FOREST GENETICS 2025

August 11–15, 2025

Ottawa, ON

38th Meeting of the Canadian Forest Genetics Association - l'Association Canadienne de Génétique Forestière

Ontario

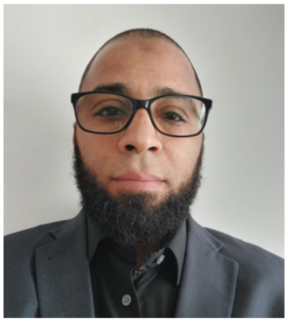
FOREST Gene Conservation ASSOCIATION

Message from the Co-Chairs

Kerry McLaven

CFGA President

Forest Gene Conservation Association



Lahcen Benomar

CFGA Vice President

Ontario Forest Research Institute

Ontario's journey to hosting Forest Genetics 2025 was anything but simple. Since the event was last held in this province in 2011, much has changed, new conversations have taken place, innovative collaborations have formed, and the nature of forest genetic resource management has continued to evolve.

Inspired by the success of the last conference (Forest Genetics 2023) in Vernon, British Columbia, enthusiasm quickly grew within Ontario, particularly among staff at the Ministry of Natural Resources (MNR), to bring the next event east. The Forest Gene Conservation Association (FGCA) joined MNR as co-hosts, with Ottawa selected as the venue for August 2025.

Ontario's long-standing history in tree breeding, genetics research, and field installations provided a rich foundation for the event. However, recent years have seen a growing disconnect between the research community, other sectors and the practical application of forest genetic resource management. The chosen theme, *Building Resilience through Forest Genetic Resource Management and Collaborative Action* aimed to bridge that gap, foster new relationships, and reignite collaboration across sectors. It succeeded beyond expectations.

From the outset, numerous organizations from Ontario and eastern Canada stepped forward to sponsor and support the event. The Province of Ontario served as the primary sponsor, joined by the FastTRAC II Project, Genome Canada, Génome Québec, Natural Resources Canada, and 18 additional partners; thank you for your generous contributions. The event's success was also made possible through the dedicated volunteer work of committee members who managed abstracts, logistics, field tours, and more.

Despite challenging economic conditions, interest in the event exceeded expectations, with over 100 participants attending from across Canada, the United States, South Korea, Israel, UK, Morocco, and Norway.

The event opened Monday with a joint workshop hosted by the Tree Seed Working Group and the Canadian Tree Nursery Association. Presentations from seed specialists across Canada were followed by a discussion about knowledge exchange priorities. The workshop generated valuable insights and sparked conversations that continued into the evening ice breaker, which had an excellent turnout.

On Tuesday, delegates entered an event space designed to reflect the southern Ontario landscape, complete with grafted butternut, native plant seeds, and sponsor exhibits. An impressive lineup of keynote and invited speakers, researchers, and students shared updates on their innovative work. Networking breaks and student poster sessions further encouraged meaningful dialogue and collaboration.

A major highlight of the week was the social dinner, held in a venue offering panoramic views of Ottawa. Delegates enjoyed an evening of networking, celebration, and connection. Wednesday continued with another full day of presentations, poster evaluations, and award ceremonies recognizing outstanding student posters and presentations, as well as undergraduate travel award recipients.

Thursday’s field tour of the Petawawa Research Forest in Chalk River, hosted by Natural Resources Canada, offered participants a firsthand look at ongoing research trials, including the recently established Adaptive Silviculture for Climate Change trial.

For those who stayed through the end of the week, a final tour at the Ferguson Tree Nursery showcased MNR’s white pine blister rust trials, MNR’s and FGCA’s realized gain trials, butternut genetic archives, grafting facilities, and the nursery’s seed facility.

Overall, Forest Genetics 2025 achieved its goal of connecting people from coast to coast, inspiring renewed commitment to forest genetic research and management in Ontario, and strengthening links between researchers and practitioners both within Ontario and beyond. From students and universities to breeders, growers, and field professionals, the future of forest genetics is clearly in capable hands.

Please read on to learn more about this impactful and inspiring event.

Acknowledgements

We would like to extend our sincere thanks to the Ontario Ministry of Natural Resources, the Forest Gene Conservation Association, and the Canadian Forest Genetics Association for their invaluable support in making Forest Genetics 2025 a success.

This event would not have been possible without the dedication, time, and expertise of our organizing and advisory committees, as well as the enthusiasm and contributions of all participants.

We are also deeply grateful to our sponsors, whose generous support helped bring this gathering of forest genetics professionals and researchers to life.

Thank you to everyone who played a role in making Forest Genetics 2025 an engaging and inspiring event.

Land Acknowledgement

We acknowledge that Forest Genetics 2025 was held on the traditional unceded territory of the Anishinaabeg, Haudenosaunee, and Algonquin Anishinaabe People.

We honour all Indigenous Peoples across Canada—past, present, and future—who have stewarded these lands and forests since time immemorial.

We are committed to respectful relationships and collaborative action in support of Indigenous knowledge, rights, and leadership in forest stewardship.

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Group photo taken on August 13, 2025, Ottawa Marriott Hotel

Program at a Glance

Monday, August 11, 2025

8:30 AM - 5:00 PM	*Growing Resilience*: *The Power of Seeds and Seedlings,* Tree Seed Working Group & Canadian Tree Nursery Association joint workshop
5:00 - 6:00 PM	Reception - Spin Kitchen & Bar, Ottawa Marriott Hotel

Tuesday, August 12, 2025

7:00 - 8:30 AM	Breakfast
8:30 - 9:00 AM	Opening: Gilbert Whiteduck, Kerry McLaven & Jennifer Dacosta
9:00 - 9:40 AM	Keynote speaker - Patrick Lenz
9:40 - 10:20 AM	Session 1: Genomic selection and tree breeding
10:20 - 10:40 AM	Break
10:40 AM - 12:00 PM	Session 2: Genomic and molecular adaptation
12:00 - 1:00 PM	Lunch
1:00 - 1:40 PM	Keynote speaker - Barb Thomas
1:40 - 2:40 PM	Session 3: Genetics of adaptation traits
2:40 - 3:00 PM	Poster session
3:00 - 3:10 PM	Break
3:10 - 3:40 PM	Invited speaker - Claire Depardieu
3:40 - 5:00 PM	Session 4: Climate change adaptation
6:00 - 9:00 PM	Social Dinner - Summit, Ottawa Marriott Hotel

Wednesday, August 13, 2025

7:00 - 8:30 AM	Breakfast
8:30 - 9:10 AM	Keynote speaker - Richard Sniezko
9:10 - 10:10 AM	Session 5: Breeding for disease resistance
10:10 - 10:30 AM	Break
10:30 - 11:00 AM	Invited speaker - Jill Hamilton
11:00 AM - 12:20 PM	Session 6: Genetic conservation
12:20 - 1:20 PM	Lunch & Guest speaker - Darren Sleep
1:20 - 2:00 PM	Keynote speaker - Igor Yakovlev
2:00 - 2:40 PM	Poster Session

2:40 - 3:00 PM	Break
3:00 - 3:30 PM	Invited speaker - Tongli Wang
3:30 - 4:50 PM	Session 7: Assisted population migration
4:50 - 6:00 PM	Closing Remarks, Awards and Prizes

Thursday, August 14, 2025

6:30 - 7:45 AM	Breakfast
8:00 AM - 3:30 PM	Tour of Petawawa Research Forest
3:30 - 5:30 PM	Travel back to Ottawa Marriott Hotel

Friday, August 15, 2025

8:45 AM - 1:00 PM	Optional visit to Ferguson Tree Nursery
1:00 - 2:00 PM	Travel back to Ottawa Marriott Hotel

Event Field Trip, Petawawa Research Forest, August 14, 2025

Tree Seed Working Group & Canadian Tree Nursery Association Joint Workshop

Monday, August 11, 2025

Dave Kolotelo, RPF

Dave has been working at the BC provincial Tree Seed Centre for the past 33 years conducting research and extension, assisting with tree seed problem solving, operational efficiency improvements and successfully avoiding management. Dave obtained a BScF from the University of New Brunswick in 1987 and a MScF at the University of British Columbia in 1991 specializing in forest genetics and tree physiology. Dave was fortunate to get this position at the BC Tree Seed Centre in 1992 after working on contract for the Douglas-fir breeding program. Dave greatly enjoys the diversity of people he deals with in the reforestation system including: cone collectors, seed orchardists, geneticists, seed researchers, processing facilities and nurseries staff. Dave is interested in tree seed science and technology, but feels more like an advocate these days for investments in research, education and infrastructure to maintain these essential services at the global level. In his spare time, Dave enjoys gardening, travelling, bicycling, hiking and beach volleyball.

Rob Keen, RPF

Rob Keen is a Registered Professional Forester and Executive Director of the Canadian Tree Nursery Association, established in 2023 to support Canadian tree nurseries' work in facilitating the nation's forest restoration efforts. Prior to establishing the Association, he served Trees Ontario for more than 20 years, first as a consultant and later as CEO, overseeing its merger with the Ontario Forestry Association, and resulting in the formation of Forests Ontario in 2014. Throughout his career, Rob has championed the sustainability and stewardship of Canada's forests, including as a Director and Chair of the Algonquin Forestry Authority and as Director of the Invasive Species Centre, and is currently a Director of Maple Leaves Forever and Chair of the Sustainable Forest Licensee, Westwind Forest Stewardship Ltd. For his work, Rob received the Clean50 Lifetime Achievement Award in the fall of 2022 and the Forests Ontario Award in 2023.

Monday, August 11, 2025

Growing Resilience: The Power of Seeds and Seedlings

Introduction

Welcome, Remembrance & Overview for the day 8:30 AM

TSWG Opening Comments by Dave Kolotelo
CTNA-ACPF Opening Comments by Rob Keen

Seed Management Across Canada

National Tree Seed Centre – Canada's Tree & Shrub Gene bank 9:00 AM
Speaker: Darren Derbowka

Conifer Seed Management in the Maritimes 9:20 AM
Speaker: Shona Millican

Seed management in Quebec: a provincial matter 9:40 AM
Speaker: Fabienne Colas

10:00 AM Break

Forest Genetic Resource Management Efforts in Ontario 10:30 AM
Speaker: Kerry McLaven

Ontario Tree Seed Genetic Archive 10:50 AM
Speaker: Brad Neary

Seed Use in Alberta 11:10 AM
Speaker: Robert Matheson

Seed use standards and practices in British Columbia 11:30 AM
Speaker: Brian Barber

12:00 PM Breakout Working Lunches

Lunches Provided
CTNA-ACPF – AGM (members only) by Rob Keen
TSWG strategy session by Dave Kolotelo

Bridging the gap between Seed Science and Operations 1:30 PM
Speaker: Dave Kolotelo

Nursery Seed Use Efficiency 2:00 PM
Speaker: Steve Kiiskila

2:30 PM Break

Prioritizing seed and seedling information needs 3:00 PM

Workshop completion 4:00 PM

CFGA Reception 5:00 PM

Tuesday, August 12, 2025

8:30 – 9:00 AM: Welcome & Conference Opening

- Gilbert W. Whiteduck, Kitigan Zibi Anishinabeg First Nation
- Kerry McLaven, Forest Gene Conservation Association & Jennifer Dacosta, Ontario Ministry of Natural Resources

9:00 – 9:40 AM: Keynote Speaker - Patrick Lenz (Natural Resources Canada)

Genomic selection: From proof of concept to optimized modelling to the inclusion of complex traits

9:40 – 10:20 AM: Session 1: Genomic selection and tree breeding
Moderator: Dan McKenney

Funda Ogut (Natural Resources Canada)
Integrating genomic selection with cutting-edge phenotyping technologies to enhance seedling resilience to future climates

Rafael Candido Ribeiro (University of British Columbia)
Incorporating climate-adaptive traits into Douglas-fir (*Pseudotsuga menziesii*) breeding programs with low-cost genomic resources

10:20 – 10:40 AM: Break

10:40 AM – 12:00 PM: Session 2: Genomic and molecular adaptation
Moderator: John Pedlar

Myles Cummins (Lakehead University)
Patterns of genotype-environment association in the eastern North American Yellow Birch (*Betula alleghaniensis* Britt.)

Suncheon Hong (Seoul National University)
Transcriptomic insights into drought stress response and recovery in *Pinus densiflora*

Meg E. Smith (University of British Columbia)
Chromosome-scale genome assemblies and analysis of genomic structural variation in Douglas-fir (*Pseudotsuga menziesii*)

Vincent Quevillon (Université Laval)
Ecogenomics of transcontinental black spruce: identifying key genes related to climate adaptation

12:00 – 1:00 PM: Lunch

1:00 – 1:40 PM: Keynote Speaker - Barb Thomas (University of Alberta)

Digital transformation of Alberta’s tree improvement programs - driven through collaboration and a need for change

1:40 – 2:40 PM: Session 3: Genetics of adaptation traits
Moderator: Betty van Kerkhof

Mina Sadeghiniaraki (Carleton University)
Integrated analysis of conifer responses to biotic and abiotic stressors: meta-analysis and gene expression insights

Edouard Desaulniers (Université Laval)
Intra-annual wood density variations in boreal conifers: Identifying novel candidate traits to select for enhanced adaptation to climate instability

Brian T. Barber (Select Seed Co. Ltd.)
The Story of Select Seed Company Ltd.: Producing tree seed for reforestation in B.C. since 1999

2:40 – 3:00 PM: Poster Session

An opportunity to explore current research and network with presenters showcasing their forest genetics projects

3:00 - 3:10 PM: Break

3:10 – 3:40 PM: Invited Speaker - Claire Depardieu (Université Laval)

Drought resilience of forests: A multi-scale perspective from genes to tree rings

3:40 – 5:00 PM: Session 4: Climate change adaptation
Moderator: Ashley Thomson

Abi Brown (University of British Columbia)
Patterns and drivers of local adaptation across species and space: a provenance trial meta analysis

Edouard Reed-Métayer (Université Laval)
Black and red spruce F1 hybrids : superior long-term vigor but intermediate dendroecological response to climate stress

Grace Gardner (Carleton University)
Identifying Local Environmental Adaptation in Jack Pine (*Pinus banksiana*) to inform Predictions of Maladaptation under Future Climate Conditions

Rakefet David-Schwartz (Volcani Institute)
Unlocking Climate Adaptation Potential: The Role of Interspecific Hybridization in Natural Regeneration of Planted Forests

Zhengyang Ye (University of British Columbia)
Using landscape genomics to define species distributions, delineate seed zones, and predict maladaptation to future climate for the interior spruce hybrid complex (*Picea glauca, Picea engelmannii*, and their hybrids)

6:00 – 9:00 PM: Social Dinner, Summit, Ottawa Marriott Hotel

Wednesday, August 13, 2025

7:00 – 8:30 AM: Breakfast

8:30 – 9:10 AM: Keynote Speaker - Richard Sniezko (USDA Forest Service)

Successes in Forest Tree Resistance Breeding and Lessons Learned

9:10 – 10:10 AM: Session 5: Breeding for disease resistance
Moderator: Pengxin Lu

Mel Lucas (Western University)
Does resilience to the mountain pine beetle come at a cost of reduced growth in lodgepole pine?

Lahcen Benomar (Ontario Ministry of Natural Resources)
Physiological characterization of white pine blister rust resistant *P. strobus* × *P. wallichiana* hybrids

Obed Asamoah (Carleton University)
Stakeholders' Perceptions: Genetically Improved Tree Species for Enhancing Forest Resilience to the Impact of Mountain Pine Beetle

10:10 – 10:30 AM: Break

10:30 – 11:00 AM: Invited Speaker - Jill Hamilton (Pennsylvania State University)

Genomics-driven monitoring for genetic conservation and breeding in forest trees

11:00 AM – 12:20 PM: Session 6: Genetic conservation
Moderator: Catherine Cullingham

Nicholas Boyce (University of Alberta)
Conservation planning for forests, tree species, and their genetic populations under climate change in Canada

Chaebin Lee (University of British Columbia)
Genome Architecture shapes Inbreeding depression: Implications for Forest Tree Populations

Aron Fazekas (University of Guelph)
25 years and Counting: The Elm Recovery Project at The Arboretum, University of Guelph

Martin Williams (Natural Resources Canada)
Building the knowledge and research capacity to preserve butternut for future generations

12:20 – 1:20 PM: Lunch & Guest Speaker - Darren Sleep (Forest Products Association of Canada)

Change before you have to: adaptive capacity in Canadian forestry

1:20 – 2:00 PM: Keynote Speaker - Igor Yakovlev (Norwegian Institute of Bioeconomy Research)

Epigenetic regulation during annual development in Norway spruce epitypes

2:00 – 2:40 PM: Poster Session

Explore current research and network with presenters showcasing their forest genetics projects. Don't forget to vote for your favourite poster!

2:40 – 3:00 PM: Break

3:00 – 3:30 PM: Invited Speaker - Tongli Wang (University of British Columbia)

Winners and losers of 43 tree species under climate change in Western Canada

3:30 – 4:50 PM: Session 7: Assisted population migration
Moderator: Aron Fazekas

Genevieve Dorrell (University of Alberta)
A Seed Selection Tool to Support Climate-Informed Reforestation in Canada

Yuhui Weng (Austin State University)
Assessing black spruce breeding zones and seed deployment in northwest Ontario

John Pedlar (Natural Resources Canada)
Variation in performance of oak species and provenances at assisted migration trials in southern Ontario

Betty van Kerkhof & Ngaire Roubal (Sault College)
Seed Transfer in Ontario

4:50 - 6:00 PM: Closing Remarks, Awards and Prizes

Thank you for joining us for Forest Genetics 2025!

Thursday, August 14, 2025
Petawawa Research Forest

Natural Resources Canada's Petawawa Research Forest (PRF) was established in 1918 and is home to over 2,000 forest research experiments and studies. The forest is located near Chalk River, Ontario, and covers approximately 10,000 hectares of land within Canada's Great Lakes – St. Lawrence Forest region. The mission of the PRF is to enhance sustainable forest management in Canada through innovative forest research by providing: a safe, secure, sustainably managed forest, accessible historic & leading-edge research data, and on-the-ground knowledge transfer experiences.

6:30 – 7:45 AM: Breakfast

7:45 – 8:00 AM: Board buses

Buses will board on Queen Street, outside of Spin Kitchen & Bar, leaving at 8:00 am sharp

8:00 – 10:30 AM: Bus from Ottawa Marriott Hotel to Petawawa Research Forest

10:30 – 11:30 AM: White Pine Provenance Trial, PRF Experiment 25-D
Presenters: Jeff Fera, Steve D'Eon and Dan McKenney

- Welcome and history of the Petawawa Research Forest
- White pine provenance trial, est. 1942, including 43 seed lots (eastern United States and eastern Canada)

11:45 AM – 12:45 PM: Lunch at PRF Silviculture building

Catered lunch provided

1:00 – 2:00 PM: Adaptive Silviculture for Climate Change Research Project
Presenter: Jeff Fera

- Operational research study focussing on "climate change ready" forest management prescriptions for the pine forests in the Great Lakes – St. Lawrence Forest region

2:30 – 3:30 PM: White Spruce Provenance Trials and Red Spruce Progeny Trials
Presenters: Steve D'Eon, Funda Ogut and Patrick Lenz

- Two white spruce provenance trials, est. 1963 and 1965, provenances from the Great Lakes – St. Lawrence Forest region
- Discussion of newly established red spruce full sib progeny trial, 39 families from Nova Scotia
- Revisiting legacy provenance trials with new research questions

3:30 PM: Concluding remarks & departure from PRF

Transportation provided back to Ottawa Marriott Hotel for 5:30 pm return

Friday, August 15, 2025
Ferguson Tree Nursery

Ferguson Tree Nursery grows high-quality, ecologically suitable trees, shrubs, and perennials from known seed sources, including native and proven non-invasive naturalized plants hardy for south-central and eastern Ontario as well as southwestern Quebec.

The plants are used by foresters, landscapers, landowners, nurseries, and conservation-minded individuals who want the most appropriate plants with the highest quality and potential of success. Ferguson Tree Nursery is a social enterprise utilizing profits to:

- *promote awareness of, and interest in, forestry (e.g., afforestation and sustainable forest management)*
- *maintain, enhance, and promote the responsible use and stewardship of the recreation and conservation lands managed by the Ferguson Forest Centre*

8:45 AM – 9:30 AM: Bus from Ottawa Marriott Hotel to Ferguson Tree Nursery

- Please meet in the foyer at 8:30 AM to board the bus to FTN for a 9:30 AM arrival
- Bus arrives at Ferguson Tree Nursery, bathroom break, welcome and tailgate safety talk before heading to the back of the property

9:45 AM: MNR Realized Gain Trial

Presenter: Lahcen Benomar

10:15 AM: Walk and talk to MNR Hybrid Pw Trial

Presenter: Lahcen Benomar

10:45 AM: FGCA Butternut Seed Orchard

Presenter: Heather Zurbrigg

11:20 AM: Tour of FTN shipping shed and seed room

Presenters: Maureen Jacques and Chris MacDonald

12:00 PM: Tour of FGCA grafting greenhouse and shade area (butternut and black ash grafts)

Presenter: Heather Zurbrigg

12:15 – 12:45 PM: Lunch

Catered lunch provided at FTN. Bathroom break at municipal building.

1:00 PM: Departure from FTN

Transportation provided back to Ottawa Marriott Hotel

Gilbert W. Whiteduck

Kitigan Zibi Anishinabeg First Nation

Speaker Biography

Gilbert W. Whiteduck is (Anishinabe) Algonquin from the Kitigan Zibi Anishinabeg First Nation community located within the Outaouais region on the ancestral territory of his ancestors. He was elected Chief of the Kitigan Zibi Anishinabeg community and served from June 2008 to April 2015. He had previously been elected to the Kitigan Zibi Anishinabeg Band Council at different intervals, for a total period of 20 years. He returned to serve on Band Council from 2020 to 2022. Mr. Whiteduck holds a B.S.W (Honors), a B. Ed, an M. Ed, a Certificate in Indigenous Law and an Honorary Doctorate which he received from the University of Ottawa in 1999 for his work in the field of education. Mr. Whiteduck was employed in the field of First Nations education for over 33 years.

Mr. Whiteduck remains active in his efforts to ensure that First Nations' voices are not only heard but understood. He continues to seek balance through ceremony and connection to elders. He walks with an understanding of the historical past that guides him in respecting the present moments with humility and love. He believes that significant groundwork remains to be completed for reconciliation to be achieved. He is optimistic that current and future generations will witness this progress within their lifetimes.

Patrick Lenz

Natural Resources Canada

Genomic selection: From proof of concept to optimized modelling to the inclusion of complex traits

Environmental changes are putting strong pressure on tree breeding programs to accelerate selection cycles and integrate diverse adaptive traits for the deployment of reforestation seedlings capable of sustaining rapid climate change and biotic stressors. Genomic selection (GS) is a powerful tool for breeders to address several aspects of this challenge. Since first proof of concept studies in boreal conifers, different genotyping resources have been created and tested in GS over the past decade. A few breeding programs have also made initial selection and deployment decisions based on GS models in Canada. At the same time, research progress has improved our understanding of the power and opportunities of different GS modelling decisions, for example: better separation of additive from non-additive effects allows for more accurate predictions based on breeding and deployment strategies and the prediction of untested crosses; better knowledge of the optimal genome coverage in markers and sample sizes required for accurate genomic predictions allows for optimized sampling strategies while limiting genotyping costs and efforts; or the use of multi-trait selection approaches that allows to study genetic correlations and take advantage of genetic covariance for the inclusion of complex traits in multiple-objective breeding. More recently, attention has focused to identify novel phenotypes that allow for efficient evaluation of insect resistance for instance, or resilience to climate anomalies as assessed from increment cores. Working with material from active breeding populations, we have developed strategies to accelerate the operational integration of these new adaptive traits into genomic prediction models. When combined, these strategies appear promising for enhancing and hastening selection for growth and adaptive traits, and thus enabling the production of high-quality seedlings for future forests.

Speaker Biography

Since 2015, Patrick is a research scientist at the Laurentian Forestry Centre in quantitative genetics and forest genomics. His current research focuses on the development of genomic breeding tools for speeding up the selection of planting stock with superior growth, resistance and wood quality. Some of the hot topics include the research on resistance traits to climate extremes, to better understand their role in adaptation and including those traits into genomic selection models.

Patrick has contributed to large-scale Genome Canada funded projects in forest genomics, such as SMarTForests and Spruce-Up. He currently co-leads the FastTRAC II project aiming at the scaling of genomic prediction for black- and red spruce breeding programs. He is an active member of the Canada Research Chair in Forest Genomics led by Jean Bousquet at Université Laval.

Barb Thomas

University of Alberta

Digital transformation of Alberta’s tree improvement programs

Building on a 5-year Genome Canada large scale applied research project, Alberta’s tree improvement (TI) sector has now embarked upon a new initiative titled ‘Best Future Forests – Advanced Forest Genomics and Integrative Resource Management System’ (BFF-AFIRMS). This initiative represents a significant advancement in Alberta's TI strategy by integrating cutting-edge forest genomics with a comprehensive digital infrastructure, specifically designed to encompass the entire conifer TI sector and revolutionize how TI decisions are made. As a centerpiece of Alberta's TI transformation, BFF-AFIRMS aims to address critical challenges such as climate change, fragmented breeding programs, and the imperative for robust data integrity, resource management and strategic optimization.

BFF-AFIRMS introduces a scalable, relational database and computational system, including growth & yield applications, tailored to Alberta’s tree improvement program needs. This system is developing, and will incorporate, a standardized genotyping platform, provide genomic selection methodologies and predictive analytics to enhance selection accuracy, reduce rotation times, and support adaptive forest management practices. Key functionalities will include dynamic pedigree reconstruction with error correction, phenotype prediction under projected climate scenarios and customizable selection tools for genetic gain estimation using genomic estimated breeding values.

Developed through a collaborative partnership among academia, government, and industry stakeholders, BFF-AFIRMS will equip Alberta’s forest sector with innovative, data-driven tools to ensure the resilience, productivity, and sustainability of future forests. The BFF-AFIRMS initiative sets the stage for a paradigm shift in TI, as Alberta shifts from fragmented, program-specific efforts, to a unified, integrated, provincial-scale approach that will shape the future of forest stewardship and resource management.

Speaker Biography

Barb R. Thomas joined the University of Alberta (UofA) in 2014, having secured an NSERC/Forest Industrial Research Chair (IRC) in Tree Improvement, which was renewed in 2020. In addition to her IRC, she led a large-scale applied Genome Canada research project entitled: ‘Resilient Forests (RES-FOR): Climate, Pests and Policy, Genomic Applications’, from 2016 to 2021. Her newest venture is focussed on the development of a computational database centre for Alberta's white spruce and lodgepole pine breeding programs in conjunction with the construction of two new SNP arrays for province wide genotyping. Prior to joining the UofA, Barb ran her own business as an industrial scientist for 17 years, leading the poplar farm research program at Alberta-Pacific Forest Industries Inc. (Al-Pac) and representing industry on various government policy/genetics related committees.

Barb's background is in horticulture, forest genetics, and ecophysiology, and she is a graduate of both UBC and the UofA. Barb is an active and founding member of Tree Improvement Alberta and sits on various other national and international Boards. Barb's primary interests lie at the intersection of science, policy, application, and climate change. Barb is currently the Associate Dean (Research), in the Faculty of Agricultural, Life & Environmental Sciences, UofA.

Richard Sniezko

USDA Forest Service

Successes in forest tree resistance breeding and lessons learned

Pathogens and pests, particularly non-native ones, continue to threaten the health of our forests. Fortunately, within each affected tree species there is usually a level of genetic resistance that can be documented and utilized in a resistance breeding program so these species will continue to be important components of forest ecosystems or managed plantings. There are now several examples of successful forest tree resistance programs with the seed being produced used for reforestation and restoration. Examples from the USDA Forest Service's Dorena Genetic Resource Center (DGRC) which has been involved in resistance breeding since the 1960s, will be used to illustrate some of the successes and lessons learned that can be helpful in guiding newer programs. The goal of these programs is to develop populations of trees with resistance that is durable and stable, while maintaining genetic variation and adaptability. The nine species of 5-needle white pines native to the U.S. (four native to Canada) are highly susceptible to white pine blister rust, caused by the fungal pathogen *Cronartium ribicola*. DGRC has screened all nine species, to varying degrees, and documented the types and levels of natural genetic resistance. Breeding programs continue for western white pine (*Pinus monticola*) and sugar pine (*P. lambertiana*), while the higher level of resistance documented in whitebark pine (*P. albicaulis*) in many areas of the Pacific Northwest should allow restoration to proceed with seed from the parent trees and/or natural regeneration. More recent programs, to develop resistance to *Phytophthora lateralis* in Port-Orford-cedar (*Chamaecyparis lawsoniana*) and to *Fusarium oxysporum* f. sp. koae in koa (*Acacia koa*) benefited from the knowledge gain in the white pine blister rust resistance program. With the increasing interest world-wide in applied forest tree resistance programs, the sharing of information from current successes can help increase the opportunity for success in newer programs.

Speaker Biography

Richard Sniezko has been Center Geneticist at the USDA Forest Service's Dorena Genetic Resource Center (DGRC) in Oregon since 1991. His work focuses on development of populations of trees with genetic resistance to non-native forest tree diseases & pests for restoration and reforestation, as well as genetic variation and gene conservation. Several of these are recognized internationally as world leadering programs in resistance. He has worked extensively with white pine blister rust caused by *Cronartium ribicola*, Port-Orford-cedar root disease (pathogen *Phytophthora lateralis*) and koa wilt (pathogen *Fusarium oxysporum*).

Some additional recent activities include providing guidance on the project to develop resistance to Rapid ‘Ōhi‘a Death in Hawaii, some genetic/gene conservation related projects with western species of ash (threatened by emerald ash borer) and setting up a new ‘sentinel’ project to help evaluate potential future pathogen and pest threats to U.S. tree species.

Richard completed his B.S. degree at Humboldt State University (1977) and his PhD at North Carolina State University (1984); prior to DGRC he worked at Oregon State University and at the Zimbabwe Forest Research Centre.

Igor Yakovlev

Norwegian Institute of Bioeconomy Research

Epigenetic regulation during annual development in Norway spruce epitypes

The establishment, maintenance, and removal of epigenetic modifications provide an additional layer of regulation beyond genetically encoded factors, by which plants can control developmental processes and adapt to the environment. Studying the annual dynamics of transcriptomes and DNA methylation in spruce epitypes can provide valuable insights into the regulatory mechanisms underlying seasonal growth, development, and adaptation of forest trees. For this, we used unique well-defined clonal epitypes of Norway spruce with a stable epigenetic memory of the temperature sum experienced during embryogenesis impacting bud phenology. Epigenetic memory is retained year after year in epitypes and affects the annual growth cycle, timing of bud set, cold acclimation, and dehardening in a predictable and reproducible manner. Epitypes refer to a group of individuals with the same genome but with different epigenomes that influence gene expression and phenotypes.

We aimed to determine whether epigenetic memory involves stable transcriptomic patterns, including small RNAs (sRNAs) and DNA methylation marks, retained through the annual cycle of development. We characterized transcriptomic (both mRNAs and sRNAs) and DNA methylation patterns in apical buds for 10 time points throughout the annual cycle of development to observe the differences between epitypes. Epitypes possessed clear differences in transcription patterns for multiple genes, especially during period of “dormancy”.

We identified the highest number of differentially expressed miRNAs during spring dormancy, bud burst, and shoot development. Because of the large size of the Norway spruce genome, we used a targeted approach to address the DNA methylation status at a single-base resolution in 3,000 selected target genes involved in the timing of phenology, the entire epigenetic machinery, and the circadian clock. We found large differences in the methylation patterns of specific genes. Methylation marks appear to be patterned throughout the annual cycle. Specific methylation states for some differentially methylated genes may be reestablished twice a year and persist or cleared in between.

Speaker Biography

Igor Yakovlev is a senior researcher and professor at the Norwegian Institute of Bioeconomy Research (NIBIO), Department of molecular biology of plants, Ås (Norway). He received his PhD at the Leningrad/Saint-Petersburg State Forest Technical Academy (Russia), studying the population structure of oak stands in the Near-Volga regions of Russia. He performed post-doctoral research at the Mary State Technical University (Russia), Lower Saxony Forest Research Institute (Germany) and Oregon State University (USA). From 2003, Igor started working at the Norwegian Forest Research Institute (recently NIBIO), studying the molecular mechanisms of the epigenetic memory formation in Norway spruce and strawberry and plant–microbe interactions.

Claire Depardieu

Université Laval

Drought resilience of forests: A multi-scale perspective from genes to tree rings

Climate change presents a significant threat to forest resilience, especially as droughts become more frequent and severe. Understanding the mechanisms that underpin this resilience is essential for anticipating ecosystem responses and adapting forest management strategies. This presentation offers a synthesis of the most promising findings from six recent scientific projects aimed at deepening our understanding of the physiological and molecular mechanisms involved in drought resilience. These projects employed, either jointly or independently, approaches from dendroecology, genomics, and transcriptomics. We will first present a large-scale dendroecological analysis conducted on 23 Canadian tree species, which reveals a gradual decline in resilience to severe, episodic drought events over the past century. We will then explore the influence of genetic and environmental factors on drought resilience by analyzing growth patterns, wood characteristics, and gene expression in white and black spruce. Our results highlight substantial intraspecific variability, with trees from different genetic sources (families, provenances) adopting diverse physiological strategies to cope with drought conditions. The combined use of genetic and dendroecological approaches has allowed us to identify the most promising genetic sources and wood traits for enhancing resilience to future climate conditions. These findings offer new insights into the relative importance of underlying physiological mechanisms in drought resilience among conifers and represent a major step forward in characterizing their genomic foundations.

Speaker Biography

Claire Depardieu is a scientist specializing in plant physiology, genomics, and environmental sciences, with a passion for studying trees and their resilience to climate change. Claire holds a PhD in Biological and Environmental Sciences (Université de Franche-Comté, France) and has completed three postdoctoral programs in bioinformatics, agronomy, and forest genomics (University of Toronto and Université Laval, Canada).

Currently a research professional with Prof. Jean Bousquet's group at Université Laval, Claire conducts research to understand the physiological and molecular mechanisms that enable conifers to withstand abiotic stresses such as drought and cold.

Claire is the author of 21 scientific articles and actively contributes to the preparation of several manuscripts and book chapters. Her work has led to nearly 50 local and international conference presentations and involvement in the development of global networks, including the international student network on climate, an international biosphere network, and an international network of living labs in forestry and agroforestry.

Jill Hamilton

Pennsylvania State University

Genomics-driven monitoring for genetic conservation and breeding in forest trees

In a rapidly changing environment, maintenance of genetic variation within and across populations is increasingly important for conservation and restoration. A species' evolutionary potential is tightly linked to both the amount and distribution of genetic variation available through which natural selection may act. While there is growing emphasis on the importance of genetics in conservation, there is a need to pair genomic monitoring with range wide ex situ conservation collections as a foundation for breeding and restoration programs. Here, I will discuss the value of combining population genomic monitoring with conservation collections to understand species' evolutionary history, and the role different evolutionary mechanisms may play influencing neutral and adaptive processes across space and time using *Fraxinus* species as a case study. The decimation of eastern hardwood forests in North America in response to the Emerald Ash Borer and its continued expansion west emphasizes the need for proactive conservation of existing genetic resources and development of new genomic resources to pair with future breeding and restoration programs. I will discuss the need to safeguard biodiversity for species at risk, proposing genomic screening of seed and living collections for use in restoration, genecology, seed orchard establishment, and breeding program development.

Speaker Biography

Jill Hamilton is Director of the Schatz Center for Tree Molecular Genetics and Ibberson Chair of Silviculture Research at Pennsylvania State University. She received her PhD at the University of British Columbia in Forestry studying adaptive introgression in forest trees, following which she completed post-docs at the University of Alberta and University of California-Davis to understand the genetic basis for adaptation across complex traits critical to forest and non-forest systems. Jill's research program integrates a foundation in evolutionary biology with conservation and restoration of natural and managed systems, leveraging population, landscape, and functional genomics alongside large-scale quantitative genetic experiments and modeling.

Tongli Wang

University of British Columbia

Winners and losers of 43 tree species under climate change in Western Canada

Climate change represents one of the most pressing global challenges, with afforestation and ecosystem restoration emerging as critical strategies for achieving carbon neutrality and biodiversity conservation. This study presents consensus projections for 43 tree species in western North America under various climate change scenarios, using Random Forest models and an extensive dataset of species occurrences and environmental variables. We analyzed potential shifts in species distributions and changes in species richness. Our results indicate diverse responses among tree species, with some projected to expand their suitable habitats while others face significant contractions. Conifers generally show more negative impacts compared to broadleaf species. Species richness patterns are projected to change, with some current biodiversity hotspots maintaining high richness while others experience declines. Novel areas of high species richness emerge, particularly in higher latitudes and elevations. Meanwhile, we developed an innovative web tool that enables users to assess species' climate suitability rankings at any location in British Columbia for the current and future periods. This tool facilitates the selection of climate-resilient tree species and provides a robust framework for species selection based on location and time period. Our study highlights the need for proactive and adaptive approaches to forest management in the face of climate change to maintain the health, diversity, and resilience of western North American forests.

Speaker Biography

Tongli Wang is an Associate Professor in the Department of Forest and Conservation Sciences at the University of British Columbia. He is working on species niche models and climate models. Tongli's work on climate niches has been published in the Science of Total Environment journal, Environmental Management, Climate Smart Agriculture, Ecology Letter, etc. His climate model serves many users, including the people here. Tongli's work also includes tree conservation and catalog work.

Guest Speaker

Darren Sleep

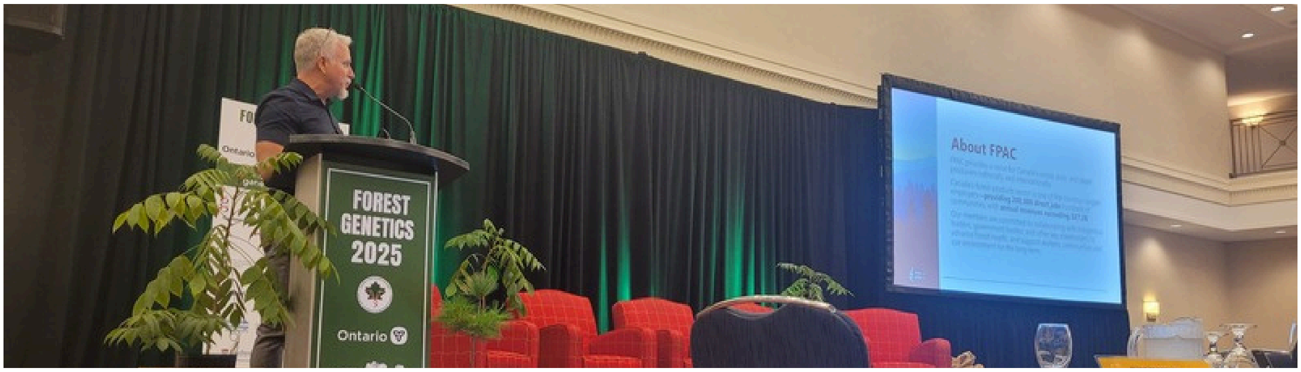
Forest Products Association of Canada

Change before you have to: adaptive capacity in Canadian forestry

Canada's forest sector must adopt a systems-level approach to climate adaptation that goes beyond tree genetics. Genomics and silviculture are an important start, but rising climate risks, market shifts, and governance complexity demand integrated strategies. Proactive forest management in partnership with Indigenous leadership is essential. Fragmented policies across various levels of government can hinder coordination, and forests' role in net-zero goals using carbon-smart practices could be compromised. Technological tools and socioeconomic support for forest communities must also be prioritized. A national adaptation strategy, Indigenous-led initiatives, and harmonized governance are key to ensuring long-term resilience, sustainability, and competitiveness in this rapidly changing environment.

Speaker Biography

Raised in the forests and fields of New Brunswick, Darren Sleep developed a profound appreciation for the natural world at a young age, exploring the Acadian forests and interacting with their diverse wildlife. After high school, he earned a BSc from the University of New Brunswick, a MSc from the University of Regina, and a PhD from the University of Guelph. Darren has since gained extensive experience working with the forest sector across North America, covering a variety of topics including rare and threatened species, protected area design, climate change, forest management, forest hydrology, and science/policy integration. Prior to joining FPAC, he served as the Lead Scientist with the Sustainable Forestry Initiative (SFI) based in Ottawa and as the Principal Scientist with the National Council for Air and Stream Improvement (NCASI) in Montreal.



Session 1: Genomic selection and tree breeding

Moderator: Dan McKenney

Integrating genomic selection with cutting-edge phenotyping technologies to enhance seedling resilience to future climates

Funda Ogut (Natural Resources Canada), Patrick Lenz, Jean Philippe Laverdière, Olivier van-Lier, Simon Nadeau, Chris Wong, Francois Van Deventer, Shona Millican, Iain Thompson, Simon Bockstette and Jean Bousquet

With climate change (CC), more intense and frequent drought events will have an impact on water availability for trees and particularly seedlings during plantation establishment. Therefore, forest managers need to increasingly consider adaptation to drought stress in reforestation strategies. However, most of the seedlings used for deployment come from breeding programs that have traditionally focused on growth and that lack efficient methods to assess resilience to biotic and abiotic stressors on hundreds or thousands of trees in breeding or production populations. Our work addresses this gap by combining advanced selection tools with high-throughput phenotyping using sensors and spectral signatures. Amongst others, results from a greenhouse experiment will be presented where two-year-old red spruce seedlings were subjected to drought stress. SNP marker data for more than 1500 seedlings are currently being processed, which will allow us to further test the efficiency of genomic selection (GS) and single-step-BLUP in this young seedling material. Compared to traditional pedigree-based selection, GS has the potential to accelerate the breeding and deployment of planting stocks which is considered critical for rapid response to climate change. The combination of improved phenotyping technologies with GS will ensure that forests continue to play a role in CC mitigation in the future, by allowing for more timely and flexible selection criteria for planting stock.

Incorporating climate-adaptive traits into Douglas-fir (*Pseudotsuga menziesii*) breeding programs with low-cost genomic resources

Rafael Candido-Ribeiro (University of British Columbia), Trevor Doerksen, Jon Degner, Marco Todesco, Tom Booker and Sally Aitken

Selective breeding has been used for decades to increase Douglas-fir growth, largely enhancing the productivity of planted forests in western North America. Recent sequencing technologies, developed for this species in the CoAdapTree project, such as a SNP-array with markers associated with climate adaptive traits, have the potential to accelerate breeding cycles and incorporate other complex traits into breeding programs. This is particularly relevant at the moment, given the observed and expected decrease in forest productivity due to climate change. Yet, considering the large number of trees screened in a breeding cycle, the cost of this technology per genotyped individual is still prohibitive for breeding programs in British Columbia (BC), urging for alternative ways to reliably assess genotypes in the breeding populations. In this study, we will compare the CoAdapTree Douglas-fir SNP-array with the newly developed massively multiplexed genotyping-by-sequencing method (Multi-GBS) in terms of quality and quantity of genomic data, and costs. Furthermore, we will use Multi-GBS to genotype 1,440 individuals from 73 natural populations, sampled from across the range of both the interior and coastal Douglas-fir varieties, and recently tested for seedling drought tolerance. GWAS will be performed with individual phenotypes and genotypes to identify and validate SNPs and candidate genes associated with drought tolerance in Douglas-fir. Finally, we will assess the presence of drought tolerance-associated alleles in the Douglas-fir breeding populations in BC. The potential of our results to inform Douglas-fir breeding and assisted gene flow as adaptive strategies for climate change will be discussed.

Session 2: Genomic and molecular adaptation

Moderator: John Pedlar

Patterns of genotype-environment association in the eastern North American Yellow Birch (*Betula alleghaniensis* Britt.)

Myles Cummins (Lakehead University), Yuanxin Ye and Ashley M. Thomson

Building climate-resilient forests requires an understanding of the genomic foundations of adaptation. As climate change accelerates, forest tree species increasingly face range shifts, maladaptation, and loss of ecosystem function. This study investigates adaptive genomic variation in *Betula alleghaniensis* (Yellow Birch), a widely distributed and ecologically important hardwood of eastern North America. Genome-wide SNP variation from 27 populations spanning the species range was analyzed using 3D-genotype-by-sequencing and two genotype-environment association (GEA) methods: redundancy analysis and Gradient Forests. The GEA approaches identified 124 putatively adaptive loci associated with key climate variables, particularly extreme minimum temperature, degree days below 0°C, winter precipitation, and precipitation as snow. Functional annotation of these loci revealed roles in stress response, transcriptional regulation, metabolism, and cellular transport. Patterns of adaptive variation indicated a latitudinal gradient tied to winter severity and duration, along with spatially heterogeneous responses to snowfall. Two distinct clusters of adaptive loci were identified; one associated with winter temperature extremeness and duration, and the other with snowfall, suggesting winter climate plays a dominant role in shaping local adaptation. Future climate projections (SSP5-8.5, 2041-2070) predict substantial shifts in adaptive alleles in the Northeastern Appalachians, Maritimes, and St. Lawrence River regions. Nevertheless, overall genetic offset across the range was relatively low, suggesting a degree of genomic resilience potentially supported by Yellow Birch's allohexaploid genome and extensive gene flow. Population-level assessments of standing genetic variation (SGV) and population adaptive indices revealed regional variation in adaptive capacity. Populations in the western Great Lakes region exhibited the highest SGV and the lowest predicted offset, likely reflecting adaptive introgression from historical hybridization with other *Betula* members. These findings highlight the roles of both neutral and adaptive processes in shaping genomic structure and underscore the importance of integrating genomic data into forest management.

Transcriptomic insights into drought stress response and recovery in *Pinus densiflora*

Sun-Cheon Hong (Seoul National University) and Kyu-Suk Kang

Pinus densiflora exhibits stage-specific transcriptional and physiological responses during recovery from prolonged drought. We investigated the molecular basis of this process by integrating time-course RNA sequencing and photosynthetic trait measurements. The seedlings underwent 33 days of drought stress, reaching water potentials below −4.4 MPa. During this period, photosynthetic traits, including Phi2, phiNPQ and Fv′/Fm′, were measured every four days to monitor stress progression. Following rehydration, RNA was extracted from leaf tissue at 0, 1, 23 and 48 hours to capture the initial transcriptional responses. Unlike previous studies that focused on the days following rewatering, our approach captured the dynamics of gene expression within the initial hours of recovery. Genes related to photosynthesis, Photosystem II assembly and chlorophyll biosynthesis were rapidly induced immediately after rehydration. PSII repair-associated genes remained enriched for up to 48 hours, suggesting a gradual, transcriptionally regulated recovery process. Importantly, photosynthetic function also recovered progressively over time, as indicated by physiological measurements. The alignment observed between the recovery of photosynthetic function and the expression of photosynthesis-related genes suggests that transcriptional regulation actively supports and reflects the physiological restoration process. By focusing on the initial rehydration period, this study sheds light on the genetic programmes that initiate drought recovery in pine trees. Our findings highlight early-response markers linked to resilience and provide valuable genetic targets for enhancing recovery capacity in forest tree breeding under climate stress.

Chromosome-scale genome assemblies and analysis of genomic structural variation in Douglas-fir (*Pseudotsuga menziesii*)

Meg E. Smith (University of British Columbia), Richard Cronn, Kailey Baesen, Sean Collins, Athena Allen, Afiya Chida, Marie Sandler, Kaede Hirabayashi, Marco Todesco, Samantha Jones, Jonathan Degner, Trevor Doerksen, Sally Aitken, Sam Yeaman, Jill L. Wegrzyn, Tom R. Booker and Amanda R. de la Torre

High-quality, chromosome-scale reference genomes are a priceless resource in contemporary genetics and genomics research. Producing chromosome-scale assemblies is particularly challenging for species like conifers whose ultra-large, ultra-repetitive genomes are difficult to resolve without long-range sequence information. In the age of high fidelity long-read sequencing, creating high-quality assemblies for these valuable species is now feasible. We present a set of chromosome-scale genome assemblies for the two varieties of Douglas-fir (*Pseudotsuga menziesii var. menziesii* and *Pseudotsuga menziesii var. glauca*). These assemblies represent 15.2Gb-15.5Gb of the estimated ~16Gb genome, of which 67.4%-94.5% is found in the first 13 scaffolds, corresponding to Douglas-fir's n = 13 haploid set of chromosomes. Using whole-genome alignment, we identified approximately 1.4Gb of structural variation between the two pseudo-haplotypes of interior Douglas-fir assemblies and the haploid coastal Douglas-fir assembly, with individual variants up to ~288kb in size, suggesting chromosomal rearrangements may be an important source of intraspecific genetic variation in Douglas-fir. Beyond providing a valuable community resource for future genetic inquiry into the species, this assembly offers an opportunity to explore the role large-scale genomic variation may play in shaping locally adapted traits in Douglas-fir, including economically and ecologically valuable traits such as climate resilience.

Ecogenomics of transcontinental black spruce: identifying key genes related to climate adaptation

Vincent Quevillon (Université Laval), Sébastien Gérardi, Patrick Lenz and Jean Bousquet

Black spruce (*Picea mariana* [Mill.] B.S.P.) is an emblematic and ubiquitous species of Canada's boreal forest, holding important ecological and economic roles. Traditionally, genetic improvement programs have focused much of their efforts on growth productivity. However, with the predicted impact of climate change on North America's boreal zone—translating into more frequent extreme weather events and significantly altered environmental conditions—the study of quantitative and molecular traits related to climate adaptation is becoming increasingly important. In the absence of common garden studies in certain regions of Canada, the assistance of molecular markers could also be useful to identify climate-associated genomic clines. Using GWAS (Genome-Wide Association Study), we aimed to identify genes whose allelic variation is associated with climate variation in black spruce. A total of 254 black spruce trees from 30 populations covering much of the species' Canadian distribution range, were sampled and genotyped for nearly 5000 SNPs located in coding regions, and representing as many distinct gene loci. Univariate and multivariate Genotype-Environment Association (GEA) approaches, RDA and LFMM, as well as an outlier method based on population differentiation (*FST*) were used to identify genes associated to climate. A total of 77 candidate genes were significantly associated to climate factors, among which 14 were corroborated by at least two statistical methods. Functional annotations for most of these genes could be retrieved for their biological roles in model plants or trees, and several of the identified genes were involved in stress responses and/or important hormonal pathways. The present results should help predicting the evolutionary trajectory of black spruce in the face of current climate change and orienting its genetic conservation strategies. Furthermore, once validated with independent population sets, such gene markers could assist the various existing black spruce breeding and assisted migration programs for more climate-resilient reforestation stocks.

Session 3: Genetics of adaptation traits

Moderator: Betty van Kerkhof

Integrated analysis of conifer responses to biotic and abiotic stressors: meta-analysis and gene expression insights

Mina Sadeghiniaraki (Carleton University), Rhiannon Peery and Catherine Cullingham

Forest ecosystems are increasingly threatened by climate-linked stressors and pathogens, necessitating a better understanding of conifer resilience. Integrating meta

-analysis and transcriptomics, this study investigates shared and species-specific defense strategies in conifers, focusing on jack pine (*Pinus banksiana*). A systematic review identified 78 recurrent stress-responsive genes across conifer species, with 52 potentially involved in both biotic and abiotic stress responses. Experimentally assessing these in jack pine via RNA-seq, mature jack pine trees were treated with *Grosmannia clavigera* (Gc), dwarf mistletoe (*Arceuthobium americanum*, Aa), and both (GcAa). Transcriptomic profiling revealed pathogen-dependent responses: Gc infection induced substantial transcriptional changes (~3,000 upregulated genes), whereas mistletoe elicited minimal response. Combined stress largely mirrored the Gc-only profile, identifying Gc fungus as a driver of defense activation. Significant overlap was observed between stress-responsive genes from the meta-analysis and those upregulated and enriched in Gc, validating conserved defense mechanisms across conifers. However, the study revealed species-specific responses; notably, suppression of monoterpene biosynthesis pathways in jack pine during Gc and GcAa treatments. This contrasts with terpenoid induction in pines like lodgepole pine (*Pinus contorta*). As jack pine is not typically exposed to Gc, its defense responses may be less refined than those of co-evolved hosts. The minimal transcriptional changes induced by mistletoe, compared to the strong Gc response, indicate distinct host reactions dependent on the specific biotic stressor. These findings advance our understanding of conifer-pathogen interactions, offering targets for genomic-guided forest management.

Intra-annual wood density variations in boreal conifers: Identifying novel candidate traits to select for enhanced adaptation to climate instability

Edouard Desaulniers (Université Laval), Claire Depardieu, Simon Nadeau, Jean-Philippe Laverdière, Funda Ogut, Martin Perron, Jean Bousquet and Patrick Lenz

This study aimed at investigating the plastic response of black spruce (*Picea mariana* [Mill.] B.S.P.) to climate anomalies based on measurements of wood density heterogeneity obtained from increment cores. We analyzed cores from more than 1029 trees representing 35 controlled crosses that had been planted in two climatically distinct sites in eastern Québec. We developed a novel automated method to quantify intra-annual wood density fluctuations (IADFs), their size and multi-year frequency, and hypothesized that families exhibiting more frequent and pronounced IADFs would demonstrate greater resilience to water stress. Results confirmed a strong correlation between earlywood IADF frequency and drought-related climate indices, suggesting that IADFs are reliable indicators for an adaptive response to moderate water stress. Moreover, our results indicate that these wood density fluctuations may support growth during challenging environmental conditions. Moderate heritability estimates were obtained for IADF traits, suggesting a good potential for their inclusion in breeding programs to enhance resilience to climate fluctuations. Nevertheless, and even if black spruce is recognized among the spruces with highest wood density, frequent IADF formation may involve trade-offs, such as reduced average wood density or increased wood heterogeneity, which could affect significantly wood quality when too severe. Overall, IADFs appear to be promising functional traits for identifying and selecting black spruce genotypes better adapted to future climate instability, and most likely in a similar way for other spruce species.

Session 4: Climate change adaptation

Moderator: Lahcen Benomar

Patterns and drivers of local adaptation across species and space: a provenance trial meta analysis

Abi Brown (University of British Columbia), Greg O'Neill and Tom Booker

Tree breeding programs, genetic improvement, and seed transfer systems depend on a robust understanding of adaptive variation within a species, more important now than ever in the era of rapid climate change. Leveraging provenance trial datasets from 17 tree species, we are looking at patterns of local adaptation across geographic, climatic, and taxonomic space. Broadly, we are looking at the role of environmental heterogeneity in driving the evolution of local adaptation. Are patterns of local adaptation predictable across species? Can patterns of local adaptation be solely attributed to environmental/climatic predictors? Are there local adaptation "hotspots" on the landscape, or are locally adapted populations diffuse across space? Predicting where populations are likely to be highly locally adapted gives us important information about the potential impact of climate change across the landscape. Understanding how the climate landscape drives local adaptation will also inform how we manage adaptive diversity in our forests in responding to future climate challenges.

Black and red spruce F1 hybrids : superior long term vigor but intermediate dendroecological response to climate stress

Edouard Reed-Métayer (Université Laval), Claire Depardieu, Patrick Lenz, Jean Bousquet and Martin Perro

Climate change imposes stresses that trees must adapt to, including more frequent severe weather events due to increased climate variability. Black spruce and red spruce are phylogenetically close species but adapted to different ecological conditions. Additionally, they form a vast natural hybrid zone where their ranges overlap. This makes them an interesting model for studying the effects of hybridization and introgression in the context of climate change, knowing that interspecific gene flow could potentially influence their adaptive capacity in their zone of sympatry. In this study, trees from rigorous controlled crosses, whose parental genetic identities were previously verified with molecular markers, were established in an interspecific progeny test and studied after 20 years. A dendroecological approach, based on the analysis of annual rings from wood cores, revealed significant differences in growth and wood density patterns between the two parental species, as well as between them and their F1 hybrids. Data analysis also showed that black spruce and red spruce exhibited similar responses to stress related to severe weather events. However, these responses varied between earlywood and latewood, indicating divergent adaptations of cambial phenology between the parental species, likely due to differential adaptations to the length of the growing season. F1 hybrids showed hybrid vigor for long-term cumulative growth under the experimental site conditions, but intermediate values for traits related to stress response. These results shall contribute to a better understanding of climate adaptation dynamics in hybrid zones and will inform on the best management of forest genetic resources in the face of upcoming climate challenges.

Identifying Local Environmental Adaption in Jack Pine (*Pinus banksiana*) to inform Predictions of Maladaptation under Future Climate Conditions.

Grace Gardner (Carleton University), Rhiannon Peery and Catherine Cullingham

The government of Canada has committed to planting more than 2 billion trees over the course of a decade to combat climate change. With reforestation being one of our biggest environmental initiatives, it is vital that planting strategies are successful in making forests resilient to future environmental conditions. Understanding the genetic basis of how tree species are adapted to their environments can inform how seedlings may be successful on the landscape. Jack pine (*Pinus banksiana*) is a conifer species widely distributed across Canada, but despite its importance to the Boreal Forest ecosystem, landscape genetic variation remains largely understudied. Implementing genotype data (SNPs) from 669 mature individuals across the species range, and historical environmental data from when these individuals were seedlings, genotype-environmental associations (GEAs) were conducted to identify genetic variation and driving environmental variables important to local adaptation. Using these newly identified genetic markers, we calculated predictions of genomic offset which indicate where jack pine will be potentially maladapted as the environmental variables driving local adaptation are predicted to change under future environmental scenarios. Approximately 30 genetic markers (SNPs) were identified as having significant association with local temperature gradients (Degree Days below 0^{0}C) and projections of genomic offsets using two different socioeconomic environmental scenarios indicate potential risk for maladaptation, particularly in the northern range extent of jack pine.

Unlocking Climate Adaptation Potential: The Role of Interspecific Hybridization in Natural Regeneration of Planted Forests

Rakefet David-Schwartz (Volcani Institute), Naomi Houminer, Yagil Osem, Amir Sherman, Ada Rozen, Hanan Sela and Joseph Riov

Generating genetic variation is crucial for species adaptation to an increasingly dynamic environment, and the establishment of hybrid zones can facilitate this process artificially. High genetic diversity offers significant potential to enhance the sustainability of man-made forests, particularly in regions experiencing degradation due to climate change. However, despite its potential benefits, our understanding of hybridization during the regeneration of man-made forests remains limited. In this study, we provide evidence of hybridization between *Pinus brutia* and *Pinus halepensis* across five distinct forests along a precipitation gradient. We examined hybridization at three key stages of forest regeneration: prior to seed dispersal, during seedling germination, and following prolonged drought conditions affecting seedling recruitment. Hybrid proportions increased from 4.7±2.1% to 8.2±1.4%, and then to 21.6±6.4%, from seeds to emerged seedlings, and from seedlings to recruited seedlings, respectively. These results suggest that hybrids exhibit enhanced traits for germination and survival under drought stress. To investigate the specific traits contributing to this advantage, we conducted common garden and physiological experiments. Our

findings revealed that hybrid seedlings outperformed pure species seedlings by exhibiting a combination of selected growth and physiological traits from both parental species. These traits include superior total biomass, root-to-shoot ratio, juvenile to total needle ratio, reduced transpiration and stomatal conductance rates, and early stomatal closure in response to drought. These results indicate that hybridization confers a fitness advantage, particularly in response to climate change-induced stress. Based on these findings, we advocate for the development of conservation strategies that support the persistence of hybrid populations, thereby fostering the emergence of adaptive genetic traits essential for climate change resilience.

Using landscape genomics to define species distributions, delineate seed zones, and predict maladaptation to future climate for the interior spruce hybrid complex (*Picea glauca, Picea engelmannii*, and their hybrids)

Zhengyang Ye (University of British Columbia) and Tongli Wang

Understanding how tree species adapt to climate is crucial for forest management under climate change. This study employs landscape genomics to investigate climate adaptation in the interior spruce complex (*Picea glauca*, *P. engelmannii*, and their hybrids) across western Canada. Using gradient forest modeling with 41,253 SNPs genotyped in 1692 natural interior spruce individuals from 252 populations, we identified winter temperature and moisture-related variables as key drivers of genomic variation. Both adaptive and neutral genetic variation showed similar patterns along climatic gradients, suggesting that population structure largely follows environmental clines. We delineated 11 seed zones based on genomic variation and climate relationships, achieving 88.2% concordance with previous genetic studies in defining species boundaries. Analysis of genetic offsets under future climate scenarios revealed potential maladaptation risks, particularly in northern and eastern British Columbia. These predictions were validated using fitness-related measurements from common-garden experiments, which showed negative correlations between genetic offsets and traits such as height and DBH. Maladaptation predictions based on genetic offsets showed some differences compared with traditional common-garden-based assessments in several regions, offering new perspectives on population vulnerability. Our results demonstrate the effectiveness of landscape genomics as a complementary approach to traditional methods for assessing climate adaptation in tree species. Our findings provide a scientific foundation for climate-smart reforestation strategies and offer practical guidance for forest management in the context of climate change.

Session 5: Breeding for disease resistance

Moderator: Lu Pengxin

Does resilience to the mountain pine beetle comes at a cost of reduced growth in lodgepole pine?

Mel Lucas (Western University), Lucas Iwamoto, Rhiannon Peery, David Coltman and Janice Cooke

Outbreaks of the mountain pine beetle (*Dendroctonus ponderosae*) have resulted in widespread mortality in the ecologically and commercially important lodgepole pine (*Pinus contorta*). Selective breeding and planting of lodgepole pine resilient to mountain pine beetle attack is one strategy to mitigate future outbreaks. However, selecting for a single trait (i.e., resilience) may have unintended consequences to other traits of interest. Here, we asked whether resilience to the mountain pine beetle comes at a cost of reduced growth in lodgepole pine. We analyzed data collected from the progeny of trees either killed by or surviving mountain pine beetle attack, for a total of 343 trees from 43 half-sibling families. We estimated pairwise relatedness among individuals using 9049 single nucleotide polymorphisms. We estimated the heritability of three components of radial growth (earlywood width, latewood width, and the proportion of latewood to total ring width) for 11 years of growth, as well as two resilience-associated traits (axial resin duct density and maternal survivorship of mountain pine beetle attack), using univariate animal models. To examine potential trade-offs individually, we estimated additive genetic correlations between resilience and each of the three radial growth metrics using bivariate animal models. Finally, we generated a complete additive genetic correlation matrix, and estimated the response to selection using the multivariate breeder's equation. This allowed us to predict the effects of selecting for resilience to the mountain pine beetle on all growth traits simultaneously, informing expectations of potential breeding efforts.

Physiological characterization of white pine blister rust resistant *P. strobus* × *P. wallichiana* hybrids

Lahcen Benomar (Ontario Ministry of Natural Resources) and Pengxin Lu

White pine blister rust (WPBR) disease, caused by an invasive fungal pathogen (*Cronartium ribicola* J.C. Fisch), has long been the primary biotic threat to eastern white pine in Canada. A hybridization program initiated in Ontario, Canada in the 1960s aimed to transfer blister rust resistance from Himalayan blue pine to eastern white pine, resulting in WPBR-resistant interspecific hybrids. Metabolic adjustments related to disease resistance may cause a trade-off with tolerance to abiotic stress (e.g. frost, heat, drought). It is, therefore, crucial to understand how the morphological and physiological traits of hybrid pines change during a multi-generation backcrossing process, as these shifts may affect their growth performance and capacity to adapt to climate change. We assessed changes in photosynthetic-related traits, needle morphology, and xylem cavitation resistance of eastern white pine and Himalayan blue pine, and their hybrids with white pine parentage ranging from 25% to 87.25%. Needle length and specific leaf area (SLA) decreased linearly by increasing eastern white pine parentage; inversely, needle density increased by increasing eastern white pine paren-

tage. However, needle diameter and stomatal density remained unchanged. The changes to needle morphology did not result in variation of light-saturated photosynthesis (Amax), mesophyll conductance (gm), maximum rate of carboxylation (Vcmax), and maximum rate of electron transport (Jmax). Photosynthetic nitrogen use efficiency (PNUE) decreased, while water use efficiency (WUEi) increased with increasing eastern white pine parentage. The trade-off between PNUE and WUEi, which resulted mainly from the change in stomatal conductance (gsw) and SLA, may shape the tolerance of interspecific hybrids to frost and drought. Also, Himalayan blue pine and hybrids were more resistant to xylem cavitation than eastern white pine. Hybrid pines recovered most of their eastern white pine morpho-physiological characteristics after two rounds of backcrossing. Consequently, WPBR-resistant interspecific hybrids should have integrated stress tolerance traits of eastern white pine enabling them to adapt to both abiotic and biotic stresses in Canadian boreal forests.

Stakeholders' Perceptions: Genetically Improved Tree Species for Enhancing Forest Resilience to the Impact of Mountain Pine Beetle

Obed Asamoah (Carleton University), Emma Neale, Vivian Nguyen and Stephan Schott

Forests contribute significantly to the economic and ecological well-being of many countries. Their resilience, especially against pest infestations like the Mountain Pine Beetle (MPB) (*Dendroctonus ponderosae*), has become a great concern in the context of climate change. In Canada, MPB infestations have devastated millions of hectares of pine forests by weakening trees and making them more susceptible to secondary infections. A genetically improved tree species with adaptive and resilient functional traits has been considered a potential tool for enhancing forest resilience and mitigating the impact of MPB. Scientific research has indeed been conducted on their biological effectiveness. However, little attention has been given to local stakeholders' perceptions of such strategies, which are critical to their acceptance and implementation. This study explored the views of key stakeholders, including forest industry professionals, conservationists, and recreational users, on using genetically improved seedlings in forest management to enhance forest resilience. From focus groups and semi-structured interviews, we gathered qualitative data from respondents from three Canadian provinces affected by MPB. Our findings revealed that, stakeholders' perceptions and attitudes towards genetically improved trees vary. This highlights the opportunities, concerns and the need to incorporate stakeholder perceptions into forest genetics in the forest resilience management plan. We recommend that policymakers and forest managers adopt collaborative governance, adaptive management, and inclusive knowledge exchange to align ecological and socioeconomic goals in forest resiliency strategies.

Session 6: Genetic conservation

Moderator: Catherine Cullingham

Conservation planning for forests, tree species, and their genetic populations under climate change in Canada

Nicholas Boyce (University of Alberta), Andreas Hamann and Scott E. Nielsen

Approximately 38% of Canada's 9.98 million km² landmass is covered by forests, totaling around 3.47 million km², with about 11% designated as protected areas. However, conservation areas only imperfectly represent Canada's forest biodiversity, and conservation efforts are managed across 13 provinces and territories, each with distinct priorities. This study provides a national overview of how different Canadian jurisdictions protect forests, tree species, and their genetic populations in the context of climate change.

The analysis utilizes level-4 ecosystem delineations (BC: BEC variants, AB: NSR variants, rest of Canada: ecodistricts), representing the finest level of what may constitute a tree population. We determine population sizes by ecosystem from forest inventory data and scaled using remotely-sensed land and tree cover data. Potential changes to species frequencies are inferred by matching historic ecosystem climates (1960s) with observed (1990s) and projected (2020s, 2050s, 2080s) climate change, using multivariate climatic distance matrices for 12 bioclimatic variables.

Results indicate that representation of forests in protected areas varies widely across jurisdictions. The highest combined diversity of species and ecological zones occurs in British Columbia, followed by Quebec and Ontario. Out of 54 tree species assessed, we identified their least protected populations of with respect to major eco zones (Level 2). Under climate change, the conservation status of western interior and boreal populations is projected to decline most severely, as these populations face the highest required migration distances necessary to track suitable climate conditions.

To support the development of an in-situ gene conservation strategy under climate change, we provide a Protected Area Selection Tool for Canada (currently under development), which identifies existing protected areas as potential assisted migration targets for tree populations that are most vulnerable to climate change or that have otherwise been identified as valuable for in-situ gene conservation efforts.

Genome Architecture shapes Inbreeding depression: Implications for Forest Tree Populations

Chaebin Lee (University of British Columbia), Brian Charlesworth and Tom Booker

Many plant species exhibit substantial inbreeding depression in experimental and natural populations, likely driven by the expression of deleterious recessive mutations. This phenomenon is especially pronounced in conifers, raising concerns for both tree breeding and conservation programs. Despite the ecological and economic importance of conifers, the fine-scale structure of their recombination landscapes remains poorly understood. Available data suggest that large portions of conifer genomes may exhibit extremely low recombination rates. This raises important questions about how recombination rate variation may influence the accumulation and expression of deleterious mutations, and shape genetic load and inbreeding outcomes. Here, I use population genetic models to examine how genome architecture —specifically recombination landscape and the distribution of fitness effects (DFE)— affects inbreeding depression in plant genomes. Parameterized with empirical estimates from plant systems, the models show that populations with distal-biased recombination landscapes experience greater inbreeding depression compared to those with uniform recombination rate along the genome, particularly when the DFE includes a high proportion of mildly deleterious mutations. In these cases, deleterious alleles may be maintained in heterozygous form within low-recombination regions through associative overdominance (AOD), potentially contributing to elevated heterozygosity in these regions. Notably, this elevated heterozygosity may not be a reliable indicator of adaptive potential, as it arises from the masking of deleterious variation rather than from increased genetic robustness. Given that conifer species likely have especially extensive non-recombining genomic regions, this mechanism may offer a potential explanation for the particularly strong inbreeding depression observed in many conifers. The findings provide both conceptual and practical insights for conservation genetics and forest tree breeding, informing strategies to mitigate inbreeding risks in small and endangered populations and to enhance the long-term sustainability of breeding and conservation strategies under climate change.

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25 years and Counting: The Elm Recovery Project at The Arboretum, University of Guelph

Aron Fazekas (University of Guelph), Sean Fox, Justine Richardson and Alison Morrison

The American elm (*Ulmus americana*) was once a keystone species in eastern North American forests and urban landscapes, prized for its towering form and resilience in diverse conditions. The arrival of Dutch Elm Disease (DED) in the 20th century, decimated our native elm populations, reshaping Ontario's natural ecosystems and urban environments. In the aftermath, surviving trees still dotted the landscape, but typically at a scale that would prevent cross-pollination. The Elm Recovery Project at The Arboretum, was launched in the late 1990s with the goal of conserving and restoring this iconic species. The project began by locating and collecting cuttings from surviving mature elms across Ontario that appeared to exhibit natural tolerance to DED. These individuals were clonally propagated and evaluated in controlled field trial programs. Today, the Arboretum maintains a genetically diverse collection of disease-tolerant elms, contributing both to conservation research and to practical restoration plantings. Ongoing work includes long-term monitoring of survival, health, and reproductive success, as well as public education and outreach. Future directions include expanding genetic trials, deepening collaborations on disease resistance genomics, and supporting municipalities, landowners, and conservation agencies in reintroducing elms to the landscape. This project serves as a hopeful model for native tree recovery in the face of invasive threats and climate uncertainty.

Building the knowledge and research capacity to preserve butternut for future generations

Martin Williams (Natural Resources Canada), Berni van der Meer, Chantelle Kostanowicz, Manuel Lamothe, Aziz Ebrahimi, Anna Conrad, Samantha Cohen, Taylor Swanburg, James Warren, Carrie Pike, Douglass Jacobs and Nathalie Isabel

Butternut, *Juglans cinerea*, is a North American hardwood species that is endangered in Canada under the Species at Risk Act 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 minimal evidence of Oc-j resistance within butternut, introgression with the introduced ornamental Japanese walnut, *Juglans ailantifolia*, is being explored. In contact zones, both species hybridize and introgress naturally, and seem to produce varying degrees of resistant progeny. Efforts are now on-going to develop strategies to protect butternut from extinction and the technologies to support them, from seed storage to high precision hybrid phenotyping. We will provide an update on our on-going contributions to research capacity and knowledge regarding this pathosystem. Specifically, we will report on the level of hybrids and introgressants within living collections in North America, which is key for the characterisation of hybrid status and to determine if any resistance is present in non-admixed butternuts. We will also discuss some preliminary phylogenetics and phenotypic data resulting from landscape-level Oc-j work. This work will be important in evaluating if current levels of resistance are enough to protect the trees. Finally, we will discuss the urgency of these efforts by providing an update on the decline of butternut in New Brunswick, one of the last regions impacted by the pathogen in North America.

Session 7: Assisted population migration

Moderator: Aron Fazekas

A Seed Selection Tool to Support Climate-Informed Reforestation in Canada

Genevieve Dorrell (University of Alberta), Nicholas Boyce, Zach Zimmerman and Andreas Hamann

Climate change adaption in forestry will need climate-informed seed transfer strategies to improve resilience, preserve genetic diversity and ensure long-term productivity, especially in northern Canada. Therefore, we developed an on-line decision support tool to help researchers and forest managers make climate-informed selections of tree species and seeds sources for reforestation. These recommendations include cross-border transfers and can also include introducing new species, but most reforestation needs can be met by matching planting sites with climate adapted seed sources from within the species' range.

For the climate informed seed sourcing recommendations, we used the 1960s (1951–1980) historic climate as a proxy for the seed source's adapted climate. We then calculated the multivariate Euclidean climatic distance of 12 bioclimatic variables of the seed source's historic 1960s climate to the target planting site's projected future climates (2020s, 2050s and 2080s) and used the climatically closest historic climates as the geographic seed source recommendations at the ecosystem level and when possible, at the seed zone level. To aid in species selection, we created tables of species' expected prevalence under the planting site's projected future climates, using species distribution models based on forest inventory data.

Based on this analysis, we created a web tool to support species and seed source selection for forest management areas of participating forest companies and government stakeholders across Canada (http://tinyurl.com/DIVERSE-SST), as well as a beta-version that supports assisted migration across the North American continent (http://tinyurl.com/NA-SST). The presentation will demonstrate the tool's applications in Canadian forest management and discuss planned improvements, including enhanced uncertainty quantification, integration of more provincial seed zones, and the consideration of orchard seed sources to support interprovincial and international seed transfer strategies.

Assessing black spruce breeding zones and seed deployment in northwest Ontario

Yuhui Weng (Stephen F. Austin State University), Paul Charrette and Pengxin Lu

Tree improvement and the deployment of genetically improved seed have been implemented by breeding zones (BZs) for black spruce in northwestern Ontario, Canada. Climate change may, however, make it rational to expand both superior tree selection and orchard seed deployment across current BZ boundaries. In this study, we assessed these feasibilities based on performances of open-pollinated families in progeny tests established in four BZs in Northwestern Ontario. In these tests, families from outside BZs were tested alongside with families from within BZs. Results showed that trees in progeny tests generally grew faster in more southerly BZs with higher overall survival rate than in northerly BZs. Within a BZ, families from southern BZs tended to have faster height growth, but with lower survival rates of unknown causes. On the other side, families from northern BZs had slower height growth in southern BZs and comparable survival. These growth patterns seemed to be consistent with results of black spruce provenance studies and suggests that deployment of improved seeds from adjacent southern BZ may be beneficial provided that causes of tree mortality are not attributable to climatic maladaptation. Across the BZs, it was shown that genetic quality of breeding populations for the next generation can be improved by 4.58%, on average, in tree height at mid-rotation ages if the top 100 trees per BZ were selected from the top 50 within-zone families in the progeny tests. In comparison, allowing selection to include the tested families from southerly BZs would lead to an average improvement of 4.95%. The implications for black spruce operational tree improvement programs are discussed.

Variation in performance of oak species and provenances at assisted migration trials in southern Ontario

John Pedlar (Natural Resources Canada), Dan McKenney, Benjamin Marquis, Kristin Sandvall, Heather Zurbrigg and Kerry McLaven

Assisted migration is an innovative method that has significant potential for adapting forests to novel climate conditions. Here we report on the growth and survival of oak species and seed sources at five assisted migration trials in southern Ontario. Each trial featured one or more oak species – including red oak (*Quercus rubra*), white oak (*Q. alba*), burr oak (*Q. macrocarpa*), and swamp white oak (*Q. bicolor*) – and seed sources from Ontario, Pennsylvania, and/or Tennessee. The trials were measured for survival and height at between 7 and 13 years after planting. For several trials and species, southern seed sources performed as well as local sources. However, southern seed sources of burr oak performed significantly worse than local sources at 2 trials in eastern Ontario. These outcomes may have been influenced by reduced quality of southern seed source planting stock at these trials. We further present novel dendroecology results for white oak from one of the trials near London, Ontario. This aspect of the work allowed us to examine detailed growth responses by each provenance to extreme weather events, such as droughts and late frosts. Early findings suggest generally similar growth patterns across provenances, with evidence of variation in growth response following an extreme drought event in 2021. Overall, our findings support previous work that suggests northward movements of seed sources of several hundred kilometers may be safe for assisted migration efforts involving (at least these) broadleaf tree species. Furthermore, the trial sites were located at the northern range limits for several oak species in this study (*Q. alba* and *Q. bicolor*), suggesting the potential for modest range expansions in this boreal-temperate transition zone. These findings help forest managers to better understand potential assisted migration outcomes under climate change.

Seed Transfer in Ontario

Betty van Kerkhof (Independent) and Ngaire Roubal

Canada's changing climate is increasing the risk that tree populations may become maladapted to the climate at their current growing locations. In response, Ontario updated its tree seed transfer policy in 2020 to reflect the evolving natural, operational, scientific, and policy environments, including a changing climate. This policy renewal was made possible through strong cooperation among federal and provincial science, operations, and policy teams. Key components of the update included a custom climate similarity analysis, identification of critical seed transfer distances, extensive engagement to assess end-user receptivity, and the development of an online interactive tool to allow users to explore seed transfer options under climate change. This presentation will highlight several factors considered during the policy update, key decisions and provide information about its usage. Our aim is to promote national awareness of seed transfer efforts in Ontario, share findings from our 2022 publication to support other jurisdictions and emphasize the need for cultural shifts in seed sourcing and management.

The First Reference Genome of *Betula lenta* Enables Comparative Genomic Analysis Across the Birch Genus

Yuanxin Ye (Lakehead University), Christian Leblanc and Ashley Thomson

Betula lenta (sweet birch or cherry birch) is an early-diverging North American species in the *Betula* genus with distinct ecological and biochemical traits. Despite its importance, genomic resources for this species have been lacking, limiting comparative and evolutionary studies across the genus.

Here, we present the first reference genome of *B. lenta*, assembled using 10X Genomics linked-read sequencing (455.8 Mb; scaffold N50 = 2.99 Mb). A total of 21,369 protein-coding genes were predicted using a combination of transcriptome, homology-based, and ab initio annotation methods, with a BUSCO completeness score of 94.1% (embryophyta_odb10). Comparative analysis revealed notable differences in gene content and organization between *B. lenta* and other *Betula* species, including gene family expansions related to secondary metabolism.

As a case study, we examined gene families involved in methyl salicylate (MeSA) metabolism—a compound found in high abundance in *B. lenta* bark. We identified expansions in SABATH methyltransferase and MES methylesterase gene families compared to *B. pendula*, suggesting potential lineage-specific diversification.

This high-quality reference genome provides a valuable resource for future ecological, evolutionary, and functional genomics research in *Betula*, and enhances our understanding of trait diversity across the genus.

Using Genomics to Estimate Jack Pine Resiliency to Mountain Pine Beetle in the Boreal Forest

Bianca Tassi (Carleton University), Rhiannon Peery and Catherine Cullingham

Jack pine serves as a cornerstone tree species in the Boreal Forest and is a newly discovered host for the mountain pine beetle. Climate change and human management in the forest may allow for continued eastern expansion of mountain pine beetle through the range of jack pine. This leads to additional questions on the suitability of jack pine as a host for mountain pine beetle across jack pine habitats in Canada. Our study investigated the genetic and spatial diversity of 198 SNP loci in jack pine, that have been identified in previous research as being associated with resilience to mountain pine beetle in lodgepole pine. A multi-locus, per individual, polygenic risk score (PRS) that estimates an individual's genetic susceptibility to a trait was calculated for jack pine, lodgepole pine, and hybrid trees using these 198 SNP loci. This was followed by spatial mapping of these scores on the Canadian landscape, and statistical analysis comparing the lodgepole and jack pine scores. The resulting map of interpolated risk scores was able to highlight various areas of vulnerability to mountain pine beetle attack. Resilience was found to be higher in jack pine on average, with lodgepole pine having a larger spread in PRS values. Areas of higher resiliency and susceptibility were estimated across jack pine sites with lower resiliency in Alberta and

Ontario. When planning conservation and management strategies, spatial patterning of loci associated with resilience can be invaluable in pinpointing vulnerable regions susceptible to the harmful impacts of mountain pine beetle infestations. This study demonstrates that PRS analysis can help identify at-risk jack pine stands to mitigate the potential spread of mountain pine beetle across the Boreal Forest.

GenARCC Overview

Patrick Lenz (Natural Resources Canada)

Globally, climate change continues to result in severe environmental disturbances with recent years being the warmest on record during the industrialized period. Within Canada, the climate continues to warm at more than double the global rate, with northern Canada expected to experience the most extreme changes. There is a growing need for science advice on the adaptation of key species to climate change, and related economic and societal implications. Genomics offers a very powerful set of tools that have the ability to rapidly assess biodiversity and ecosystem health, and to help predict how species and ecosystems will respond to climate change. In April 2022 the Government of Canada Genomics Research and Development Initiative launched 'GenARCC' (Genomic Adaptation and Resilience to Climate Change). Through the use of genomic tools, GenARCC aims to inform climate change adaptation for the protection of Canada's biodiversity, ecosystem resiliency, food security, and health. The GenARCC team is using their expertise to quantify genetic diversity, monitor ongoing spatial and temporal climate associated change, and predict future vulnerability of species and populations to climate change across forest and tundra, agricultural, aquatic and coastal ecosystems. This broad and collaborative approach is designed to inform policy and regulatory decision-making, as well as climate mitigation strategies relevant to a wide range of end-users.

Advancing black spruce (*Picea mariana*) breeding through genomic selection: a comparative analysis of models using pedigree and genomic marker information

Jesse Milani (Lakehead University), Ashley Thomson and Patrick Lenz

The integration of genomic selection (GS) into forest tree breeding holds promise for accelerating genetic gains in long-lived species like black spruce (*Picea mariana*). This study evaluates the performance of genomic prediction models in estimating breeding values for key growth traits in a black spruce progeny trial established in the Lake Nipigon West (LNW) breeding zone, Ontario. Utilizing phenotypic data from 400 open-pollinated families measured at ages 5 and 10, and genotypic data from 672 individuals across 70 families, we compared traditional pedigree-based (ABLUP), genomic-based (GBLUP), and hybrid (HBLUP) best linear unbiased prediction models. Two genotyping platforms—RADseq (10,626 SNPs) and SNP chip arrays (16,217 SNPs)—were employed and merged to construct robust genomic relationship matrices. Results demonstrated that HBLUP provided the most accurate heritability estimates, particularly for growth rate and stem volume, while early height traits exhibited low heritability across all models, likely due to environmental influence. Both GBLUP and HBLUP outperformed ABLUP in predictive ability and genetic gain, with the highest annual gains observed under genomic models. Our findings underscore the efficacy of integrating genomic information into operational breeding programs to enhance selection accuracy and shorten breeding cycles. We advocate for the continued development of GS in conifers through high-density genotyping and incorporation of ecological covariates. This research contributes to a growing body of evidence supporting GS as a transformative tool for improving the genetic quality and adaptive potential of black spruce under changing environmental conditions.

Breeding for genetic resistance to blister rust in eastern white pine

Pengxin Lu (Ontario Ministry of Natural Resources), Darren Derbowka and Lahcen Benomar

White pine blister (caused by *Cronartium ribicola* J.C. Fisch.) continues to be a top threat to the regeneration of eastern white pine (*Pinus strobus* L.) in Ontario, especially at more northerly sites. Breeding for genetic resistance to the exotic pathogen has been undertaken in Ontario since the 1940s. A breeding strategy of interspecific hybridization followed by backcrossing was consequently adopted after limited progress from breeding within *P. strobus*, possibly due to lack of meaningful resistance alleles. Ontario's breeding objectives included developing white pine genotypes that can withstand heavy blister rust challenge while maintaining morphological, physiological and growth characteristics of *P. strobus*, with an exotic genomic composition less than 6.25% by pedigree.

Among many interspecific hybrid crosses created between *P. strobus* and other five-needle pine species, those with *Pinus wallichiana* A.B Jacks showed promises in surviving heavy blister rust infection in artificial disease inoculation experiments and good growth and adaptation in field research trials established across Ontario. After several rounds of backcrossing and selection, Ontario is now close to reaching its breeding objectives with the third-generation backcrosses. The ability to retain strong disease resistance in multi-generation backcrossing may suggest that genetic resistance conferred by *P. wallichiana* is major-gene resistance which can be further studied using genomic approaches and genetic markers developed can be used to guide future mating designs. Whereas progressive improvement on morphological, anatomic, physiological and growth traits along with the backcrossing may suggest codominance on these traits by the species. Somatic embryogenesis, which is successfully well developed for *P. strobus*, provides an effective and powerful tool to realize genetic gains by propagating elite genotypes vegetatively to retain excellent tree form, disease resistance, wood quality and growth rate.

Best Future Forests: Genomic-Driven Tree Improvement in Alberta

Katherine Eaton (University of Alberta), Charles Chen, Lee Woodham and Barb Thomas

Tree Improvement in Alberta is operationally complex, with more than 20 breeding programs independently managed by government, private industry, and cooperatives. There is an urgent need for a centralized data-sharing system, to support collaborative, evidence-based decision-making. In addition, there is growing interest in incorporating new predictive frameworks, such as climate-based seed transfer (CBST) and genomic selection (GS), in order to shorten breeding cycles, optimize gain across multiple objectives, and improve selection accuracy. To fully harness the genomic potential of

Alberta's key economic forest species (lodgepole pine and white spruce) a new approach to information management is essential in the face of increasing climatic uncertainty.

To address the evolving needs of Alberta's forestry sector, the Best Future Forests initiative was created in 2024 between the University of Alberta, the Government of Alberta, Tree Improvement Alberta, and Oklahoma State University. A key objective of this initiative is the development of a centralized resource management system, consisting of a relational database, high-performance algorithms, and a dedicated computing cluster. Best Future Forests aims to transform Alberta's forestry sector by streamlining data submission, curation, and computation, with a novel focus on leveraging high-through genotyping and predictive analytics. Computational workflows include pedigree error correction, genomic estimated breeding values (GEBV), genotype-environment interactions (GxE), and the incorporation of genetic gain into growth and yield models. The system promotes transparency and reproducibility by prioritizing open-source tools for both information management (PostgreSQL) and analytics (R, Python).

As a response to the critical need for sustainable forestry practices in the face of climate change, and to position Canada's leadership at the forefront, Best Future Forests will provide stakeholders with a transformative, convergent solution to explore genomic adaptation scenarios, next-generation seed orchard design, as well strategic planting and harvesting based on genetic gain and future growth potential.

Assessing the Genetic Variation of Resilience to Climate Anomalies in Red Spruce

Juliette Bourgeois (Université Laval), Claire Depardieu, Simon Nadeau, Sébastien Gérardi, Simon Bockstette, Patrick Lenz and Jean Bousquet

Red spruce (*Picea rubens Sarg.*) is a conifer native to the temperate forests of eastern North America, whose populations have significantly decreased since the 1960s. This decline is likely due to the combined effects of climate warming, air pollution, and logging practices. The species' reported sensitivity to harsh climatic conditions raises questions about its adaptive capacity in the face of ongoing rapid environmental change. This research project aims to assess the resilience of red spruce to current climatic conditions by analyzing its physiological responses to extreme weather events (e.g., drought, early or late frost), and by estimating the intraspecific genetic variability influencing these responses, including the degree of introgression with black spruce. To achieve this, approximately 1,700 red spruce trees were cored and genotyped for many thousands of SNP markers from the exome. These trees belong to a first generation polycross trial series that was established about 30 years ago across 16 common garden sites in Nova Scotia. The dendrochronological data analysis conducted as part of this study will allow for the correlation of annual growth ring characteristics with site-specific severe weather events. Genetic parameters, such as heritability, will be estimated for novel phenotypes linked to resilience under climate anomalies. By providing new insights into genetic diversity and mechanisms underlying resilience and adaptation, this research will contribute to the development of sustainable management strategies for red spruce forests and tree breeding programs in the context of climate change.

Assisted gene flow expected to have limited effect on lumber quality in eastern Canadian white spruce

Isabelle Duchesne (Natural Resources Canada), Patrick Lenz, Martin Girardin and Nathalie Isabel

White spruce (*Picea glauca* [Moench] Voss) is among the most productive tree species in eastern Canada and is extensively reforested across the entire country. It is thus a candidate for assisted gene flow in response to expected climate gradients to mitigate the impacts of environmental change on forest growth. Genetic improvement programs for this species have been established in most provinces, with the goal of enhancing the growth and adaptive traits of reforested seedlings. However, despite the economic importance of white spruce for the wood-processing industry, wood traits have rarely been considered in genetic studies, and studies on the quality of lumber at rotation age are nearly absent. In this study, we evaluated the effect of provenance origin on lumber production and quality at rotation age in two white spruce provenance trials established in contrasting environments in eastern Canada. Based on more than 100 felled trees, which resulted in close to 1000 pieces of lumber, we found that volume production on the southernmost site was almost twice as much as on the northern site. Provenance had a significant influence on growth but had no effect on lumber stiffness and wood density, which are crucial characteristics for the structural use of wood. Only a small provenance effect was recorded for lumber strength in the first bole. Altogether, management strategies aiming to efficiently sequester carbon should primarily maximize volume productivity at northern sites, as moving seed sources north still reduces provenance productivity. Given the important genetic control of wood quality traits, breeding programs should exploit the high within-provenance variation to prevent decreases in lumber stiffness due to augmented productivity and shortened rotation cycles.

Optimizing marker coverage for genomic prediction accuracy and estimation of genetic parameters

André Soro (Université Laval), Jean-Philippe Laverdière, France Gagnon, Simon Nadeau, Martin Perron, Funda Ogut, Jean Beaulieu, Patrick Lenz and Jean Bousquet

Genomic selection (GS) is increasingly used in forest tree breeding, offering the potential to accelerate genetic gain by enabling higher selection intensities through large-scale screening of young candidate trees and leveraging multi-trait selection including for complex traits. GS also reduces the need for extensive long-term field-testing and speeds up selection cycles, providing additional flexibility to tree breeding programs in the context of rapid climate change. However, the still relatively high cost of genotyping large numbers of individuals for up to tens of thousands of genome-wide molecular markers remains an important financial challenge for conventional tree breeding programs, while the actual need for very high-density SNP genotyping arrays remains an understudied topic in typical conifer breeding programs. We conducted a study on three widely planted spruce species in the northern hemisphere, Norway spruce (*Picea abies*), white spruce (*Picea glauca*), and black spruce (*Picea mariana*) to determine the optimal marker coverage required to maximize the accuracy of genomic prediction models and the precision of genetic parameters considering several growth and wood quality traits of contrasted heritability.

Our results show that heritability estimates increase with the number of markers, reaching a plateau for approximately 6,000 to 8,000 well distributed SNPs on the genome. This pattern was consistent across the three species. Similarly, the predictive ability of GS models improved with marker coverage up to this threshold, with only marginal gains in accuracy beyond it.

This study identified optimal marker coverages for genomic selection of various traits in spruces, aiming for a balance between maximized prediction efficiency and minimized genotyping effort. These findings support the operational implementation of GS in tree breeding programs targeting multiple traits, especially in the context of rapidly changing environmental conditions.

From common gardens to genes, to microbiomes. What's driving local climate adaptation in black spruce?

Anna Fijarczyk (Natural Resources Canada), Etienne Robert, Benjamin Marquis, Patrick Gagné, Manuel Lamothe, Patrick Lenz, Martin Girardin, Christine Martineau and Nathalie Isabel

Black spruce (*Pinus mariana* [Mill.] B.S.P.) is a tree species of great economic importance and a major component of boreal forest in Canada. Black spruce is widespread throughout the country and originated from multiple distant glacial refugia, two factors facilitating the heterogeneous distribution of genetic diversity and local adaptation. We aim to integrate genomics, phenotype modeling, and microbiome associations to understand the local adaptation of black spruce to the environment and predict its fitness and productivity to future climate. Here we leverage genomics, phenomics, and microbiome sequencing in 40 years-long common garden experiments to study i) genetic variation underlying local adaptation to climate, ii) the utility of locally adapted variants and common garden phenotypes to predict the black spruce fitness to future climate conditions, and iii) associations between the trees and beneficial and pathogenic microbes in the climate gradient. With up to 1500 trees in 68 populations and around 30,000 single nucleotide polymorphisms, we found genetic structure largely corresponding to three glacial refugia with extensive gene flow between them. Genetic clusters also differed in climate, with climate moisture index, frost probability, and photoperiod being the strongest determinants of allele distribution. Variants associated with environmental factors predicted higher genetic offset (higher genomic vulnerability) to future climate for populations from the Central-East part of the black spruce distribution. Microbiome analyses also allowed us to identify key beneficial and pathogenic microbes associated with black spruce. Comparison of phenotypic and genetic models and inclusion of additional relevant phenotypes such as resistance to drought events will allow us to identify populations with high and low vulnerability to environmental change.

Improving Early Detection of Oak Wilt with Quantitative PCR

Cailyn Carscadden (Ontario Ministry of Natural Resources), Sharon Reed and Sandy Smith

Oak wilt, an invasive species currently in the United States, was detected in Ontario in Niagara Falls and Springwater in the spring of 2023. Oak wilt is a fungal disease that attacks the vascular system of oak trees, capable of killing red oak trees in as little as two weeks in severe cases. Developing early detection methods is key to identifying new oak wilt locations and identifying areas where it is likely to spread next. This project proposes use of the recently developed TaqMan qPCR assay with sap beetle collections from the lower peninsula of Michigan and southern Ontario to identify high risk areas of oak wilt spread through space, the variation in oak wilt spread through time, and the detection rates of oak wilt on specific vectors. Analysis of these data will quantify spore loads from insect collections with Lindgren funnel traps to improve surveyors ability to interpret results of eDNA surveys.

Standing genetic variation shapes the adaptive and carbon sequestration potential of a widespread boreal conifer in a warming climate

Etienne Robert (Natural Resources Canada), Patrick Lenz, Yves Bergeron, Guillaume de Lafontaine, Olivier Bouriaud, Nathalie Isabel and Martin Girardin

Black spruce is a keystone species of the north American boreal forest and is a candidate for assisted gene flow as a way to maintain the health and carbon sequestration potential of boreal forests under climate change. The species is shaped by significant standing genetic variation, including an important phylogeographic structure, which is composed of three main lineages inherited from recolonization after the last glaciation. Local adaptation and standing genetic variation (along with phenotypic plasticity) are interconnected and may play a role in the adaptive potential of the species to future climate. In this study, we explored the influence of standing genetic variation on black spruce adaptation to climate and on growth projections under climate change. To do so we assembled dendroecological and genomic data of trees from more than 60 populations growing in four 40-year-old common gardens. Using a random forest algorithm, we modelled aboveground biomass as a function of climate while accounting for local adaptation and the phylogeographic structure of the species. We then projected the biomass accumulated after 40 years of growth under two climate change scenarios (SSP2-4.5 and SSP5-8 .5) and at two time-horizons (2060 and 2100) at the population scale. We found that high summer and autumn temperatures negatively impact black spruce growth. Additionally, projections revealed a decline in biomass production by the end of the century as a result of warming, suggesting a maladaptation of the species to future climate and a decrease of its carbon sequestration potential. The growth response to climate change was heterogeneous among populations with notable differences between lineages as the western lineage was more impacted than central and eastern lineages. This demonstrates the importance of considering standing genetic variation, notably associated with the phylogeographic structure, when projecting species' response to climate change.

Exploring the genetic diversity of Moroccan wild rose and their contribution to improving climate change resilience of *Rosa damascena*

Karim Saghir (National Institute of Agricultural Research), Younes Abbas, Fatima Gaboun, Nezha Lebkiri, Driss Iraqi, Abdelhakim Taha, Mohamed Fokar, Rabha Abdelwahd and Ghizlane Diria

Rosa genus is among the most extensive plant genera, with more than 200 terrestrial species and over 18,000 hybrid cultivars. Research has shown this genus is predominantly found in temperate and subtropical zones of the Northern Hemisphere in Europe, Asia, Middle East, North America and North Africa. In Morocco, fifteen species of wild roses, predominantly found in the northern half of the country, particularly in the Atlas and the Rif Mountains.

With the climate changes the world has witnessed in recent decades, many crops have seen a gradual decline in productivity, which negatively impacts countries' economies. Morocco is one of the world's leading cultivators and producers of Damask roses, alongside Turkey, Iran, Bulgaria, France, and China. However, the lack of rainfall in recent years has adversely affected yields and, consequently, the region's economy. To address this issue, we must turn to wild roses, as they are better adapted to climate changes. Thus, the objectives of this study are: i) To study wild roses in order to preserve them as a natural heritage, and thus preserving forest biodiversity, ii) To select species with high genetic and morphological diversity, as well as strong antioxidant properties, and guide their use in a breeding program with Damask roses.

This study described the genetic diversity of Moroccan wild rose, revealing significant variation within this genus. Eleven distinct species were identified, highlighting the rich biodiversity of Moroccan rose populations in forest ecosystems. The antioxidant properties of rose fruits were also analyzed, demonstrating their potential ecological and therapeutic value. These results provide insights into the genetic composition, species distribution, and functional characteristics of Moroccan wild roses, contributing to conservation and sustainable use strategies and establishing a breeding program with *Rosa damascena* to produce more productive hybrids that are resistant to climate change.

Left to right: Veronica Pacholczak, Ayla Chin, Nicholas Boyce, Genevieve Dorrell, Yuanxin Ye and Bianca Tassi (missing Grace Gardner)

Travel Awards

Funding for these students to attend the conference was provided by Forest Genetics 2025 sponsors, whose generous donations helped to support students with an interest in forest genetics. This year, funding recipients were selected based on a review of proposals submitted by eligible students from across Canada. The award covered conference registration fees (including field trips and the social dinner), round-trip economy transportation, double-occupancy accommodation, and meal costs not included in the conference program.

Student	University
Ayla Chin	University of Alberta
Veronica Pacholczak	Lakehead University

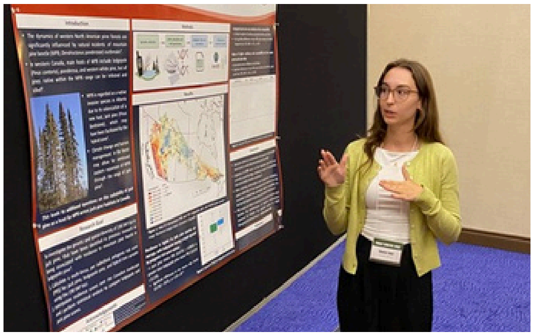
Poster and Presentation Awards

Award	Prize	Winner	University
Carl Heimburger Award for Best Oral Presentation First Place	$1,000 CAD	Grace Gardner	Carleton University Ottawa, Canada
Carl Heimburger Award for Best Oral Presentation Second Place	$250 CAD each	Genevieve Dorrell & Nicholas Boyce	University of Alberta Edmonton, Canada
Gene Namkoong Award for Best Poster	$500 CAD	Yuanxin Ye	Lakehead University Thunder Bay, Canada
People's Choice Award for Best Poster	$200 CAD	Bianca Tassi	Carleton University Ottawa, Canada

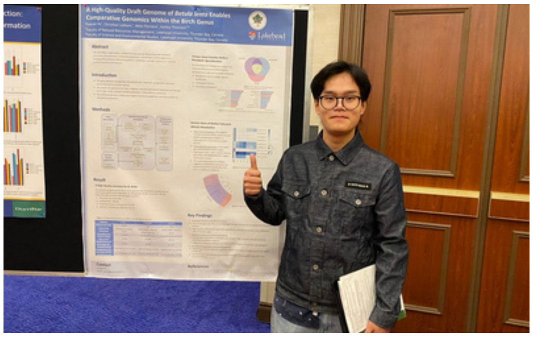
Grace Gardner

Genevieve Dorrell

Nicholas Boyce



Bianca Tassi



Yuanxin Ye

Thursday, August 14, 2025
Petawawa Research Forest

Natural Resources Canada's Petawawa Research Forest (PRF) was established in 1918 and is home to over 2,000 forest research experiments and studies. The forest is located near Chalk River, Ontario, and covers approximately 10,000 hectares of land within Canada's Great Lakes–St. Lawrence Forest region. The mission of the PRF is to enhance sustainable forest management in Canada through innovative forest research by providing a safe, secure, sustainably managed forest; accessible historic and leading-edge research data; and on-the-ground knowledge transfer experiences.

As part of Forest Genetics 2025, attendees spent a beautiful, sunny day at PRF to learn more about Canadian Forest Service provenance trials and adaptive silviculture work.

White Pine Provenance Trial, PRF Experiment 25-D

Presented by: Jeff Fera, Steve D'Eon and Dan McKenney

Attendees were welcomed with a history of the Petawawa Research Forest, proceeding to a white pine provenance trial, established in 1942. The trial includes 43 seed lots from the eastern United States and eastern Canada.

The trial raised many questions and discussions about activities moving forward.

Adaptive Silviculture for Climate Change Research Project

Presented by: Jeff Fera

The Adaptive Silviculture for Climate Change (ASCC) operational research study was the first established in Canada and focuses on "climate change ready" forest management prescriptions for the pine forests in the Great Lakes – St. Lawrence Forest region.

These treatments will help forest managers for decades to come.

White Spruce Provenance Trials and Red Spruce Progeny Trials

Presented by: Steve D'Eon, Funda Ogut and Patrick Lenz

The group visited two white spruce provenance trials established in 1963 and 1965, using provenances from the Great Lakes – St. Lawrence Forest region.

Adjacent to that, a newly established red spruce full sibling progeny trial was visited, containing 39 families from Nova Scotia.

Researchers are revisiting legacy provenance trials with new research questions, showing how valuable these trials are decades later.

Friday, August 15, 2025
Ferguson Tree Nursery

Ferguson Tree Nursery grows high-quality, ecologically suitable trees, shrubs and perennials from known seed sources, including native and non-invasive naturalized plants hardy for south-central and eastern Ontario as well as southwestern Quebec. The plants are used by foresters, landscapers, landowners, nurseries and conservation-minded individuals who want the most appropriate plants with the highest quality and potential of success. Ferguson Tree Nursery is a social enterprise utilizing profits to:

- promote awareness of, and interest in, forestry (e.g., afforestation and sustainable forest management)
- maintain, enhance and promote the responsible use and stewardship of the recreation and conservation lands managed by the Ferguson Forest Centre

This optional half-day field tour saw 25 attendees and included a sunny and informative walk around several Ministry of Natural Resources (MNR) and Forest Gene Conservation Association (FGCA) initiatives on the property.

Ministry of Natural Resources Hybrid Pw Trial

Presented by: Lahcen Benomar and Pengxin Lu

The genetic resistance program for white pine blister rust (WPBR) was initiated in Ontario in the 1950s by Dr. Carl C. Heimburger and aimed to transfer major gene resistance from Himalayan blue pine to eastern white pine. This field trial was established in 2006 to compare the growth performance of 45 WPBR-resistant hybrid pine families (*Pinus strobus* × *Pinus wallichiana*) with varying levels of eastern white pine parentage, ranging from F1, F2, BC1, BC2.

Ministry of Natural Resources Realized Gain Trial

Presented by: Lahcen Benomar and Pengxin Lu

Ontario's eastern white pine tree improvement program began in the 1980s with clonal seed orchards that are now managed by the FGCA, MNR, SFLs and partners for seed production.

Realized genetic gain trials for first-generation orchards were established to mitigate information loss. This trial was planted in 2008 with 3,456 seedlings from 9 seed sources, including 5 seed orchards.

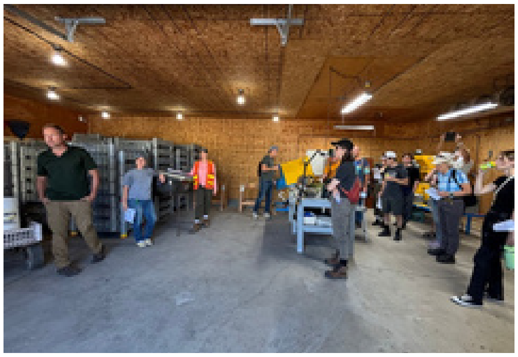
Forest Gene Conservation Association Butternut Seed Orchard

Presented by: Heather Zurbrigg and Briana Heuving

FGCA shared an overview of the FGCA butternut archiving program, which has been been archiving the genetics of healthy butternut trees that are showing signs of tolerance to the butternut canker since 2008. Participants toured FGCA's oldest butternut orchard, one of six in the program, that have representative grafts of over 200 parent butternut trees.

Tour of Ferguson Tree Nursery Seed Facility

Presented by: Maureen Jacques and Chris MacDonald



Ferguson Tree Nursery staff gave participants an overview of appropriate seed storage and handling—an essential step in successful seed collection. Part of the demonstration included showcasing the equipment on-site used for seed cleaning and processing, as well as examples of optimal seed storage conditions.

Tour of Forest Gene Conservation Association Grafting Greenhouse and Shade Area (Butternut and Black ash grafts)

Presented by: Heather Zurbrigg

The tour included visits to structures built by FGCA as part of the butternut archiving program, where staff have grafted thousands of butternut. More recently, the FGCA has added other species to their repertoire including black ash, black spruce and white pine. FGCA works with many different partners to help with species recovery, forestry and conservation.

Conference Venue: Ottawa Marriott Hotel

Participants

Younes Abbas
Sultan Moulay Slimane University

Obed Asamoah
Carleton University

Brian Barber
Select Seed Co Ltd

Sarah Barker
Forests Canada

Jeff Barton
Northeast Seed Management Association

Jarmila Becka Lee
Forest Gene Conservation Association

Lahcen Benomar
Ontario Ministry of Natural Resources

Hailey Blacquiere
J. Frank Nursery

Simon Bockstette
Nova Scotia Department of Natural Resources

Juliette Bourgeois
Université Laval

Nicholas Boyce
University of Alberta

Abigail Brown
UBC - Vancouver

Rafael Candido-Ribeiro
UBC - Vancouver

Cailyn Carscadden
University of Toronto, Ontario Forest Research Institute

Patrick Carty
Natural Resources Canada

Paul Charrette
Superior-Woods Tree Improvement Association

Ayla Chin
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Ian Cochrane
Rideau Valley Conservation Authority

Colin Cordell
Forest Gene Conservation Association

Catherine Cullingham
Carleton University

Myles Cummins
Lakehead University

Jennifer Dacosta
Ontario Ministry of Natural Resources

Rakefet David-Schwartz
Agriculture Research Organization, Volcani Institute

Claire Depardieu
Université Laval

Darren Derbowka
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Genevieve Dorrell
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Mike Downing
Pépinière de Harrington

Sarah Drabble
Somerville Seedlings

Katherine Eaton
University of Alberta

Sionaid Eggett
The Ontario Woodlot Association

Aron Fazekas
University of Guelph

Benjamin Filewod
Natural Resources Canada

Kaylen Foley
Canadian Tree Nursery Association

Brent Forbes
Somerville Seedlings

Scott Formaniuk
Coast to Coast Reforestation Inc.

Adam Gambioli

Grace Gardner
Carleton University

Stephen Goodfellow
PRT Growing Services

Andreas Hamann
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Jill Hamilton
Pennsylvania State University

Eden Harbec
Somerville Seedlings

Briana Heuving
Forest Gene Conservation Association

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Suncheon Hong

Nina Hunt
Forest Gene Conservation Association

Kyu-Suk Kang
Seoul National University

Rob Keen
Canadian Tree Nursery Association

Steven Kiiskila
Arbutus Grove Nursery

Dave Kolotelo
Tree Seed Working Group

Mebarek Lamara
Université du Québec en Abitibi-Témiscamingue

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UBC - Vancouver

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Maara Packalen
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John Pedlar
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Evan Pilkington
Vineland Research and Innovation Centre

Vincent Quevillon
Université Laval

Edouard Reed-Métayer
Université Laval

Dave Richardson
Forestart Limited

Paul Richardson
Pineneedle Farms Inc.

Ryder Robinson-Tod
University of Alberta

Olivia Rodrigo
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Ngaire Roubal
Sault College

Mina Sadeghiniaraki

Jeff Sharp
St Clair Region Conservation Authority

Darren Sleep
Forest Products Association of Canada

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UBC - Vancouver

André Soro
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Sammy Tangir
Kawartha Land Trust

Bianca Tassi
Carleton University

Barb Thomas
University of Alberta

Ashley Thomson
Lakehead University

Francois van Deventer
The Atlantic Tree Improvement Council

Betty van Kerkhof

Simona Wagner
Forêt Capitale Forest

Tongli Wang
University of British Columbia

Stefan Weber
Forest Gene Conservation Association

Yuhui Weng
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