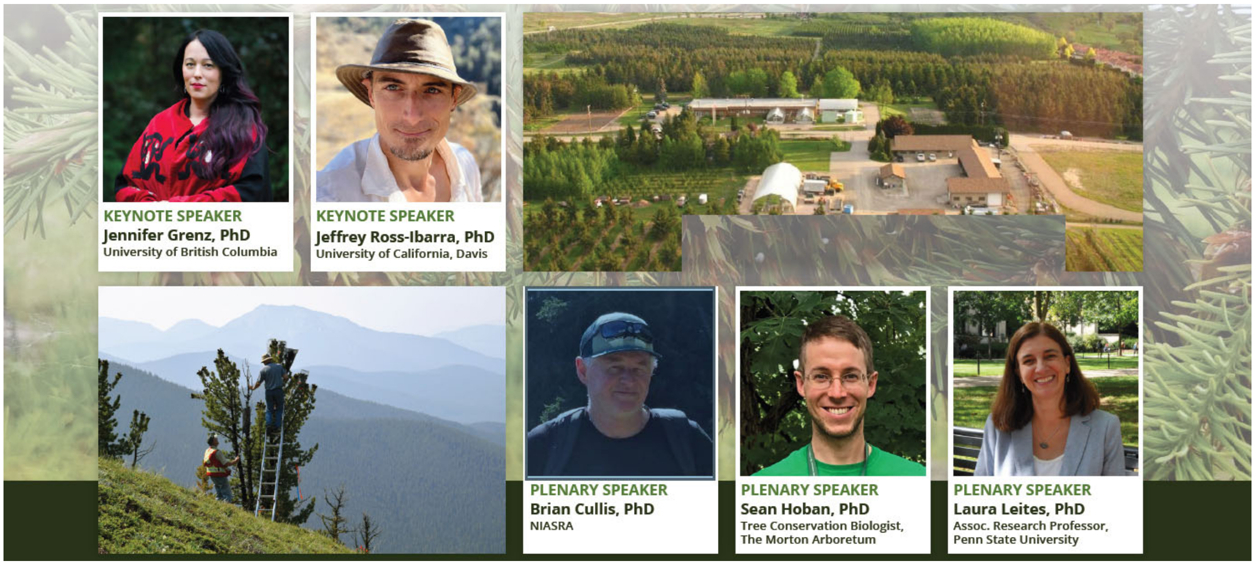
Forest Genetics 2023
Discovery & Innovation in Changing Climates



KEYNOTE SPEAKER
Jennifer Grenz, PhD
University of British Columbia

KEYNOTE SPEAKER
Jeffrey Ross-Ibarra, PhD
University of California, Davis

PLENARY SPEAKER
Brian Cullis, PhD
NIASRA

PLENARY SPEAKER
Sean Hoban, PhD
Tree Conservation Biologist,
The Morton Arboretum

PLENARY SPEAKER
Laura Leites, PhD
Assoc. Research Professor,
Penn State University

July 10 - 14, 2023
Prestige Vernon Lodge
Vernon, British Columbia, Canada

Canadian Forest Genetics Association • Association canadienne de génétique forestière

Co-hosted by

WFGA
Western Forest Genetics Association

MESSAGE FROM THE CO-CHAIRS

Brian T. Barber, RPF
President
Canadian Forest Genetics Association

Nicholas Ukrainetz, PhD, RPF
President
Western Forest Genetics Association

The Western Forest Genetics Association (WFGA) and the Canadian Forest Genetics Association/ l'Association canadienne de génétique forestière (CFGA) are pleased to co-host a third meeting in as many years in beautiful British Columbia.

We are excited to hold this in-person conference in Vernon, BC, located in the North Okanagan and the traditional and unceded territory of the Syilx Okanagan People. The North Okanagan is also the hub of BC's interior tree breeding and climate change and adaptation research, and BC's interior seed orchards.

Over 100 participants from across Canada, USA, Europe and Asia will attend the conference. These include a number of undergraduate, masters, and Ph.D students. Please take the time to meet and inspire our next generation of forest genetics scientists and practitioners.

The conference will take place at the Prestige Vernon Lodge. It is preceded by meetings of the CFGA Tree Seed Working Group and Canadian Poplar and Willow Council of Canada on Monday, July 10.

Please join us for registration and reception in the lodge's picturesque atrium on Monday evening, July 10. The conference kicks-off at 8:00 Tuesday morning with our first Keynote Speaker, **Dr. Jennifer Grenz**, followed by several plenary, concurrent and poster sessions. The conference banquet will be held Tuesday evening at the Vernon Seed Orchard Company, with spectacular views of the Okanagan Valley.

The field trip on Wednesday includes visits to the BC Ministry of Forests' Kalamalka Forestry Centre and Bailey Road Seed Orchards, and PRT Growing Service's Armstrong Nursery and Seed Orchards. Scientific talks resume on Thursday, and conclude with our second keynote speaker, **Dr. Jeffrey Ross-Ibarra**. A post-conference field tour (sold out) will take place on Friday.

The in-door sessions will not be livestreamed, but recorded so persons unable to attend the conference, and registrants interested in catching all the concurrent sessions, can watch the video recordings later at their convenience.

This in-person event would not have been possible without the generous support of our sponsors and contributions from many volunteers and service providers.

In particular, we would like to express our thanks and appreciation to **Sonia Serrambana**, Conferences and Accommodations UBC, and **Greg O'Neill**, program committee lead, and for their time and energy.

We hope you enjoy the conference and reconnecting with ‘old’ colleagues and meeting new ones. Please also take the time to enjoy some of the many local attractions during your stay in the sunny Okanagan Valley. It’s cherry season!

ACKNOWLEDGEMENTS

Program Committee: Greg O’Neill, Sally Aitken, Brian Baltunis, Nicolas Feau, Miriam Isaac-Renton, Barb Thomas, and Alvin Yanchuk.

Conference and post-conference field tours: Krista Copeland, Marie Vance and Dan Gaudet

CFGA Tree Seed Working Group Meeting; Dave Kolotelo and Melissa Spearing

CFGA Undergraduate Student Travel Award Committee: Ashley Thomson, Nathalie Isabel, Dave Kolotelo, Patrick Lenz, and Barb Thomas.

Student Award Adjudication: Andreas Hamman

Finances: Conferences and Accommodations UBC; Shona Millican, Treasurer, CFGA; Richard Zabel, Western Forestry and Conservation Association for WFGA; Meaghan’s Bookkeeping

Service Providers: Prestige Vernon Lodge; Conferences and Accommodations, UBC, Caorda Web Solutions, Fairwinds Creative, New Horizons Productions, Showtime Event & Display, Avalon Event Rentals, VistaPrint, Gumtree Catering, Vernon Catering, Bluestar Coachlines, Johnston Meier Insurance, Anne-Marie Hague, and Christopher Thomson (name tags).

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GENE $500

Centre for Forest Biology
University of Victoria

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PROGRAM AT A GLANCE

Monday, 10 July

08:00 - 16:00	Tree Seed Working Group (separate registration required)
16:00 - 19:00	Conference registration - Hotel atrium
17:00 – 18:00	Reception - Hotel atrium

Tuesday, 11 July

08:00 – 08:20	Introductions – Ballroom 1
08:20 – 09:00	Keynote speaker: Jennifer Grenz – Ballroom 1
09:00 - 10:00	Session 1 - Population and quantitative genetics/collection and analysis of progeny test data – Ballroom 1
10:00 - 10:20	*Break*
10:20 - 11:40	Session 2a - Genetic conservation – Ballroom 1
	Session 2b - Forest Health – Ballroom 3
11:40 - 12:40	*Lunch – Ballroom 2*
12:40 - 13:20	Plenary speaker: Brian Cullis – Ballroom 1
13:20 - 14:20	Session 3a - Collection and analysis of progeny test data – Ballroom 1
	Session 3b - Seed transfer and provenance test analyses – Ballroom 3
14:20 - 15:40	Poster session – Okanagan room
15:40 - 16:20	Plenary speaker: Sean Hoban – Ballroom 1
16:20 - 17:00	Session 4a - Genetic conservation – Ballroom 1
	Session 4b - Seed, seed orchards and seedlings – Ballroom 3
18:30	Banquet - Vernon Seed Orchard Company

Wednesday, 12 July

08:45 – 17:00	Conference field tour

Thursday, 13 July

08:00 - 08:40	Plenary speaker: Laura Leites – Ballroom 1
08:40 - 10:00	Session 5 - Seed transfer and provenance test analysis – Ballroom 1
10:00 - 10:20	*Break*
10:20 - 12:00	Session 6a - Seed transfer and provenance test analyses – Ballroom 1
	Session 6b - Interdisciplinary research/population and quantitative genetics – Ballroom 3
12:00 - 13:00	*Lunch – Ballroom 2*

13:00 - 14:20	Session 7a - Genomic tools – Ballroom 1
	Session 7b – Other forest genetics related topics – Ballroom 3
14:20 - 14:40	*Break*
14:40 - 15:40	Session 8a - Genomic tools – Ballroom 1
	Session 8b - Seed transfer and provenance test analyses – Ballroom 3
15:40 - 16:20	Keynote speaker: Jeffrey Ross-Ibarra – Ballroom 1
16:20 - 17:00	Session 9 – Population and quantitative genetics – Ballroom 1
17:00 - 17:20	Closing remarks and student awards

Friday, 14 July

8:15 – 17:00	Optional field trip (meet in the Vernon Lodge parking lot)

DETAILED PROGRAM

Monday, July 10

8:00 Tree Seed Working Group (separate registration required)

16:00 Conference registration opens
17:00 Reception
Sponsored by: Select Seed Company Ltd.

Tuesday, July 11

8:00 Introductions

Welcome to the territory of the Syilx Okanagan People
Elder from the Okanagan Indian Band

Welcome from the City of Vernon
Councillor Akbal Mund

8:20 Keynote Speaker:
Reclaiming forest genetics as a practice of indigenous land stewardship
Jennifer Grenz
Sponsored by: Forest Genetics Alberta Association

Session 1: Population and quantitative genetics/collection and analysis of progeny test data

9:00 Genomic tools for species restoration: the case of American chestnut
Jason Holiday

9:20 Genetic signatures differentiate progeny of mountain pine beetle-killed lodgepole pine from progeny of survivors
Janice Cooke

9:40 Selection in the presence of variety by environment interaction: using factor analytic linear mixed models to define interaction classes
Alison Smith

10:00 Break

Session 2a: Genetic conservation

10:20 Predicting fundamental climate niches of forest trees based on species occurrence data
Yueru Zhao

10:40 Ne port in a storm: genetic diversity in BC reforestation
Hayley Tumas

11:00 Assessment of the impact of climate change on endangered conifer tree species
Wenhuan Xu

11:20 Moving forward to protect and recover the endangered North American butternut
Martin Williams

Session 2b: Forest health

10:20 Local adaptation of trees to forest pests
Dawei Luo

10:40 Determining the role of *ophiostomatiod* fungal pathogens in overcoming lodgepole pine defenses during mountain pine beetle mass attack
Colleen Fortier

11:00 Examining the transcriptional response to multiple attacks by *Hylobius abietis* on *Picea sitchensis* in the UK
Barley Rose Collier Harris

11:20 Growth and survival of western white pine seed sources in the face of white pine blister rust and a changing climate: age 15 results from six trials in western Washington
Richard Sniezko

11:40 Lunch

12:40 Plenary Speaker:
A model-based design approach for the design of selection experiments using ODW
Brian Cullis
Sponsored by: Weyerhaeuser

Session 3a: Collection and analysis of progeny test data

13:20	Phenotyping coastal Douglas-fir progeny trials with drone-mounted multispectral, thermal, and LiDAR sensors to scan for environmental resilience *Olivia Waite*
13:40	Genetic parameters of *Fagus sylvatica* (L.) open-pollinated progeny trials in a gradient of site fertility and climatic conditions *Vasyl Mohytych*
14:00	Genetics of wood quality traits in a *Pinus contorta* progeny test *Trevor Doerksen*

Session 3b: Seed transfer and provenance test analyses

13:20	Universal response function for interior spruce (*Picea glauca*, *Picea engelmannii*, and their hybrids) and its spatial validation *Zhengyang Ye*
13:40	Safe seed transfer of *Pinus brutia* in Türkiye *Greg O'Neill*
14:00	Spruces (*Picea* spp.) in Icelandic forestry *Mai Duong*

14:20	Poster session *Sponsored by: Mosaic*

15:40	Plenary Speaker: Conserving genetic diversity of trees and other plants without DNA data - simple but useful metrics *Sean Hoban* *Sponsored by: Washington State Department of Natural Resources*

Session 4a: Genetic conservation

16:20 Continuous cover forestry and genetic diversity: a case study of England's Douglas-fir and western redcedar plantations
Laura Guillardin

16:40 What does the future hold? Aiming the National Tree Seed Centre's research and conservation strategy towards 2030 (and beyond!)
Melissa Spearing

Session 4b: Seed, seed orchards and seedlings

16:20 United States Forest Service and Washington Department of Natural Resources tree seed orchard restoration collaboration in Washington State
Claire Ellwanger

16:40 DNA methylation differences in somatic embryogenesis competence of *Abies nephrolepis*
Chae-Bin Lee

18:00 Bus departure from Prestige Vernon Lodge

18:30 Banquet dinner: Vernon Seed Orchard Company

Wednesday, July 12: Conference field tour

8:45	Load buses – Vernon Lodge parking lot
9:00	Travel to Kalamalka Forestry Centre
9:30	Tour of Kalamalka Forestry Centre
11:30	Lunch
12:30	Travel to Bailey Seed Orchard
13:00	Tour of Bailey Seed Orchard
14:30	Travel to PRT Armstrong
15:00	Tour of PRT Armstrong
16:30	Travel to Prestige Vernon Lodge
17:00	Arrive at Prestige Vernon Lodge

Thursday, July 13

8:00	Plenary Speaker: Forest trees adaptation to climate: Building on the legacy of genecology to anticipate responses to climate and guide seed movement *Laura Leites* *Sponsored by: Forest Genetics Council of BC*

Session 5: Seed transfer and provenance test analyses

8:40	dwreml: An R package for fitting the linear mixed model *Brian Cullis*
9:00	Balancing risk and benefits of assisted migration to address climate change *Andreas Hamann*
9:20	Establishing Monarch Butterfly overwintering sites for the future: *Abies religiosa* upper altitudinal limit expansion by assisted migration *Cuauhtémoc Sáenz-Romero*
9:40	Multispectral vegetation indices from drone remote sensing quantify clinal adaptation to climate in provenance tests of *Picea englemannii x glauca* *Samuel Grubinger*
10:00	Break

Session 6a: Seed transfer and provenance test analyses

10:20	Coastal grand fir common garden, multiple environment genecology trials: 40-year results *Charles Cartwright*
10:40	Testing climate-based seed transfer guidelines for jack pine (*Pinus banksiana* Lamb.) in northeast Ontario *Dennis Joyce*
11:00	Inter- and intraspecific variation in photosynthetic and functional traits in the two most important Central European broadleaved tree species: *Fagus sylvatica* and *Quercus robur* in relation to drought *Marzena Niemczyk*
11:20	Phenotypic and genomic signals of climate adaptation in western larch: informing assisted migration and climate-based breeding *Beth Roskilly*

11:40 The penalty of the height growth syndrome in tree breeding and forest management
Deogratias Rweyongeza

Session 6b: Interdisciplinary research/population and quantitative genetics

10:20 Measuring the phenotype and growth performance of improved and unimproved seedlings of *Pinus contorta* under commercial greenhouse conditions (A Study using High-Throughput Phenotyping Technology)
Sarun Khadka

10:40 Social Acceptability of Genomic Selection for Pest Resistance
Valerie Berseth

11:00 Second-generation co-operative genetic gain trials in the US Pacific Northwest
Keith Jayawickrama

11:20 Physiological and Transcriptomic Responses to Drought in Ponderosa Pine
Adam Gilewski

12:00 Lunch
Sponsored by: Canadian Wood Fibre Centre

Session 7a: Genomic tools

13:00 Implementing genomic selection in Norway spruce
Funda Ogut

13:20 Optimizing genomic selection for application: The importance of accurate estimation of genetic merit and disentangling of additive from non-additive effects
Patrick Lenz

13:40 Comparative transcriptome analysis reveals putative genes involved in cone development of Korean red pine (*Pinus densiflora*)
Dayoung Lee

14:00 Identification and classification of potential disease resistance genes across the North American, European, and Asian white pine species
Akriti Bhattarai

Session 7b: Other forest genetics related topics

13:00	Managing adaptability in a breeding program while balancing gain and diversity *Trevor Walker*
13:20	Assembly and annotation of the black spruce genome provide insights on spruce phylogeny and evolution of stress response *Theodora Lo*
13:40	Tree improvement increases the growth of white spruce (*Picea glauca*): evidence from 15-year-old operational plantations in Alberta *shes Bhandari*
14:00	Advancing White Spruce Genomics: Long-read genome assembly of white spruce enables improved annotation and generation of a chromosome-scale epigenetic map *Irem Yucel*
14:20	Break

Session 8a: Population and quantitative genetics

14:40	Current and future adaptive genetic variation associated with drought tolerance and cold hardiness in Douglas-fir (*Pseudotsuga menziesii*) *Rafael Candido*
15:00	Comparative and population genomics of the *Cronartium harknessii*-pine pathosystem *Laura Manerus*
15:20	Genomics of western redcedar: towards improved genetic resilience in a self-compatible conifer *Tal Shalev*

Session 8b: Seed transfer and provenance test analyses

14:40	Climate adaptation of selected coastal Douglas-fir: resilience to drought and frost under different levels of competition *Fleur Damen*
15:00	Assisted migration poleward rather than upward in elevation minimizes frost risks in plantations *Zihaohan Sang*
15:20	The early bud gets the cold: Diverging spring phenology drives exposure to late frost in a *Picea mariana* [(Mill.) BSP] common garden *Claudio Mura*

15:40	Keynote Speaker: A Tale of Two Teosintes: admixture, archaeology, and a new model of the origins of maize *Jeffrey Ross-Ibarra* *Sponsored by: Huallen Seed Orchard Co*

Session 9: Population and quantitative genetics

16:20	Identifying the genetic basis of convergent local adaptation in conifers *Tom Booker*
16:40	Genomic offset of *Populus tremuloides*, a keystone species in North America *Melanie Zacharias*
17:00	Closing remarks and student awards

Friday, July 14: Post conference tour (Separate registration required)

8:15	Load vehicles – Vernon Lodge Parking Lot
8:30	Travel to Deep Creek AMAT site
9:30	Deep Creek AMAT site
10:10	Travel to the Western Larch trial
10:30	Western Larch progeny test
11:10	Travel to the Barnes Creek clone bank
12:10	Lunch and drone demo – Barnes Creek clone bank
13:10	Travel to the Barney Site
13:30	Western redcedar Barney progeny trial
14:15	Travel to realized gain trial
14:45	Lodgepole pine realized gain trial
15:30	Travel to Vernon
17:00	Arrive at the Prestige Vernon Lodge

MAP OF THE VENUE

KEYNOTE SPEAKERS

JENNIFER GRENZ, PHD

University of British Columbia

Reclaiming Forest Genetics as a Practice of Indigenous Land Stewardship

Learning Indigenous languages and spending time with Elders and plant knowledge keepers has made clear that plant breeding and the care of plant genetics have been essential to the practice of Indigenous Land Stewardship within so-called British Columbia. Numerous plant species have multiple names within Indigenous languages, all differentiating them by plant characteristics, uses, and growing sites. Modern genetic tools are filling in knowledge gaps and painting a picture of the importance and desirability of certain tree species demonstrating purposeful introductions as plants and seeds were moved with traveling Indigenous Peoples. I will share how working on land-healing efforts, such as the reclamation and revitalization of Indigenous food systems with St'at'imc and Tsimshian communities, and Cowichan Tribes, as well as the recovery of major climatic events such as wildfire, have brought to light the importance of place-based-plants. As native plant nurseries are on the rise, questions are being raised about the potential impacts of introducing "outside" plants and trees to the lineages of culturally important plant relations. I bring a cautionary message, that we need to work carefully to ensure that restoration efforts are not inadvertently contributing to the continued erasure of the purposeful shaping of Indigenous lands by Indigenous Peoples since time immemorial, while sharing how reclamation of this little recognized dimension of Indigenous land stewardship, could offer hope for climate resiliency.

Speaker Biography: Jennifer has a B.Sc in Agroecology and a PhD in Integrated Studies in Land and Food Systems from the University of British Columbia. Her scholarly interests revolve around invasive species management, ecological restoration, and science communication, and she brings with her nearly two decades of experience providing consulting services and on-the-ground management of invasive species for all levels of government and working with Indigenous communities on creating food security plans and land healing initiatives. Jennifer is a proud Nlaka'pamux woman of mixed ancestry whose family comes from the Lytton First Nation (though she grew up on the coast of BC).

JEFFREY ROSS-IBARRA, PHD

University of California, Davis

A Tale of Two Teosintes: admixture, archaeology, and a new model of the origins of maize

Jeffrey Ross-Ibarra is an evolutionary geneticist at the University of California Davis with a background in ethnobotany and population genetics. His group works on plant evolution, using maize and its wild relatives as a model system to investigate questions from genome architecture to local adaptation and experimental evolution. Recent work from the group ranges from studying the nonequilibrium dynamics of background selection on genetic diversity, to methods to detect selection on transposable elements, to the role of gene flow in local adaptation and convergent evolution.

INVITED PLENARY SPEAKERS

BRIAN CULLIS, PHD

National Institute of Applied Statistics Research Australis (NIASRA)

A model-based design approach for the design of selection experiments using ODW

The success of a plant improvement program is based on its ability to maintain high levels of genetic gain. From a purely statistical perspective, maintenance of genetic gain relies on the use of near optimal experiment designs and appropriate methods of analyses. The natural phenotyping instrument for selection in the advanced evaluation phase is a multi-environment trial (MET). The analysis of METs has received wide attention for many years, culminating in the use of a single-step factor analytic mixed model by many plant breeding programs in Australia and elsewhere. There is, however, a dearth of literature concerned with the design of single and multiple selection experiments. There is a long history concerned with the design of experiments for fixed treatment effects, but these designs are not appropriate for selection experiments. In this talk we present a model-based approach for the design of single and multiple selection experiments. Our approach is model-based and hence allows for the use of genetic relatedness for each stage in the design process. The construction of optimal or near-optimal designs is achieved using the R package, ODW. We illustrate our ideas using two MET datasets.

Speaker Biography: Brian Cullis is a Senior Professor at the National Institute for Applied Statistics Research, Australia, and Professor of Biometry at the University of Wollongong having been appointed to this position in July 2011 after working as a biometrician for more than 30 years with NSW Department of Primary Industries. He has led numerous large-scale industry projects and has extensive experience in the management of large teams of applied statisticians working across multiple research and consulting projects on behalf of the Centre for Biometrics and Data Science for Sustainable Primary Industries, and in his previous role as Director of Biometrics in the NSW Department of Primary Industries.

His interests relate to the application of statistical approaches to the analysis of agricultural and biological data. He has co-authored more than 210 refereed papers. Much research involves the application and development of linear mixed model techniques. He is a co-developer of the ASReml and ASReml-R software systems. He has successfully supervised over 25 Masters and PhD students and has trained, developed and mentored the majority of statisticians currently supporting the grains industry within Australia.

He was the recipient of the E.A. Cornish award in 2015, an award for recognition of a member in the Australasian Region who has given long-time service to the Biometric Society and to the advancement of biometry. He is a past Co-Editor of Biometrics and past Associate Editor of the Australian and New Zealand Journal of Statistics and is currently Co-Editor for Frontiers in Plant Science (Plant Bioinformatics) and Associate Editor of the Journal of Agricultural Science, Cambridge.

SEAN HOBAN, PHD

Tree Conservation Biologist, The Morton Arboretum

Conserving genetic diversity of trees and other plants without DNA data - simple but useful metrics

There is a pressing need to assess the genetic diversity status, and loss or maintenance of adaptive capacity, for large numbers of threatened tree species, quickly. However, DNA based studies remain expensive and time consuming, and we lack genetic data for the vast majority of species. I will present several solutions to this challenge, which use non-genetic data. The first approach regards "indicators" for genetic diversity, based on minimum effective population sizes and conserving genetically distinct populations, which build on principles already in use in forestry. These indicators were presented by Hoban, Laikre, and colleagues in 2020; are being tested and improved at the national scale; and have been recommended by the recent Convention on Biological Diversity (CBD) COP15 agreement. The second approach regards ecogeographic summaries of how much of a species' range is conserved ex situ and in situ. This approach has been used for a decade in the seed bank and botanic garden community to measure progress in safeguarding genetic diversity and in prioritizing species and populations. Lastly I will mention the use of simulations for understanding and improving conservation of genetic diversity, including its uses in the planning of germplasm collections. Although these approaches have many imperfections, I argue that they help identify species experiencing genetic erosion, assist in planning interventions for such species, and make genetic concepts and issues approachable to non-geneticists.

Speaker Biography: Sean Hoban is a Tree Conservation Biologist at The Morton Arboretum in Chicago USA. Sean also has a leading role in the IUCN Conservation Genetic Specialist Group, GEO BON, and the Coalition for Conservation Genetics. He has a PhD from University of Notre Dame, and performed a postdoc with the ConGRESS project and another postdoc at NIMBioS. He has more than 80 publications and currently focuses on developing science-based advice for ex situ collections like botanic gardens, and for bringing knowledge on adaptive capacity of populations to national and global policy. He also has interests in seed dispersal, macrogenetics, hybridization, and population size change over time. You can read more about his group at hobanlab.com.

LAURA LEITES, PHD

Associate Research Professor, Pennsylvania State University

Forest trees adaptation to climate: Building on the legacy of genecology to anticipate responses to climate and guide seed movement

At a time when genomics and advanced new technologies propel our knowledge of forest tree species adaptation to climate, a centuries-rich legacy of genecology studies is still providing a solid knowledge foundation and answers to pressing new questions about the potential fate of species under a changing climate. In this talk, I will summarize how this legacy has led to the reanalysis of old provenance trial data across biomes, and around the globe, to anticipate species responses to climate change. I will discuss the main findings related to intraspecific variation in responses to climate, and highlight knowledge gaps that future re-analyses of old provenance trial data could help fill in. I will also provide examples of re-analyses, focusing on temperate broadleaf deciduous and conifer species with distributions in eastern North America. Finally, I will discuss how provenance trial data is informing the delineation of climate-smart seed zones and its associated challenges.

Speaker Biography: Dr. Laura Leites is an associate research professor of quantitative forest ecology at Penn State University where she leads the Quantitative Forest Ecology Lab. She holds a Doctorate in Natural Resources and a Master of Science in Forest Resources from the University of Idaho, and a Bachelor of Science in Agronomy from the Universidad de la República in Uruguay. Her research program focuses on understanding adaptation to climate in forest tree species and their potential responses under a changing climate. Current studies include modeling populations responses to climate change and using these models to guide seed movement for reforestation and restoration. Leites is also an Equity Leadership Fellow in the Office of the Vice Provost for Educational Equity where she leads initiatives to foster greater equity and inclusion across the university.

DAY 1: TUESDAY, JULY 11

SESSION 1: POPULATION AND QUANTITATIVE GENETICS/COLLECTION AND ANALYSIS OF PROGENY TEST DATA

GENOMIC TOOLS FOR SPECIES RESTORATION: THE CASE OF AMERICAN CHESTNUT

Jason Holliday, Joanna Malukiewicz, Alexander Sandercock and Jared Westbrook

Introduction of the fungal pathogen *Cryphonectria parasitica* to North America in the early 20th century led to the functional extinction of American chestnut (*Castanea dentata*), a catastrophic loss from ecological, economic, and societal perspectives. Two approaches to developing disease resistant chestnut populations currently show promise: introgressive hybridization with resistant Asian *Castanea* species, and genetic modification. While each of these approaches shows promise, they each present ongoing challenges. For example, the hybrid breeding program has generated families with intermediate resistance, but was predicated on a three-gene resistance model that is incorrect. This, coupled with low trait heritability, has complicated the selection process. By contrast, overexpression of an oxalate oxidase (OxO) transgene yields robust resistance, but multiple generations of outcrossing will be needed to recover genetic diversity. We have generated multiple population and functional genomic datasets to address these challenges. First, we developed a genomic prediction model trained on progeny-test data, which we used to select the top 1% of backcross families. To aid in diversifying transgenic lines, we sequenced whole-genomes of ~350 wild C. dentata stump sprouts from across the historical species range, and applied a variety of modern population genomic tools to understand patterns of neutral and adaptive variation. These results will guide ex situ conservation of wild germplasm for breeding with transgenic lines. Finally, while OxO-based resistance should be durable, this is not certain. We are therefore seeking additional candidates for transgenic manipulation by integrating RNA-seq of a blight canker development time series in resistant and susceptible species, whole-genome comparative analysis of all Castanea species, and QTL mapping within the hybrid breeding program. I will summarize results from each of these projects, which support our long-term goal of developing disease resistant, locally adapted American chestnut populations for restoration of the species.

GENETIC SIGNATURES DIFFERENTIATE PROGENY OF MOUNTAIN PINE BEETLE-KILLED LODGEPOLE PINE FROM PROGENY OF SURVIVORS

Janice Cooke, Rhiannon Peery, Catherine Cullingham, Joshua Miller, David Coltman, Staffan Lindgren and Dezene Huber

Over the past two decades, mountain pine beetle (MPB; *Dendroctonus ponderosae* Hopkins) has caused substantial mortality over more than 28 million hectares of pine forests in western North America. Lodgepole pine (*Pinus contorta* Dougl. ex Loud. var. *latifolia*) has been the main species affected by this epidemic. Even under severe outbreak conditions, however, some surviving lodgepole pine remain on the landscape. Did surviving trees have host quality traits that enabled them to avoid being successfully detected, attacked and colonized by MPB, or were these survivors just lucky? To address this question, we used large-scale DNA genotyping to identify genetic signatures that differentiate progeny of surviving lodgepole pine from progeny of lodgepole pine in the same stand that were killed by mountain pine beetle in central British Columbia during the hyperepidemic of the mid 2000s. A common garden experiment of F1MPB-killed and F1MPB-survivor individuals was established using seeds extracted from cones from MPB-killed killed parents and cones collected from survivor parents that had been produced following the outbreak, collected from four sites in northcentral British Columbia that sustained significant MPB mortality. A total of 481 individuals were genotyped at ca. 14000 high quality single nucleotide polymorphisms (SNPs), and the resulting dataset was analyzed using quantitative and population genomic approaches. Minor allele frequency analyses revealed significant reductions in lodgepole pine standing genetic diversity at most of the sampled sites, suggesting that MPB exerts selection pressure on host pines under hyperepidemic conditions. The calculated F1MPB-killed/F1MPB-survivor phenotype heritability value was high, indicating there is a genetic component to survivorship. Genomic selection in tandem with GWAS, were used to identify loci that predict survivorship. Loci that showed significant genotype-environment associations were removed from this data set to generate a list of candidate loci that represents a genetic signature for MPB resilience.

SELECTION IN THE PRESENCE OF VARIETY BY ENVIRONMENT INTERACTION: USING FACTOR ANALYTIC LINEAR MIXED MODELS TO DEFINE INTERACTION CLASSES

Alison Smith and Brian Cullis

Plant breeding multi-environment trials (METs) are an important component of identifying superior varieties as they allow an assessment of variety by environment interaction (VEI). A key consequence of the presence of VEI is that it is both statistically invalid and biologically meaningless to base variety selections on measures of overall performance across all environments in the MET. In this presentation we address the issue within the framework of a single-step linear mixed model analysis in which a factor analytic model is used for the variety effects in each environment. The numerous advantages in analysing MET datasets using this approach are widely known and the method is used extensively in Australian plant breeding programmes and in the National Variety Trials system. Our approach for variety selection involves the formation of groups of environments, called interaction classes (iClasses), within which there is minimal crossover VEI. It is then valid to obtain predictions of variety performance across the environments in each iClass. These predictions can then be used not only to select the best varieties within each iClass but also to match varieties in terms of their patterns of VEI across iClasses. We introduce a new graphical tool, called an iClass Interaction Plot, to display this information in a clear and illuminating manner. The idea of forming groups of environments with minimal VEI is not new. However a key distinction with our approach is that iClasses are formed on the basis of the fundamental parameters of the factor analytic model, namely the environment loadings, so are a direct consequence of the model used for analysis. We demonstrate the methods using a commercial MET dataset.

SESSION 2A: GENETIC CONSERVATION

PREDICTING FUNDAMENTAL CLIMATE NICHES OF FOREST TREES BASED ON SPECIES OCCURRENCE DATA

Yueru Zhao, Tongli Wang and Greg O'Neill

Species climate niche models (CNMs) have been widely used for assessing climate change impact, developing conservation strategies and guiding assisted migration for adaptation to future climates. However, the CNMs built based on species occurrence data only reflect the species' realized niche, which can overestimate the potential loss of suitable habitat of existing forests and underestimate the potential of assisted migration to mitigate climate change. In this study, we explored building a fundamental climate niche model using widely available species occurrence data with two important forest tree species, lodgepole pine (*Pinus contorta* Dougl. ex Loud.) and Douglas-fir (*Pseudotsuga menziesii* Franco.), which were introduced to many countries worldwide. We first compared and optimized three individual modeling techniques and their ensemble by adjusting the ratio of presence to absence (p/a) observations using an innovative approach to predict the realized climate niche of the two species. We then extended the realized climate niches to their fundamental niches by determining a new cut-off threshold based on species occurrence data beyond the native distributions. We found that the ensemble model comprising Random Forest and Maxent had the best performance and identified a common cut-off threshold of 0.3 for predicting the fundamental climate niches of the two species, which is likely applicable to other species. We then predicted the fundamental climate niches of the two species under current and future climate conditions. Our study demonstrated a novel approach for predicting species' fundamental climate niche with high accuracy using only species occurrence data, including both presence and absence data points. It provided a new tool for assessing climate change impact on the future loss of existing forests and implementing assisted migration beyond the forest species' native range for better adapting to future climates.

NE PORT IN A STORM: GENETIC DIVERSITY IN BC REFORESTATION

Hayley Tumas, Nicholas Ukrainetz, David Kolotelo, Marie Vance, Trevor Doerksen, Alvin Yanchuk, Jonathan Degner, Dragana Obreht Vidakovic and Sally Aitken

Forest landscapes in British Columbia are a mosaic of natural and reforested stands, with over 60% of seed for reforestation produced by breeding programs. Tree breeders must balance genetic gain against genetic diversity by managing population size and relatedness in orchards. Climate change has further elevated the importance of stand and landscape-level genetic diversity for resiliency and the continued supply of forest ecosystem benefits. As more of the landscape is harvested and replanted, and as breeding generations advance, questions arise regarding the impacts of breeding and reforestation policy on genetic diversity at multiple scales across forest landscapes. In BC, genetic diversity is monitored and regulated for operational use by estimating seedlot effective population size (Ne) from qualitative pollen and seed production. However, the accuracy of these estimates, how well estimates reflect genetic diversity in mature stands, or the consequences of genetic diversity policy minimums on forest landscape-level genetic diversity are still unclear. Here we use genomic data for three widely planted BC conifers, lodgepole pine (*Pinus contorta* ssp. *latifolia* Engelm.), interior spruce (*Picea glauca, P. engelmannii*, and their hybrids), and coastal Douglas-fir (*Pseudotsuga menziesii* var.

menziesii) to examine genetic diversity in BC forestry at multiple scales and stages. We compare genomic and qualitative estimates of Ne, compare genetic diversity in natural and selectively bred seedlots, and examine the shift in genetic diversity from orchard to maturing stands. We find that current methods accurately estimate Ne, and that, although Ne is significantly lower in selectively-bred seedlots, natural regeneration may substantially buffer genetic diversity in planted stands. These results inform a landscape genetic simulation model to assess the effect of forest management policy and landscape deployment on landscape-level genetic diversity. Results will be used to evaluate whether changes are needed to policies or practices to maintain forest health, productivity, and economic benefits.

ASSESSMENT OF THE IMPACT OF CLIMATE CHANGE ON ENDANGERED CONIFER TREE SPECIES

Wenhuan Xu and Tongli Wang

Climate change results in the habitat loss of many conifer tree species and jeopardizes species biodiversity and forest ecological functions. Delineating suitable habitats for tree species via climate nichemodel (CNM) is widely used to predict the impact of climate change and develop conservation and management strategies. However, the robustness of CNM is broadly debated as it usually does not consider soil and competition factors. Here we developed a new approach to combine soil variables with CNM and evaluate interspecific competition potential in the niche overlapping areas.We used an endangered conifer species - *Chamaecyparis formosensis* (red cypress) - as a case study to predict the impact of climate change. We developed a novel approach to integrate the climate niche model and soil niche model predictions and considered interspecific competition to predict the impacts of climate change on tree species. Our results show that the suitable habitat for red cypress would decrease significantly in the future with an additional threat from the competition of an oak tree species. Our approach and results may represent significant implications in making conservation strategies and evaluating the impacts of climate change, and providing the direction of the refinement of the ecological niche model.

MOVING FORWARD TO PROTECT AND RECOVER THE ENDANGERED NORTH AMERICAN BUTTERNUT

Martin Williams, Manuel Lamothe, Aziz Ebrahimi, Berni van der Meer, Anna Conrad, James Warren, Carolyn Pike, Douglass Jacobs, Keith Woeste and Nathalie Isabel

Butternut, *Juglans cinerea*, is a North American hardwood species that is endangered in Canada under the species at risk act (SARA) due to an exotic fungal pathogen (*Ophiognomonia clavigignenti-juglandacearum* (Oc-j)). Discovered in the late 1960s, the pathogen has decimated butternut populations in the US and in Canada. With no cure and minimal evidence regarding resistance to the pathogen within the species, Can-US efforts are now on-going to develop strategies to protect butternut from extinction; from seed storage to high precision phenotyping in order to develop a backcross breeding program to capture resistance genes from Japanese walnut (*Juglans ailantifolia*). The latter was introduced as ornamental since the late 1800. In contact zones, both species hybridize and introgress naturally, producing offspring with varying resistance to Oc-j. As a first step, hybrid identification using pre-selected SNP markers from nuclear (34 SNPs) and chloroplastic regions (2 SNPs) and obtained in previous sequencing efforts will be conducted. The SNP panel has been developed to discriminate four *Juglans* species and their hybrids. It will be used to detect the presence of Japanese walnut as one of the parental species. Chloroplast DNA markers have been integrated in the panel to detect the direction of the cross. We will report on the level of interspecific hybridization/introgression detected in both the reference samples used in the SNP validation process and to characterize a subset of putatively resistant individuals, which are part of living collections planted across the US and Canada. The genotyping project is part of a bigger effort to protect and restore the species and includes several activities such as ex situ cryoconservation and pathogen landscape genomics, which will also be discussed.

SESSION 2B: FOREST HEALTH

LOCAL ADAPTATION OF TREES TO FOREST PESTS

Dawei Luo, Greg ONeill, Tongli Wang, Deogratias Rweyongeza, Peter Ott, Nicholas Ukrainetz and Richard Sniezko

The detection of local adaptation of forest tree species to pests is a new opportunity to address forest health concerns exacerbated by climate change. From an extensive network of provenance and progeny trials, we compiled forest health data for 14 pests of six native tree species in western North America. The data came from 25 series of field trials replicated at 195 locations in British Columbia, Alberta and Yukon Territory (Canada) and USA Pacific Northwest. We developed transfer functions (TFs) to 1) investigate the extent of local adaptation for resistance to forest pests; 2) identify climate transfers associated with increased incidences of pest infection; and 3) demonstrate the calculation of safe seed transfer distances to avoid unintended increase in forest insects and diseases. Infections of many insects and diseases were strongly related to transfer distances in mean summer precipitation (MSP), mean coldest month temperature (MCMT), mean annual precipitation (MAP), frost free period (FFP) and mean warmest month temperature (MWMT). Tree populations showed local adaptation for resistance against most of the pests we investigated. Consequently, we quantified safe transfer distances for a combination of tree species and pests using a pooled transfer function (PTF). Under the same climate gradients, the resistance to *Endocronartium harknessii* and *Dendroctonus septosporum* were positively related, live crown ratio was negatively affected by both *E.harknessii* and *Dothistroma septosporum* while was positively correlated to *D. Ponderosae* for lodgepole pine (*Pinus contorta* var. *latifolia*). These findings indicated the feasibility and necessity of including forest health to applying assisted migration to address climate associated health risk.

DETERMINING THE ROLE OF *OPHIOSTOMATOID* FUNGAL PATHOGENS IN OVERCOMING LODGEPOLE PINE DEFENSES DURING MOUNTAIN PINE BEETLE MASS ATTACK

Colleen Fortier, Antonia Musso, Maya Evenden and Janice Cooke

The current mountain pine beetle (MPB; *Dendroctonus ponderosae*) outbreak continues to be a major threat to lodgepole pine (*Pinus contorta* var. *latifolia*) forests in Alberta. MPB utilize an effective mass attack strategy to overwhelm host tree defenses and promote MPB colonization. MPB vector several *Ophiostomatoid* fungi, including the necrotrophic pathogen *Grosmannia clavigera*, which are introduced to the pine host during MPB mass attack. These fungi invade the host's sapwood during MPB colonization, resulting in the classic blue staining of the wood. Several studies have demonstrated that these *Ophiostomatoid* fungal associates provide nutrition to developing MPB. However, the role of these fungi in MPB attack success is much less clear and has been the subject of debate. To test the hypothesis that *Ophiostomatoid* fungi contribute to overwhelming host defenses during MPB mass attack, we compared defense hormone responses of mature lodgepole pine trees mass attacked by MPB to trees inoculated with *G. clavigera*. We reasoned that if *Ophiostomatoid* fungi contribute to MPB's ability to overwhelm host defenses, we should see hormone profiles consistent with attack by an herbivorous insect plus a necrotrophic fungal pathogen. Alternatively, if these fungi do not contribute to MPB's ability to overwhelm host defenses, then we should see hormone profiles consistent with attack only by an herbivorous insect. Our analyses revealed that while *G. clavigera* inoculation led to increased levels of both jasmonate and ethylene in host trees, MPB attack led to increased levels of only jasmonate. We also studied phenolic defense gene expression and chemical profiles as an early marker of lesion development and found unique host phenolic defense responses to *G. clavigera* inoculation that were not present during MPB mass attack. Taken together, our results indicate that *G. clavigera* does not play a major role in MPB overcoming host defenses during mass attack.

EXAMINING THE TRANSCRIPTIONAL RESPONSE TO MULTIPLE ATTACKS BY *HYLOBIUS ABIETIS* ON *PICEA SITCHENSIS* IN THE UK

Barley Rose Collier Harris, John MacKay, William Hoaen, George Mackay and Roger Moore

Hylobius abietis (L.) is a major native pest to UK and European forestry. Mature weevils feed on the bark of conifers and cause the death of saplings by ring barking. Without treatment over 50% of seedlings die, which has a large economic impact. Currently, most seedlings are protected with the regular application of an acetamiprid-containing pesticide until they are large enough to survive. This pesticide is due to be banned for commercial use in the UK. *Picea sitchensis* (Bong.) Carriére (Sitka spruce) makes up over 50% of UK forestry and is heavily impacted by *H. abietis* so research into integrated pest management, including resistance breeding, is vital.

Conifer species have been shown to transcriptionally respond to insect attacks including *Pinus sylvestris* to *H. abietis*, and Sitka spruce to *Pissodes strobi*. The objective of this study is to examine the transcriptional responses of Sitka spruce when exposed to different numbers of *H. abietis* exposures. To determine, if *H. abietis* elicits a transcriptional response in Sitka spruce, how that response varies over a time course and if previous exposure to the insect primes the tree"s inducible defences.

Clonal cuttings from 4 individuals from the UK breeding population of Sitka spruce were used. There were three treatments, no exposure, a single period of three-day exposure to *H. abietis*, or two three-day periods of exposure a month apart. Samples of bark tissue were taken directly after exposure, 5 days later and a month later. RNA was extracted, sequenced by Illumina sequencing and analysed to look for differentially expressed genes (DEGs).

Gene lists show over 3000 DEGs between treatments and different expression profiles over a time course allowing us to see if inducible defences are primed by previous wounding from *H. abietis*. Analysing these shows enrichment and over-representation of particular gene ontologies or KEGG pathways.

GROWTH AND SURVIVAL OF WESTERN WHITE PINE SEED SOURCES IN THE FACE OF WHITE PINE BLISTER RUST AND A CHANGING CLIMATE: AGE 15 RESULTS FROM SIX TRIALS IN WESTERN WASHINGTON

Richard Sniezko, Dan Omdal, Rachel Brooks, Robert Danchok, Emily Boes, Benjamin Wilhite and Angelia Kegley

Western white pine (WWP, *Pinus monticola*) is a long-lived conifer with a wide geographic distribution in western North America. It has typically been designated as a genetic generalist, suggesting that seed sources may grow and survive well over a relatively wide geographic area. However, it is also very susceptible to white pine blister rust (WPBR) caused by the non-native, invasive fungal pathogen *Cronartium ribicola*. Several regional programs to develop WPBR-resistant populations, using seedling inoculation trials, have been underway for >50 years. A network of WWP field trials in the Pacific Northwest has been established over the last three decades to examine efficacy of the resistance to blister rust. Survival, growth and WPBR infection in six 15-year-old trials in western Washington is examined here to provide updates on the potential utility of this species. These trials include up to 36 common seedlots planted during winter 2006/2007 and originating from three regional WPBR resistance programs. Seedlots with major gene resistance and quantitative resistance from a range of seed zones as well as a susceptible control were included. The trials have been assessed four times since 2011 and provide an overview of some of the dynamics of WPBR infection and resistance as well as WWP growth throughout western Washington. Although summary and analyses of the data are just beginning, an initial look of the data indicates that in 2011 the susceptible control varied from ~10 to ~90 percent WPBR infection over the six sites (four sites having <35%) and continued to increase over time, reaching 60 to 100 percent infection by 2021; in contrast, infection varied widely amongst the resistant seedlots. Other mortality factors have also been observed. Growth has generally been good with some trees exceeding 10 inches DBH. Pollen and cone production have also been evident during the last several assessments.

SESSION 3A: COLLECTION AND ANALYSIS OF PROGENY TEST DATA

PHENOTYPING COASTAL DOUGLAS-FIR PROGENY TRIALS WITH DRONE-MOUNTED MULTISPECTRAL, THERMAL, AND LIDAR SENSORS TO SCAN FOR ENVIRONMENTAL RESILIENCE

Olivia Waite, Nicholas Coops, Miriam Isaac-Renton, Jake King, Alex Liu and Samuel Grubinger

As the climate continues to warm and becomes more variable, tree breeders are keen to ensure their genetic selection programs can tolerate novel pressures due to mismatch between photoperiod and temperature regimes as well as altered timing and severity of precipitation and drought. Though there is urgent need to assess climate-adaptive traits in tree breeding programs, many existing forest phenotyping approaches are labor-intensive and slow processes. To help screen reforestation programs for trees that can cope with future climates, we use drone-mounted sensors to acquire data with high spatial, temporal, and radiometric resolution. We evaluate differences in spectral reflectance as proxies for stress and differences in crown temperatures as proxies for water balance and evapotranspiration. In this presentation, we describe our developed data collection, quality-control and analysis pipeline to process and analyze large volumes of laser scanning, multispectral (10 bands, 444nm -842nm), and thermal data (800nm-1400nm), to reliably assign responses to individual tree crowns within two coastal Douglas-fir progeny trials in coastal British Columbia. We evaluate how these proxies acquired from bi-weekly field campaigns over a growing season compare to climate data from an on-site climate logger. Phenotypic indices are calculated at the individual tree level and averaged at the family level to quantify rank changes. We discuss the ability of these phenotypic indices to detect meaningful differences at the family level. These new technology approaches remove a number of existing phenotyping bottlenecks that restrict sample size and data collection frequency, allowing for the faster detection of climate-resilient traits and uptake into tree breeding programs. This work offers potential to better inform genetic selections to maintain long-term forest health and productivity in future climates.

GENETIC PARAMETERS OF *FAGUS SYLVATICA* (L.) OPEN-POLLINATED PROGENY TRIALS IN A GRADIENT OF SITE FERTILITY AND CLIMATIC CONDITIONS

Vasyl Mohytych, Vasyl Mohytych, Marcin Klisz, Jan Kowalczyk, Eduardo Pablo Cappa and Marzena Niemczyk

Fagus sylvatica (FS) is a broadleaved tree species of high economic importance in European forests. Despite previous studies indicating high intra-population variability, individual selection is rarely used in this species. We aimed at analysing genetic parameters for growth traits (diameter and tree height) of open-pollinated (OP) progeny of FS, while accounting for site fertility and climatic conditions. We studied three series (each consisting of four experimental sites) of 10-year-old OP progeny trials in north-western Poland, with a total of 189 families and 74,374 seedlings planted across a gradient of site fertility and climatic conditions. To account for environmental heterogeneity within sites, we tested models using three approaches: a priori block design, and a posteriori B-spline and autoregressive residuals. Heritability and genetic correlation were estimated using a multi-trait-multi-site model. Phenotypic values for progeny growth traits and their genetic parameters were analysed in relation to the site fertility and climatic transfer of the tested material. Our results showed considerable spatial variability that affected the estimated genetic parameters within each site. Notably, models using a B-spline and an autoregressive approach produced more accurate estimates of genetic parameters than models using an a priori block design. Single-site-narrow-sense heritability for growth traits ranged from 0.03 to 0.24 and varied most among fertile sites. Genetic correlations between sites (0.20-0.81 for diameter and 0.34-0.81 for tree height) revealed significant effects of genotype-by-environment interaction in each series tested. Specifically, on less fertile sites, the heritability of growth traits was more constrained by site fertility than by climate. In contrast, progeny on fertile sites exhibited higher heritability but also a local adaptation pattern to precipitation, with climate transfer significantly affecting heritability and tree performance. Therefore, our findings emphasize the importance of considering both site fertility and precipitation transfer to increase the genetic gain from individual selection of FS.

GENETICS OF WOOD QUALITY TRAITS IN A *PINUS CONTORTA* PROGENY TEST

Trevor Doerksen, Fatih Temel, Trevor Doerksen, Nicholas Ukrainetz and Julie Cool

Assessment of wood quality of standing trees in progeny tests relies on indirect, non-destructive methods such as pilodyn penetration and acoustic velocity (AV) measurements. The value of these methods for wood quality assessment largely depends on how precise they predict wood quality traits such as wood density, modulus of elasticity (MOE), and/or modulus of rupture (MOR) at the rotation age. We sampled a lodgepole pine (*Pinus contorta*) progeny test in BC interior 1) to investigate quantitative genetics of growth and wood quality traits, and 2) to examine reliability of pilodyn and AV measurements in predicting MOE and MOR. Bison Creek progeny test was established in 1988 with 285 open pollinated lodgepole families where each family was represented by a four-tree row-plot in each of seven replications. The trees were measured for height (ages 5, 10 and 11), diameter (ages 10, 11 and 32) and Pilodyn penetration (age 10). AV was measured on 339 trees belonging to 72 families (one to eight trees per family) in three replications (reps. three, four and six) before felling at age 32. Resistograph measurements were taken on 533 trees from a separate set of 50 families (six to 11 trees per family) in five replications (reps. one to five). Logs were transported to the laboratory, scanned for size and form, and sawn into boards. The dimensions and grade of each board produced were recorded before being subjected to MOE and MOR tests. A linear mixed model approach is employed to investigate genetic correlations between direct and indirect assessment of wood quality traits, and to provide insight on reliability of non-destructive wood quality assessment methods.

SESSION 3B: SEED TRANSFER AND PROVENANCE TEST ANALYSES

UNIVERSAL RESPONSE FUNCTION FOR INTERIOR SPRUCE (*PICEA GLAUCA, PICEA ENGELMANNII*, AND THEIR HYBRIDS) AND ITS SPATIAL VALIDATION

Zhengyang Ye, Tongli Wang and Greg ONeill

Ecological models, including various forms of population transfer and response functions, have been widely employed to predict the performance of forest trees under future climate conditions. However, the accuracy of model predictions remains a challenge due to the lack of systematic model optimization and validation processes. In this study, we explored a series of candidate universal response functions (URFs) based on comprehensive provenance trials for interior spruce, a tree taxon of great ecological and economic importance in British Columbia. We first developed URFs with various number of climate variable and their combinations, evaluated and validated these models with conventional statistical methods. Although these models showed high predictive power and performed well in statistical validation, the map visualizations of these models varied substantially. Therefore, we further conducted a pixel-wise spatial validation against site productivity data to identify the model with the best performance. Our results revealed that: 1) interior spruce showed a relatively weak among-population variation, indicating modest productivity gain potential from seed transfer; 2) To include a certain number of climate variables was important for a good ecological model; 3) conducting a spatial validation could be critical to ensure the credibility of ecological models; and 4) The current interior spruce habitat would be mostly vulnerable to anthropogenic climate change, largely due to temperature rise, with a major upslope shift was predicted.

SAFE SEED TRANSFER OF *PINUS BRUTIA* IN TÜRKIYE

Greg O’Neill and Fatih Temel

Red pine (*Pinus brutia* Ten.) is the most important forest tree species in Türkiye, covering 5.1 million ha (23% of total forests), and accounting for 9.3 million m3 (34%) of annual timber production. Over 50 million red pine seedlings are produced annually (~20% of total forest tree seedling production) for artificial regeneration, and industrial plantations. The country’s six current seed zones, developed in the absence of provenance test data, are based on relative humidity during the vegetation period, and are partitioned into two to six sub-zones within each main zone (22 in total) on the basis of the length of vegetation period. In 1988, a comprehensive provenance testing program was initiated where 50 red pine populations from Türkiye and Northern Cyprus were tested on 26 sites in Türkiye and Northern Cyprus. Trees in these tests were measured for survival, growth and form at ages three, five, 10 and 20. We used population mean growth data from these provenance tests to develop transfer functions from which safe seed transfer distances were calculated. On average, DBH at age 20 (DBH20) had the strongest relationship with the transfer distances. For each site growth relative to local population was calculated and plotted across all climatic transfer distances for all sites. Transfer distances for summer precipitation (PPT_sm), mean warmest month temperature (MWMT) and annual heat moisture index (AHM) were found to have significant relationship with DBH20. Red pine seed sources can be transferred within 105 mm PPT_sm, 10 °C MWMT and 36 units AHM without sacrificing volume growth more than 5% compared to that of local seed source. Implications of these findings for a climate-based seed transfer system and assisted migration for red pine will be discussed.

SPRUCES (*PICEA* SPP.) IN ICELANDIC FORESTRY

Mai Duong, Aðalsteinn Sigurgeirsson, Brynjar Skúlason and Mariana Tamayo

The Icelandic Forest Service (Skógræktin) established spruce (*Picea* spp.) experimental plots throughout Iceland in 1995/1996 to assess provenance selection for afforestation. Our research aimed to guide forest management in choosing origin seeds that worked best in Iceland. We used data on height and survival collected in 2018 from two types of sites: frost-prone and protected (i.e., non-frost-prone). Comparisons of 40 provenances, mainly from western Canada and southern Alaska, were conducted. At frost-prone sites, white spruce (*Picea glauca*) and its hybrids grew well, whereas at protected sites, Sitka spruce (*P. sitchensis*) and its hybrids performed best. One provenance stood out as suitable for both frost-prone and protected sites: a Sitka spruce mixed with Lutz spruce (*P.* x *lutzii* Little) from Iniskin Bay, Alaska. Latitude and environmental conditions of the provenances were important factors in determining survival and growth. To further enhance provenance testing, genetic analysis will help identify genes that favor performance in protected and frost-prone sites in Iceland. Moreover, having sites that are a mix of frost-prone and protected to evaluate provenances would be beneficial and strengthen forest management decisions. Iceland as a novel location represents the northern bounds of the spruce distributional range, and thus has implications for climate change research.

SESSION 4A: GENETIC CONSERVATION

CONTINUOUS COVER FORESTRY AND GENETIC DIVERSITY: A CASE STUDY OF ENGLAND'S DOUGLAS-FIR AND WESTERN REDCEDAR PLANTATIONS

Laura Guillardin, John MacKay, Gary Kerr, Barley Rose Collier Harris and Ella Glover

Pseudotsuga menziesii (Douglas fir) is native to western North America and commonly planted in many parts of Europe for its high timber value. In England, it is usually found in even-aged pure stands but transformation towards more diversified woodlands using a Continuous Cover Forestry (CCF) approach may increase the ability of these forests to face ongoing environmental shifts. However, plantations may lack genetic diversity; therefore, their natural regeneration may result in a limited gene pool being transmitted to the offspring and thus negatively affect the ability to face potential environmental changes. We performed a forest survey to analyse the species diversity and composition of four stands across the South of England and categorised the stands among the different CCF transformation stages. To assess the genetic diversity of these CCF sites, we genotyped both canopy trees and natural regeneration. We used a locus-specific PCR on a high-throughput platform to genotype 80 SNPs recovered from publicly available SNPs datasets. Our results showed a high level of genetic diversity within the Douglas fir plantations in England, with an overall mean observed heterozygosity of 0.48. The genotypic comparison between generations revealed no differences in heterozygosity, we did however find substantial differences in effective population size (Ne). This genetic diversity indicator also varied among sites, detecting higher Ne in sites that show higher levels of species diversity. These findings shed light on the vulnerability of such populations and highlight the need for comprehensive and effective genetic conservation strategies to ensure the continued viability of these woodlands in the face of ongoing environmental changes.

WHAT DOES THE FUTURE HOLD? AIMING THE NATIONAL TREE SEED CENTRE'S RESEARCH AND CONSERVATION STRATEGY TOWARDS 2030 (AND BEYOND!)

Melissa Spearing, Donnie McPhee and Lucie Lavoie

Proactive solutions require proactive measures, but high-quality seeds of known origin should be "first, last and always" (C.W. Yeatman). Since 1967, the National Tree Seed Centre (NTSC) has been collaborating with many jurisdictions, researchers, and practitioners to improve the sustainable use of Canada's forest genetic resources (FGR). The challenge we face is keeping up with emerging FGR threats and technologies while being adequately equipped to sustain our long-term collections. To this end, the NTSC has developed a 10-year strategic plan designed to meet both traditional and emerging stakeholder needs, but it is far from written in stone. We need to know: what do you see in your crystal ball and what actions can we prioritize in advance? This presentation will cover new NTSC priorities and deliverables for the next decade, as guided by NTSC collaborators to date. We will share highlights since the 2019 CFGA conference including new MOUs, increased NTSC staffing, equipment and facility capacity, interactive training delivered, in-house seed conservation milestones and species prioritized by a national seed supply chain study. We have always worked to recognize, strengthen, and complement jurisdictional FGR programs, but players" knowledge extension needs are rapidly changing. Your collective wisdom is needed more than ever to see what is coming and how to hit some of these moving targets together.

SESSION 4B: SEED, SEED ORCHARDS AND SEEDLINGS

UNITED STATES FOREST SERVICE AND WASHINGTON DEPARTMENT OF NATURAL RESOURCES TREE SEED ORCHARD RESTORATION COLLABORATION IN WASHINGTON STATE

Claire Ellwanger, Vicky Erickson, Erin Baumgart, Jeff DeBell and Jeff deGraan

There is growing recognition of the need for increased reforestation capacity in the Pacific Northwest to aid recovery from larger and more frequent forest fires. The foundation of any reforestation effort is a reliable and genetically appropriate seed supply. The United States Department of Agriculture, Forest Service (USFS) has 25 seed orchard sites in Washington that can help meet this need. However, after decades of budget limitations, these orchards need restoration work to reduce vulnerability to loss from fire and insect outbreaks, and to restore them to a condition favorable to seed production. Staff with expertise in genetics and seed production from both the USFS and Washington State Department of Natural Resources (DNR) have been collaborating on a plan to restore these seed orchards to a more productive condition, so that both organizations can have access to a more reliable seed supply.

The Good Neighbor Authority and similar programs allow the USFS and DNR to work together on restoration and forest health projects on National Forest lands. Genetics program staff from both organizations are working together to create the specific plans for each orchard. The on-the-ground implementation is being done as part of the larger ongoing landscape restoration work in each area.

Restoration activities in orchards will include (1) thinning trees to keep crowns well separated, carefully planned to maintain genetic diversity, (2) pruning trees and remove tall shrubs to minimize ladder fuels, (3) minimize concentrations of ground fuels. A management zone of 300 feet or more around the perimeter of each orchard will be treated to create and maintain a shaded fuel break.

Initial projects are planned for implementation during the summer of 2023. This model could be applied to other regions where seed needs of federal and state agencies overlap.

DNA METHYLATION DIFFERENCES IN SOMATIC EMBRYOGENESIS COMPETENCE OF *ABIES NEPHROLEPIS*

Chae-Bin Lee, Ye-Ji Kim, Dayoung Lee and Kyu-Suk Kang

Somatic embryogenesis is a highly effective method for producing artificial seeds in woody plants, and it also provides an opportunity to study plant cell totipotency. Somatic embryos are regenerated by dedifferentiation of somatic cells to embryogenic callus, and subsequent redifferentiation to somatic embryos. The acquisition of embryogenic competence is the critical process in somatic embryogenesis, but its molecular mechanisms are not yet well understood. Recent studies suggest that epigenetic regulation plays a vital role in the acquisition of embryogenic competence. *Abies nephrolepis* (Trautv. ex Maxim.) Maxim., an evergreen coniferous tree that inhabits the subalpine zone, is threatened by habitat loss in South Korea and requires ex-situ conservation efforts. Here, we used Methylation-Sensitive Amplification Polymorphism sequencing (MSAP-seq) to investigate differentially methylated sites (DMS) in embryogenic callus (EC) and non-embryogenic callus (NEC) of *A.*

nephrolepis. Zygotic embryos were used as explants to induce callus. Induced embryogenic callus and non-embryogenic callus derived from the same explant were selected as one set for MSAP-seq analysis, and five sets were analyzed. Our results suggest that acquisition of embryogenic competence is potentially regulated by epigenetic modifications at DNA sites related to cell division and structure, stress responses, transcription, kinase activity, and transposable elements. Based on DMS sequences screened in this study, further studies on methylation of non-coding sequence and multi-omics approaches may enhance our understanding of plant regeneration mechanisms.

DAY 2: TUESDAY, JULY 12 – CONFERENCE FIELD TOUR

KALAMALKA FORESTRY CENTRE

The Kalamalka Forestry Centre was established in 1976 as the provincial tree improvement hub for the Interior of British Columbia. Mild, dry winters and hot, dry summers characterize the Vernon area, stimulating conifer reproduction, which is essential for both seed production and tree-improvement research. The site is 73 hectares and is divided between seed orchards (32 hectares) and research (41 hectares). On the research side, the site accommodates offices, laboratories, greenhouses and breeding arboreta for the Douglas-fir, western larch, Interior spruce, ponderosa pine and western redcedar breeding programs, as well as genecology and pest resistance research trials.

BAILEY SEED ORCHARD

The Bailey Seed Orchard is located along HWY 97 south of Vernon, British Columbia, on an east-facing slope overlooking Kalamalka Lake. It was established in 1995 to expand provincial seed production operations in the Okanagan Valley. Warm, dry summers stimulate reliable reproduction for the orchards located on the site: Douglas-fir, ponderosa pine, western white pine, lodgepole pine and paper birch.

PRT ARMSTRONG NURSERY

PRT's focus on container grown seedlings and continuous innovation has made them one of the largest container grown forestry seedling nurseries in North America. They grow a diverse range of species and stock types for spring, summer and fall planting.

DAY 3: THURSDAY, JULY 13

SESSION 5: SEED TRANSFER AND PROVENANCE TEST ANALYSES

DWREML: AN R PACKAGE FOR FITTING THE LINEAR MIXED MODEL

David Butler and Brian Cullis

The average information (AI) algorithm for efficient residual maximum likelihood (REML) estimation of variance components has proven highly effective in the analysis of data arising from the biological sciences. However, as problem size and model complexity have increased, a key computing step, the assembly and solution of the mixed model equations (MME) using traditional tools, has become a significant time constraint. With falling memory costs, these methods have become compute-bound and are limited in their extent to exploit parallel processing opportunities. The dwreml package implements the AI algorithm for REML estimation, and leverages advances in equation solver technology that take advantage of sparsity and parallelism. In particular, dwreml uses the MUMPS (MUltifrontal Massively Parallel Sparse direct solver) library to solve the MME. The dwreml package offers a familiar R user-interface based on ASRreml-R and we illustrate its use in crop breeding applications, with an emphasis on highlighting elapesd times for key steps in fitting the linear mixed model. It is intended that dwreml become available in the public domain.

BALANCING RISK AND BENEFITS OF ASSISTED MIGRATION TO ADDRESS CLIMATE CHANGE

Andreas Hamann

How reliably can we guide forest resource management through assisted migration of species and their populations in reforestation? Such management interventions tend to entail the risks of unintended consequences, and several conditions should be met before implementing assisted migration to address climate change. We bring together results from genetic field trials, remote sensing, tree ring research, and landscape ecology to develop assisted migration prescriptions for western North America. Our intention is to develop more dependable guidelines by synthesizing information from a variety of modeling, experimental and empirical research with the help of multi-criteria decision support tools.

ESTABLISHING MONARCH BUTTERFLY OVERWINTERING SITES FOR THE FUTURE: *ABIES RELIGIOSA* UPPER ALTITUDINAL LIMIT EXPANSION BY ASSISTED MIGRATION

Cuauhtémoc Sáenz-Romero, Legna A. Pérez-Cruz, Patricia Herrejón-Calderón, Verónica Osuna-Vallejo, Arnulfo Blanco-García, Roberto Lindig-Cisneros, Angel Endara-Agramont, Leonel Lopez-Toledo, Guadalupe Joaquin-Juan and Ana Laura Cruzado-Vargas

Projections of climatic change indicate a grim scenario for *Abies religiosa* (oyamel, sacred fir) forest inside the Monarch Butterfly Biosphere Reserve (MBBR), at the Mexican Transvolcanic Belt (MTVB): a total loss of the suitable climatic habitat by the decade centered in year 2090. Because A.

religiosa is the tree species on which exclusively stay the overwintering Monarch butterfly (*Danaus plexippus*) colonies, it is urgent to tests the feasibility of shifting upwards in altitude *Abies religiosa* beyond its contemporary natural upper altitudinal limit, which is about 3500 m. Since the MBBR has its summits at about 3550 m of altitude, it is needed to shift to a higher mountain outside of the MBBR, in this case, to Nevado de Toluca extinct volcano (summit: 4690 m). It was established in early July 2021 four *A. religiosa* provenance tests at contrasting altitudes at Nevado de Toluca: 4000 Timberline), 3800 and 3600 m (testing upper altitude species range expansion) and at 3400 m (reference site). Planting of *A. religiosa* seedlings was done under existing shrubs serving as nurse plants. After 18 months of field planting (evaluation February 2023, after two growing seasons), the overall survival is 76% (excluding mortality by gophers). A fitted linear regression of average survival per provenance per site against climatic transfer distance on Mean Annual Temperature (r2 = 0.39, p = 0.0009), suggest an additional 8.7 % mortality for every 1 °C of transfer toward colder sites at higher altitudes. Even when survival seems to be acceptable so far, seedlings appear to be very stressed, apparently due to a dry season November – February more dry than usual, where still happen very cold (near or below °C) temperatures at night.

MULTISPECTRAL VEGETATION INDICES FROM DRONE REMOTE SENSING QUANTIFY CLINAL ADAPTATION TO CLIMATE IN PROVENANCE TESTS OF *PICEA ENGLEMANNII* X *GLAUCA*

Samuel Grubinger, Nicholas Coops and Greg ONeill

As climate change progresses, accurate quantification of local adaptation becomes essential to inform breeding programs, seed transfer systems, and assisted migration policies. Field-assessed diameter and height have historically been used to assess climate adaptation. However, adaptive differences may not be evident in these traits, and growth measured in young trials may obscure risky adaptation strategies. Remotely sensed vegetation indices utilize key wavelengths to quantify canopy traits related to foliar stress, phenology, and photosynthetic and photoprotective pigments.

We detail a methodology for generating multispectral data (10 bands, 444 nm – 842 nm) from common-garden trials using commercially available drone, sensor, and photogrammetry technology. We analyze summer reflectance at six provenance test sites spanning Mediterranean, maritime, continental, and subarctic climates in British Columbia and Alberta, Canada, containing 126 disparate populations of interior spruce (*Picea glauca* x *englemannii*). We use best linear unbiased prediction and principal components analysis to quantify adaptive clines as correlations between 15 spectral traits and transfer distances along principal components (PCs).

Highly significant ($P < .05$) clines were evident for spectral traits at all sites for all PCs; clines were stronger for spectral indices than for field-assessed height at all sites along two of three PCs. Clines in vegetation indices related to the red edge, carotenoids, and greenness varied in importance along PCs representing different dimensions of climate. We discuss the physiological basis for these relationships and their implications for forest genetics policy. Traits linked to foliar physiology can elucidate responses to divergent climate pressures, e.g. temperature and aridity.

This work reveals local adaptation to climate which is not evident in field-assessed growth traits. Our findings indicate great potential for spectral traits as indicators of local adaptation and utility in breeding and seed transfer systems for maintaining growth and genetic gains while selecting optimally adapted genotypes for changing climates.

SESSION 6A: SEED TRANSFER AND PROVENANCE TEST ANALYSES

COASTAL GRAND FIR COMMON GARDEN, MULTIPLE ENVIRONMENT GENECOLOGY TRIALS: 40-YEAR RESULTS

Charles Cartwright

The performance of 24 coastal grand fir IUFRO provenances was followed in common garden, multi-environment, wild site trials over 40 years. The populations represent much of the coastal range of the species, from Southern Oregon (42.467° N) to Northern Vancouver Island (50.333° N). The continentality of the environments, from which seed was sourced, ranged from marine settings (5 m elevation) to well up into the Cascade Mountains (945 m elevation). The test sites were of more restricted distribution, located from 48.7626° N to 50.2604° N, and 121.6744° W to 125.8436° W, plus from 15 m to 345 m elevation. Three of the trials were in seed zones where the species is planted, but a fourth was on more maritime ground. Early in the study susceptibility to needle disease, stem defect, and frost damage were scored, but after age 10 years only height, diameter breast height, and survival were monitored. Measuring a wide range of seed sources through a rotation on varied environments was planned to assist in development of seed transfer guidelines, and selection of provenances superior in disease resistance and wood volume production. Variation in the growth traits was significant for provenance effects on all sites, as were among-site differences, (genotype by environment interaction). Selection of faster growing provenances for volume gains can be recommended. For seed transfer, broadened guidelines are logical based on the results across test sites. Over time cumulative insults of changing climate and disease are followed through use of various functions. The modifications to the shape of these curves as the trees aged were used to help assess how to account for a changing climate. The use of more southerly seed sources of this species to compensate for climate change, (assisted migration), has considerable utility.

TESTING CLIMATE-BASED SEED TRANSFER GUIDELINES FOR JACK PINE (*PINUS BANKSIANA* LAMB.) IN NORTHEAST ONTARIO

Dennis Joyce

The objectives of this work are to develop climate niche and ecological genetic models to guide the development and testing of climate-based seed transfer guidelines for the managed forest land base in northeast Ontario. A presence and absence dataset derived from more than 41,000 inventory and ecological ground plots east of the 95th meridian was appended with estimated climate variables and analyzed with Random Forests to develop a realized climate niche model for eastern North American jack pine (*Pinus banksiana* Lamb.). The resulting 200 classification trees had an overall error rate of 14.9%. Errors of omission (false negatives) were slightly lower at 13.6%. The mapped climate niche documented the geographic extent of the contemporary distribution. Under the IPCC RCP6.0 scenario, approximately 39 percent if the contemporary niche space is projected to be susceptible to range recession by mid-century. Edaphic constraints will likely constrain the projected 32% geographic increase due to emergent suitable habitat. Height growth data from a common garden study of 97 seed sources from Northeast Ontario resulted in an ecological genetic model with an R-square of 0.61. Seed zones derived from the genetic model were projected into mid-century to function as seed deployment zones. The seed zones derived directly from the ecological genetic model are viewed as seed procurement zones. To test the veracity of mid-century projections, the managed forest land base in northeast Ontario was used as a case study. Genetically improved seed lots from the Michigan's Lower Peninsula, Northwest Ontario, and NE Ontario tree improvement programs are included in two transfer trials in Northeast Ontario. The merits of the interlocking block design are discussed.

INTER- AND INTRASPECIFIC VARIATION IN PHOTOSYNTHETIC AND FUNCTIONAL TRAITS IN THE TWO MOST IMPORTANT CENTRAL EUROPEAN BROADLEAVED TREE SPECIES: *FAGUS SYLVATICA* AND *QUERCUS ROBUR* IN RELATION TO DROUGHT

Marzena Niemczyk, Piotr Wrzesinski, Tomasz Wojda, Vasyl Mohytych and Szymon Krajewski

Drought is a major contributor to ecological change and species distribution shifts. Rising temperatures are expected to increase the vapor-pressure deficit (VPD) and soil drought. To support forest management decisions regarding tree species and provenance selection, we conducted a drought experiment in a controlled forest environment with the two most important Central European broadleaved tree species: *Fagus sylvatica* (FS) and *Quercus robur* (QR). The selected provenances of the focal tree species ranged from 44 to 54° north latitude. We used one-year-old seedlings in a randomized complete block design with three treatments: drought, water deficit (50% of control), and control (optimal irrigation). We monitored gas exchange during a 60-day drought treatment and measured the functional traits of the photosynthetic apparatus in response to drought stress during the drought phase and a 30-day regeneration period. First, we modeled the assimilation and stomatal responses of the two species as a function of VPD and soil moisture. We then analyzed the repeatable measurements of the traits with linear mixed models. Interspecific differences were more pronounced than intraspecific variation in measured traits. We found statistically significant differences in assimilation (Anet) and stomatal conductance (gs) between species. QR was characterized by higher Anet and gs values, while transpiration was comparable to FS. Responses of individual provenances to drought and during the regeneration period were more nuanced. In general, QR regenerated fully after the drought period. It was also characterized by a significantly higher number of stomata per unit area, suggesting that it may be evolutionarily better adapted to environmental water limitation.

PHENOTYPIC AND GENOMIC SIGNALS OF CLIMATE ADAPTATION IN WESTERN LARCH: INFORMING ASSISTED MIGRATION AND CLIMATE-BASED BREEDING

Beth Roskilly, Brandon Lind, Dragana Obreht Vidakovic, Sam Yeaman and Sally Aitken

Climate niche modelling projects that areas of future suitable climate for western larch (*Larix occidentalis* Nutt.) have already expanded beyond and contracted within its current range and will continue to do so in the coming decades, making it a desirable candidate for assisted migration. Based on both modelling and trial plantings, western larch was the first conifer species to be approved for operational planting outside of its current range in British Columbia. We analyzed data on growth, bud phenology, drought tolerance, and cold hardiness of 52 natural populations and 28 breeding families in a seedling common garden to understand climate adaptation and transfer risks in western larch. We found high phenotypic variance within populations and low differentiation among populations for all traits (VPOP =1-13%). Geographic variables were stronger predictors of phenotypic variation among populations than climatic variables. Greater height growth potential was found in eastern populations, which appear to have evolved faster growth rates to compensate for shorter growing seasons. Consistent with adaptation to seasonal frost risks, bud break was later in eastern populations and bud set was later in populations from higher elevations. Fall cold hardiness exhibited non-significant population differentiation and weak clinal variation with cold temperatures. We found strong global adaptation to drought but no signal of local adaptation. We also analyzed genotype-environment associations using 1.48 million SNPs in pooled exome-capture sequence data from 44 natural populations. We found only 61-189 SNPs associated with the top five temperature- and moisture-related climate variables, further signaling weak local adaptation. Weak signals of local adaptation to climate in western larch and high adaptive genetic variation within populations suggest that seed transfer limits could be less conservative than other sympatric conifer species and supports the prospect of assisted migration for this species.

THE PENALTY OF THE HEIGHT GROWTH SYNDROME IN TREE BREEDING AND FOREST MANAGEMENT

Deogratias Rweyongeza, Andy Benowicz, Robert Stronach, Robert Matheson and Tammy Decosta

Foresters use parameters such as Site Index (SI) based on height-age relationship to define site quality and predict growth and yield of a forest stand. In cold climates such as in Canada, height might be the only realistic trait related to yield a breeder can measure in the first 20 years of a progeny trial. Thus, the breeders' use of height is both a practical necessity and a need to align with forest management planning practices. Timber yield is measured in volume estimated from height, diameter at breast height (DBH) and tree taper. As products of a growth process, height and DBH are allometrically related with high but not perfect correlation. However, height and DBH are not equally correlated with tree volume. Therefore, selection for height may not pick all the best clones leading to a penalty in volume genetic gain. We analyzed height, DBH and volume of 24-year-old trees in a progeny trial of 125 families of white spruce on 3 sites in northern Alberta. The Alberta ecologically based individual tree volume equations were used to estimate the volume. We found that (i) in all Natural Subregions, volume was more correlated with DBH than height; (ii) selection for height led to 4% - 5% loss in volume genetic gain compared to direct selection on volume; and (iii) volume genetic gain was 1.9 - 2.0 times height genetic gain when trees were selected for height and 2.0 – 2.2 times DBH genetic gain when trees were selected for DBH. This supports the current height-volume conversion practice in Alberta. It also underscores the need to exercise caution when selecting trees based on height at a young age.

SESSION 6B: INTERDISCIPLINARY RESEARCH/POPULATION AND QUANTITATIVE GENETICS

MEASURING THE PHENOTYPE AND GROWTH PERFORMANCE OF IMPROVED AND UNIMPROVED SEEDLINGS OF *PINUS CONTORTA* UNDER COMMERCIAL GREENHOUSE CONDITIONS (A STUDY USING HIGH-THROUGHPUT PHENOTYPING TECHNOLOGY)

Sarun Khadka and Barb R. Thomas

Image-based high-throughput plant phenotyping (HTP) in the greenhouse has the potential to alleviate the challenges of acquiring a large amount of phenotypic data manually. The forest sector can utilize this technology with potential to advance into a machine-learning platform for efficient monitoring of their seedling crops. The objectives of this study are: i) to compare phenotypic characteristics, including height and aboveground biomass using canopy cover, of improved and unimproved seedlings of *Pinus contorta* using HTP versus manual measurements at the end of the growing season; ii) to compare the growth performance of improved and unimproved seedlings at three stages of growth including germination, before and after thinning, and at lifting using HTP; and iii) to determine the survival rate and growth performance at lifting of the seedlings transplanted into empty cavities at the time of thinning. Seedlings from nine seedlots (four improved and five unimproved) are being measured through photo imaging at the PRT Beaverlodge greenhouse from germination in Feb, 2023 and re-measured approximately every 10-days until hot-lifting in July, 2023. A GoPro camera attached to a telescopic pole is being used to take images of seedlings growing in 411B styroblocks using the time-lapse mode to capture images every 0.5 sec. A modified tripod with a flat platform is used to slide the pole over the rows of styroblocks. All images will be processed using Agisoft Metashape software to obtain height, canopy cover and orthomosaic images of each seedlot. Similarly, the processed images will be further analyzed with the use of ArcGIS Pro to determine the NDVI and to observe needle growth in each seedlot. This research aims to explore the differences between improved and unimproved seedlots by investigating whether their height and growth performance differences can be obtained using a non-destructive method.

SOCIAL ACCEPTABILITY OF GENOMIC SELECTION FOR PEST RESISTANCE

Valerie Berseth, Jenna Hutchen, Emma Neale, Vivian Nguyen and Stephan Schott

Over the past two decades, mountain pine beetle (*Dendroctonus ponderosae*, MPB) has killed more than 18 million hectares of pine forests in western Canada. Decision-makers are evaluating reforestation strategies and seeking innovative solutions to increase forest resiliency, including using genomics to select for MPB resilience in trees. However, there may be barriers related to the social acceptability of genomics and conflicting management objectives. Understanding risk perceptions and preferences among diverse forest users and managers is vital to identifying socially desirable responses to mitigate large-scale pest disturbances. The goal of this research is to assess risk perceptions and preferences for risk mitigation approaches, such as genomic applications or natural solutions, among forest users and managers. We conducted semi-structured interviews (N=14) with

MPB experts and forest management professionals across five provinces and federal agencies and a series of stakeholder workshops in Quesnel, British Columbia (N=13). Interviews and workshops covered MPB risks, forest health and resilience, and views on forest management approaches, including selective breeding for pest resistance. We use inductive analysis to identify emerging themes and patterns in responses and compare across groups (forest managers and forest users). We find that views of the suitability of genomic approaches for mitigating future risks of pest disturbance vary across groups. Forest managers identified practical and institutional barriers to implementing genomic selection for pest resistance, including uncertainty and changing environmental conditions. Forest users emphasized the importance of socially robust decision-making processes regarding novel genomic technologies and consideration for local knowledge in forest management. Both groups expressed multi-faceted views of the meaning of forest health and resilience. These findings can provide decision-makers with alternative strategies and their perceived relative strengths and weaknesses contribute to a growing body of interdisciplinary research on the social context in which genomic tools for managing forests are evaluated.

SECOND-GENERATION CO-OPERATIVE GENETIC GAIN TRIALS IN THE US PACIFIC NORTHWEST

Keith Jayawickrama and Terrance Ye

Accurate measurement of changes in yield with genetically improved stock requires comparison of improved and unimproved stock planted as block-plots, which simulate actual stands. There are little data on the growth of very high genetic gain Douglas-fir and western hemlock planted in competition with similar crosses, on productive ground and managed intensively. Such plantations are expected to grow at rates beyond the limits of the data used to build current growth models. Our current yield improvement knowledge is based on first generation trials initiated in 1992 and 2003. It was therefore timely to establish another iteration of genetic gain investigation. The objectives were to: (1) Compare realized and predicted genetic gains for seed lots similar to those being produced, from second-generation seed orchards. (2) Produce data sets that represent tree growth using intensive silvicultural management coupled with top genetic improvement (i.e., the upper limit of coastal Douglas-fir and western hemlock tree growth currently achievable) and (3) Visually demonstrate the impact of Douglas-fir and western hemlock breeding programs and of using high-gain reforestation stock.

The trials used a small number of well-tested, high-gain crosses from 2nd-cycle trials, so that average gain levels were higher and the seedlots were genetically more homogeneous than the improved lots used in the older gain trials. Two genetic gain levels were tested – the unimproved base population vs. a mix of the best, reliably tested crosses. Only one spacing, similar to operational stand density, was used. The original intention was to establish all the sites without fencing, to be more representative of operational plantations, but this had to be modified on two locations due to excessive browse. The sites were established between 2017 and 2020 (eight each for Douglas-fir and western hemlock). Early results show large yield improvements for the elite treatment over the unimproved.

PHYSIOLOGICAL AND TRANSCRIPTOMIC RESPONSES TO DROUGHT IN PONDEROSA PINE

Adam Gilewski, Jim Mattsson and Marie Vance

Ponderosa pine (*Pinus ponderosa*) is a drought-tolerant tree species of key importance for the BC interior's increasingly hot and dry forests. BC's only A-class seed orchard contains selections based on volume at rotation age, but their performance under drought conditions is unknown. A comparison of half-sib family responses to well-watered and drought conditions revealed that: (1) families with high growth generally did not experience greater reduction in growth in response to drought than slow-growing families, (2) drought-stressed seedlings that grew well had higher water potentials and lower water use efficiencies, (3) fast growing individuals within the drought treatment had intermediate transcriptomic responses in needles relative to trees that grew poorly under drought stress. Additionally, hydroponic experiments showed that mild osmotic stress stimulated rather than inhibited root growth, and that some families were not inhibited by strong osmotic stress. Finally, we have generated a highly-complete assembly of multiple ponderosa pine transcriptomes and identify drought regulated genes, as well as strong correlations between gene expression and growth within the drought treatment. In summary, we found that some families previously selected for growth have high drought tolerance and can be used for deployment and further selection for drought resistance. Moreover, high growth and water potential together with smaller transcriptomic changes and low water use efficiency under drought stress indicate both access to and transpiration of water. We hypothesize that this is accomplished by a drought avoidance strategy such as root growth accessing deeper water.

SESSION 7A: GENOMIC TOOLS

IMPLEMENTING GENOMIC SELECTION IN NORWAY SPRUCE

Funda Ogut, Patrick Lenz, Chen DING, Josh Sherrill and Jean Bousquet

Norway spruce (*Picea abies* [L.] Karst) is a non-native conifer species frequently planted in Eastern Canada. Due to its superior growth, it outcompetes native spruce species, leading to higher volume yields in plantations while showing similar wood properties compare with white spruce. However, white pine weevil tends to attack Norway spruce causing death of leader shoots and hence growth reduction, stem deformation, and lower commercial value of saw logs. Genomic selection (GS), using SNP molecular markers can help to accelerate selection of weevil resistant genotypes combined with growth. GS analyses in a clonally replicated progeny trial established by JD Irving Ltd. in different regions of New Brunswick provided a proof of concept of the ability of GS to increase selection intensity and to improve prediction accuracy of genetic merit in multi-varietal forestry. To continue implementation of GS, a second Norway spruce full-sib progeny trial established across four sites was used to quantify heritability of growth and weevil resistance traits. Narrow sense heritability estimates were ranging from 0.17 to 0.23 and pooled additive genetic correlations between sites were ranging from 0.51 to 0.87 for breast height diameter and weevil attack, respectively indicating strong to low genotype-by-environment interaction. Based on those results and particularities of the experiment, the development of a GS training population and strategies for prediction model validation will be discussed aiming at genotyping 1920 trees from this Norway spruce breeding population using 50K SNP array for Norway spruce, Thermo-Fisher Axiom Microarray of the Conifer Consortia. Using a larger SNP marker (50K) data on a large, structured breeding population to implement GS and other genomic methods will provide valuable information to breeders to select high-yielding and weevil resistant genotypes at the seedling stage and understand trait architecture contributing genetic variation.

OPTIMIZING GENOMIC SELECTION FOR APPLICATION: THE IMPORTANCE OF ACCURATE ESTIMATION OF GENETIC MERIT AND DISENTANGLING OF ADDITIVE FROM NON-ADDITIVE EFFECTS

Patrick Lenz, Simon Nadeau, Salvador Gezan, Jean Bousquet, Jean Beaulieu, Funda Ogut, Martin Perron and Jean-Philippe Laverdière

Ten years after the first proof of concept studies, several breeding programs in North America have used genomic selection for operational decisions and conducted selections based on genomic-estimated breeding or genetic values. Still, many programs rely on additive breeding values to evaluate genetic merit, seeming to neglect the role of precisely estimating genetic effects and the potential of non-additive effects for enhancing genetic gains. Using two large comprehensive datasets of more than 4000 trees from 146 full-sib families of white spruce (*Picea glauca* [Moench] Voss), we evaluated the effects of increasing sampling on genomic selection model accuracy, and of including dominance on the estimation of genetic merit.

Higher heritability was estimated for wood traits than for growth. Wood quality was mainly under additive genetic control while for growth traits, considerable non-additive components were found.

Also, for growth traits, genomic-based models partitioned additive and dominance effects into roughly equal parts, while pedigree-based models overestimated the non-additive component. Resampling simulations led to the conclusion that genomic-based models require smaller sample sizes to produce accurate estimates of genetic variances compared with pedigree models. When prediction was conducted on the same families on which the model was trained, pedigree- and genomic-based models lead to similar predictive abilities of breeding and total genetic values. Nevertheless, genomic-based models outperformed pedigree-based ones when prediction was applied to unphenotyped families, which can be used for mating allocation and the maximisation of total genetic value for clonal or elite family propagation.

COMPARATIVE TRANSCRIPTOME ANALYSIS REVEALS PUTATIVE GENES INVOLVED IN CONE DEVELOPMENT OF KOREAN RED PINE (*PINUS DENSIFLORA*)

Lee, Dayoung, Kim, Ye-Ji, Kim, Yang-Gil, Lee, Chae-Bin and Kang, Kyu-Suk

The development of reproductive structures in gymnosperm has not been studied much compared to angiosperm. *Pinus densiflora* is an important native species used for reforestation and timber production and it occupies the largest area as a single species in Korea. It adapts well to dry and barren environments and is widely distributed throughout East Asia. In this study, reproductive (female and male cone) and vegetative (shoot apex, needle, stem, root) tissues of *P. densiflora* were sampled and total RNA was extracted. After Illumina sequencing of cDNA libraries, a single de novo reference transcriptome of *P. densiflora* was generated. Reads were mapped on the assembled transcriptome to quantify the gene expression level and differentially expressed genes (DEGs) were then identified. Functional annotation and pathway mapping were performed as well as gene co-expression network analysis. Finally, quantitative real-time PCR (qRT-PCR) was used to verify the expression levels of DEGs. Hierarchical cluster analysis indicated that the tissues of *P. densiflora* were clustered into several groups yielding two clearly separated sex-specific gene expression. 25307 genes were identified as DEGs in the 10 types of tissues and among these genes, 4212 genes showed sex-biased expression between early female and early male cones. We further investigated putative genes associated with cone development of *P. densiflora*. Finally, we confirmed that the relative expression profiles of DEGs using RNA-seq platform were consistent with qRT-PCR approach. Our results suggest that many biological and physiological factors contribute to the differences in gene expression of female and male cones of *P. densiflora*. Furthermore, this study could help us understand the mechanism of cone development in gymnosperm, especially in *Pinus* species.

IDENTIFICATION AND CLASSIFICATION OF POTENTIAL DISEASE RESISTANCE GENES ACROSS THE NORTH AMERICAN, EUROPEAN, AND ASIAN WHITE PINE SPECIES

Akriti Bhattarai and Jill Wegrzyn

The white pines are susceptible to a devastating disease known as white pine blister rust (WPBR) caused by the fungus *Cronartium ribicola*. Major resistance loci have been identified in four North American species, and candidate genes for these loci have been categorized as NLRs. These are a major class of disease resistance genes consisting of an N-terminal domain, nucleotide-binding domain (NB-ARC), and leucine-rich repeat domain (LRR). NLRs are also candidates for quantitative resistance in white pines through loci contributing partial resistance, and these associated genes can be identified through their characteristic domains. Existing transcriptomic resources (Illumina RNA-Seq reads sourced from NCBI) for 22 species were reassembled de-novo using Trinity, SOAPdenovo-Trans, and rnaSPADES before frame selection with Evigene. InterProScan and RGAugury were used for protein domain analysis while NLR-Annotator was used to scan the coding sequences for NLR-associated motifs. Combining the results of these methods, a total of 6427 potential NLRs were identified in the white pine transcriptomes, ranging from 177 to 581 per species. The identified domains and motifs were used to annotate potential NLRs and classify them into subfamilies based on their N-terminal domain. The genome assembly and annotation is available for two of the white pine species, *P. lambertiana* and *P. albicaulis*. To identify additional NLRs, NLR-Annotator was run on the whole genome sequences and the gene annotations were used with the protein domain scanning methods. The identified NLRs were also compared to candidate genes for the major resistance loci Cr1 in *P. lambertiana*. The final set of identified NLR genes will provide a catalog for the exploration of genes related to quantitative resistance and allow for a more comprehensive evaluation of potential disease resistance genes.

SESSION 7B: OTHER FOREST GENETICS RELATED TOPICS

MANAGING ADAPTABILITY IN A BREEDING PROGRAM WHILE BALANCING GAIN AND DIVERSITY

Trevor Walker and Fikret Isik

In addition to the balance between gain and diversity, forest tree breeding programs must also ensure that adaptability is maintained when choosing the trees and crosses to breed. Maintaining adaptability can be a challenge when there are undesirable genetic correlations within the species, such as for cold-hardiness and growth rate in *Pinus taeda*. Breeding zones have traditionally been used to maintain adaptability, but the rigid demarcations will result in a sub-optimal crossing plan when the adaptability variation is clinal. For example, a breeding zone strategy will generally exclude crosses among trees that may have similar provenance origins, but are separated by the zone boundary, such as the upper coastal plain and lower piedmont. Further, provenance origins become difficult to define after a few cycles of breeding, especially when trees from wide crosses are selected for breeding. A better approach is to permit crosses among all individuals while applying constraints that require mating trees from across the range and discourage wide crosses in a mate selection algorithm. Using the NC State University *P. taeda* breeding program as an example, we demonstrate this approach and evaluate the gain, diversity, and adaptability consequence for different scenarios for managing cold hardiness. The scenarios are evaluated using the MateSel algorithm, which has grown in popularity among livestock, aquaculture, and plant breeding programs.

ASSEMBLY AND ANNOTATION OF THE BLACK SPRUCE GENOME PROVIDE INSIGHTS ON SPRUCE PHYLOGENY AND EVOLUTION OF STRESS RESPONSE

Theodora Lo, Lauren Coombe, Kristina Gagalova, Rene Warren, Carol Ritland, Nathalie Pavy, Steven Jones, Joerg Bohlmann, Jean Bousquet, Inanc Birol and Ashley Thomson

Globally, forest health is declining due to the vulnerability of trees to increasing biotic and abiotic stresses associated with climate change. One species of interest is black spruce (*Picea mariana* [Mill.] B.S.P.), as it is a dominant conifer species in the North American boreal forest that plays important ecological and economic roles. Adaptive variation of clinal nature in relation to climate change have been reported in black spruce. Studies utilizing recently developed genomic resources have played a critical role in advancing our understanding of the genomic basis of adaptive variation in forest trees. Here, we present the first genome assembly of *P. mariana* with a reconstructed genome size of 18.3 Gbp and NG50 scaffold length of 36.0 kbp. A total of 66,332 protein-coding sequences were predicted in silico and annotated based on sequence homology. We analyzed the evolutionary relationships between *P. mariana* and five other spruces for which complete nuclear and organellar genome sequences were available. The phylogenetic tree estimated from mitochondrial genome sequences agrees with biogeography; specifically, *P. mariana* was strongly supported as a sister lineage to four North American spruce taxa, followed by the European *P. abies*. In phylogenetic trees estimated from nuclear and chloroplast genome sequences, mixed topologies with weaker statistical support were obtained, indicative of ancient reticulate evolution affecting these two genomes. Clustering of protein-coding sequences from the six *Picea* taxa and two *Pinus* species resulted in 34,776 orthogroups, 560 of which appeared to be specific to *P. mariana*. Analysis of these specific orthogroups and dN/dS analysis of positive selection signatures for 497 single-copy orthogroups identified gene functions mostly related to plant development and stress response. The *P. mariana* genome assembly and annotation provides a valuable resource for forest genetics research, especially in relation to climate adaptation.

TREE IMPROVEMENT INCREASES THE GROWTH OF WHITE SPRUCE (*PICEA GLAUCA*): EVIDENCE FROM 15-YEAR-OLD OPERATIONAL PLANTATIONS IN ALBERTA

shes Bhandari, Bradley D. Pinno and Barb R. Thomas

The timber producing forest land base in Alberta, Canada is decreasing due to the increase in allocation of land to other uses such as energy development and conservation areas while the demand for forest products is increasing. Tree improvement, implemented in Alberta since 1975, can be one of the potential options for increasing forest productivity to meet this increasing demand of forest products. To investigate the operational effect of tree improvement programs on white spruce productivity, we compared tree and stand level performance at age 15 between stands planted with improved and unimproved seedlots. In 18 stands, for all trees diameter at breast height (DBH), total height, crown width, and branch diameter were measured in 100 m2 circular plots. White spruce trees in improved stands had 17% greater DBH and 17% greater height compared to unimproved stands. The growth of white spruce was negatively affected by competition from other species but this relationship did not vary between improved and unimproved stands. On average, tree improvement increased the site index of white spruce by 2 m compared to unimproved stands.

ADVANCING WHITE SPRUCE GENOMICS: LONG-READ GENOME ASSEMBLY OF WHITE SPRUCE ENABLES IMPROVED ANNOTATION AND GENERATION OF A CHROMOSOME-SCALE EPIGENETIC MAP

Irem Yucel, Rene Warren, Lauren Coombe, Kristina Gagalova, Theodora Lo, Vahid Akbari, Nathalie Pavy, Joerg Bohlmann, Jean Bousquet, Steven Jones and Inanc Birol

White spruce (*Picea glauca*) is a conifer native to the northern temperate and boreal forests of North America and is a resilient tree that tolerates variations in climatic conditions. As a result, it is often used as a model for studying the genetic makeup and adaptability of conifer trees. The previous genome assembly of *P. glauca*, generated using short and linked-read sequencing data, had over 2.4 million scaffolds with an NG50 length (a measure of assembly contiguity indicating that at least half of the expected genome size is in pieces at least the NG50 length) of 131 kbp. Here, we introduce an improved assembly of P. glauca, built using long nanopore sequencing reads and scaffolded with linked-read sequencing data, representing one of the most contiguous (NG50 length = 2.3 Mbp) and gene-complete (56.1% complete BUSCO genes in the embryophyta lineage) genomes of this size (~20 Gbps). By organizing the genomic scaffolds into linkage groups using a previously developed genetic map, we assigned 64.7% (equivalent to 12.9 Gbps) of the white spruce genome assembly to its twelve chromosomes. Our new assembly was annotated using BRAKER2, which predicted 66,775 genes with a mean length of 18 kbp. Using orthogroup inference, we found 2,237 white spruce-specific genes that were enriched in gene ontology terms related to bacterial defence and tissue damage. We then leveraged the epigenetic information inherent in the long-read sequencing data to complete methylome analysis using NanoMethPhase and found 320,946,144 CpG sites and 12,698 quality-filtered allelic differentially methylated regions. We found that 1,459 annotated genes intersect with DMRs and that these are enriched in genes prompting plant responses to external damage and pathogen infection.We anticipate that our chromosome-scale white spruce genome assembly and the epigenetic map will be invaluable resources for furthering conifer research.

SESSION 8A: POPULATION AND QUANTITATIVE GENETICS

CURRENT AND FUTURE ADAPTIVE GENETIC VARIATION ASSOCIATED WITH DROUGHT TOLERANCE AND COLD HARDINESS IN DOUGLAS-FIR (*PSEUDOTSUGA MENZIESII*)

Rafael Candido-Ribeiro, Brandon Lind, Mengmeng Lu, Pooja Singh, Dragana Obreht Vidakovic, Sam Yeaman and Sally Aitken

Drought is playing an increasing role in driving tree mortality in temperate forests. Climate change is also disrupting long-known patterns of local adaptation to cold temperatures in temperate species. However, little is known about the genetic architectures of traits contributing to population adaptation to climate and how this could affect adaptability, tree breeding and reforestation under future conditions. Here we conducted a case-control genome wide association study with 20 provenances (80 seedlings/provenance) from both interior (var. *glauca*) and coastal (var. *menziesii*) Douglas-fir varieties to identify genetic variants associated with drought tolerance and fall cold hardiness. Differences in allele counts between phenotypic extremes (ten tolerant cases and ten intolerant controls pooled per provenance) were tested for over 1.5 million SNPs. We identified 359 drought-tolerance candidate genes (transcriptional contigs) for var. *menziesii* and 468 for var. *glauca*, with an overlap of just eight genes between the two varieties. Furthermore, 65 cold-hardiness associated genes were identified for var. *menziesii* and 412 for var. *glauca* (with two overlaps). Among the identified genes, 16 overlapped between cold and drought tolerance for var. *glauca* and only one for var. *menziesii*, indicating weak pleiotropy that varied between varieties. The current distribution of the top drought-tolerance and cold-hardiness identified variants was predicted across the species range based on Gradient Forest models trained with the allele frequencies of the same variants observed in 73 natural provenances and their climate of origin. Genomic offsets under future climatic conditions were also estimated based on the same variants. Hargreaves reference evaporation (mm) and continentality (°C) are the two main climate variables driving the distribution of the identified adaptive variants in coastal and interior Douglas-fir respectively. We will also present results on the effects of two generations of breeding for growth on the genetic architecture of drought tolerance and cold hardiness in Douglas-fir.

COMPARATIVE AND POPULATION GENOMICS OF THE *CRONARTIUM HARKNESSII*-PINE PATHOSYSTEM

Laura Manerus, Rhiannon Peery and Janice Cooke

Lodgepole pine (*Pinus contorta* Dougl. ex Loud var *latifolia*) and jack pine (*Pinus banksiana* Lamb.) form a mosaic hybrid zone where their ranges overlap in Alberta and the Northwest Territories. Lodgepole pine, jack pine, and their hybrids are hosts for *Cronartium harknessii* (J.P Moore) Meinecke, the causative agent of western gall rust. Lodgepole pine is more susceptible to C. *harknessii* than jack pine, while hybrids show an intermediate susceptibility. Recently, we have described two genetically distinct variants of C. *harknessii*: a more virulent western variant whose range overlaps with lodgepole pine, and a less virulent eastern variant whose range overlaps with jack pine. A comparison of whole genomes assembled from representative samples of C. *harknessii* eastern and western variants has revealed significant structural differences. The objective of this present study is to conduct a fine-scale analysis of the population structure of C. *harknessii* across the lodgepole x jack pine hybrid zone. We hypothesize that the more virulent western variant of C. *harknessii* will be more prevalent on lodgepole x jack pine hybrids than the less virulent eastern variant, and that structural differences in the genomes of C. *harknessii* variants present a barrier to introgression between these variants. To test these hypotheses, we extensively sampled sporulating C. *harknessii* galls and pine host foliage across a transect spanning from genetically pure lodgepole pine in western Alberta across the hybrid zone to genetically pure jack pine in eastern Alberta. Host pine ancestry will be ascertained using species-discriminating single nucleotide polymorphisms (SNP). C. *harknessii* genotypes will be evaluated using previously published microsatellites together with a variant-discriminating diagnostic PCR assay that we are developing through mining of the C. *harknessii* whole genome sequences. The results from this study will help us better understand how co-evolution has shaped this pathosystem.

GENOMICS OF WESTERN REDCEDAR: TOWARDS IMPROVED GENETIC RESILIENCE IN A SELF-COMPATIBLE CONIFER

Tal Shalev, Carol Ritland, Omnia Gamal El-Dien, Lise van der Merwe, Matias Kirst, Alvin Yanchuk, John Russell and Joerg Bohlmann

Western redcedar (WRC; *Thuja plicata*) is an ecologically, culturally, and economically important tree species in North America. By creating genomic resources for important trees such as WRC, we aim to develop a better understanding of their biology and improve breeding for growth and resilience to pests and climate change in operational forestry. We present novel transcriptome, genome, and single nucleotide polymorphism (SNP) resources for WRC. We found that genetic diversity is low for a continuous tree species of its range size, likely due to range expansion from a single glacial refugium and its unique self-compatibility. Unique selfing lines revealed that WRC's adaptability and responsiveness to selection may be due to balancing selection as a result of its demography. Further, not only does WRC show limited inbreeding depression for growth, terpene chemistry, or dendrochronological traits, but appropriate selection intensity can mitigate the effects of inbreeding for growth traits. Using a genomic selection (GS) approach, we identified thousands of loci putatively associated with growth and specialised chemistry traits in WRC, with substantial variation in effect sizes of loci between different traits. These results have been used to develop custom SNP sets for improving GS in operational breeding, and for the application of GS to growth, foliar and heartwood chemistry and durability, and drought resistance traits.

SESSION 8B: SEED TRANSFER AND PROVENANCE TEST ANALYSES

CLIMATE ADAPTATION OF SELECTED COASTAL DOUGLAS-FIR: RESILIENCE TO DROUGHT AND FROST UNDER DIFFERENT LEVELS OF COMPETITION

Fleur Damen, Jonathan Degner, Sally Aitken and David Montwe

As an important commercial tree species in British Columbia, coastal Douglas-fir (*Pseudotsuga menziesii* var. *menziesii*) has been subject to recurrent selection to enhance productivity. However, it is important to know if selection for volume yield has affected Douglas-fir's susceptibility to extreme weather events, and how such effects are modulated by competition. As climate projections for coastal Douglas-fir forests in the Pacific Northwest predict more frequent and extreme weather events such as heat and drought, maintaining resilience is critical. In 1996, the British Columbia Ministry of Forests established five replicated realized gain trials comprising four initial planting densities and three levels of genetic gain for timber volume. By comparing tree-ring widths across all factorial combinations of site, genetic gain and planting density, we evaluate the effects of selection and competition on growth resilience following years with extreme weather events. We further investigate which climate extremes and seasonal climate variables have the greatest influence on Douglas-fir growth variability. We predict that genetically selected individuals are less resilient to extremes, but that increased competition has a negative effect on resilience. Moreover, we hypothesize that summer precipitation has a strong influence on coastal Douglas-fir growth patterns, while temperatures during the period of cold acclimation may influence growth in the following growing season. Preliminary results suggest that secondary growth is limited by high temperature and low precipitation in June. With climate and planting density as the primary drivers of Douglas-fir growth variability, selection of the best adapted trees for reforestation and flexibility in operational planting densities can ensure that future Douglas-fir forests are resilient to climatic extremes and can continue to provide their ecological, economic, and cultural functions.

ASSISTED MIGRATION POLEWARD RATHER THAN UPWARD IN ELEVATION MINIMIZES FROST RISKS IN PLANTATIONS

Zihaohan Sang, Andreas Hamann and Sally Aitken

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. (Reference: https://doi.org/10.1016/j.crm.2021.100380).

THE EARLY BUD GETS THE COLD: DIVERGING SPRING PHENOLOGY DRIVES EXPOSURE TO LATE FROST IN A *PICEA MARIANA* [(MILL.) BSP] COMMON GARDEN

Claudio Mura, Valentina Buttò, Roberto Silvestro, Annie Deslauriers, Guillaume Charrier, Patricia Raymond and Sergio Rossi

Under climate change, the increasing occurrence of late frost, combined with earlier growth reactivation, could increase the risk of frost damages on developing buds and leaves. Species with large distribution areas can exhibit intra-specific variability in bud phenology, resulting in a different susceptibility to frost damages. This study analysed the effects of a late frost event occurring in a common garden of black spruce (*Picea mariana* (Mill.) BSP) in Simoncouche (48°12'N; 71°14'W), QC, Canada. We tested the hypothesis that provenance-specific patterns in phenology drive the exposure of vulnerable tissues to frost and explain observed differences in damage.

We measured 371 trees, planted in 2014 and originating from five different provenances located along a temperature gradient between 48 and 53° N. Phenological measurements of bud break for the apical bud were performed from 2015 to 2021. Frost damages were measured by counting the proportion of damaged buds on each tree. Phenological phases and frost damage levels were analysed by ordinal regressions.

After an early and warm spring, temperatures <0°C occurred between 28 and 30 May 2021, reaching a minimum of -1.9°C. At the time of frost occurrence, the buds of trees from the southern provenances were mostly still closed, while trees from the northern provenances had more exposed shoots. Northern provenances showed more frequent and more severe damages compared to the southern ones. We found a significant correlation between the progression in bud break and severity in frost damage.

Our study provides field-based evidence that phenological differences between provenances influence the risk of frost damage. When compared under the same conditions, northern black spruce provenances reactivate earlier than southern provenances resulting in higher risks of late frost damage. Our findings point to ecotypic differentiation in black spruce phenology, and highlight the importance of provenance selection in forest management under climate change.

SESSION 9: POPULATION AND QUANTITATIVE GENETICS

IDENTIFYING THE GENETIC BASIS OF CONVERGENT LOCAL ADAPTATION IN CONIFERS

Tom Booker, Michael Whitlock, Sally Aitken, Sam Yeaman, Pooja Singh, James Whiting, Mengmeng Lu, Brandon Lind and Dragana Obreht Vidakovic

Studying local adaptation provides a window into the process of evolution, yielding insights about the nature of evolvability. Conifers are a great model for studying convergent evolution as they often inhabit large spatial ranges that encompass wide environmental heterogeneity to which they exhibit strong local adaptation. If the same or similar genomic regions were repeatedly involved in local adaptation in distinct conifer lineages, it would inform us about constraints to diversification. A potentially powerful method to identify locally adaptive genetic variation is the genotype environmental association (GEA) study. In GEA studies, correlations between allele frequency and environmental variables that are presumed to reflect selection gradients are examined for many markers across the genome. In this presentation, I will describe a comparative population genomics analysis of conifers from both North America and Europe. In our study, we apply novel GEA methods and tests for convergent evolution to data from 7 species, representing roughly 200 million years of evolution. Our novel methods allow us to quantify the extent of convergent evolution among pairs of species and to identify gene orthologs with evidence of convergent evolution over deep time. I will describe results from our analyses and discuss what we can infer from them.

GENOMIC OFFSET OF *POPULUS TREMULOIDES*, A KEYSTONE SPECIES IN NORTH AMERICA

Melanie Zacharias, Ilga Porth, Roosje Goessen, Nathalie Isabel and Christian Anton Wehenkel

Quaking aspen (*Populus tremuloides* Michx.) is an important keystone species with a wide distribution range over North America. It exists in a wide variety of environmental settings and plays a crucial role for many ecosystem services. To investigate the genetic offset of the species when facing climate change, we analysed over 900 non-clonal, diploid individuals of *P. tremuloides* sampled across its wide distribution range. The sampled populations represent different ecological conditions, across Canada, the US down to central Mexico, including drier regions like the Prairies, western U.S. or Texas. We use gradient forest, a random forest learning approach, to identify potential maladaptation under climate change in *P. tremuloides* by comparing its current genomic composition to the one predicted to be necessary in the future. For identifying the environmental variables driving the genetic clustering, we use a full dataset of around 10,200 prefiltered SNPs and a subset of 290 SNPs which we already associated with environmental variables. The objective is to identify which environmental variables have an influence on the allele frequency changes and to further know how individual *P. tremuloides* populations are equipped for a changing climate by calculating their genetic offset. We will be able to identify environmental variables over the distribution range which have an influence on the genetic composition and to predict the genetic equipment of *P. tremuloides* populations to cope with future climate conditions.

POSTER ABSTRACTS

SIMULATING EARLY SPRING CONDITIONS IN TWO SUGAR MAPLE PROVENANCES

Denise Alano, Claudio Mura, Sergio Rossi, Annie Deslauriers, Patricia Raymond and Guillaume Charrier

In temperate and boreal forests, trees follow an annual cycle of defoliation and reappearances of leaves, or budbreak, that follow the seasonal changes of the environment. Budbreak is a process that is controlled by many factors, including photoperiod and temperature. Two particular temperatures affect budbreak: chilling, which corresponds to the accumulation of cold during the autumn and winter, and forcing, which is the accumulation of warm temperatures related to the spring. The current predictions of global climate change indicate an increase of 1,8°C to 6,3 °C of the mean annual temperatures before the end of the century. These changes could affect spring phenology in two different and contrasting ways. First, the warmer spring temperatures will advance the timing of budbreak. Secondly warmer winters will reduce chilling, possibly delaying budbreak. Moreover, trees can exhibit intra-specific variations in budbreak that also affect budbreak timings. In the present study, we test the impact of different chilling durations on the time to budbreak of sugar maple saplings from two provenances in Quebec. A total of 144 maple saplings were exposed to natural chilling conditions during the winter. We simulated early spring conditions by transferring the sapling to warm conditions and measuring the time to budbreak. Our results show that there is a significant difference of the mean amount of days it takes for saplings to complete budbreak depending on both their provenance and the amount of chilling. Saplings from the southern provenance complete budbreak earlier than those from a southern provenance. Studying the length of budbreak is important since during this time, and afterwards, trees are more susceptible to damage caused by late frosts, a possible frequent occurrence thanks to climate change. Our study also showcases the importance of taking into consideration the provenance of trees when thinking of applying assisted migration efforts.

PERFORMANCE OF SIBERIAN LARCH IN ALBERTA

Andy Benowicz, Deogratias Rweyongeza and Jodie Krakowski

Siberian larch (SL, *Larix sibirica* Ledeb.) is known for its fast growth, high strength decay-resistant wood, and tolerance to low temperatures, low intensity fires, and drought. SL distribution in its native Russia covers locations with climatic conditions similar to those in the Canadian Prairie Provinces. In Alberta 24 SL trials were planted in 15 climatically diverse locations from 1980 to 1998. Survival and growth of SL were compared to two most important conifer species native to Alberta: lodgepole pine (LP; *Pinus contorta* var. *latifolia* Engelm.), and white spruce (WS, *Picea glauca* (Moench) Voss) at 12 and 10 trial locations, respectively. The average data age was 18 years (range: three to 27). Based on all available data from all tests, the average LS stem volume per unit area was 378% and 64% greater than that of Sw and Pl, respectively. The best seed sources for Alberta were mature trees growing in Alberta and Saskatchewan but whose initial provenances are unknown. The Russian Altai Mountain source grew well at high elevations while the Finnish Raivola source performed well in the northern, low elevation area. Open-pollinated progeny tests of 58 families planted in five diverse locations yielded individual tree narrow-sense heritabilities and family mean heritabilities for height at age 15 of 0.15 and 0.59, respectively. The type B between-site genetic correlation was 0.44 indicating a strong genotype × environment interaction. SL has performed very well in Alberta and its growth can be further improved by selection and breeding from appropriate seed sources.

EXPLORATION OF CLIMATE AS A POTENTIAL FACTOR DRIVING SEX DISTRIBUTION OF MATURE ASPEN TREES IN AN ACTIVE TREE IMPROVEMENT REGION IN ALBERTA

Raiany Dias de Andrade Silva and Barb R. Thomas

Trembling aspen (*Populus tremuloides* Michx.) is a diecious clonal tree species native to North America that is found on primarily upland sites. In diecious species, sexes are often expected to perform differently, based on the theory that females allocate more resources to reproduction than males. Current literature also indicates a possible connection between environment and sex distribution in *Populus* spp. where female trees appear to be more sensitive to drought, due to differences in anatomical traits of xylem between males and females. Consequently, female clones may be more prevalent on sites with moister environments than males, while male clones may be found in either moist or dry environments. If female aspen are more drought sensitive, we would predict that a gradient of differential moisture availability would result in a differential distribution of male and female aspen clones on the landscape. In this study, we described the distribution of mature (older than 50 years) male and female aspen within an active tree improvement region in central Alberta and explored climate as a potential factor driving the distribution of sex. To explore this, 12 mature aspen stands, in four different areas, were selected and a minimum of 19 trees per stand were sampled. Data collected include: DNA analyses, using a 2 cm phloem punch; diameter at breast height; wood density, ring growth, and stand age, assessed using a 5mm increment core, and a Resistograph was also used to determine wood density. Sex was determined with the use of the TOZ19 gene sequence, which is only present in males. Climate data (precipitation, evapotranspiration, temperature, and climate moisture index) were obtained with the BioSIM software for each study site. Results are being explored and will be presented at the Conference.

COMPOSITION OF THE DOUGLAS-FIR (PSEUDOTSUGA MENZIESII) FOLIAR MYCOBIOME AND ITS ROLE IN SWISS NEEDLE CAST SEVERITY FOR A BREEDING POPULATION

Emma Hayward, Paul de la Bastide, Joey Tanney, Jürgen Ehlting and Jonathan Degner

Fungal pathogens of trees are an essential component of forest ecosystems as an ecological driver of diversity and natural selection; however, they can also have devastating effects. My research aims to better understand *Nothophaeocryptopus gaeumannii*, the causal agent of Swiss Needle Cast (SNC), a disease infecting Douglas-fir (*Pseudotsuga menziesii*). This pathogen infects the needles of its host and is associated with defoliation and is endemic throughout the range of Douglas-fir. In the Pacific Northwest of the US and Canada, a rise in incidence and severity of SNC has been observed in the past few decades, which is thought to be linked to climatic changes and forestry practices. There is a genetic component to SNC tolerance, enabling selection of SNC resilient genotypes for reforestation. However, fungal load is not correlated with needle loss suggesting a more complex relationship. Our research investigates whether there are other fungal endophytes involved in this interaction. We used fungal culturing and ITS amplicon metagenomics to characterize the foliar mycobiome of a general combining ability population with a high incidence of SNC from the provincial Douglas-fir breeding program. Phenotype data (i.e., incidence of fungal fruiting bodies in their needles and degree of needle loss) was collected for this population to understand the relationship between the foliar mycobiome community composition and SNC symptom severity. *N. gaeumannii* was found to have a slight but negative correlation with the second must abundant OTU, belonging to the genus Rhizosphaera. Preliminary analyses suggest a great diversity of fungal species across individual trees covering 20 taxonomic orders of Ascomycetes and seven Basidiomycetes. However, no significant differences in foliar mycobiome composition were observed when comparing tree families. As a consequence of mycobiome composition similarity, the impact of these communities could not account for the observed variability in SNC severity.

COMPARING DNA ISOLATION METHODS FOR FOREST TREES: QUALITY, PLASTIC FOOTPRINT, AND TIME- EFFICIENCY

Laura Guillardin

Genetic and genomic studies are seeing an increase in sample sizes together with a wider range of species investigated in response to environmental change concerns. In turn, these changes may come with challenges including the time and difficulty to isolate nucleic acids (DNA or RNA), the sequencing cost and environmental impacts of the growing amount of plastic waste generated in the process. Pseudotsuga menziesii var. menziesii (Mirbel) Franco (PM), Tsuga heterophylla (Raf.) Sarg. (TH) and Thuja plicata Donn ex D.Don (TP) are conifer species found in diverse woodlands both as natives and naturalized exotics. Our study was carried out whilst investigating their genetics to understand their population structure and potential for adaptation.

In the present study, we compared two different DNA isolation methods, i.e., spin-column DNeasy plant mini kit (QIAGEN), and temperature-driven enzymatic cocktail Plant DNA Extraction (MicroGEM). The quantity of recovered DNA and the quality of DNA were assessed along with the plastic footprint and time needed for three tree species. Both methods were optimised and proven to provide enough DNA for each studied species. The yield of DNA for each method depended on the species: QIAGEN showed higher yield in PM and TH, while TP recovered similar amount of DNA for both methods. The DNA quality was investigated using DNA barcoding techniques by confirming species identity and species discrimination. No difference was detected on the PCR amplification of the two barcoding loci, (rbcL and trnH-psbA), and the recovered sequences between DNA isolation methods. Measurement of the plastic use and the processing time per sample indicated that MicroGEM had a 52.64% lower plastic footprint and was 51.8% faster than QIAGEN.

QIAGEN gave higher yields in two of the species although both methods showed similar quality results across all species. However, MicroGEM was clearly advantageous to decrease the plastic footprint and improve the time efficiency. Overall, MicroGEM recovers sufficient and reliable DNA to perform common downstream analyses such as PCR and sequencing. Our findings illustrate the benefits of research and efforts towards developing more sustainable methods and techniques to reduce the environmental footprint of molecular analyses.

DROUGHT RECOVERY IN WESTERN LARCH POPULATIONS

Martin Henry, Beth Roskilly and Sally Aitken

Western larch (*Larix occidentalis* Nutt.) is an ecologically and economically important species. As climate changes, it's important to understand how western larch populations respond to drought stress. Western larch is also a strong candidate for assisted migration, as areas of suitable habitat are predicted to expand under future climates. Understanding local adaptation to drought will help inform climate-based management and conservation strategies. A seedling common garden experiment was conducted for two years to test how provenances differ in drought resistance and recovery. In 2021, 52 natural populations were subjected to drought and well-watered (control) treatments to analyze drought resistance. In 2022, drought recovery among populations was analyzed under well-watered conditions. Heights were measured four times over the course of each season. Our results suggest drought continues to affect height growth in the recovery season. Overall, height growth in the recovery season was reduced by 20% in the drought treatment compared to the control treatment. Variation among populations in height growth was low in the control treatment (VPOP = 0.11) and was strongly reduced in drought treatment in the recovery year (VPOP = 0.007). Drought resistance, measured as the rate of decline in chlorophyll fluorescence in the drought year, was a weak predictor of height growth in the recovery year (R2 = 0.08, p = 0.05). Populations with greater drought resistance had higher growth in both the drought year and recovery year. Height growth in the recovery year was correlated with height growth during the drought year (r = 0.52, p < 0.001) indicating most populations maintain their height growth rank between years. Understanding local adaptation and responses to drought over multiple seasons can help inform future management strategies for this species under changing climates and increasing drought conditions.

ASSESSING THE ACCURACY OF CLIMATEAP-GENERATED BIOLOGICALLY RELEVANT VARIABLES

Jing Jiang, Tongli Wang, Wenhuan Xu, Shiyi Zhang and Lei Zhang

Climate data quality significantly affects the reliability of ecological modeling. In the Asia-Pacific (AP) region, low-quality climate data hinders ecological modeling, impacting forest genetics research. This study validates biologically relevant variable data generated by ClimateAP, a software developed in 2017 for high-quality climate data in the AP region, benefiting researchers in forest genetics, health, and ecological niche modeling. We compared ClimateAP's prediction accuracy with the commonly used WorldClim gridded data using univariate regressions on 48 monthly variables from 2,366 weather stations Landforms, classified as mountainous or flat based on elevation, slope, ruggedness, and Topographic Position Index, were subjected to separate regression analyses. Random Forest (RF) models were used for climatic niche modeling of *Cunninghamia lanceolata*, a coniferous species that possesses a sizable genome at 11.6 Gb and Polymorphism Information Content (PIC) at 0.53. A comparative analysis of climatic niche models using ClimateAP and WorldClim data was performed. ClimateAP explains a minimum of 94.74%, 97.77%, 96.89%, and 94.40% of monthly maximum, minimum, average temperature, and precipitation variances, respectively, outperforming WorldClim in 37 biologically relevant variables. ClimateAP attains higher Adjusted R-squared and lower RMSE values for 12 monthly minimum temperature variables, and consistently improved Adjusted R-squared and reduced RMSE values for precipitation across all landforms. Its temperature data yields lower Adjusted R-squared values in high-elevation, rugged, and mountainous areas but higher values in mid-slope drainages, plains, open slopes, and upper slopes. Using ClimateAP improves the occurrence prediction accuracy for *Cunninghamia lanceolata* from 77.90% to 82.77%. The study validates ClimateAP"s biologically relevant climate data based on weather station observations, demonstrating improved data quality, especially in non-mountainous regions. The results suggest that

ClimateAP can enhance climatic niche modeling for tree species with large genomes and high genetic diversity, providing a better understanding of tree species adaptation and resilience compared to gridded data.

GENETIC VARIATION OF BIOMASS, ACORN PRODUCTION AND PHYSIOLOGICAL TRAIT AMONG FAMILIES IN *QUERCUS ACUTA* AND *Q. GLAUCA* SEED ORCHARDS

Ye-Ji Kim, Chae-Bin Lee, Dayoung Lee, Wookyung Song, Hyun Seok Kim and Kyu-Suk Kang

The distributions of warm-temperate tree species gradually shifts northward due to climate change, and thus the Korea Forest Service is promoting the development of new tree species to expand carbon absorption. In particular, *Quercus acuta* and *Q. glauca* are increasingly being focused on because they have superior carbon uptake capacity and can adapt to environmental stress caused by climate change. This study evaluated the genetic variation and heritability on biomass, seed yield, and physiological traits of the two tree species. Seedling seed orchards of *Q. acuta* and *Q. glauca* were established in Jeju Island, and these seed orchards will be the base populations for future selection and the second generation seed orchard. The results showed that the average biomass of *Q. acuta* was 146.74 kg/tree with a heritability of 0.55, while *Q. glauca* had a slightly higher biomass of 159.02 kg/tree and a heritability of 0.77. *Q. acuta* had an average seed production of 80.55 seeds/tree with a heritability of 0.57, whereas *Q. glauca* produced 211.25 seeds/tree with a heritability of 0.59. Net photosynthetic rate and water use efficiency were also evaluated, resulting that *Q. glauca* had higher rates of both traits. Correlation analysis showed that leaf area and periphery of both species were positively correlated with acorn yield, weight and length. Net photosynthetic rate was positively correlated with the DBH in *Q. acuta*, whereas chlorophyll content was positively correlated with growth traits and negatively correlated with seed size in *Q. glauca*. Acorn yield was negatively correlated with physiological traits (Nitrogen and Chlorophyll contents), but positively correlated with leaf area and periphery in *Q. glauca*. The study provides valuable information for future breeding programs of these tree species (i.e., breeding value estimation), which will help to enhance forestry carbon sequestration and adaptability to environmental stress caused by climate change.

PRACTICAL CONSIDERATIONS FOR DRONE-BASED DATA COLLECTION ON FOREST RESEARCH TRIALS

Jacob King, Alex Liu, Miriam Isaac-Renton, Olivia Waite and Lise van der Merwe

Once new drone-mounted remote sensing tools have been validated, there is major potential for broad deployment of these scalable technologies. In BC alone, hundreds of forest genetics trials can be re-assessed using these tools, for traditional traits like tree size, as well as novel climate-adaptive traits and tree health assessment.

Over the last year, in partnership with UBC, we have collected multispectral, thermal and LIDAR data at bi-weekly intervals under a range of weather conditions at six BC Ministry of Forests genetics research trials ranging in age from 5-25. This includes data acquisition for two iconic coastal conifers from the Cupressaceae and Pinaceae families: Western redcedar (*Thuja plicata*) and Douglas-fir (*Pseudotsuga menziesii*).

Based on what we have learned, we would like to provide an overview of considerations for forest genetics programs intending to use drone-based data collection on forest research trials. This will cover best practices and practical considerations for field campaigns, for example, optimal times of year and day to collect data, age of trials, brushing requirements, ground control points, flight parameters and field validation. For data processing, we will cover the level of technical knowledge required, along with proprietary software and IT specifications that are needed. We will also cover drone and sensor set-ups and costs as well as maintenance programs and longevity. From a client's perspective, we will also discuss how drone collection and data processing could be contracted.

DOES THE SELECTIVE BREEDING OF LODGEPOLE PINE ALTER ITS ABILITY TO RESPOND TO CLIMATE CHANGE?

Valerie Russell

Decades of field-based provenance trials have demonstrated the local adaptation of lodgepole pine (*Pinus contorta* var. *latifolia*) provenances to climate change. Seedling common gardens can provide results on provenance differentiation, especially for adaptive traits such as cold hardiness and phenology that are difficult to phenotype in the field. However, it's important to establish how consistent results from these seedling trials, especially those conducted in locations that are outside of species ranges, are with longer-term field results. In 2013, lodgepole pine seeds from 105 natural and 20 selectively bred seedlotsfrom various climates were planted in common garden beds at UBC to investigate the growth, phenology, and cold hardiness traits of the seedlings. The seedling study analyzed phenotypic traits of 2- and 3-year-old seedlings that had been grown outside of their natural range. Seedlings from the same seedlots were also planted within the var. *latifolia* range at Alex Fraser Research Forest (located near Williams Lake, BC) and have been growing there for 10 years. I will present results of analyses of height growth, tree health, and visible injury from abiotic or biotic causes for lodgepole pine provenances and selectively bred seedlots in relation to the climate of origin, and whether the seedlots are from natural stands or selectively bred. I will also present the results of analysis of phenotypes of the Alex Fraser trees to results from seedlings from the same populations and seedlots grown in a common garden at UBC. Finally, I will assess the extent to which genomic composition (positive effect alleles) predicts field performance.

FIRST DOCUMENTATION IN LIMBER PINE OF VIRULENCE TO MAJOR GENE RESISTANCE TO WHITE PINE BLISTER RUST, AND TOOL TO MONITOR ITS SPREAD

Richard Sniezko

The nine 5-needle pine species native to the U.S. and Canada are highly susceptible to white pine blister rust (WPBR). Virulent races of the rust have developed previously, notably to the major gene resistance (MGR) present in sugar pine and western white pine. MGR has also been documented in limber pine and southwestern white pine. This study reports on a new *Cronatium ribicola* virulent race (designated vcr4), which can overcome limber pine with MGR. Limber pine MGR parent trees have previously been documented in several seed families from Alberta in seedling trials, using Oregon rust races. However, three Alberta parental trees (pf-503, pf-508, and PF2015-0070) previously identified as MGR from seedling inoculation trials are infected with WPBR, and we hypothesized that a race of rust virulent to Cr4 genotypes had arisen at those sites. To test for virulence against Cr4

MGR, aeciospores were collected from one of the infected parents, pf-503, and used to inoculate Ribes in a growth chamber. Limber pine seedlings, including (1) canker-free seedlings that survived prior trials, (2) seedlings from known Cr4 families and (3) known susceptible families were inoculated with basidiospores from the Ribes infected with the putative vcr4 race. All inoculated seedlings were successfully infected, developing disease spots on the needles and cankers on the stems, indicating that the spores collected from tree pf-503 are virulent (vcr4) against Cr4. SNP-based genotyping further confirmed that MGR of the pf-508 and PF2015-0070 families was controlled by Cr4 and that it appears vcr4 is also present at sites in Alberta 40 km apart. Following sequencing and assembly of the fungal race transcriptome and genome, we are currently developing DNA markers to monitor the migration patterns of WPBR by identifying the *C. ribicola* virulent genotypes against resistance genes of white pines.

GENETIC DISSECTION AND POTENTIAL APPLICATION OF LIMBER PINE QUANTITATIVE DISEASE RESISTANCE FOR MANAGEMENT OF WHITE PINE BLISTER RUST (WPBR)

Richard Sniezko

White pine blister rust (WPBR) is a deadly non-native invasive fungal disease of five-needle pines that causes serious economic and ecological impacts to ecosystems in North America. We dissected complex genetic architecture in limber pine using a genome-wide association study (GWAS). Two-year-old seedling progeny of 60 Alberta parent trees were inoculated under controlled conditions in 2018 and needles sampled for DNA genotyping. Disease development was assessed five times from 2019 to 2022. Three seed families had canker-free rates from 3% to 30%, suggesting quantitative disease resistance (QDR) might be present, or possibly that those trees were the result of pollination of a susceptible parent tree with pollen from parent trees with major gene resistance. A set of candidate genes with putative plant disease resistance functions and defense responses were selected for targeted sequencing. Using single nucleotide polymorphisms (SNPs) of candidate genes, GWAS was performed using both general linear model (GLM) and mixed linear model (MLM) models. Nineteen SNPs, distributed on *Pinus* consensus linkage groups (LG) 1, 2, 4, and 5, were significantly associated with quantitative traits for limber pine QDR to WPBR ($p < 1e\text{-}6$). These QTLs co-located with candidate genes encoding nucleotide-binding site and leucine-rich repeats (NBS-LRR) proteins, leucine-rich repeat receptor-like kinases (LRR-RLKs), calcium-dependent phosphotriesterase (CaPTE), and glutamate receptor (GluR2), which may play roles in limber pine QDR against WPBR. These SNP-based QTLs were not linked to the Cr4-controlled major gene resistance (MGR) that was genetically mapped on LG8. Canker-free QDR appears to be rare in seedling families of limber pine. This is the first confirmation of its frequency, facilitated with genomic resources to eliminate the possibility that these canker-free seedlings were due to MGR. Pyramiding QDR with MGR with the aid of molecular markers may become an effective strategy for breeding for durable resistance in limber pine restoration.

GENETIC VARIATION IN LEAF TRAITS ASSOCIATED WITH LOCAL ADAPTATION TO CLIMATE IN YELLOW BIRCH

Ashley Thomson, QingLai Dang, Ashley Maloney and Piumi Maheshika

Understanding variation in functional traits of hardwood trees is crucial for the conservation and management of North American temperate forests under climate change. In this study, we examined provenance variation of yellow birch (*Betula alleghaniensis* Britton) in traits related to drought resistance in hardwood tree species. We examined the diameter, biomass, leaf morphology, and stable carbon isotopes in trees of ten seed sources from Canada and the Northern USA grown in a common garden. Analysis of variance (ANOVA) showed significant variation in tree height and leaf width, but there was no significant difference in root collar diameter among the different provenances. Significant leaf morphometric variables (average horizontal width, horizontal width, maximum perpendicular width, perpendicular width 1, and perpendicular width 2) were strongly and positively correlated with one another but were not significantly correlated with seedling growth. Both temperature and heat-moisture indices were strong predictors of leaf width, with seedlings originating from warmer, drier climates having narrower leaves than those from cooler, drier climates. The lack of significant correlations between seedling height growth and any of the climate variables suggests that the growth of yellow birch may be more influenced by local site factors, such as soil pH, soil moisture, and light availability, than climate variables.

CONTINUING THE SEARCH FOR WHITE PINE BLISTER RUST RESISTANCE IN FOXTAIL PINE (*PINUS BALFOURIANA*)

Benjamin Wilhite, Richard Sniezko, John Gleason, Emily Boes, Robert Danchok and Angelia Kegley

Foxtail pine (*Pinus balfouriana*) is a high elevation 5-needle pine species endemic to California with two geographically disjunct sub populations in the Klamath and southern Sierra Nevada mountains. In addition to threats stemming from climate change and its limited geographic range, foxtail pine is susceptible to the non-native, invasive fungus *Cronartium ribicola*, the causal agent of white pine blister rust (WPBR). In the first seedling inoculation trial at Dorena Genetic Resource Center (DGRC) in 2015, 100 percent of seedlings were cankered and all but two died. Subsequently, three additional trials were initiated at DGRC, and another in Placerville, CA. The trials aim to (1) test the effectiveness of varying levels of inoculum density to detect and characterize WPBR resistance, (2) greatly expand the existing number of families tested for WPBR resistance and (3) compare field results to seedling inoculation trial results. To examine the effect of inoculum density, 19 and 7 families (3 of which were in both) were sown in 2018 and 2019, respectively. Seedlings were inoculated at three spore densities. Level and severity of infection has been assessed, including mortality. Another 2019 trial included 150 families from throughout the range of foxtail. Early assessments of the trials, still in progress. indicate that infection (needles and stem) and mortality are extremely high, and summary/analysis is underway to determine what levels of resistance may be present. A subset of 19 families, including some of the best and worst rated from the 2015 trial (highest and fewest needle spots and cankers), were planted at two field sites (OR and CA) to monitor the durability and effectiveness of resistance in a field setting. The high susceptibility of foxtail pine documented here provides key information to help assess the future viability of this species and in planning conservation efforts.

PREDICTING THE GLOBAL FUNDAMENTAL CLIMATE NICHE OF LODGEPOLE PINE FOR CLIMATE CHANGE ADAPTATION

Yueru Zhao and Tongli Wang

The widely used species-occurrence-based models that predict the realized climate niche of plants can be too restrictive and do not reflect among-population variation in assessing climate change impact and guiding assisted migration for adaptation to future climates. To mitigate this deficiency, this study built a fundamental climate niche model for lodgepole pine (*Pinus contorta* Dougl. ex Loud.) based on 20-year tree height from wide-ranging provenance trials as a case study. The model was built through comparisons and optimizations of two candidate models, universal response function (URF) and universal transfer function (UTF), with linear and linear mixed-effect forms, against varying sample sizes based on the comprehensive provenance trials. We found that URF and UTF models had similar performances, while URF models were more straightforward in identifying optimal provenances for planting sites. Linear mixed-effect models did not show clear advantages over linear models in our case but prevented including additional predictors, which are often critical. We selected the linear model of URF and predicted the fundamental climate niche of lodgepole pine on a global scale and revealed a great potential of using this species for climate change adaptation beyond its native distribution, representing a significant step in forest genecology. Our study presented a new approach for assisted migration at the species and the population levels to optimize adaptation and productivity under a changing climate.

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