas-fir. Prior to working on Douglas-fir, he conducted research on breeding and genetics of perennial grasses and grain wheat.

Low-density SNP Genotyping in Douglas-fir using Targeted Genotyping-by-sequencing

Co-authors : Anna Magnuson, Gancho Slavov, Glenn Howe

Douglas-fir is an ecologically and economically important species used for reforestation and to understand the ecological genetics of forest trees. Simple sequence repeat (SSR) markers are routinely used by Douglas-fir breeders to identify mis-labelled genotypes in seed orchards, measure pollen contamination, and determine parentage in breeding programs. Furthermore, there is an increasing interest in using single nucleotide polymorphic (SNP) markers to practice genomic selection. We previously developed a high-density genotyping array for Douglas-fir that can be used to genotype about 28K SNPs on a contract basis, but this number of SNPs is not needed for many applications. Also, a change from SSRs to SNPs is desirable because (1) SNP genotyping is more easily outsourced, (2) automated genotyping procedures are more robust for SNPs than for SSRs, and (3) it is easier to interpret the resulting marker genotypes. The specific objectives of this study were to: (1) develop a new, low-cost genotyping approach that can be used by Douglas-fir breeders on a contract basis, (2) develop bioinformatic tools to generate high quality genotyping data, and (3) develop a framework genetic map for SNP markers. In collaboration with RAPiD Genomics LLC (https://rapid-genomics.com/), we evaluated a new, lower-cost approach for genotyping SNPs in Douglas-fir that is based on targeted genotyping-by-sequencing (GBS). We developed a custom SNP calling program that is suitable for genotyping populations of closely related trees. To evaluate SNP performance, we applied our custom SNP calling pipeline to data generated from foliage collected from open-pollinated trees growing in Oregon and New Zealand. Overall, we demonstrated that we can genotype at least 3,500 SNPs at a call rate greater than 90%, as long as samples with low DNA concentrations are excluded. Our results also indicate that SNP call rate was highly influenced by sequence read depth, false positive rate (FPR), and likelihood of identifying heterozygotes (pHet). To develop a framework genetic map for Douglas-fir, two large full-sib families were genotyped and processed using our custom SNP calling pipeline. We also compared the performance of GBS genotyping with genotyping using our Axiom genotyping array. The availability of a lower-cost genotyping approach will enhance the management of Douglas-fir and accelerate Douglas-fir breeding programs.

Key words : Douglas-fir, SNPs, low-cost, genotype, pipeline

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Milos Ivkovich is a Data Analyst with Tree Breeding Australia (TBA), the national not-for-profit body for tree breeding and genetic improvement in Australia. He obtained his PhD degree in Forestry from the University of British Columbia, Canada, and worked previously as a research scientist with CSIRO, Australia. He specialised in quantitative genetics, economic breeding objectives and wood properties of radiata pine. He currently works on development and maintenance of TBA's DATAPLAN and TREEPLAN systems, and their application in tree improvement programs in Australia.

Scaling of Estimated Breeding Values in Australian Pinus radiata Breeding Program

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Tree Breeding Australia (TBA - http://www.treebreeding.com) manages the Australian tree improvement programs for radiata pine (*Pinus radiata*) and blue gum (*Eucalyptus globulus*), and supports programs in shining gum (*E. nitens*) and southern pines (*P. elliotii x caribaea*). TBA uses the TREEPLAN genetic evaluation system for estimating breeding values (EBVs) and total genetic values (EGVs) for all families and genotypes in the breeding program. The system uses all trial performance and pedigree information available to produce performance estimates for all plantation regions in Australia.

In *P. radiata* , TREEPLAN currently uses data on up to 34 selection criteria (SC) from 264 progeny trials in the analysis. The SC represent different traits, ages of measurement, and site types. The data for each trait in each trial are divided by an estimate of the trial trait additive genetic standard deviation, so that the SC EBVs are in units of additive genetic standard deviations. EGVs are similarly scaled, with non-additive genetic variances expressed as a ratio to the additive variance. Stand harvest age traits (or breeding objective traits – BO) are predicted from the SC. Measurement of stand harvest age traits is not routinely done as the rotation length is long, and pedigree structure of the trials does not allow estimation of the SC-BO genetic correlations and variances needed. The correlations are currently derived from SC age-age correlations, and the BO additive variances based on assumed additive coefficients of variation (CVa). For use in economic selection indices, we wish to derive the best estimate of the harvest-age stand-trait CVa to allow the estimates of seedlot performance to be appropriately scaled for the stand traits in question under commercial plantation silviculture conditions.

There is now accumulated a considerable amount of block-plot trial data usually with family mix treatments that can be used for an estimation of the growth BO EBV scaling factor. Harvest-age values of the block-plot stand traits can be predicted using industry customized growth models. The relationship of harvest-age mean annual increment in volume (MAI) with unit-scaled growth BO EBVs, provides the scale the EBVs. This approach was tested using 12 trials of *P. radiata* with latest measurements between 15 and 25 years. Additionally, more than 30 block-plot trials with early-age measurements allowed estimation of the relationship of basal area and EBVs at age 10 years. In all cases the unit scaled EBVs were positively correlated with large plot growth at measurement age. The ability of the growth models to predict growth in the plots was variable, which made predictions of harvest age values problematic. The estimate of CVa for harvest-age volume MAI was around 14%. Methodologies for incorporating genetic gains into growth and yield modelling, and forest valuations are discussed.

Key words : Pinus radiata; Realised genetic gains; Growth and Yield Modelling.

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Leader of the development of tree breeding program for main commercial tree species in Latvia (hemiboreal zone, Europe), now being implemented in practice, producing seed material for regeneration of ~10000 ha annually. Currently main research topics are related to forest adaptation (natural disturbances: wind and fire) – development of forest wind resistance models and recommendations for establishment and management of resilient stands. Assessment and modelling of carbon balance in old-growth forest and forest originating from improved plant material. Associated professor in Forestry faculty, director of PhD program Forest Sciences. Lead auditor of forest management (FSC, PEFC). Member of the board in two Forest sector research companies.

Performance of lodgepole pine provenances in hemiboreal forests of Europe, Latvia

Co-author : Raits Rieksts-Riekstiņš[1]
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Lodgepole pine (*Pinus contorta* var. latifolia Engelm.) has been extensively introduced in Scandinavia on less productive sites. Under a changing climate, it also has a high potential in the eastern Baltic region; still, its performance there has scarcely been reported. We have assessed the performance of 36 Canadian provenances (origin 50°–63°N and 115°–132°W) in 14 trials in western Latvia (56°–57°N, 22°–24°E) during 1979–1994. The trials had a randomised complete-block design with 4–8 replications and 12–48 tree plots of 3–13 provenances. Most of the provenances were represented in less than four trials. Height, stem diameter at breast height, and diameter of the thickest branch up to 2 m height were measured on each on each tree in each trial multiple times at the age of 10 to 29 years. The presence of spike knots and wildlife damage (browsing by cervids) were recorded as binary variables. Stem straightness was evaluated according to three grades (straight, slightly curved, and curved).

Tree dimensions showed notable provenance and provenance-by-environment variation, implying that local selection by provenance can be applied for improved yield. Southern provenances showed the best height growth, while southwestern (more oceanic) provenances excelled in diameter growth. Most of the quality traits were affected by provenance or provenance-by-environment interaction, yet the variation was lower than for the growth traits. The probability of wildlife damage showed significant variance by provenance, while the probability of spike knots and survival showed significant interaction variance; yet, the magnitude of the variances were lower than for heights and diameter at breast height. Mean proportion of damaged trees in trials older than 20 years was 9%, however it varied notably and significantly between the locations.

Yield of lodgepole pine was on average 25% higher than that of Scots pine (*Pinus sylvestris* L.) at the same age and site conditions (control lots of the trials), demonstrating a significant potential in use of selected materials of this species to diversify and improve the yield in production forests.

Key words : *Pinus contorta* var. *latifolia*; transfer; growth traits; spike knots; browsing damages

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Dr. Keith JS Jayawickrama has been Director of the Northwest Tree Improvement Cooperative (NWTIC) based at Oregon State University since June 2000. The primary species of interest for NWTIC is coastal Douglas-fir, with an equally advanced program in western hemlock. NWTIC and Dr. Jayawickrama support tree improvement work for over 60 entities in the Pacific Northwest; improvement work is also underway for Noble fir, western red cedar, coast redwood, sugar pine and white fir. Before NWTIC Dr. Jayawickrama worked with radiata pine improvement in New Zealand and Chile, and obtained his graduate education at North Carolina State University.

Updates on Cooperative Genetic Improvement for Coastal Douglas-fir in western Washington, western Oregon, and NW California

Co-author : Terrance Ye[1]

[1] Oregon State University

This presentation provides an update of cooperative tree improvement in the US PNW after the previous 2.02.05 Work Group meeting in 2013.

Second-cycle breeding and testing has progressed well and is largely complete, with final measurements completed on 111 of 115 tests established by 2012 (the remaining four are scheduled this fall). The great majority of the 115 tests were successful and provided very good data; only two were lost due to wildfires, and one abandoned due to high mortality. A new second cycle breeding program is being developed for hotter and drier areas in western WA, southern Oregon, and NW California; sites are to be planted starting in 2023. This program aims to serves sites as high as 1,500 or 1,800 meters since they tend to have the most precipitation. Third-cycle breeding and testing has proceeded largely according to the model used the second cycle. A slight consolidation of breeding zones (compared to the second cycle) took place, selections were organized in sublines of 10-15 trees with all relatedness confined to within those sublines, with each parent used in one to three pair crosses (no polymix testing). Crossing has proceeded quite rapidly, with staff at one orchard complex regularly completing 150-200 crosses per year. Test establishment started in 2017; 19 sites have been planted (one lost in its first season due wildfire) and 17 more are due to be planted this coming winter (early 2022). One series to be planted in 2022 is to include supplementary drought hardiness sites (short-term trials at narrow spacing under droughty conditions).

Realized genetic gain and reliable rotation-age projections remain of great interest to co-operators. Age-20\21 data were obtained from the oldest series (in the North Oregon Cascades) and used for projections through rotation age and for development of growth multipliers; we plan to obtain age-30 data in 2023-24. Age-17 data were obtained for the second series (located in the Washington Coast). A third series of trials was established on the South Oregon Coast with elite tested second-cycle crosses compared to unimproved seed. Seed orchard development and management has continued, with additional elite "1.5-generation" and second cycle orchards established or expanded, including plans for orchards for NW California. For some areas second cycle orchards are meeting all or most of the seed needs, and first-generation orchards have been removed or converted to low-intensity management. The use of orchard seed is now standard for reforestation with very limited use of wild seed.

The large wildfires in 2020 and extreme temperatures (up to 47C in Oregon) of the June 2021 heat dome underscored risks posed by climate change, with the heat dome causing widespread damage in young plantations and some progeny tests. This has given additional impetus to establish pilot Assisted Migration studies. Another current area of research is the comparison of data from aerial and ground-based LiDAR, with standard measurement techniques, in PNW tree improvement trials.

Testing and deployment of coastal redwood in California and Oregon

Co-authors : Sara Lipow,Tim Truax

Coastal redwood (Sequoia sempervirens) is an iconic, awe-inspiring yet enigmatic species with some of the largest living trees on earth; in the right conditions redwood completely dominates forest stands. Native to the north and central California coast (where it was once heavily used for construction and is now used for outdoor timbers) and the very southern tip of Oregon, its potential as an exotic outside its range is not fully understood. While a common view is that coastal redwood depends on coastal fog and is sensitive to frost, planted and natural stands and isolated trees can be found on harsh droughty sites, cold areas, northern latitudes, and high elevations; it has been grown far from California in Europe, South America, Asia, and New Zealand. Infrequent natural seed production (and reliance on sprouting) might be one factor that slowed its spread in western North America following glaciation.

There is currently interest by some Oregon forest growers in planting coastal redwood, and the next decade could witness substantial planting of this species. Perceived advantages include high growth rates far exceeding coastal Douglas-fir in some plantations, good log prices in the recent past, resistance to laminated root rot and Swiss Needle Cast disease, capacity to sequester enormous amounts of carbon including below-ground storage, and inexpensive regeneration from coppicing. Climate change could expand the area suitable for redwood in Oregon. Potential disadvantages could include limited processing capacity and demand by Oregon sawmills, frost damage, sensitivity to widely used herbicides, risk of peeling by black bears, negative public reactions to planting a non-native species, and limited research and experience on aspects such as spacing. Limited wild and orchard seed has led to limited availability of seedling planting stock, and there are also few facilities capable of reliably producing clonal propagules.

Tree improvement of coastal redwood dates to the 1970s and include some of the early work in modern clonal forestry and the development of rooted cutting and tissue culture protocols. Important efforts include Simpson's (now Green Diamond's) long-standing program, contributions by Louisiana Pacific, Pacific Lumber, Soper-Wheeler, Humboldt Redwood, Mendocino Redwood, and other companies, and research by prominent scientists such as Dr Bill Libby. A rangewide collection led to 180+ clones being established in the "Kuser trials" (in the USA and overseas) in the late 1980s and early 1990s. Several seed orchards were developed but are currently either abandoned or mostly inactive.

A new Redwood Tree Improvement Cooperative (RWTIC) was established in 2019 (with 18 members by 2021), aiming to test 500+ new selections across a range of sites in California and Oregon as clones. This effort has already resulted in testing 47 existing production clones on five sites in Oregon in 2020, planting clonal spacing trials 2020, and developing 180 new clones for outplant in 2023. Developing a new Oregon "landrace" (or multiple landraces) could be one outcome of this effort, in addition to a more stable and broad-based long-term tree improvement effort benefiting many forest growers in both states.

Key words: Testing, clonal forestry, California, Oregon

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I am an assistant professor at the University of Agriculture in Krakow, Poland. My scientific interests focus on bark beetles biology and ecology. as well as protection in forest management. I conduct studies relating to the improvement of techniques for reducing the occurrence of harmful bark beetles pests based on testing the innovative techniques for the gender identification and the analysis of the impact of logging residues utilization methods on the development and reproductive success of insects. The ecological aspects of my work include the impact of dead wood quality and quantity structure and fires on entomofauna biodiversity.

Biotic threats to key Pacific Northwest Species in Western and Central Europe

Co-authors : David Shawn[1], Gabriela Ritokova[1], Mee-Sook Kim[3]

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Biotic threats to Pacific Northwest (PNW) tree species grown in Europe can influence their utility in forestry. Key PNW tree species, including Douglas-fir (*Pseudotsuga menziesii*), grand fir (*Abies grandis*), lodgepole pine (*Pinus contorta*), and Sitka spruce (*Picea sitchensis*), are proposed for climate change resiliency, and ecological and economic relevance in Western and Central Europe (WCE). Climate and global plant trade-induced challenges for successfully growing these tree species in WCE are discussed.

Major insect and pathogen pests of PNW tree species within their native North American range pose a potential threat if introduced into WCE. For example, the most damaging root disease in the PNW is the mortality-causing laminated root rot (LRR), caused by *Coniferiporia sulpherascens*, and Douglas-fir and grand fir are highly susceptible hosts. Armillaria root disease (*Armillaria solidipes*) causes major damage to PNW conifers, and it can also be found as part of a root disease complex in trees weakened by LRR. Root diseases can also predispose trees to bark beetle attacks, including Douglas-fir (*Dendroctonus pseudotsugae*) and grand fir (*Scolytus ventralis*). Further examples of a native insect pests are *D. ponderosae*, a mortality agent of lodgepole pine, and *Pissodes strobi,* which causes severe stem deformations in Sitka spruce.

Native WCE insects and pathogens also pose a threat to health of the non-native trees. For example, PNW tree species that show close phylogenetic relationship to European trees are frequently susceptible to native WCE insects. *Lymantria monacha* is a major defoliating pest of conifers in Central Europe, and it may become a threat for Douglas-fir and Sitka spruce stands throughout their planted range to in northern WCE, as summers warm. Sitka spruce is also a potential host for *Ips typographus*, responsible for the Norway spruce (*Picea abies*) tree mortality in many European countries.

In addition, low impact insects and pathogens in the PNW could pose severe impacts on forest health condition in WCE, due to differences in climate and lack of natural enemies, e.g., predators and parasites. The recent European introduction of Douglas-fir needle midge *(Contarinia pseudotsugae*), a native PNW pest with low impact factor in PNW, is an indicator of potential issues that could arise in the next decade.

The successful establishment of key PNW forest tree species in WCE will depend on phytosanitary regulations that prevent the introduction of insect and pathogen pests into Europe. Unknown relationships among PNW tree species in WCE and invasive alien species (IAS) from different regions pose a challenge for the management of European forest health. Because of the complex and dynamic interactions of diverse environmental factors with potential biotic threats, regular monitoring for emerging insects and pathogens is required to identify potential threats to introduced tree species, especially if their use becomes commonplace.

Key words: Introduced conifers, forest insect, forest pathogen, climate change, pest management

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Jaroslav Klápště is a Scientist at Scion (New Zealand Forest Research Institute Ltd.). He graduated from the Czech University of Life Sciences in Prague with MSc in Forestry and PhD in Dendrology and Forest Tree Breeding. After graduation, he successfully applied for a postdoctoral fellowship at the University of British Columbia focused on statistical genomics. He was involved in one of Genome Canada's Large-Scale Applied Research Projects, where he worked on statistical genomic analysis (GWAS and genomic selection) to deliver genetically improved plant stock for bioethanol production. In addition, he also participated in several small-scale genomic projects in co-operation with the British Columbia Ministry of Forests, Lands and Natural Resource Operations, to implement genomic selection in the current breeding programme for Interior spruce and Douglas-fir. Currently, he works at Scion on projects focused on the implementation of genomic selection in NZ forest tree breeding programmes

Genomics-enabled radiata pine breeding in New Zealand

Co-authors : Ahmed Ismael[1], Mark Paget[2], Natalie Graham[1], Grahame Stovold[1], Heidi Dungey[1], Gancho Slavov[1]

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Tree improvement is a slow process as the breeding cycles of forest trees are inherently long. This issue is becoming urgent in the light of accelerating global environmental changes and consequent need for drastic social transformation, with forest ecosystems, and particularly fast-growing plantations, expected to play an essential role. Genomic selection (prediction of unobserved phenotypes from a genome-wide set of markers) can shorten the time needed to complete the breeding cycle and thus increase genetic gain per time unit. Furthermore, genomic data can be used to better manage genetic diversity and minimise inbreeding, thereby increasing both the effectiveness and sustainability of breeding programmes. Thus, the development of appropriate, lower-cost genotyping platforms has been a major research priority over the last decade. As part of a collaboration between the Radiata Pine Breeding Company (RPBC) and Scion, we have developed several genotyping strategies based on (1) a combination of exome capture and genotyping by sequencing, (2) an Affymetrix single-nucleotide polymorphism (SNP) array, and (3) highly-multiplexed amplicon re-sequencing around target SNPs. These platforms were used to genotype ~30k trees from the RPBC breeding populations, enabling large-scale pedigree reconstruction and genomic prediction. We substantially improved the accuracy of pedigree information and demonstrated that genomic prediction and single-step genomic evaluation would be effective across populations, including field trials that have not been genotyped, as well as within previously untested families.

Key words: Genomic selection, GBLUP, single-step genomic evaluation, radiata pine, pedigree reconstruction

SEED / SEED ORCHARDS

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Dave has been working at the British Columbia provincial Tree Seed Centre for the past 30 years conducting research and extension, assisting with tree seed problem solving, operational efficiency improvements and successfully avoiding management. Interests include tree seed science and technology with an emphasis on conifers from reproductive biology to seedling production. Chair of the Canadian Tree Seed Working Group and Coordinator of IUFRO 2.09.00 and 2.09.03 which several of us are trying to revitalize. Feeling more like an advocate these days for investments in research, education and infrastructure to maintain these essential tree seed services globally.

Deployment Bottlenecks: Cone and Seed Processing, Storage and Inventory Management

The Tree Improvement Delivery system has resulted in large gains in volume, and in some cases pest resistance, for Pacific Northwest conifers. Current emphasis is to further explore pest traits, impacts of climate change and to reduce the breeding generation time. These are all important initiatives that should further increase successes already achieved through tree breeding programs. The focus of this talk is focus on some of the basic steps of the delivery system have been taken for granted. Without further investments in awareness and education (leading to succession); research, and infrastructure, these areas will erode and be significant bottlenecks in the delivery of genetic gain. Cone and seed processing and seed storage are potential bottlenecks due to the lack of investment in maintaining or upgrading facilities. This highly specialized business area is also suffering from difficulties in succession and loss of knowledge due to mortality or retirement. Cone and seed processing practices are the most important determinant of seedlot germination! This greatly impacts seed use efficiency and deployment potential of our valuable breeding efforts. The history and status of cone seed processing in the Pacific northwest and its species' elsewhere will be reviewed as well as some specifics of their processing.

The potential needs of cone and seed processing and storage facilities based on increased reforestation scenarios will be discussed. This bottleneck could be very large due to the various reforestation programs being invested in, or promised, to aid in carbon sequestration or to deal with the increased amount of forested land suffering catastrophic losses. Modernization of cone and seed processing and storage facilities and increased efficiency of seed utilization will be critical. What can we borrow from advancements in agricultural seed processing and which technologies are pipe dreams to incorporate with Pacific Northwest conifers? Examples of adapted technologies and methods used, and 'not in our lifetime' ones will be discussed.

Climate change will likely also impact the desire for inter-jurisdictional exchange of genetic material. Some jurisdictions have sophisticated seed management systems while others are basically running by the seat of their pants and subject to the current availability of cone crops. This has efficiency implications, but also implications for adaptability and post-planting success of the plantations being established. Land tenure systems and reforestation responsibilities, and their introduced walls, greatly influence the desire to exchange information and seed. The potential benefits of a common deployment 'language' and existence of land vs. tenure-based seed management systems will be promoted.

Key words : Cone & Seed Processing; Seed Management Systems

PROVENANCE TRIALS
SPECIES INTRODUCTION

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Introduction, tree breeding and use of PNW Conifers in Sweden

Forests in Nordic countries are generally poor in tree species. During the search to find new tree species, the focus has often been on the tree species-rich forests in PNW. The Swedish forestry has long hoped that new tree species will be able to remedy the industry's increased need for timber. There has been a need to use new tree species to improve a generally poor forest condition, as during the last century, or as today, to maintain forest production when extensive forest pests affect the production and survival of native tree species. However, an increasing element of non-native tree species in Swedish forestry has often been limited by new legislation and in a similar way, the new forest environment certification is also very restrictive to the use of non-native tree species.

Climatic differences, but also regional differences in the forestry's ownership structure, have affected the interest and conditions for the introduction of new tree species in different parts of Sweden. During the introduction of non-native tree species during the last century much effort was devoted to identifying suitable provenances and to developing silvicultural practices. The most promising species have also gained attention in tree improvement programs where genetically well adapted trees from the best performing provenances/families were selected for seed production and breeding activities.

Lodgepole pine (*Pinus contorta*, LP) is by far the most planted exotic tree species in Swedish forests. The species outstanding performance in harsh areas in northern Sweden, on sites where regeneration with native species had failed, gave Swedish foresters a tool to regenerate such problematic areas in this part of the country. A large-scale introduction of LP started in the second half of the last century and was accompanied by thorough collections of seed material and comprehensive research. Significant breeding activities began at the end of the 1970s, when a seed orchard program was initiated with intention to make Sweden self-supporting with genetically good LP base material and seed sources.

Douglas fir (*Pseudotsuga menziesii*, DF) is a highly valued tree species in many countries in Northern Europe. However, it is still not being used in Swedish forestry on a large scale but the climate change challenge could reinforce interest in regenerating forest land with DF in southern Sweden. Douglas fir has been planted in Sweden during the last century, usually using coastal provenances from PNW, but to a very limited extent. DF can grow well in southern Sweden, but during the first years after planting it is prone to both abiotic and biotic damages. Grafted seed orchards were used as a first step of capturing the genetic gain by forward selection of plus trees within the best open pollinated families in good provenances. Seedling seed orchards, established after seed collection from the same plus trees, were presented as an alternative low-cost method for mass propagation, and would also serve as clone archives for the breeding population in a low budget breeding program for mass propagation.

Key words : Non-native species, Douglas fir, Lodgepole pine

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Dr. Jun-Jun Liu has worked at the Canadian Forest Service since 2000. As a research scientist he is in charge of research projects on white pine blister rust (WPBR). His works focus on genomics-assisted breeding of western white pine, whitebark pine, and limber pine; molecular genetics of host-pathogen interactions; as well as fungal pathogenomics in the WPBR pathosystems. In recent years, he also leads several other forest research projects, including genetic resistance of western redcedar and hemlock to root and butt rot diseases, and genomic breeding to enhance Douglas-fir drought tolerance. He has contributed to more than 120 research papers in peer-reviewed journals.

Genomics-assisted breeding of western white pine resistance to white pine blister rust

Co-author : Richard A. Sniezko[1]

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White pine species, including western white pine (*Pinus monticola* Dougl. Ex D. Don), are important components in North American forests, providing a wide range of economic, social, ecological, and environmental benefits. However, many white pine forests have been seriously damaged in the last 100+ years following the accidental introduction and fast spread of white pine blister rust (WPBR), caused by the exotic fungus *Cronartium ribicola* (J.C. Fisch.). Resistance screening is considered the key step for breeding improvement and future use in reforestation and restoration. With the recent advances in developing genomic resources, genomic approaches have potentials to increase selection accuracy of resistant genotypes and to shorten breeding cycles in forest breeding.

With application of next-generation sequencing (NGS) and high-throughput genotyping technologies, we developed genomics resources and selection tools for genomics-assisted breeding of western white pine. RNA-seq was performed to generate white pine reference transcriptome and SNP database using open-pollinated families with phenotypic segregation of major gene resistance, controlled by Cr2 for HR-like resistance against *C. ribicola* avirulent pathotype (Avcr2). A total 34,595 genes were assembled from RNA-seq data due to their expression in needle and stem tissues. Gene annotation revealed 736 genes encoding proteins with NB-ARC domain as R candidate genes, including 257 full-length NB-ARC sequences. Future functional verification will determine if any of them plays a role as Cr2 or other unknown R gene in MGR or quantitative resistance (QR) against WPBR or other pathogens and pests.

Over 455K SNPs were detected within 21,769 functional genes with polymorphism coverage of at least 50 times in both resistant and susceptible bulked samples and used for identification of DNA markers with practical application for resistance screening in breeding programs. Genome-wide association for extreme-phenotypes (XP-GWAS) showed that 90 genes with 264 SNPs were significantly associated with MGR-phenotypes using a cut-off of p-values at 1.1e-07 as corrected by Bonferroni method. Among them, 53 genes with 134 SNPs were further detected as the most significantly associated genes with SNP allele frequencies > 45% in resistant seedlings but

< 5% in susceptible samples by association genetic mapping with allele frequency directional difference (AFDD). In addition to those genes previously mapped on Pinus consensus linkage group-2 (LG-2), this study provided more *Cr2*-associated genes as targets for development of genomics-assisted breeding tools.

SNPs of two *Cr2*-associated genes with NB-ARC domain (snp41490-1778M and snp58688-82Y) were developed into TaqMan-based selection tools, and genotyped using >1,200 samples originating in Oregon, Washington, and British Colombia. The allele-A and C of snp41490-1778M were associated with *Cr2* and *cr2*, respectively. This marker showed genotype-phenotype matching rates at 95% and 86% within samples originated in US and Canada, respectively. The snp58688-82Y allele C and T were associated with *Cr2* and *cr2*, respectively. In all 490 samples native to Canada, no allele C was detected, consistent with reports of conventional resistance screening that *Cr2* was not present in Canadian natural stands. Therefore, our genomics work provides powerful genomics-assisted tools for accurate prediction of *Cr2*-resistance in wild parental trees across the western white pine's landscape.

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The focus of Greg O'Neill's research is on understanding the nature and distribution of adaptive variation of BC's tree species and applying this understanding to reforestation practices to help ensure BC's forest plantations remain healthy and productive in new climates. Greg manages two large, long-term forest genetics field trials (the Assisted Migration Adaptation Trial, and the Interior Spruce Climate Change / Genecology Provenance Trial. Greg is a professional forester with degrees in biology, forest ecology and forest genetics. He has worked in environmental consulting, international development, seedling production, and for the last 20 years in the Forest Genetics section of the British Columbia government.

Genecology of Forest Health Traits in western North American conifers

Co-author : Nicholas Ukrainetz [1]

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Constraining seed movement appears to provide a low-cost strategy to help control the incidence of pest infection in forest plantations. While the degree of acceptable seed movement is typically determined using growth-based transfer functions, we observed moderately strong transfer functions – evidence of local adaptation - in all four host-plant systems that we examined (Dothistroma needle blight, western gall rust and Lophodermella needle cast in lodgepole pine, and Swiss needle cast in Douglas-fir). Minor health concerns were observed among populations transferred short distances, and a moderately steep decline in tree health was noted among populations transferred moderate or long climate distances in one or both climate directions.

These findings support the contention that a carefully developed seed transfer system can help ensure that plantations are both productive and healthy. They also highlight the potential for improving seed transfer systems by broadening the scope of evaluated traits to include forest health, and demonstrate again the value of provenance tests in providing solutions to forest management challenges.

Key words: Forest health, adaptation, transfer functions, climate, pests

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I am a Research Director at INRAE Val de Loire, Orléans, France. I study adaptation of forest trees to climate in natural and artificial forest tree populations. My investigations of evolutionary adaptation and adaptive phenotypic plasticity are based essentially on annual rings and wood formation studies. I am also co-director (with A. Martinez-Meier of INTA, Argentina) of the International Associated Laboratory between INRAE, France, INTA, Argentina and University of Huanta, Peru, FORESTIA. I am also a Scientific Officer of the INRAE International Relationships for Latin America, and since 2020, in charge of the International Priority Program "Adaptation of forests and agroforests to climate change". Finally, I am an elected member of the INRAE scientific council.

Potential of adaptation to drought in Douglas-fir: twenty years of research efforts

Co-authors : Thibaud Chauvin, Britez Manuela Ruiz Diaz, Guillermina Dalla Salda, Anne-Sophie Sergent, Alejandro Martinez Meier

Over the last 60 years, Douglas-fir became the most important introduced tree-species in France. The material planted in France comes mainly from a low number of seed orchards originating from a temperate and humid coastal fragment of the natural range. During the last 30 years, French Douglas-fir stands have suffered diebacks associated to drought and heat waves. During the last 20 years, we developed genetic, dendroecological and ecophysiological studies of the Douglas-fir evolutionary and plastic adaptation to drought. We revealed the key-roles played by wood density, wood anatomy and resistance to cavitation. Cavitation process, tree-ring microdensity and anatomy traits were found to be interrelated, genetically variable, related to survival, and linked to climate variation in the natural range. We developed original methods to estimate norms of reaction and phenotypic plasticity of ring variables to climate. We used common garden experiments to show that variable climatic selection pressures in the natural area had shaped local adaptation: origins from the warmer and drier parts of the natural range show higher wood density and resistance to cavitation, and have more efficient cell wall pits. These trends are completed by high intra-provenance variation, contrasting genetic variation of ring density features and multifaceted associations among the variables at different local, geographical and time scales. The observed responses to climate change suggest that in France the current plantations may cross their adaptive threshold when global warming exceed 2°C.

Key words: Douglas-fir, adaptation, phenotypic plasticity, drought, wood, cavitation

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Dr. Silvio Schüler is biologist working at the Austrian Research Centre for Forests BFW, Vienna. He started his scientific career as population geneticist on forests trees. Later he got strongly involved in provenance research, where he established new trial series for hardwood species but mainly used provenance data to understand local adaptations to climate and climate extremes and to improve seed provenance recommendations. Since 2017 he is head of the Department of Forest Growth, Silviculture and Genetics, where he aims at developing integrated silvicultural strategies (incl. genetic knowledge) to support forest adaptation to climate change.

Will climate change result into a new era of introductions of conifers? A case study about needs, opportunities and risks in Austria

Co-authors : Debojyoti Chakraborty[1], Stephanie Salzmann[1], Katharina Enigl[2], Matthias Schlögl[2], Christoph Matulla[2], Katharina Lapin[1]

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Since more than 100 years, Pacific Northwest Conifers have been introduced and utilized around the world. Given their high productivity and adaptive capacity to a wide range of environmental conditions many of them belong to the most successful timber species in the world. However, while forest industries heavily depend on timber from PNW conifers, environmental concerns about negative environmental effects increased and led to more critical views on non-native conifer production. At the same time, climate change started to affect both native and non-native forest communities, compromising vital forest ecosystem services including timber production and carbon sequestration. Austria has a forest cover of close to 50% and thanks to a vital wood industry it belongs to the top-ten sawn wood exporting countries. Due to large timber resources in native Norway spruce, PNW conifers so far played only a marginal role in Austria's wood production. Species such as Douglas-fir were mainly planted under climate conditions that were not suitable for Norway spruce production. With ongoing climate change, forest owners and timber industries evaluate the expansion of Douglas-fir production and the introduction of further conifers from the Pacific Northwest and elsewhere. Both, the expansion of Douglas-fir production and the stronger utilization of other species require new strategies for seed sourcing and genetic improvement. Moreover, new introductions will also require a stronger risk-based approach to avoid the transmission on new pest and diseases as well as potentially invasive species.

Key words: species introduction; provenance selection; invasion risk; climate change adaptation

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Developing and Using White Pine Blister Rust-Resistant Populations of Pinus monticola, P. albicaulis and P. lambertiana

The non-native, invasive fungal pathogen *Cronartium ribicola*, cause of white pine blister rust (WPBR) has caused high mortality, greatly impacting the white pine (5-needle pines) species of the Pacific Northwest U.S. and Canada. The use of these species in reforestation and restoration has been limited in the past due to the presence of WPBR. Due to the threat from WPBR and other factors, one of these species, *P. albicaulis*, has been designated as 'endangered' in Canada and has been proposed for listing as 'threatened' in the U.S. Major programs to develop genetic resistance to WPBR have been undertaken in western white pine (*Pinus monticola*), sugar pine (*P. lambertiana*), and whitebark pine (*P. albicaulis*), with the programs for two of the species underway for more than five decades. These regional programs in the PNW U.S. are based at Dorena Genetic Resource Center (DGRC), but DGRC works with a range of federal, state, tribal and private cooperators to make progress in developing resistance and to get it out for reforestation and restoration. Major gene resistance (MGR) is available in two of the species (P. monticola, P. lambertiana), and quantitative resistance (QR) is present in all three species. The level of QR varies by species and breeding programs are underway to increase the level of QR in P. monticola and *P. lambertiana*. The level of QR in *P. albicaulis* is high enough to begin restoration plantings of this ecologically important keystone species. To be usable, resistance must be durable (persists even with evolution of the pathogen), stable (over environments and under a changing climate) and of a high enough level to ensure survival that meets land manager's needs. Field trials to confirm resistance levels and its durability and stability have been established for all three species and results are encouraging. Seed orchards have been established by a range of co-operator's and seed from these orchards are currently in use in Oregon and Washington for *P. monticola* and *P. lambertiana*. These applied resistance programs represent some of the most advanced tree resistance programs for non-native diseases in the world, and the lessons learned can be invaluable to helping ensure the success of future forest tree resistance programs with other species.

Key words: Cronartium ribicola, white pine blister rust, genetic resistance, white pines

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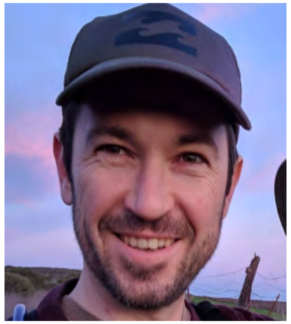
Port-Oford-cedar (POC, *Chamaecyparis lawsoniana*) and resistance to Port-Orford-cedar root disease and Stigmina foliage blight.

Port-Orford-cedar ((POC, *Chamaecyparis lawsoniana*) is a large, long-lived forest tree species native to southern Oregon and northern California. It has also been widely used in horticultural plantings around the world (often referred to as Lawson's cypress). The most damaging, wide-spread disease to POC in the U.S. (and Europe) is POC root disease, caused by *Phytophthora lateralis*, a non-native pathogen. In addition, in some environments Stigmina foliage blight, caused by *Pseudocercospora thujina* (formerly *Stigmina thujina*) can also severely impact trees. A large-scale applied resistance program to develop populations of POC with resistance to *P. lateralis* was begun in 1997 and based at the USDA Forest Service's Dorena Genetic Resource Center. The program has divided the range of the species into 13 breeding zones, with a goal of establishing containerized seed orchards with resistant parents to provide seed to land managers in the Pacific Northwest U.S. The program has been fast moving and very successful, identifying both major gene resistance (MGR) and quantitative resistance (QR) in POC. Containerized seed orchards have been established for many of the breeding zones and are producing abundant seed crops now being used in reforestation and restoration, with consideration also being given to resuming future horticultural use. Partners and cooperators have been invaluable contributors to the success of the program. Current efforts focus on breeding to increase the level of resistance and developing orchards for additional breeding zones. The use of containerized seed orchards has been very successful for this species, and orchard parents can readily be replaced as new data from resistance screening is available. Stigmina foliage blight had been noted as problematic on POC at several locations throughout the world but has been little studied. Fortuitously, in 2014, some trees in a large clone bank for the *P. lateralis* resistance program established at USDI Bureau of Land Management's Tyrrell orchard site showed foliage blight providing an opportunity to assess parent trees from throughout the geographic range of POC for susceptibility/impact from the foliage blight. Very large differences have now been documented in this clone bank that can provide some guidance to choosing seed sources and on potential 'assisted migration' for moving seed sources under climate change.

Key words: *Phytophthora lateralis*, Stigmina foliage blight, Port-Orford-cedar, *Chamaecyparis lawsoniana*, genetic resistance

CLIMATE / GENECOLOGY



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Joe Stewart is currently a postdoctoral research ecologist at UC Davis where he works on decision support tools for climate-smart reforestation. Though these days he mostly spends time crunching data, fitting models, and building tools, his years of field experience spanned taxonomic and ecosystem categories. He first fell in love with the field of ecology after he saw how relatively simple math can predict vegetation dynamics. His favorite tree species to read a book under include *Populus tremuloides, Quercus agrifolia, Pinus albicaulis, and Platanus racemosa.*

Optimizing Assisted Gene Flow for Forests

The climate is changing faster than tree populations are expected to naturally evolve or disperse, leading to a mismatch between the climate that tree populations are adapted to and the climate they experience (Climate-Adaptation Mismatch, CAM), manifested by decreased growth and survival. The California Department of Forestry and Fire Protection has funded an effort to combat CAM by developing preliminary reforestation guidelines for sourcing seeds adapted to the climate of their planting location (assisted gene flow). These preliminary guidelines are contained in California's Climate-Adapted Seed Tool (CAST). CAST uses climate-transfer functions fit to provenance test data to inform seed sourcing decisions for reforestation projects. Climate-transfer functions in CAST use Bayesian, multidimensional, asymmetric, bell-shaped curves to fit response variables (i.e. growth, survival) to climate transfer distances (e.g. temperature, precipitation). This talk with examine four sub-topics. (1) Transfer functions fit to different species (e.g. *Pinus contorta*, *P. ponderosa, Pseudotsuga menziesii*) tend to be similar, but can show significant differences in shape. Likewise, transfer functions fit to trees of different ages can differ in shape and steepness. For species with limited (or non-existent) provenance test data, how can we best use existing data to inform assisted migration? (2) Transfer functions fit to different combinations of climate variables tend to show strong agreement for shorter geographic transfer distance but begin to disagree when geographic transfer distance becomes large. How should we best either account for this uncertainty or constrain geographic transfer distances to optimize assisted gene flow? (3) Climate change projections indicate the climate of the 21st century will likely continue to be non-stationary, warming as time progresses. Non-stationary climate creates a tradeoff between optimizing seed selection for near-term climate, growth, and *survival*, and optimizing over longer timeframes. I will discuss approaches for optimizing over both near-term and long-term climate projections. (4) Provenance test data suggests that CAM has already led to declines in the productivity and survival of natural forests. In California, in the absence of assisted gene flow, we estimate that CAM has already caused a 5-10% decline in tree growth rates and a 0.7-0.8% decline in survival. By 2030, growth is expected to decline by 9-18%, with a 1-2.5% decline in survival. By 2050, growth is expected to decline by 21-32%, with a 2-7% decline in survival. Decisions we make today will impact California's forest for subsequent generations.

Key words: Assisted Gene Flow, Provenance Test, Climate Adaptation

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MOLECULAR

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Hayley Tumas is a postdoc in the Department of Forest and Conservation Sciences at the University of British Columbia, Canada with Sally Aitken. She obtained her PhD in Forestry and Natural Resources at the University of Georgia (USA) studying conservation genetics of a foundational salt marsh plant. Her work in forest genetics began with her postdoc at the University of Oxford with John MacKay where she developed a high-density linkage map for Sitka spruce. Her research has traversed elevations from coast to mountains, as she now examines genetic diversity in three conifers at multiple spatiotemporal scales of forest management in BC.

A SNP marks the spot: a high-density linkage map for UK Sitka spruce (*Picea sitchensis* [Bong.] Carr.)

Co-authors : Joanna Ilska[2], John Woolliams[2], Paul Mclean[3], Joan Cottrell[4], Gustavo Lopez[4], Gregor Gorjanc[2], Mateja Janes[2], Jean Bousquet[5], Sebastien Gerardi[5], Jerome Laroche[5], Brian Boyle[6], John Mackay[1]
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Harnessing the power of genomic data will be crucial for the future of forest tree breeding and conservation. The size and complexity of conifer genomes is limiting the use of innovative genomic methods, like genomic prediction, that have already been successfully applied to other species. Next generation sequencing capabilities that could deal with these massive genomes continue to develop, but generally still lack resolution and structural data. Genetic linkage maps can help bridge this gap and provide useful information for breeding and climate adaptation studies. Sitka spruce (*Picea sitchensis* [Bong.] Carr.) is the number one timber producing species in the United Kingdom as well as being an ecologically and culturally important species in its native range across the Pacific Northwest of North America. Here we develop a SNP array using exome capture based on the white spruce (Picea glauca (Moench) Voss) transcriptome. We then use a combination of genomic markers from the SNP array and restriction-site associated DNA sequencing (RAD-seq) to develop a high-density linkage map for Sitka spruce. Genotypes from two full-sib families of approximately 300 individuals each from the UK breeding population were used in LepMap3 to group and position markers on chromosomes. The resulting map, with 21, 571 markers across 12 chromosomes, is the highest density map for Sitka spruce and among the densest maps across conifer species. In comparison to maps from other, closely-related species, our map has high (>80%) synteny. Using a previously developed white spruce map and markers based on the white spruce transcriptome as scaffolds, we generate an integrated white and Sitka spruce map that places more genes than either individual map. This Sitka spruce linkage map represents an important and valuable resource that can be used in the development of efficient breeding practices for Sitka spruce abroad or in conservation genetic research in the species' native range.

Key words: genetic map, *Picea sitchensis, Picea glauca*, exome capture, Europe

MOLECULAR

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Marcela van Loo heads the Unit of Provenance Research and Breeding at the Institute of Forest Growth, Silviculture and Genetics at the Austrian Forest Research Centre in Vienna (Austria). Her current research and projects focus on provenance research, tree responses to biotic and abiotic stress, and forest and population genetics, especially adaptation processes, responses to drought stress and interactions to pathogens in planted native and non-native tree species such as spruce, black pine, white oaks, beech, and Douglas-fir. Her studies include long-term observations in permanent plots, manipulated experiments in nature and experimental designs under controlled conditions in growth chambers.

Whole-exome sequencing unravels genomic signals of climatic adaptation in Douglas-fir

Co-authors : Jan-Peter George[2], Michael Grabner[3], Sandra Karanitsch-Ackerl[3], Konrad Mayer[3], Michael Stierschneider [4], Lambert Weissenbacher[1], Silvio Schüler[1]

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Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco) is attracting attention outside its natural range, including Europe, due to its ability to cope with climate warming and drought. Throughout its natural range, it grows along steep gradients of different climates, which is expected to result in spatially varying selection and adaptation to local climatic conditions. However, signals of climatic adaptation can often be confounded because unraveled clines covary with signals caused by neutral evolutionary processes such as gene flow and genetic drift. Consequently, our understanding of how selection and gene flow have shaped phenotypic and genotypic differentiation in trees is still limited.

A 40-year-old Austrian common garden experiment showing a strong association between growth traits and seed source climate, represented by 16 Douglas-fir provenances covering a north-to-south gradient of approx. 1,000 km, was analyzed. Genomic information was obtained by exome capture, resulting in an initial genomic dataset of >90,000 single nucleotide polymorphisms. We used a restrictive and conservative filtering approach that allowed us to include only SNPs and individuals in the environmental association analysis (EAA) that were free of potentially confounding effects (LD, relatedness among trees, heterozygosity deficiency, and deviations from Hardy–Weinberg proportions). We used four conceptually distinct genome scan methods based on F_{ST} outlier detection and gene–environment association in order to disentangle truly adaptive SNPs from neutral SNPs.

A relatively small proportion of the exome showed a truly adaptive signal (0.01%–0.17%) when population sub-structuring and multiple testing were taken into account. Nevertheless, the unraveled SNP candidates revealed significant relationships with climate at the provenance origins, strongly suggesting that they have featured adaptation in Douglas-fir along a climatic gradient. Two SNPs were found independently by three of the employed algorithms, and one of them is located in close proximity to an annotated gene involved in circadian clock control and photoperiodism, as also found in *Populus balsamifera*.

Key words: Douglas-fir, climatic adaptation, common garden experiment, exome capture, environmental association analysis

CLIMATE / GENECOLOGY

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Marie Vance is a Research Scientist at the Kalamalka Forestry Centre in Vernon, British Columbia (BC), with the BC Ministry of Forests, Lands, Natural Resource Operations and Rural Development. Marie's primary focus is on assembling new tree improvement programs for ponderosa pine and interior western redcedar. Marie graduated in 2011 from the University of Neuchâtel, Switzerland, with an MSc in Plant Ecology and Physiology and completed a PhD in the Centre for Forest Biology at the University of Victoria, BC, in 2019.

Drought screening in ponderosa pine

Ponderosa pine occupies the hottest and driest forested habitat in British Columbia. As climate change proceeds, this species' climate niche will undergo a major northward expansion. Within its current distribution, drought-tolerant ponderosa pine trees will be challenged by warmer mean annual temperatures, earlier snowmelt, reduced summer precipitation and more frequent drought events. Breeding for drought tolerance is therefore an important part of BC's climate change adaptation strategy. In the fall of 2019, ten raised-bed progeny trials were established at the Kalamalka Forestry Centre in Vernon, BC, using 20 open-pollinated families collected from the only provincial seed orchard with tested parents. Half of the beds were droughted during the summers of 2020 and 2021. Phenological, morphological and physiological traits were assessed. Significant differences in carbon isotope ratio, water potential and height growth were observed between treatments. Family-level variation was observed in, e.g., height growth. In the fall of 2020, a paired field test was established at the Kalamalka Seed Orchard on a south-facing slope in a grassland habitat. The results of this work will be used to develop large-scale screening methods to maintain and/or improve the physiological adaptation of tree species that we know will face increasingly harsh environmental challenges.

Key words: Ponderosa pine, Drought screening, Climate change

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Dr. Walther is a plant physiologist and expert in somatic embryogenesis (SE) of conifers. She works at the Humboldt-Universität zu Berlin on the implementation of SE as a biotechnology to produce elite plant material of hybrid larch and Douglas fir for German foresters. Therefore, she was involved in the establishment of a well-characterised and cryopreserved clone collection of several hundred genotypes of both species. Further, she is interested in the transition of plant cells to an embryogenic state and investigates the influence of hormones and stress factors.

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Andrea Rupps is leading the team 'Plant Development' in the department Plant Systematics and Biodiversity. Her main research is motivated by unravelling regulatory mechanisms of the artificial process 'somatic embryogenesis' in conifers as well as to unearth its potential. Hereby, her current work focuses on the molecular mechanisms leading to the initiation and regulation of somatic embryogenesis (how and why can an already differentiated cell return to the embryogenic state?), the development of somatic embryos (are there deviations to zygotic embryos?) and practical optimisations of the whole process chain (is somatic embryogenesis an alternative to seed propagation and/or for material production?). As Climate change requires an adaptation to a fast altering environment, her intention is to exploit the untapped advantages of the system and to offer alternatives and characterised material for forestry and for production of important wood substances.

Vegetative propagation of Pseudotsuga menziesii by refined somatic embryogenesis and its application in multilateral field trials

Co-author : Andrea Rupps[1]
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Douglas-fir (Pseudotsuga menziesii (Mirb.) Franco) is native in the forests of North West America and has been successfully introduced into other areas of a similar climate. Due to its drought tolerance, timber quality and yield, Pseudotsuga even became one of Europe's most important non-native tree species. In recent times breeding programs had been established in seed orchards in combination with somatic embryogenesis (SE) as the preferred vegetative propagation method. Although many protocols exist, several problems concerning the in vitro process remain: for example, the limited number of genetic backgrounds that respond to the initiation stimuli and the accumulation of non-embryogenic callus cells during subculture. To overcome these bottlenecks and to capture high-value genotypes with superior characteristics, we tested the influence of the genetic background of the explants, the cone harvest time and the basal media for SE initiation. This way we were able to increase induction frequencies and decrease unwanted callus growth on specific genotypes using abscisic acid (ABA). Histological studies revealed the location of SE competent cells in the (sub)epidermal cells of the basal hypocotyl. As part of our multilateral project MULTIFOREVER (funded by ForestValue), the resulting Douglas-fir somatic seedlings were planted in the first multi-site trial in Europe at three sites: in Germany (HUB, SBS), France (FCBA) and Sweden (UPSC/SLU in partnership with Linnaeus University), partly in clonal mixtures and in reference to seedling standards. The deployment of tested, high-performance varieties ('multi-varietal forestry') can contribute to optimized wood production and also enable more dynamic diversity management.

Key words: Douglas fir, somatic embryogenesis, induction, Abscisic acid, multi-varietal forestry

FOREST HEALTH

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Geoff Williams is currently the International Sentinel Network Coordinator working with collaborators across the world through International Programs in the USDA Forest Service collecting data on pests and pathogens that impact US species abroad. Geoff completed an M.S. at the University of Idaho on crown foliage allocation in western larch (Larix occidentalis) and his Ph.D. from Purdue University focused on the microbiome and nematodes in Thousand Cankers Disease of Eastern black walnut (Juglans nigra). He was awarded a Fulbright to study forest pathology and entomology in Esquel, Argentina (Patagonia). He lives in Eugene, OR and enjoys hiking, brewing, and gardening.

A Sentinel Network Information Platform for N. American Woody Flora: Leveraging Established *ex situ* Plantings of PNW Conifers and Integration with Parallel Efforts

Co-author : Richard A. Sniezko[1]

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In the U.S., *nonindigenous* pathogens and insect pests of native forest trees are those that first arrived in the U.S. since European colonization but originated elsewhere. Operationally, nonindigenous pathogens and insect pests are considered *invasive* when they spread unabetted; causing damage to novel, native host tree species; displacing other organisms; disrupting ecological processes; incurring costs to natural resources; and/or threatening the sustainability of ecosystem services and functions. The costs incurred by invasive pathogens and insect pests of forest trees are high, extend far beyond traditional markets, and they threaten global sustainability along with landscape destruction and climate change. However, such pests typically remain unknown until they have already become difficult to control or manage. Furthermore, specific risks of future invaders are difficult to quantify, complicating the adoption of allowable trade measures to prevent their introduction. For example, emerald ash borer had already become widely established in Michigan by the time it was first discovered there.

With respect to protecting U.S. natural resources, *sentinel trees* are trees that may be used for monitoring to provide early detection, identification, and study of potentially invasive nonindigenous pathogens and insects that may present a threat to native U.S. tree species. *Ex patria* sentinel trees are trees native to the U.S. growing abroad and can provide a basis for proactive biosecurity; serve as monitoring resources for future threats; aid and reduce risk uncertainty; and jumpstart the development of effective pest and disease management tools. For example, *Phytophthora austrocedri* is known to cause disease on U.S. Cuppressaceae spp. in the United Kingdom and *Cronartium* pini causes disease on U.S. *Pinus* spp. in Eurasia. Further demonstrating the potential of sentinel trees in risk assessments and reductions, it was recently recommended to ban importation of Pinus seedlings to prevent introduction of C. pini, and the risk to *Pinus* spp. in the U.S. was mapped via Spatial Analytic Framework for Advanced Risk Information Systems (SAFARIS) using climatic and host distribution data.

In addition to parallel efforts to establish new plantings and to survey botanical gardens, *U.S. native species have been established abroad > 100 years in plantations such as introduction, progeny and provenance trials that could be used as sentinels.* Gathering information through literature review and international outreach, we will build a user-interface-accessible database of hosts, GIS locations and ages of plantations, observations of pathogens and pests, and damage. Sentinel trees in genetically diverse plantations can also provide pre-invasion information on resistance. Any available metadata on genetics, provenances and variation in damage will be included. The database will be integrated with the European Plant Protection Organization (EPPO) Global Database, Center for Agriculture and Biosciences International (CABI) Invasive Species Compendium, North American Invasive Species Network (NAISN), Botanical Garden Conservation International-International Sentinel Plant Network (BGCI-ISPN), SAFARIS, and other efforts, databases, and tools. A proof-of-concept will be completed for focal U.S. species including pacific northwest *Pinus*, Cuppressaceae, and *Pseudotsuga menzeisii.* Potential end-users include plant protection organizations, forest health advocates, policymakers, forestry practitioners, entomologists, pathologists, industry professionals, land managers, landowners, and the public.

Key words: invasive species, forest pathogens, forest pests, resistance, risk assessment

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POSTERS

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Andrew is a geneticist with the US Forest Service in Olympia, Washington. He has a bachelor's degree in forestry from U.C. Berkeley, M.S. in forest science from Oregon State University, and a Ph.D. in forest sciences from the University of British Columbia. He is the Zone Geneticist for western Washington and northwest Oregon and is also the Project Leader for the USFS Whitebark Pine Restoration Program in the Washington and Oregon. His professional interests include population and conservation genetics of forest trees and native plants, and conservation/restoration of rare or threatened trees. He also works with botanists and foresters providing guidance on seed movement guidelines and genetic issues relative to trees and herbaceous native plants.

Seed source evaluation trials to evaluate the feasibility of operational assisted migration

It is well established that trees and plants are locally adapted to their environment, and this adaptation is driven by local climate. This knowledge led to the development and implementation of seed zones for forest trees and native plants under the general concept that "local is best". However, due to climate change, there is a growing body of evidence that this assumption may no longer be valid.

Geneticists with US Forest Service Pacific Northwest Region and Pacific Northwest Research Station are installing a series of seed source evaluation trials on National Forest lands in Washington and Oregon. Working with the National Forests to identify areas in need of restoration either due to timber harvesting, wildfire, or other disturbance, the goal of these trials is to evaluate the success of seedlots that evolved under different climate regimes that match predicted future climates of the planting site (preadapted) and to assess whether assisted population migration is feasible alternative. One of the uncertainties regarding assisted migration is whether using seed sources "preadapted" to a future climate (i.e., warmer) will suffer from frost damage in the current climate.

The Seedlot Selection tool (www.seedlotselectiontool.org)/sst) was used to identify seed sources where the current climate is a close analog to the future climate of the planting site. Four time periods are utilized: present – "local" seed source (1961-1990), near-future (2011-2040), mid-century (2041-2070), and late-century (2071-2100). The Seedlot Selection Tool helps identify appropriate seed sources (geographic areas) that match the climate of the planting site in these future time periods. Once appropriate seed sources were identified, the Regional seed inventory was reviewed to determine which specific seedlots were available for use. To select specific seedlots for each time period, climatic transfer distances between the planting site and the candidate seedlots was calculated for the near-term and long-term future climates of the planting site. Current and future data on climate variables of interest for the planting site and for all seedlots currently in inventory at the Bend Seed Extractory and at JH Stone Nursery were included in this analysis. Appropriate seedlots are identified by finding the smallest climatic transfer distance between the seedlot and the planting site for the future climate while remaining within an acceptable transfer limit for cold temperatures in the near-term to avoid risk of cold damage.

Seedlings will be grown and outplanted using the same nursery protocols and planting specifications as seedlings established in "operational" reforestation projects (e.g., stock type, culling standards, tree spacing, planting season, planting technique, etc.). Randomized 1.5-acre blocks of each seedlot will be replicated at least 4 times across the landscape to reduce the impact of local environmental variation on measured variables.

While these trials are not intended to be intensively measured for adaptive traits, survival and growth will be monitored regularly to determine if differences develop among seed sources, and which seed sources perform the best over time. With a randomized block design, statistical analysis can be conducted on survival and growth data to assess differences among seed sources.

Key words: Climate change, assisted migration, reforestation, seed source trial

Establishment of white pine blister rust resistant seed orchards for whitebark pine in the Pacific Northwest

Whitebark pine is a keystone species in high-elevation ecosystems in western North America. It has been severely affected by the combined impacts of successional replacement due to fire suppression, outbreaks of bark beetles, climate change, and most critically the introduced disease white pine blister rust. A considerable investment has been made in the US Forest Service Pacific Northwest Region in the last ~15 years to identify individual whitebark pine trees with some level of resistance to white pine blister rust. To-date, approximately 150 trees have been identified. These individual trees are at risk of loss from fire, insect attack, windthrow, and other disturbances, making in-situ conservation challenging. In an effort to preserve these resistant genotypes, scion from these "elite" parent trees has been grafted onto rootstock and these clones have been outplanted in ex situ clonal conservation banks at multiple tree seed orchards already established in Washington and Oregon. A secondary, but equally important, objective of these outplantings is to serve as seed orchards for production of rust resistant seed for future restoration or reforestation work. Seed orchards can help meet this need for reliable, easily accessible source of rust resistant seed will be one key factor in any successful restoration work throughout most of the range of WBP.

The range of whitebark pine in the Pacific Northwest Region was divided into four geographic areas: eastern and western Washington and Oregon. Each geographic area will be represented in two ex situ plantings to buffer against catastrophic loss or failure at any one site. Approximate 100 ramets from 26 clones from western Washington were outplanted in October 2020. Survival though summer of 2021 has been above 90%. Approximately 150 ramets from 34 clones from western Oregon and 80 ramets from 20 clones from eastern Oregon were outplanted in June of 2021, approximately 50 ramets from 19 clones from western Washington and 90 ramets from 30 clones from western Oregon were outplanted in October 2021. Ramets from eastern Washington and eastern Oregon will be outplanted in fall of 2022. Scion from additional elite rust resistant parents will continue to be collected each fall/winter to add genetic diversity to these ex situ conservation plantings in the future.

Key words: Whitebark pine, seed orchard, ex situ conservation, white pine blister rust

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Dr Amanda De La Torre obtained her PhD at the University of British Columbia in Vancouver, Canada and later worked as a postdoctoral researcher at Umea University in Sweden, and the University of California-Davis in the US. She is currently an Assistant Professor in Forest Genomics at Northern Arizona University (Arizona, US) and the Director of the NAU Forest Genomics Lab. Dr. De La Torre has extensive experience in the use of genomic resources for conservation, management, breeding and restoration of forest tree species, with an emphasis on conifers. Her research in population, quantitative and comparative genomics, molecular evolution and local adaptation to climate has been published in top scientific journals such as PNAS, Molecular Biology and Evolution and New Phytologist. Synergistic activities include being a world coordinator for the International Union of Forest Research Organization (IUFRO) working party in Tree Genomics, a member of the board of directors for the North American Forest Genetics Society (NAFGS), and associated editor in several peer-review Genetics journals.

Differences in growth, heat and drought tolerance among advanced-generation hybrids and coastal Douglas fir families

Co-authors : Samuel Compton[1], Aalap Dixit[1], St.clair Jb[2]

[1] Northern Arizona University, [2] USDA Forest Service

We used a greenhouse common garden study to investigate variation in height, carbon isotope discrimination, and electrolyte leakage among 115 Douglas fir families (with an average of 22 seedlings per family) representing either coastal or advanced-generation hybrid varieties. Genome-wide association was performed among traits and genotypes. We found an increase in water use efficiency and photosynthetic capacity in advanced-generation hybrids, suggesting lower stomatal conductance in comparison to coastal Douglas fir. Hybrids were also more heat tolerant than coastal Douglas fir families. Several new candidate genes associated with heat tolerance and involved in the inositol phosphate metabolic pathway were reported. This information about differences in drought and heat tolerance among Douglas fir families may be useful for selecting families in a changing climate, and for assisted migration and large-scale reforestation projects.

Key words: Carbon isotope, height, electrolytic leakage, hybrids, Douglas fir

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My name is Omnia Gamal El-Dien and I am currently working as a sessional instructor in applied statistics (Faculty of Forestry, UBC) and an NSERC PDF (Michael Smith Laboratories, UBC) in Quantitative Forest Genomics with Drs. Joerg Bohlmann and Alvin Yanchuk. I did my Ph.D.in Forest Quantitative Genomics with Dr. Yousry El-Kassaby at UBC. My Ph.D. and postdoctoral research are in fitting complex genomic prediction models (Genomic Selection) to reduce the length of the breeding cycle of trees. I have also worked as a research scientist and data analyst at the BC Ministry of Forest with Dr. Alvin Yanchuk.

Genomic Selection in western redcedar breeding program in BC: from proof of concept to application

Co-authors : Tal Shalev[1], Matias Kirst[2], Lise Van Der Merwe[3], Alvin Yanchuk[3], Carol Ritland[1], John H. Russell[3], Joerg Bohlmann[1]

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Western redcedar (WRC, *Thuja plicata*), a major ecological and commercial conifer species in BC, is renowned for its natural wood durability. The species current breeding strategy is lengthy for measuring desired attributes (~25-year breeding cycles). Genomic Selection (GS), predicting phenotypes from genomic data, has created a paradigm shift through speedy evaluation and improved selection accuracy; however, in conifers GS is in its infancy due to the lack of advanced testing and validation. WRC's unique biology, including long-distance linkage disequilibrium and precocious reproduction makes it an ideal species to evaluate the application of GS in conifers as it is expected to reduce the breeding cycle to 2 years. Here, we present one of the first GS applications at the operation level with two-stage approach of model validation and multi-traits early selection at the seedling phase.

Using Capture-Seq genotyping technology of target genic and non-genic regions, we genotyped 113 parent trees, 1520 F1 trees (training population: 19-year- old, 26 PX families collected from 3 sites progeny test) and 3000 F1 seedlings (target population: 1-year-old, 168 FS families). These populations share 26 parents (training population female parents). After filtration, 45K high quality SNPs were used, we divided these SNPs into three groups (genic-coding, genic-non-coding and intergenic). The training population was phenotyped for several traits related to growth, heartwood thujaplicins and lignans (late expressed traits underlie wood durability) and foliar monoterpenes (early expressed trait underlie deer browse resistance), while the target population was phenotyped for only foliar monoterpenes.

First, we constructed the genomic relationship matrix (G matrix) to convert the 26 PX families to 447 full-sib families, and identify pedigree errors. The paternity assignment revealed significant unequal male contribution (range: 7-187 offspring/male).

Second, we compared the traditional pedigree analysis (ABLUP, using original PX pedigree) and genomic analysis (GBLUP) in the training population using all traits. The GBLUP analysis outperformed the ABLUP and resulted in increased breeding values accuracies and expected genetic gain. We also compared different SNPs groups using GBLUP.

Third, GS prediction models were fitted for 8 growth, foliar monoterpenes, and heartwood thujaplicins and lignans attributes. These models were validated first in the training population using a random ten-fold cross validation. Moreover, across-generations, -environments, -time validation and effect of relatedness were assessed. In the second stage of model validation, we independently validated those models in the target population for foliar monoterpenes, taking advantage of assessing it at the seedling target population. The prediction accuracy (PA), correlation between measured and predicted phenotypes, ranged between 0.08 (removing relatedness) and 0.99 (parent trees predicting training population) depending on the attribute, validation type and the used reference to estimate PA. The average PA is around 0.7.

Finally, we used the validated models to predict growth and wood traits for the seedling target population and constructed a multi-traits selection index (growth, heartwood thujaplicins and lignans, and foliar monoterpenes) for early selection and selected the best ≈ 100 seedlings for breeding population development and possible seed orchard establishment.

Key words: Western redcedar, Genomic Selection, multi-traits early selection, paternity assignments, and pedigree errors

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Xiali Guo has graduated from South China Botanical Garden, Chinese Academy of Sciences. During her Ph.D. period, as a visiting scholar, she studied at the University of Quebec in Canada for one and a half years. Her research interests include the study of mechanisms behind xylem formation and bud phenology. Her research concerns the study of the effects of nitrogen deposition on xylem formation of broadleaf species and the role of auxin evolved during the xylem formation of conifer species in subtropical forests. Her current research focuses on the bud phenological adaptation mechanism of sugar maple and black spruce.

Common-garden experiment reveals clinal trends of bud phenology in black spruce populations from a latitudinal gradient in the boreal forest

Climate warming is modifying the movement of air masses over Northern latitudes, producing warming and cooling events across the boreal regions. These new conditions changes may mismatch plant phenology from weather conditions and affect the growing period of trees. Understanding the processes of local adaptation in bud phenology can help to predict the response of plants to these rapid and unexpected environmental changes. Our study monitored bud burst and bud set weekly during four growing seasons in black spruce [*Picea mariana* (Mill.) B.S.P.] saplings planted in a common garden and originating from five provenances representing the whole latitudinal distribution of the closed boreal forest in Quebec, Canada. We compared the variance in bud phenology among populations and years and analysed the relationships with temperatures at the origin sites. Bud burst and bud set occurred in mid-May and mid-July, respectively, with a large variability among provenances and between the study years. A delayed bud phenology was observed in the provenances from warmer sites, with bud burst and bud set being 1.1 and 1.4 days later for every additional degree in mean annual temperature at the origin site respectively. Populations with earlier bud bursts also showed earlier bud sets, thus the growing season was similar among provenances. The heritability of bud set was higher than that of bud burst, with estimates of 0.26 and 0.21 respectively. On average, variance in bud phenology among provenances reached 5.3%, which was higher than that within provenances (2.6%). The factor year explained 37.7%–69.7% of the variance in bud phenology. The findings demonstrate the evolutionary response to climate variations in the boreal biome. Endogenous and environmental components have different effects on the phases of bud burst and bud set. This complex interaction among drivers of bud phenology may prevent reliable predictions of changes in the growing season under changing climate. An earlier growth reactivation due to higher spring temperatures could result in higher frost risks to the developing buds. Despite a longer period for photosynthesis expected for the evergreen black spruce under warmer conditions, the period spent for bud development could remain unchanged.

Key words:Picea mariana, bud burst; bud set; ecotype, global warming

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Diāna Jansone got her Master's degree in University of Latvia in Botany and Ecology. Now is a Ph.D student in the Latvia University of Life Sciences and Technologies in Forest faculty. Ph.D thesis topic – ''Influence of meteorological factors on radial increment of introduced tres species in Latvia''. Since 2017 works as a research assistant in Latvian State Forest Research Institute ''Silava''. Research is related to the assessment of climate change impacts on tree species, dendrochronology and tree radial increment.

Growth of Sitka Spruce and Douglas Fir in European hemiboreal forests, Latvia

Climate is an important factor affecting tree growth. Due to changing climate, trees need to adapt to the new conditions or migrate. The rate of climatic change can exceed the rate of natural tree migration. Therefore, to fasten migration rate, assisted migration can be used. Study in European hemiboreal forests in Latvia was done to analyze two introduced tree species (Sitka spruce *Picea sitchensis*, Douglas fir Pseudotsuga *menziesii*) radial growth and compare it to native coniferous specie (Norway spruce *Picea abies*). To measure tree ring width, 60 core samples were taken from each site (2 cores per one tree). Analysed measurements from 1 – 34 years of age. All analysed conifers showed similar tendency – faster growth at early age and lower over the age of 30. Douglas Fir had the highest rates of annual DBH (diameter at breast height). When analysed cumulatively, Douglas Fir showed higher rates of DBH increment followed by Norway Spruce. Sitka Spruce showed the lowest increase. First results indicate that Douglas Fir may be suitable for growth in Latvia. Although this study needs further research to analyse the sensitivity of these species to various meteorological factors.

Key words: Species introduction, dendrochronology, climate change, *Picea sitchensis*, *Pseudotsuga menziesii*

BREEDING PROGRAMS

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Dr. Keith JS Jayawickrama has been Director of the Northwest Tree Improvement Cooperative (NWTIC) based at Oregon State University since June 2000. The primary species of interest for NWTIC is coastal Douglas-fir, with an equally advanced program in western hemlock. NWTIC and Dr. Jayawickrama support tree improvement work for over 60 entities in the Pacific Northwest; improvement work is also underway for Noble fir, western red cedar, coast redwood, sugar pine and white fir. Before NWTIC Dr. Jayawickrama worked with radiata pine improvement in New Zealand and Chile, and obtained his graduate education at North Carolina State University.

Diverse Pacific Northwest Forests for the 21st Century – Developing Secondary Conifers

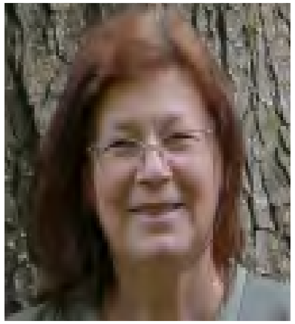
Co-author : Mike Crawford
[1] Bureau of Land Management

There have been very large investments in improving coastal Douglas-fir, the primary species in western Oregon and Washington, and interest remains high with 3rd cycle programs well underway and rapid progress in seed orchards. Work in western hemlock also keeps pace, with 3rd cycle tests about to be established; this species is often preferred in areas affected by Swiss Needle Cast disease.

Landowners are also interested in planting a diversity of secondary conifers, due to the diverse environmental conditions in which reforestation takes place in this region (from dry to very wet, from sea level to 2,000 meters) and the varied markets to serve (domestic and export, framing, large timbers, panels, and outdoor use) and with very minimal planting of hardwood species. Planting a variety of conifers on appropriate sites should enhance the resilience of forests under changing climatic conditions, fluctuating log markets, and the possible introduction of diseases and pests. Some sites west of the Cascades are too hot and dry to support pure Douglas-fir stands, while laminated root rot affects significant areas and causes mortality in Douglas-fir and some other conifers. High-elevation areas with heavy wet snow tend to favour Noble fir more than Douglas-fir.

- Seed orchards have been established for Noble fir, western white pine, sugar pine, high elevation western hemlock, and western red cedar, some within the last decade. These are being actively managed.
- There is interest in developing high monoterpene seed sources for western red cedar to reduce damage from deer browse.
- Introducing coastal redwood to the warmer wetter parts of Oregon shows promise; a cooperative testing program has been formed.
- There is a modest demand for weevil-resistant Sitka spruce for areas closest to the ocean and subject to strong winds.
- Consistent seed supplies are also sought for Ponderosa pine, incense cedar, Pacific Silver fir and white fir. There are plans to establish the first-ever seed orchard for white fir, serving the Cascades and Sierras of southern Oregon and northern California.
- Successful disease resistance breeding programs supported by the US Forest Service and the Bureau of Land Management offer the promise of re-introducing more sugar pine, western white pine, and Port Orford cedar back to the landscape, after decades of disease impacts to these native species.

Key words : Seed orchards, Secondary Conifers



PROVENANCE TRIALS
SPECIES INTRODUCTION

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Dr. Georgeta Mihai is senior researcher and the head of Silvobiology Laboratory at the National Institute for Research and Development in Forestry (Bucharest, Romania). She has a forestry and quantitative genetics background. Since 1990 she is working in the field of research and has participated and coordinated several national and international research projects on forest genetics, tree breeding and the management of the forest genetic resources (e.g. GENCLIM, TehMol, TEEBREEDEX, NNEXT). Her research is focused on assessing the intraspecific genetic variation and adaptive capacity of forest species in context of climate change, and development the breeding program for coniferous species. Currently she is involved in revision of the provenance regions for forest reproductive material in Romania, development of the genetic basis to advance to new breeding generations and establishing the most appropriate breeding strategies for European larch, Silver fir and Norway spruce.

Could Douglas fir be an alternative species in a changing climate? Comparative analysis with local Norway spruce in western Romania

Co-authors : Alin-Madalin Alexandru[1], Marius-Victor Birsan[2]
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The most recent climate change scenarios show that Southern and Eastern Europe will be affected by a significant increase in temperature and drought frequency by the end of the 21st century. Romania has already recorded very high temperatures and long periods of drought over the last decades, the most affected regions being the south, west and east of the country. Norway spruce, the most widespread coniferous species outside the natural distribution area, exhibited high sensitivity to decrease of water availability, and weak adaptive capacity at lower elevations.

Considering that successful forest management requires suitable species and high-quality reproductive material for reforestation, the aim of this study was to evaluate and compare the growth and drought response of Douglas fir (Pseudotsuga menziessi var. menziesii) and Norway spruce in two stands installed at the end of the 19th century in western Romania. These are mixed stands with Douglas fir, Norway spruce and deciduous species, and are among the oldest Douglas fir plantations in Romania. The stands are located in highly contrasting site conditions, on high-productivity site conditions for European beech at an altitude of 880 m, and low-productivity site conditions at an altitude of 460 m, respectively.

The growth traits, wood characteristics and drought parameters (resistance, recovery, resilience and relative resilience) of Douglas fir and Norway spruce trees have been analyzed and compared. The climate-growth relationship was determined using growth response functions over the period 1938–2017. Also, to simulate the potential impact of climate change on Douglas fir in this region, the RCP4.5 scenario was used over two periods: 2021–2050 and 2071–2100.

Results reveal that Douglas fir has an exceptional growth capacity, overcoming the Norway spruce since the early ages in both site conditions. The highest growth performances have been obtained on the low productivity site. Analyzing response to drought events, considerable differences were found between species. Results highlight the high resistance and relative resilience to extreme droughts of Douglas fir compared to Norway spruce. Norway spruce displayed higher resilience to extreme droughts while both species recorded a similar recovery capacity. However, autumn-winter temperatures play an important role in the adaptation of Douglas fir to site conditions in Romania. The developed models used to assess the climatic conditions of Douglas fir suitability in Romania show good survivability for the western-most part of the country (Banat Plain). The use of proper provenances of Douglas fir for site conditions, in mixture with native deciduous species, could be an option for climatically exposed sites because it could increase the value of these stands and their capacity to adapt to climate change. Therefore, the conservation of the most valuable stands of Douglas fir should have priority, since they can be used as potential seed sources for ecosystem restoration.

Key words: Douglas fir, Norway spruce, climate-growth relationship, response to drought, climate change

BREEDING PROGRAM

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Mirko Liesebach studied forest science. At the end of the 1980th he worked as an assistant in various forest divisions of the Federal Ministry for Food, Agriculture and Forestry. Since 1990, he has been researching in the field of forest genetics and tree improvement at the Federal Research Centre for Forestry and Wood Products (Grosshansdorf and Waldsieversdorf, DE), the Research and Training Centre for Forests, Natural Hazards and Landscape (Vienna, AT), the Northwest German Forest Research Institute (Hann. Münden, DE), and the Thünen Institute of Forest Genetics (Grosshansdorf). Since 2008, he is as senior scientist head of unit for provenance research and forest tree breeding and forest genetic recourses. He is active in several national and international organisations and committees.

The German breeding concept on Douglas-fir – current status

Co-authors : Katharina Liepe[1], Heike Liesebach[1], Christoph Rieckmann[1], Volker Schneck[1]

[1]Thünen Institute of Forest Genetics

From the 1980th up to now the proportion of natural regeneration and planting has inverted from 20 % and 80 % to 85 % and 15 %, respectively. The number of forest tree breeding institutions is decreasing continuously in Germany. Therefore, a breeding workshop was held in 2011 to receive an overview on the present status. Four invited speakers gave an overview on the forest tree breeding activities in their countries followed by the analysis of the situation in Germany from different points of view. As a result of this workshop a concept on forest tree breeding in Germany was prepared.

The concept is focusing on six species and species groups including Douglas-fir. With substitutes of the 'Waldklimafonds', a joined grant program of the federal ministries of agriculture and environments, the realisation of the concept could be started in 2014. Depending on the breeding progress the strategy for the 6 species and species groups varies from selection of stands over the establishment of seed orchards, the creating of parents of families and the selection of clones.

Additional to existing regions of provenance we start to delineate breeding zones taking climate change into consideration.

The breeding activities will be completed by evaluation of the genetic diversity and pollination structure, and in a revised seed orchard concept.

The evaluation of the provenance trials resulted in 3 breeding zones for Douglas-fir in Germany. For the establishment of the breeding populations, the plus trees were mainly selected in provenance trials. This has the great advantage that the growth of a provenance and the plus trees selected can be directly compared to other provenances at the same site. Furthermore, a genetic fingerprint was created for each plus tree.

A breeding population with 150-300 plus trees was compiled for each of the 3 breeding zones. Each plus tree is secured with 3 copies in one of the breeding populations (clone archives) at 2 locations each. The archives form the basis for the seed orchards to be established.

In population genetic studies, minimum requirements for seed crop populations and seed orchards were determined. The results have been incorporated into the development of a seed orchard concept. Using the latest software, the genetic fingerprint data of the plus trees are used to determine how many clones are required for a genetically diverse seed orchard and how the genetic structures of the seed can be optimised by distributing the clones in the seed orchard in order to reduce inbreeding depression.

A project has started in October to produce graftlings to establish 2 seed orchards for one breeding zone.

PROVENANCE TRIALS SPECIES INTRODUCTION

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I am working as a senior scientist in Natural Resources Institute Finland (Luke) with main area of responsibility in Scots pine breeding. I have also been involved in defining the deployment areas of the native conifers in Finland. My current tasks include testing of exotic tree species. This work has been more topical now, as exotics are seen as one solution to adapt to the climate change.

Pacific Northwest Conifers in Finland

Co-authors : Matti Haapanen[1]

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Finland has only two native conifers of commercial importance, Scots pine (*Pinus sylvestris* L.) and Norway spruce (*Picea abies* Karst.). Therefore, many experiments to assess the wood production potential of exotic trees both from East Asia and North America were established during the 20th century, especially in the 1920's and 1930's. Recently the relevance of exotic tree species has been discussed in relation to mitigating the effects of global warming on forests.

Lodgepole pine (*Pinus contorta* ssp. *latifolia* Dougl. Ex Lond.) and Douglas-fir (*Pseudotsuga menziesii* var. glauca) are among the most intensively studied PNW conifers. The best performing provenances of these species originate from the inland parts of British Columbia.

Lodgepole pine produces more stem biomass and has better resistance against some insects and fungi than the native Scots pine. This led, together with the concurrent Swedish enthusiasm for this species, to a limited commercial interest for planting lodgepole pine in Finland in 1970's and 1980's. However, the stem quality of lodgepole pine is inferior to that of Scots pine due to its thick branches. Stem breakages due to snow and wind are also common. The area of lodgepole pine stands is currently somewhat below 10 000 hectares. Today, the interest in lodgepole pine in Finnish forestry has vanished.

A few successful Douglas-fir stands from the pre-war era have helped to keep the interest in this species alive. However, results from field experiments and operational plantations are generally not very encouraging. The mostly flat terrain of Finland and the abundance of poorly drained soils are not optimal for Douglas-fir, resulting in poor growth and quality. Many trials have also been terminated at an early age because of extensive frost damages and mortality. Douglas-fir is sometimes considered as a potential tree species for Finnish forestry as it appears to be more drought-hardy and thus less threatened by the ongoing climate warming than the native spruce. However, the potential seems to be restricted to a few site types in southern Finland. The total area of Douglas-fir plantations in Finland is just a few hundred hectares.

Other PNW conifers tested in Finland include, e.g., western redcedar (*Thuja plicata*), western hemlock (*Tsuga heterophylla*), Sitka spruce (*Picea sitchensis*), subalpine fir (*Abies lasiocarpa*), black spruce (*Picea mariana*), white spruce (*Picea glauca*) and Engelmann spruce (*Picea engelmannii).* The first three of these have shown adequate performance only on the southern coast of Finland, whereas the rest are hardy in the whole of Finland. However, none of them has proven any benefits over the native conifer species. These PNW conifers are mostly found in arboreta and their commercial importance in Finland is insignificant, as it is for all the exotic tree species.

Key words:Douglas-fir, lodgepole pine, species introduction, provenances, Finland

CLIMATE / GENECOLOGY

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I am a PhD student in the department of Renewable Resources at the University of Alberta. My research interests are broad and mainly focus on applying statistical models to investigate plant-climate interactions of North American boreal tree species, with the goal of predicting and mitigating climate change impacts. I graduated from Albert-Ludwigs-University Freiburg, Germany in 2019 with dual MSc degrees in Forest Sciences. I am now working on adaptation of tree species to climate environments, and researching the risks and opportunities for assisted migration to address climate change.

Should we plant trees at higher latitudes or at higher elevations to compensate for climate change? An evaluation of frost risks

When assisted migration is used to address climate change, tree seedlings may have to be moved to substantially colder environments in anticipation of climate warming over their life span. Here, we evaluate frost risks for four economically important forest tree species of western Canada, Douglas-fir (*Pseudotsuga menziesii*), lodgepole pine (*Pinus contorta*) , interior spruce (*Picea glauca*, *P. engelmannii*, and their hybrids), and western larch (*Larix occidentalis*), when moved to adjacent northern and higher elevation seed zones that are cooler by approximately 2 °C. Changes to risks of damaging frosts among seed zones are evaluated during two 30-day periods, after dormancy release in spring and before onset of dormancy in fall, assuming a temperature-dominated day of bud break and a critical photoperiod-controlled onset of dormancy in fall. Based on daily interpolated climate data between 1980 and 2019, we find that late spring and early fall frost risks do not change significantly for transfers toward the north (<1 percentage point in most cases). In contrast, moving planting stock toward higher elevation generally leads to a substantial increase in exposure to unseasonal frosts (late spring frosts: 0.5% to 9.4%, early fall frosts: 0.8% to 17.1%). We conclude that transfers toward the north are preferable to transfers up in elevation in reforestation of these tree species in western Canada.

Key words: Frost risk; assisted migration; climate change; latitude transfer; altitude transfer

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FOREST HEALTH

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Dr Sniezko is Center Geneticist at the USDA Forest Service's Dorena Genetic Resource Center in Oregon. His work focuses on development of populations of trees with genetic resistance to non-native forest tree diseases & pests, as well as genetic variation and conservation. He has worked with white pine blister rust (*Cronartium ribicola*), Port-Orford-cedar root disease (*Phytophthora lateralis*) and koa wilt (*Fusarium oxysporum*) among others. He is coordinator of IUFRO 2.02.15 (Breeding and Genetic Resources of Five-needle Pines) and a deputy coordinator 7.03.11 (Resistance to Insects and Pathogens).

Searching for White Pine Blister Rust Resistance in Foxtail Pine (Pinus balfouriana)

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Foxtail pine (*Pinus balfouriana*) is an endemic pine native to California. It has a disjunct range with 480 km between the northern and southern subspecies. One subspecies is in northern California (North Coast and Klamath Mountains), and the other in the southern Sierra Nevada range. Like all North American white pine species, it is very susceptible to white pine blister rust (WPBR), caused by the non-native, invasive fungal pathogen *Cronartium ribicola*. Very little prior investigations of genetic resistance to WPBR have been undertaken, but they suggested it was perhaps the most susceptible of the white pine species of the U.S. A concerted effort to examine foxtail pine for resistance to WPBR started in 2014, with seedling screening trials beginning in 2014, 2018 and 2019. The 2014 trial seem to confirm the very high susceptibility of foxtail pine, the 2018 trial will examine variation under lower inoculum density levels, while the 2019 trial is examining 150 seedling families in a range-wide screening trial that includes both subspecies. These three trials were undertaken at the USDA Forest Service's Dorena Genetic Resource Center, but two additional trials are also underway at the Region 5 screening facility in Placerville, CA. In addition, two field trials of 20 families were established in 2021, one in northern CA, one in southern OR, to provide validation of seedling screening results, examine durability of any resistance found, and provide a look at adaptive differences in families of foxtail pine from both subspecies.

Key words: *Cronartium ribicola*, white pine blister rust, genetic resistance, foxtail pine, *Pinus balfouriana*

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Genetic variation and climate response of radial growth of Larix olgensis at four trails in northeast China

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Larix olgensis is one of the most important timber species in northeast China. Previous studies on *L. olgensis* had mostly focused on evaluation of genetic variation using natural forests, but comparative studies on provenance trails at different sites are still rare. Thus, the objective of this study was to evaluate the age trends of genetic variation parameters in radial growth of different provenances and growth-climate relationship in different locations. In the present study, tree-ring cores of 10 *L. olgensis* provenances were sampled from four representative trail sites in 2019 (Cuohai, CH; Jiagedaqi, JGDQ; Liangshui, LS; Mao'ershan, MES). The results of ANOVA show that significant differences in DBH at different ages were detected among provenances at four sites, except for 10, 11, 37, and 38 years at LS. The genetic variation parameters in different sites at the young age were generally higher than those at the mature period. Age-age correlations among different sites show that the early selection for DBH could be made at the age of 12 years at JGDQ and LS, while the ages for early selection at CH and MES were 10 and 11 years old, respectively. The results of growth-climate relationships show that temperature and precipitation played key roles in the radial growth of larch. At CH, radial growth showed significant correlations with August temperature (positive) of the current year, and with previous May temperature (negative) and November temperature (positive), and previous December precipitation (positive). The current June temperature (negative) and precipitation (positive) were important factors affecting the radial growth at JGDQ. July temperature of the current year had a negative relationship with larch growth at LS, while there were no significant correlations between radial growth and climatic factors at MES. The results reported in this study provide a valuable insight about early selection for different sites and can serve as a reference for future breeding and improvement research.

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Terrance Ye earned his Ph.D. in forest biology and management from University of Alberta in 2003. He is currently working at the Department of Forest Ecosystems and Society, Oregon State University, and as a quantitative geneticist for the Northwest Tree Improvement Cooperative (NWTIC). His research interests focus on the fields of breeding strategies for US pacific northwest tree species, methodology in quantitative genetics, host-pathogen interaction, and genomic selection.

Early Assessment on Realized Genetic Gains from Second-Cycle Western Hemlock Tree Improvement

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Western hemlock (Tsuga heterophylla (Raf.) Sarg.) is an economically important tree species in western North America. First-cycle testing started in 1975 with 1,500 parents from five separate zones tested. The best selections went into seed orchards and were also used as the parents in a second-cycle breeding program in 1992; 539 full-sib families were tested in this cycle.

Through the joint effort of the Stand Management cooperative and the Northwest Tree Improvement Cooperative, trials were established in Oregon and Washington in 2017 and 2018 to verify the realized genetic gain in large block-plot settings at operational spacing over a longer time span (the rankings had been obtained in single-tree plots at a narrower spacing). Two genetic entries were included, i.e., the unimproved seedlot comprising two woodsrun checklots and the improved seedlot (= a mix of nine top-performing second-cycle full-sib families). The tests are growing at four sites on a regular grid with 10' spacing. Each site had ten plots (except for one site with six) distributed randomly, with equal numbers of plots for unimproved and improved seedlots.

Total height (HT, cm), diameter at breast height (DBH, mm), and crown width (CW, cm) were measured for all trees after five growing seasons. Volume index (VOL) was calculated as HT x DBH x DBH / 100,000. Data was analyzed using two fixed linear models based on (1) plot means, and (2) individual tree measurements. Model 1 includes the following effects: population mean, site, genetic type, their interaction, and residual. Model 2 includes all effects in model 1 plus family within genetic type as well as its interaction with site. Realized genetic gains were calculated as percentage increase of improved materials over unimproved.

Overall, the improved seedlot performed significantly better than the unimproved seedlot, with realized gain being 22.5% for HT, and 19.3% for DBH, 73.2% for VOL, and 12.2% for CW. These values were up to 200% higher than age-10 predicted genetic gains in progeny tests. In addition, all full-sib families had higher growth rate and crown width than the unimproved materials at family level.

Significant site by seedlot interaction was found for HT and VOL at plot level, and for all traits at family level. The size of the realized gains was higher or lower depending on site; however, realized gains were strongly positive at each site for HT, DBH and VOL.

There were also large differences in realized gain between the highest- and lowest-gain tested families (i.e., 45% for HT, 44% for DBH, 130% for VOL, and 50% for CW), suggesting large possible gain in the next breeding cycle of western hemlock.

The results confirmed that tree improvement programs for western hemlock have been very effective in the US Pacific Northwest.

Key words: *Tsuga heterophylla*, realized genetic gain, tree improvement

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