

PROCEEDINGS OF THE THIRTY-SIXTH MEETING OF THE CANADIAN FOREST GENETICS ASSOCIATION

PART 1 Minutes and Member's Reports
PART 2 Symposium

Applied Forest Genetics – Where do we want to be in 2049?



Génétique forestière appliquée - où voulons-nous être en 2049?

COMPTES RENDUS DU TRENTE-SIXIÈME CONGRÈS DE L'ASSOCIATION CANADIENNE DE GÉNÉTIQUE FORESTIÈRE

1^{re} PARTIE Procès-verbaux et rapports des membres
2^e PARTIE Colloque



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Proceedings of the Thirty-sixth Meeting of the Canadian Forest Genetics Association

Includes preliminary text and articles in French.
Contents: Part 1 Minutes and Member's Reports. Part 2 Symposium

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- 1 Forest genetics – Congresses.
- 2 Trees – Breeding – Congresses.
- 3 Forest genetics – Canada – Congresses.
- I Atlantic Forestry Centre
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Comptes rendus du trente-sixième congrès de l'Association canadienne de génétique forestière

Comprend des textes préliminaires et des articles en français.
Sommaire : 1^{re} partie Procès-verbaux et rapports des membres. 2^e partie Colloque

CODAGE

CODAGE

- 1 Génétiques forestières – Congrès.
- 2 Arbres – Amélioration – Congrès.
- 3 Génétiques forestières – Canada – Congrès.
- I Centre de foresterie de l'Atlantique
- II Titre : Génétique forestière appliquée - où voulons-nous être en 2049?
- III Titre : Comptes rendus du trente-sixième congrès de l'Association canadienne de génétique forestière

PROCEEDINGS
OF THE
THIRTY-SIXTH MEETING
OF THE
**CANADIAN FOREST GENETICS
ASSOCIATION**

PART 1

Minutes and members' reports

Lac Delage, Quebec
August 19 – 23, 2019

Editors

D.A. McPhee and J.D. Simpson

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Spruce Up

COMPTES RENDUS
DU
TRENTÉ-SIXIÈME CONGRÈS
DE
**L'ASSOCIATION CANADIENNE DE
GÉNÉTIQUE FORESTIÈRE**

1^{re} PARTIE

Procès-verbaux et rapports des membres

Lac Delage, Québec
19 au 23 août 2019

Éditeurs

D.A. McPhee et J.D. Simpson

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BUSINESS MEETING MINUTES



36th Business Meeting Minutes of the Canadian Forest Genetics Association

Patrick Lenz chaired the 36th Business Meeting of the CFGA/ACGF held at Lac Delage, Québec August 22, 2019

424 Attendance

Greg Adams (NB)
 Brian Barber (BC)
 Jean Bousquet (QC)
 Fabienne Colas (QC)
 Janice Cooke (AB)
 Marie Deslauriers (QC)
 Yousry A. El-Kassaby (BC)
 Michele Fullarton (NB)
 Claude Gagné (QC)
 Nathalie Isabel (QC)
 Dennis Joyce (ON)
 Christopher Keeling (QC)
 Dave Kolotelo (BC)
 Patrick Lenz (QC)
 Donnie McPhee (NB)
 Martin Perron (QC)
 Ilga Porth (QC)
 Barb Thomas (AB)

425 Approval of Minutes of the 35th Meeting

Minutes of the 35th meeting in Edmonton were presented as written and sent to members by the 2017 meeting organizers.

426 Membership

426.1 Honorary Membership

Dave Kolotelo had nominated Dale Simpson at the 2017 meeting. To respect CFGA bylaws, nominations need a 60-day notice and signatures of four sponsors, which was sent to the Secretary after the 2017 business meeting.

Motion: That the nominated Honorary Member be duly elected.
 Moved by: Dave Kolotelo
 Seconded by: Michele Fullarton
 Carried

426.2 Active Membership

The following individuals were nominated as follows:

Ken Elliot – nominated by Pengxin Lu
 Ngaire Roubal – nominated by Barb Boysen
 Melissa Spearing – nominated by Barb Boysen
 Omnia Gamal El-Dien – nominated by Michele Fullarton
 Ashley Thomson – nominated by Patrick Lenz
 Julie Godbout – nominated by Patrick Lenz
 Miriam Isaac-Renton – nominated by Patrick Lenz
 Justin Whitehill – nominated by Nathalie Isabel
 Raju Soolanayakanahally – nominated by Nathalie Isabel
 Jean-Marie Sobze – nominated by Nathalie Isabel
 Clara Schortemeyer – nominated by Greg Adams
 Josh Sherril – nominated by Greg Adams

Motion: That the nominated Active Members be duly elected.
 Moved by: Dave Kolotelo
 Seconded by: Michele Fullarton
 Carried.

426.3 Active Member's Obligations, etc.

The Chair reminded members to update mailing and contact information with the secretary in case of changes and to send their (short) activity report to the Editor.

In a following discussion it was agreed that the way of reporting on members' activities has to change. Reports and proceedings need to be published in a timely manner, which was not the case in recent years for diverse reasons. The current way of reporting seems outdated. Members spend a lot of time in writing reports, but they are not read or rarely cited. Assembling reports and editing is also time consuming for the Editor, in addition to regular professional duties. Several members suggested that the CFS should be lobbied for taking on the commitment again, as it was in the past, to support the Editor and Secretary services of the organization. Other suggestions were made on streamlining reporting into a bullet-point format and/or using an online reporting tool for easier and timely updating.

It was agreed to task the next executive with analyzing the situation and to come up with suggestions for facilitating reporting on activities and keeping member lists updated.

It was also suggested to honor the careers and accomplishments achieved by deceased and retired members to the forest genetics community.

Motion: To publically recognize deceased or retired members.
 Moved by: Patrick Lenz
 Seconded by: Brian Barber
 Carried.

427 Chair's Report

Preparing the 36th CFGA meeting

We chose the Manoir du Lac Delage for its proximity to nature, and the calmness and serenity because we felt it would be the perfect environment for discussions and exchanges around our chosen theme: "Applied forest genetics – Where do we want to be in 2049?" Apart from keeping people together at the end of the day and supporting the building of the group, the venue was also a cost-efficient alternative to Old-Québec hotels.

Development of a common vision

The meeting was a successful conference with several positive comments received. We had a great attendance of over 110 regular participants for this joint meeting with the "Tree Seed Working Group", the "GE³LS", and the "Poplar and Willow Council of Canada". The inclusion of GE³LS aspects throughout the sessions was a primer in the conference's history and led to interesting discussions about social acceptance, including the public and politics into genetics research.

Potential need for continued training

The co-chairs suggest fostering training workshops around specific topics in the future – whether during regular meetings or apart in order to stimulate exchange and knowledge transfer within the Association.

Budget overview

This is the final 2019 CFGA budget

	Debits	Credits
REVENUE		
Partners		\$ 19,287.01
Registrations		\$ 64,238.00
CFGA seed money		\$ 10,000.00
TOTAL		\$ 93,525.01
EXPENSES		
Hotel packages (IT and audiovisual equipment)	\$ 50,111.93	
Guest speakers and invited students	\$ 12,198.23	
Student awards	\$ 800.00	
General administration	\$ 5,728.78	
Activities	\$ 3,440.63	
Liability insurance	\$ 1,165.76	
Reimbursement of CFGA seed money	\$ 10,000.00	
TOTAL	\$ 83,445.33	
NET SURPLUS		\$ 10,079.68

Nathalie Isabel and Patrick Lenz
Co-Chairs

428 Treasurer's Report

The Treasure's financial report was presented by Michele Fullarton.

Financial Statement June 2017 – June 2019

Holdings – June 30, 2017

Cash balance	\$ 7,514.10
---------------------	--------------------

Credits

Interest (GIC)	\$ 285.00
CFGGA 2017	
Repayment of Seed Money	\$ 7,404.64
Surplus from conference	\$ 9,703.82
Cash from Rate Riser GIC	\$ 10,000.00

Credits	\$ 27,393.46
---------	--------------

Total Credits	\$ 34,907.56
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Debits

Seed Money for CFGGA 2019	\$ 10,000.00
Web Hosting (annual fees for Carleton Communications)	\$ 142.80
Interac Fee	\$ 1.50
GoDaddy (Domain renewal for 2 years)	\$ 138.94

Total debits	\$ 10,283.24
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Holdings – June 30, 2019

Cash	\$ 24,624.32
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Total Holdings	\$ 24,624.32
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Motion: That the financial statement is accepted as presented.
 Moved by: Dave Kolotelo
 Seconded by: Patrick Lenz
 Carried.

429 **Editor's Report**

The business meeting minutes and activity reports can be submitted in September 2019 for publication of the CFGA 2019 conference proceedings along with any additions to active membership and their contact information.

A request was initiated in 2017 for Active Member reports to be included in the 2017 conference proceedings but a limited response was forth coming. For the 2019 conference proceedings, a link to a website for work conducted for your report could also be included (i.e., publications or laboratory link....).

The State of Forest Genetic Resources (FGR) Report 2020 is being amalgamated by Dr. Tannis Beardmore and Kathleen Forbes. With this in mind, who better to contact than the active members of CFGA whose jurisdictional input is vital in conducting a panoramic vision for Canada. If you have not been contacted and would like to participate, there are some general questions that we would like your input for. It is not a daunting task but having the perspective from across all jurisdictions is vital in understanding how Canada manages our FGR and the future we envision in Canada. Your participation is greatly appreciated and will be acknowledged in the report. (Request for input to FAO report and details will be sent to members after the meeting.)

Once the 2019 Conference has concluded, could an electronic copy of the program with abstracts and any pictures be sent to me to be included in the 2019 proceedings?

After 2020, I will no longer be the editor for CFGA, so a new editor should be nominated at the 2019 business meeting.

Kathleen Forbes

430 **Education Committee**

We had strong student participation in this conference. They presented 7 talks and 11 posters.

Seven universities were invited to send a student to attend the conference. University of Moncton was not able to provide a student for sponsorship. Following discussions at the 2017 meeting, sponsorship of undergraduate students was particularly encouraged. The conference Co-chairs mentioned that most conference sponsors wish to support students, which provides a rationale for fund-raising for future conferences. Five sponsored students attended the 2019 conference with only one graduate student:

Alicja Muir	University of Northern British Columbia (poster)
Dreama Galbraith	University of New Brunswick

Kiera Stewart-Shepherd	University of Alberta
Lyne Touchette	Université Laval (poster)
Rafael Candido Ribeiro	University of British Columbia (poster)

The CFGA Gene Namkoong Award (\$300) is presented to a student for the best poster. The winner was Rafael Candido Ribeiro from The University of British Columbia for his poster “Drought Tolerance in Douglas-fir: Are Populations Locally Adapted?”

The CFGA Carl Heimburger Award (\$500) is presented to a student for the best oral presentation. The winner was Hughes La Vigne from Université de Sherbrooke for her presentation “The DeLeaves Drone, A Device for Efficient Tree Canopy Sampling”.

Chris Keeling

431 Working Group Report

431.1 Tree Seed Working Group

Dave Kolotelo referred to discussions during the Tree Seed Workshop and the presentation held during the regular meeting summarizing the main outcomes of the workshop. The workshop had seen strong and encouraging participation during this conference. Three Tree Seed Bulletins were published since the last meeting and he further encouraged people to submit articles. Dave also reported on reflections on putting together a series of webinars presenting current topics in the tree seed field and that would be accessible to all members.

Dave Kolotelo
Chair

432 Old Business

432.1 Exchanges Between CFGA, WFGA and SFTIC

The purpose of this was for better coordination of meetings and potential collaboration.

Patrick Lenz reported on discussions led with the other association during the last year as mandated during the last business meeting. In summary, all organizations would like to combine forces, but regional meetings remain highly important for local exchange and momentum. This is more important as many organizations have travel restrictions.

432.2 Formation of North American Forest Genetics Association

David Neale requested that this idea be presented to the CFGA members. Nathalie Isabel and Patrick Lenz provided an update on the creation of a North American Forest Genetics Association, which will provide a unified voice for forest geneticists. A first meeting is planned in June 2020. More news to come.

433 New business

433.1 Activities and Projects for Incoming Executive

The new executive will include the following points into their reflections and suggestions for the next business meeting:

- 1) Need to incorporate / register CFGA as a not-for-profit organization and implications for the by-laws,
- 2) Cooperative insurance for meeting organizers, and
- 3) Options for more permanent websites and mailing lists.

434 Future meetings

434.1 Location of the 2021 Meeting

Vernon, BC joint with WFGA

434.2 Location of the 2023 Meeting

Ontario or Atlantic Canada?

435 Election of New Executive

435.1 The following slate of officers will serve as the executive for the next CFGA/ACGF meeting

Chairperson:	Brian Barber
Vice-Chairperson:	Nick Ukrainetz
Executive Secretary:	Michele Fullarton
Treasurer:	Michele Fullarton
Editor:	Donnie McPhee following retirement of Kathleen Forbes in 2020

435.2 Regional representatives

To support reflections and suggestions for changes to the Association.

Atlantic region:	Donnie McPhee and Michele Fullarton
Quebec:	Patrick Lenz
Ontario:	Ken Elliott and Ashley Thomson
Alberta:	Barb Thomas
British Columbia:	Brian Barber
TSWG:	Melissa Spearing

436 Adjournment

Motion: That the 36th business meeting of the CFGA/ACGF be adjourned.

**ACTIVITY REPORTS
FROM ACTIVE MEMBERS**

NEW BRUNSWICK TREE IMPROVEMENT UPDATE

Michele Fullarton and Chris Hennigar

**Kingsclear Provincial Forest Nursery
Department of Energy and Resource Development
Island View, NB**

Keywords: breeding, second-generation, GA4/7, third-generation, seed orchard, black spruce, jack pine, white spruce, red spruce, Norway spruce, tamarack, NBTIC.

The New Brunswick Tree Improvement Council (NBTIC) was formed in 1976. It is comprised of industrial, scientific and government agencies, and the objective of the Council is to provide well adapted, improved seed for reforestation. The Department of Energy and Resource Development (DERD) coordinates the NBTIC activities, and is responsible for breeding and growing of test material. The Seedling Production section of DERD is currently growing 14.2 million seedlings in 2019 for Crown land reforestation, with 95 % of the seed coming from seed orchards. The tree improvement program continues to focus on the main reforestation species: white spruce (*Picea glauca*), black spruce (*Picea mariana*), red spruce (*Picea rubens*), and Norway spruce (*Picea abies*). Other species include: white pine (*Pinus strobus*), balsam fir (*Abies balsamea*), jack pine (*Pinus banksiana*), and tamarack (*Larix laricina*).

SEED ORCHARDS AND SEED PRODUCTION

Orchard establishment for NBTIC members currently stands at 306 ha comprised of 7 coniferous species. These orchards are meeting the reforestation demands for Crown land. Seed production in 2017 was excellent for balsam fir with almost 500 kg of seeds produced. The seed is available for purchase by private Christmas tree growers. In 2018, the crop was not very good, with only 11,000 l collected.

TREE BREEDING, TESTING AND SELECTION

Third-generation jack pine selections and further breeding are on hold due to a reduction in demand for this species, although 40 selections were made to establish a third-generation orchard. DERD continues to follow the breeding strategies for black spruce and jack pine that were adopted in 1993. Clones were uniformly deployed to breeding groups and breeding conducted in a positive assortative mating design. A total of 23 sub-lines was established for black spruce and 21 for jack pine. Full-sib breeding and testing is now completed. Data from seven series of black spruce full-sib tests were analyzed, and the information used to begin third-generation plus tree selections. Forty-nine trees for seed orchards were selected and grafting started in 2019. A new third-generation population will be field-checked in 2019 and a breeding garden and new orchards established in the next 2 to 3 years. A breeding strategy is now in place for advanced generations. Second-generation white spruce breeding, for the past five years, has been supplemental mass pollination on orchard clones to establish tests to evaluate clones for future roguing. Pair-mating started in 2013 using an updated breeding strategy.

In the NBTIC program, three hundred and sixty-seven tests have been planted on 406 ha located throughout the province. In 2019, the second series of second-generation white spruce full-sib progeny tests was

established. These will be used for third-generation selections. In addition, a second series of red spruce open-pollinated tests of orchard clones was established. This test series will be used for orchard roguing.

NBTIC DATA ANALYSIS AND RESEARCH

The *FastTRAC* project completed the genomics selection analysis in March of 2018. Consequently, these results were used by DERD and J.D.Irving, Limited to plan orchard roguing and for optimizing our breeding program. There are plans in place to hire a data analyst to take care of data needs in both Nova Scotia and New Brunswick (government agencies). This is still in the planning stages.

PUBLICATIONS AND REFERENCES

Fullarton, M.S. 2018. NBTIC Twenty-seventh biennial report 2016–2017. NB Department of Energy and Resource Development. 18 p.

NATIONAL TREE SEED CENTRE

Donnie McPhee and Katie Burgess

**Canadian Forest Service
Natural Resources Canada
Fredericton, NB**

The National Tree Seed Centre (NTSC) celebrated its 50th anniversary in 2017 at the same year Dale Simpson retired after managing the Centre since its move to Fredericton in 1996. The NTSC's mission remains to safeguard Canada's forest genetic resources. It does this in the face of climate change, invasive species and other threats by acquiring, evaluating, preserving, and providing a national collection of genetic resources to assist in securing the forest biological diversity that underpins the sustainable development of Canada's forests. The Centre's aim is to store seeds of tree and shrub species from throughout their ranges with representative collections from each ecoregion they naturally exist in. This report covers activities during 2017 and 2018. The NTSC provides seed to research programs in Canada and abroad for a wide array of purposes (Fig. 1). Seven hundred and eighty-eight seedlots representing 54 species were provided free of charge for research purposes over this two-year period. Ongoing activities include: collecting and processing seeds; conducting tests such as germination, moisture content, and 1,000-seed weight; and setting up and evaluating research trials.

Most of the collection effort focuses on collecting seeds from a minimum of 15 trees in a population and keeping the collections separate by individual tree. Many of the accessions donated or purchased are bulk collections from natural populations. Seed is stored at -20°C primarily in two categories: Seed Bank, where seeds are available for research and Gene Conservation. During the two-year period, the NTSC inventory rose by 300 seedlots from 53 species. NTSC staff collected 68.3% of these while 24.3% were donations from collaborators including: Parks Canada (Banff, Point Pelee), University of Guelph Arboretum, British Columbia Ministry of Forests, Confederacy of Mainland Mi'kmaq, Urban Forest Associates, Forest Gene Conservation Association of Ontario, New Brunswick Department of Energy and Resource Development, Nature Conservancy Canada Newfoundland and Labrador, and Unama'ki Institute of Natural Resources. Purchased seeds represented 5.7% and 1.7% was collected in collaboration with the Unama'ki Institute of Natural Resources in Cape Breton, NS.

Currently, 7,341 seedlots from 148 species exist in Seed Bank. The Gene Conservation collection also continued to grow with over 5,770 seedlots including seven species listed by the Species at Risk Act. Seed in this collection conserves natural genetic variation through collections from species or populations that are unique or threatened as well as samples from seedlots that were initially collected for Seed Bank. The Seed Centre also has a cryogenic facility. Most of the material stored is tissue arising from somatic embryogenesis under a butternut (*Juglans cinerea*) conservation program, led by Tannis Beardmore. Butternut, is listed nationally as endangered due to butternut canker caused by an exotic disease (*Sirococcus clavignenti-juglandacearum*). Butternut seeds are recalcitrant, however, the embryonic axis is tolerant to desiccation and freezing. This is the only *ex situ* conservation collection of butternut in North America. Currently the cryogenic collection consists of 32,500 axes (e.g., root-shoot embryos) and an additional 10,000 nut tissue samples for future DNA and chemical analyses.

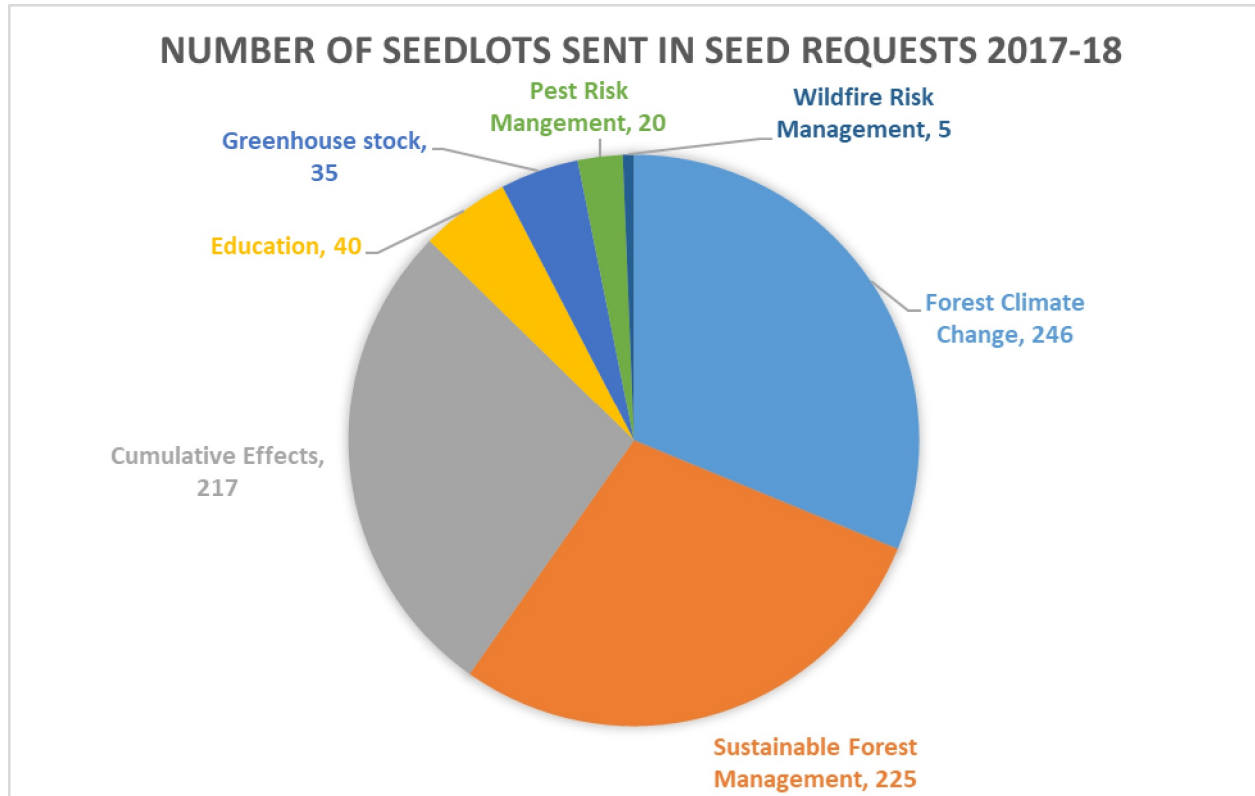


Figure 1. Number of seedlots sent in seed requests by various categories, 2017–2018.

Beginning in 2004 the NTSC has been leading efforts for conservation of ash seeds due to the threat imposed by emerald ash borer (*Agrilus planipennis*) and its expanding range in Canada. There is an opportunity to collect and store seed to conserve the genetic variability of native ash species so that the material will be available for research and/or restoration planting after the insect infestation has passed through. There was a reasonable seed crop in 2018 that resulted in over 71 collections made by NTSC staff with a few donated from Ontario and Quebec. About 951 seedlots from five species are in storage.

Germination testing of seedlots in storage is an integral part of the Seed Centre's annual activities. For most species, germination tests are conducted every ten years. During the two-year period, 1,404 tests were completed using Petawawa Germination Boxes. The data not only provide an indication of the quality of each seedlot but when combined with previous test data they provide an indication of the long-term storage potential for a species. This is particularly important when seed is being stored long term for genetic conservation purposes.

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BUTTERNUT CONSERVATION RESEARCH

Martin Williams, Kathleen Forbes and Tannis Beardmore

**Canadian Forest Service
Natural Resources Canada
Fredericton, NB**

Butternut, (*Juglans cinerea*), also called white walnut, is an uncommon hardwood species that is endangered in Canada under the Species at Risk Act (SARA) due to what is thought to be an exotic fungal pathogen (*Ophiognomonia clavigignenti-juglandacearum* (Oc-j)). Oc-j was discovered in 1967 (Renlund 1967) and described in 1979 (Nair et al. 1979). This pathogen has decimated butternut populations in the United States (US) and in Canada. New Brunswick (NB), which is one of 3 jurisdictions within butternuts' natural range and considered the species' most northeastern part of its range, was the last province infected by the pathogen in 1997 (Harrison et al. 1998). Based on mortality in the US and in Ontario, predictions are that butternut could be extinct within the next century if disease resistance is absent (COSEWIC 2017). A recovery strategy was published in 2010 (Environment Canada, 2010). To support this recovery our work has focussed on 3 aspects of butternut research for conservation: 1) to evaluate the spread of the disease in the province of NB since appearance, 2) a range-wide (US-Canada) evaluation of genetic variation to guide an *ex situ* conservation strategy, and 3) to develop *ex situ* seed collections and cryostorage to safeguard the remaining genetic diversity.

To assess the disease spread in NB, over 600 trees were assessed for canker and tree health across the range and found that the canker was present throughout all its range in the province (Williams et al. 2019a) which was not the case in 2010. Out of these trees surveyed, approximately 75% are infected (Williams et al. 2019b). Although many trees are cankered, many trees are still considered vigorous but that could change very quickly on rich sites (riparian and flood plain) which are beneficial to pathogen viability.

High tree vigour has enabled us over the last 6 years to implement an *ex situ* program for the collection of butternuts to capture the remaining diversity before it is too late. Even though butternut are sub-orthodox in seed storage behaviour (Bonner 1990), where they can withstand drying and cold temperatures, their viability over time under these conditions is still very low (2–3 years) due to lipid oxidation. To overcome this problem, cryostorage of embryogenic axes (EAs) which includes the embryo and part of the cotyledons was established (Beardmore and Vong 1998) and more recently, an in vitro propagation method was published (Williams et al. 2019b). Presently, the *ex situ* program has focussed its efforts on NB provenances and has cryobanked 329 seedlots (individual trees and bulks) for a total of 35,000 EAs. Recent germination of a few seedlots shows that the EAs are still viable for up to 6 years after cryostorage.

Most of the mother trees have been genotyped using available microsatellite markers (Hoban 2008; McCleary 2009). Genotyping is beneficial: 1) to confirm *Juglans cinerea* maternal background to minimise the introgression of japanese walnut (*Juglans ailantifolia*) alleles in the collection and 2) to provide a range-wide population genetics assessment of butternuts for *ex situ* conservation planning. A range-wide study (US/Canada) is presently on-going to evaluate the potential presence of a designatable unit in part of Canada's native range. This could lead to a designatable unit determination for the species, a factor that is essential in a recovery/action plan for the conservation and restoration of the species. Finally, in July 2019, a group of researchers from the US and Canada met at Purdue University to discuss the status of butternut across North America and approaches to restore butternut including the prospect of resistance breeding. These efforts to save the species from probable extinction are on-going and will hopefully be successful in providing a moving forward strategy for species restoration (Pike et al. in preparation).

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**TREE IMPROVEMENT PROGRESS
AT THE DIRECTION DE LA RECHERCHE FORESTIÈRE**

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Keywords: white spruce, white pine, Norway spruce, black spruce, jack pine, hybrid larch, hybrid poplar, tamarack, Septoria canker, controlled crosses, tree improvement, tree selection, provenance tests, progeny tests, climate change adaptation, molecular certification, forest yield, wood properties, seed orchards, low-cost breeding strategy.

INTRODUCTION

Through its breeding programs, the Ministère des Forêts, de la Faune et des Parcs (MFFP) aims to increase high-quality wood yields for major reforestation species while maintaining a high level of diversity, to help reduce pressure on natural forests, to select varieties better adapted to local climate conditions expected in the coming decades, and to help implement appropriate *in situ* or *ex situ* measures to conserve forest genetic resources.

An article relating the history of tree improvement at the Direction de la recherche forestière (DRF) was produced for the journal “Histoires forestières du Québec” to mark our organization’s 50th anniversary in 2017.

WHITE SPRUCE TREE IMPROVEMENT

Martin Perron and André Rainville

As part of our collaboration on the *FastTRAC* project (rapid tests for evaluation and selection of conifers), we produced the first operational recommendation based on genomic predictions in the summer of 2018. A first culture was initiated, as a step toward the deployment of new multi-clonal and multi-family varieties of the 30 best white spruce (*Picea glauca*) clones out of 3,171 genotyped clones classified for 6 traits of interest. These 30 clones represent 15 families from 20 parents in the MFFP’s clone bank.

In addition, researchers and other MFFP staff participated in the cost-benefit analysis of the use of forest genomics in the context of operational deployment in Quebec.

Quebec’s white spruce genetic improvement program was revised to implement the 2nd breeding cycle. Following our participation in the [FastTRAC project](#), our strategy now considers the integration of genomic selection using the GBLUP method for elite populations and a 5-year breeding cycle (2020–2024). It will target short-term genetic gains (2–3 breeding cycles) for growth, modulus of elasticity (MoE), and resistance to abiotic and biotic stresses (e.g., drought). For the moment, we expect to follow this same strategy for the 3rd breeding cycle (2025–2029). The main breeding population will be managed using a simpler strategy, probably involving open pollination.

CLIMATE CHANGE ADAPTATION MEASURES

Martin Perron and André Rainville

Our collaboration with Laval University continued on the study of the impacts of climate change on white spruce, using the plantation network of the realized gains project, particularly to update the deployment area for second-generation orchards.

LARCH TREE IMPROVEMENT

Martin Perron

In 2017, 16 trees per taxon (*L. decidua*, *L. kaempferi*, hybrids *L. decidua* × *L. kaempferi* and *L. kaempferi* × *L. decidua*) derived from Experiment 1 (Perron 2008, [DOI:10.1515/sg-2008-0043](https://doi.org/10.1515/sg-2008-0043)) were selected on the basis of their breeding value for 5-year height as well as the absence of defects and disease. Top grafting on mature trees was used to accelerate flower production and to eliminate transplant culture. In the spring of 2018, two grafts were produced for 22 of the 64 trees selected the previous fall. The difference in phenology between the two sites (a progeny trial and a breeding orchard) prevented the completion of grafting for the rest of the trees. This was our first attempt to use top grafting at different sites. Due to limited resources, we modified our sampling strategy and selected 64 parents based solely on 5-year height growth, instead of the two-step strategy which involved the production of greater number grafts based on 5-year results, followed by a final selection based on 10-year results. In 2017, the operational deployment of the MEH 20-20 variety resulting from Quebec's larch breeding program was the focus of a report on "La semaine verte", a television program targeting the general public.

BLACK SPRUCE TREE IMPROVEMENT

Mireille Despons

Researchers have demonstrated the effectiveness of an indirect and non-destructive *in situ* selection method for density and MoE in black spruce (*Picea mariana*). Since MoE is a highly heritable wood property, this finding suggests that significant genetic gains could be obtained from the second-generation selections. Improving MoE (also called "rigidity") ensures that timber is both flexible and resistant to deformation, and could increase the quality and value of many processing products.

We used measurements from two clonal tests to prescribe the thinning of the black spruce clonal seed orchard supplying the Côte-Nord region and the Réserve faunique des Laurentides (eastern balsam fir bioclimatic subdomains), taking into account both tree growth and wood quality. These same two clonal tests were also used to produce recommendations for the spruce-moss and the western balsam fir-white birch domains.

A study on the effectiveness of genomic selection on wood properties in black spruce, carried out in collaboration with researchers at Laval University, the Laurentian Forestry Centre (Natural Resources Canada), and the DRF, indicates that the integration of this method could accelerate genetic gains during future selections for this species.

In 2018, we completed controlled crosses with selected trees from about 15 half-sib progeny trials of the northern temperate zone. A second-generation population of 200 full-sib families will be tested in progeny trials to evaluate multiple traits (growth, wood properties, adaptation to climate change, and assisted migration).

NORWAY SPRUCE TREE IMPROVEMENT

Marie-Josée Mottet

Geneticists continued to contribute to the *FastTRAC* project by collaborating on several transfer activities related to genomic selection models for growth, wood quality and white pine weevil resistance in Norway spruce (*Picea abies*).

A new generation of Norway spruce resistant to white pine weevil is under development. Recently, polycross matings were made in a new breeding population derived from trees selected in open-pollinated family tests. A second part of this population will consist of trees selected in full-sib family tests. The first phase of this selection process is planned for 2019–2020 in the 20-year-old tests.

HYBRID POPLAR IMPROVEMENT PROGRAM

Pierre Périnet and Marie-Josée Mottet

In 2018 we revised the list of hybrid poplar clones recommended for Quebec on the basis of their resistance to Septoria canker (*Sphaerulina musiva*). In addition, as part of a collaboration between the DRF and a Chilean poplar research centre (Universidad de Talca), canker-resistant hybrid poplar clones from Quebec were established in vitro and exported to Chile to test their local resistance.

Populus suaveolens is a critical species for Quebec's poplar breeding program. In the winter of 2018, we conducted intraspecific crosses between Japanese and Chinese provenances in a greenhouse using flowering twigs harvested from trees cultivated and selected in Quebec. This advanced generation of almost 300 families will compose a new population and enable us to improve this species and obtain new hybrids.

A study conducted at the Université du Québec en Abitibi-Témiscamingue (UQAT), with the participation of the DRF, documented phenotypic and genotypic correlations between anatomical, physical, and mechanical wood properties of different hybrid poplar clones.

WHITE PINE TREE IMPROVEMENT

Marie-Josée Mottet

Results from genetic tests established several years ago by Natural Resources Canada have led to recommendations allowing white pine (*Pinus strobus*) seed sources from southern Quebec to be used in the western balsam fir-white birch bioclimatic subdomain. This provides a short-term response to the recent demand for white pine seedlings in the Lac-Saint-Jean region.

In addition, we are undertaking a study on the phenology and the reproductive capacity of trees included in the second-generation seed orchard (V2) located in Berthierville. Since the orchard includes trees from southern regions outside Quebec, this could represent a first step toward white pine assisted migration.

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RECENT ADVANCES IN TREE PRODUCTION BY SOMATIC EMBRYOGENESIS IN QUEBEC

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In Quebec, the annual production target is around 150 million plants of coniferous and deciduous species. Seed and seedling production is managed provincially, as it is for research and development on tree improvement. The seedlings needed for reforestation for the entire province are produced by a total of 19 forest nurseries, 6 public and 13 private.

Somatic embryogenesis (SE), through the propagation in large quantities of the most productive clones, allows the deployment of white spruce (*Picea glauca*) somatic plants that yield considerable gain. Work at the Saint-Modeste public forest nursery has led to major advances toward scaling up this technique and the production of somatic plants has been conducted here at an operational level since 2013. In 2018, the first million plants produced by somatic embryogenesis was delivered to be planted in public forests. Communication efforts have been made to increase social acceptance of this elite product and understanding of the possibilities offered in terms of genetic gain and growth. There are plans to maintain the communication and outreach activities.

Somatic plants represent an elite product under development. Until recently, the selection of clones was based on height measurements in clonal tests. Since 2018, thanks to the collaboration of Quebec's Ministry of Forests, Wildlife and Parks in the *FastTRAC* project, clone selection can be done by genomic selection. Among several advantages, genomic selection allows to increase the selection pool to clones that were not included in clonal tests. In order to effectively produce multi-clonal varieties with the desired characteristics, ongoing work aims to identify the clones that perform best both in the field and under laboratory conditions. But it's not as easy as it seems. The first plants selected by genomics will be delivered in 2023.

The maintenance of genetic diversity in the plantations is a constant concern. That's why the Saint-Modeste public forest nursery has developed an approach to ensure that each seedling lot to be planted in the forest consists of a mixture of 20 to 30 distinct clones. In order to ensure a uniform distribution of clones, the recommended method implies that we act as early as possible in the cultivation of plants. Thus, at the soil transfer step, i.e., when the seedlings leave the laboratory for cultivation in a greenhouse, clonal traceability is maintained for all of the seedlings. A small proportion of the plants will remain traceable until their delivery, while the vast majority will be mixed when they leave the greenhouse. This mixing is carried out by calculating the proportion of each clone in a volume of 90 containers, which is the number of containers moved during delivery between the greenhouse and the field. Numerous other operations which take place before plant delivery (removal of mother plants, cuttings, transplanting of cuttings, delivery truck loading)

will also contribute to the random mixing of clones throughout the volume.

In addition, it is planned to gradually but rapidly increase the production of white spruce somatic plants to reach an annual delivery of 4 million plants within the next few years. The implementation of automation systems in the Saint-Modeste nursery is underway. The existing production is indeed very labor intensive, and automation of specific processes will be an efficient way of reducing costs and time production. For white spruce, the stages of maintenance, maturation, and germination have been identified as the critical stages to be improved, since they all require a lot of handling and equipment.

ORAL AND POSTER PRESENTATIONS

Tremblay, L.; Gingras, J.; Carles, S.; Bérubé, S.; Gagné, C. 2019. Somatic embryogenesis: a cutting-edge technique to propagate and deploy white spruce. Poster presentation at the Canadian Forest Genetic Association Conference, 19–23 August 2019, Lac Delage, Quebec.

Carles, S.; Gagné C. 2019. Overview of the production system of forest seed and tree seedlings in Quebec. Oral presentation at the Canadian Forest Genetic Association Conference, 19–23 August 2019, Lac Delage, Quebec.

Tremblay, L.; Gingras, J.; Carles, S.; Bérubé, S.; Gagné, C. 2019. L'embryogenèse somatique : une technique d'avant-garde pour reproduire et déployer des épinettes blanches d'élite. Poster presentation at the Carrefour Forêts 2019, 2 au 4 avril, Québec, Qc.

FOREST GENOMICS AND GENETICS AT UNIVERSITÉ LAVAL

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Keywords: conifers, chloroplast DNA, comparative genomics, deciduous trees, functional genomics, gene expression, gene flow, genogeography, genome mapping, genome scans, genome sequence, genomic selection, genomics-based biosurveillance, insect pests, mitochondrial DNA, molecular ecology, molecular breeding, phylogeography, population genomics, quantitative genetics, SNPs, spruces, spruce budworm, stem-borers, structural genomics, transcriptomics, tree breeding, tree pathogenic fungi, tree physiology, wood quality.

MAIN RESEARCH ACTIVITIES AND PROJECTS

This report summarizes our main research efforts in forest genomics and genetics over the 2017–2019 period. The Genome Canada LSARP (Large-Scale Applied Research Program) project Spruce-Up - Advanced spruce genomics for productive and resilient forests, made significant progress. The 5-year project extending from Fall 2016 to 2021 was also supported by Genome Quebec, Genome BC, and Genome Alberta. It has been co-led by J. Bohlmann Univ. of British Columbia (UBC) and J. Bousquet (Univ. Laval) and involves many other Canadian academics from Univ. Laval (N. Gélinas, J. Beaulieu, A. Achim, E. Bause, B. Boyle), UBC (G. Bull, I. Birol, S. Jones), Univ. of Alberta (J. Cooke), and Univ. of Toronto (I. Ensminger). It also involves scientists from other Canadian research organizations such as Natural Resources Canada (NRCAN) (team of N. Isabel), the Canadian Wood Fibre Centre (CWFC) (team of P. Lenz), and the Ministère des forêts, de la faune et des parcs du Québec (MFFPQ) (team of M. Perron and A. Rainville). Several collaborators worldwide also participate in the project, including scientists from the Max Planck Institute for Chemical Ecology in Germany (team of A. Hammerbacher) and the Univ. of Oxford in England (team of J. Mackay). The goals of the project are to pursue the development of biomarkers, genomic selection (GS) models and socio-economical assessments for improving traits related to spruce budworm (*Choristoneura fumiferana*) resistance, nutrient use efficiency, resilience to drought stress, biomass for carbon sequestration, crown morphology, wood stiffness and various other traits related to spruce wood quality. New precision-phenotyping methods are also being developed including isotopic determination and drone-assessment of drought stress response using sensors and lidar-assessment of crown morphology. At the same time, efforts are also directed towards improving the contiguity of spruce genome sequences and their annotation, and developing new genotyping tools. The target species are: eastern white spruce (*Picea glauca*), interior spruce, (*P. glauca* x *engelmannii*), and Sitka spruce (*P. sitchensis*). The Univ. Laval component of the project, in collaboration with NRCAN, CWFC, and MFFPQ, has involved over two dozen postdocs, graduate students, and research associates. This project has already resulted in a large number of scientific publications and new genomic resources (see <https://spruce-up.ca/en/> and list below).

The Genome Canada project *FastTRAC* – Fast Tests for Rating and Amelioration of Conifers, launched in spring 2015 under the Genomics Applied Partnership Program (GAPP) of Genome Canada was completed with success in the Spring of 2019. It received additional support from Génome Québec, FPInnovations (FPInnov.), CWFC, MFFPQ, J.D. Irving, Limited (JDI), NRCAN, the New Brunswick Tree Improvement

Council (NBTIC), and the New Brunswick Department of Economic Development. The project was co-led by J. Bousquet from Univ. Laval and G. Smith from CWFC, and involved scientists and practitioners from Univ. Laval (J. Beaulieu), CWFC (P. Lenz, Y.-S. Park), MFFPQ (M. Perron, M.-J. Mottet, A. Rainville, and M. Campagna), JDI (G. Adams, A. McCarthy, and S. Milican), NRCan (N. Isabel), NBTIC (M. Fullerton), and FPInnov (F. Robichaud). Its goal was to bring genomic selection (GS) to the operational scale for eastern white spruce and Norway spruce (*P. abies*) advanced breeding programs in Quebec and New Brunswick. Growth, wood density, and resistance to white pine weevil (*Pissodes strobi*) attacks were the targeted traits of deploying high accuracy GS predictive systems (see <https://fasttracproject.ca/en/home/> and list below). Additional funding was also obtained from the Forest Innovations Program of the Canadian Wood Fibre Centre of Natural Resources Canada to foster the uptake of the forest genomics technology by the end-users.

Under the leadership of J. Bousquet, the Canada Senior Research Chair in Forest Genomics, which was established in 2001 at the inception of the Canada Research Chair (CRC) program, has been and will be pursuing its activities until 2022 at the Institute for Systems and Integrative Biology and the Forest Research Centre through an exceptional third 7-yr period. The group includes the affiliated members I. Porth and J. Beaulieu (Univ. Laval), N. Isabel (NRCan), P. Lenz (CWFC), M. Perron (MFFPQ), and J. Mackay (Univ. of Oxford). During the period, many senior research associates and postdoctoral fellows contributed to the research program, including L. Benomar and N. Pavy (ongoing), G. de Lafontaine (now associate professor and CRC at Univ. du Québec), J. Godbout (now researcher at MFFPQ Research Branch), and J. Prunier (now researcher at CHU de Québec Hospital Research Centre). Many MSc and PhD students have also been supervised during the period including M. Lamara (now associate professor at Université du Québec), G. Otis-Prud'Homme (now researcher at MFFPQ Research Branch), A. Sahli (now bioinformatician at Wellcome Trust Centre for Human Genetics, U.K.), J. Stival Sena (now postdoc at NRCan), and J. Laoué, J.-P. Laverdière, I. Rashidi and A. Soro (ongoing).

The Genome Canada LSARP project BioSafe (Biosurveillance of alien forest enemies), launched in the Fall of 2016 until 2021, has also been progressing well. It is led by R.C. Hamelin (UBC – Univ. Laval) and I. Porth (Univ. Laval) with additional funding from Genome BC and Génome Québec. It involves C. Duff from the Canadian Food Inspection Agency (CFIA) as co-leader and end-user, with many other Canadian scientists from Univ. Laval (L. Bernier, C. Landry, and R. Levesque), UBC (V. Griess), Univ. of Victoria (W. Hintz, P. Constable), McGill Univ. (M. Blanchette), and Univ. of Western Ontario (B. Sinclair). It also involves scientists from other Canadian research organizations such as NRCan (M. Cusson, D. Dousset, P. Tanguay, A. Roe, and M. Boyland), FPInnov (A. Uzunovic), the CFIA (G. Bilodeau and B. Day), Agriculture and Agri-Food Canada (P. Bouchard), and provincial forest ministries of Québec, Manitoba, Saskatchewan, British Columbia, and Alberta as end-users. Several collaborators worldwide also participate in the project, including scientists from the Beijing Forestry Univ. (J. Shin), the *Phytophthora* Genome Consortium (B. Tyler), the USDA (M. Keena and N. Havill), and Penn State Univ. (K. Hoover). The goals of the project are to pursue the development of genomics-based tools for prevention and early detection in biosurveillance programs of four top priority pests and pathogens as immediate threats to Canadian forests, related industries, and ecosystems provisions. The specific objectives are to provide: 1) accurate species identification, 2) assignments to source populations and knowledge regarding the invasion pathways of the species, 3) identification of fitness and outbreak-related epidemiological traits that can impact invasion outcome of the species in question, and therefore 4) reduce uncertainty of invasion outcomes and inform decision support systems to speed up and improve decision-making for forest invasive alien species mitigation and management. The four targeted pests are the Asian longhorned beetle (*Anoplophora glabripennis*), the Asian gypsy moth (*Lymantria disparasiatica*), Dutch elm disease related *Ophiostoma* fungi, and the sudden oak death related oomycete *Phytophthora ramorum*. Currently, 4 postdocs, 4 PhD students, and 2 research assistants are involved in the project at Univ. Laval. Our group has already published or submitted many papers from this project (see <https://www.biosafe-genomics.com/> and list below).

For the period 2018–2021, I. Porth also received funding from FRQ-NT (Fonds de recherche québécois en nature et technologies) to undertake a bilateral collaborative research project with Mexico (CONACYT matching funds) about the study of the *Populus tremuloides* genome throughout North America to detect signals of adaptation to local climate and soil. More than 20 PIs are involved in this project including those from Mexico. Presently, there are two graduate students (Roosje Goessen, co-supervised with J. Bousquet and N. Isabel, and L. Touchette co-supervised with J.-M. Beaudoin) and two technical staff (I. Giguere and F. Larochelle) involved in this project at Univ. Laval. For the 2019–2024 period, I. Porth also obtained funding from the Canadian Foundation for Innovation (CFI) to support the acquisition of new tools and instruments for her “Tree Biology and Plant Functional Genomics Lab” at the Institute for Systems and Integrative Biology of Univ. Laval.

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ADVANCES IN FOREST GENOMICS AT THE CANADIAN FOREST SERVICE, QUEBEC REGION

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Keywords: white spruce, black spruce, eastern white pine, larches and poplars, *Picea glauca*, *Picea mariana*, *Pinus strobus*, *Larix* spp. and *Populus* spp., adaptation, geographic origin, long distance gene flow, wood quality, climate change, pedigree, introgression, SNPs, gene and QTL mapping, population genetics, GEA, hybrid zones.

The group was strongly involved in the Genome Canada funded projects leveraged by internal and GRDI funds, *Spruce-Up* and *FastTRAC*, whose goal was the development of genomic breeding tools. In collaboration with our university partners (Univ. Laval, Univ. of British Columbia, Univ. of Toronto, and Univ. of Alberta) and stakeholders (province of Québec (MFFP), province of New Brunswick, New Brunswick Tree Improvement Council, and J.D. Irving, Limited (JDI)), we mainly supported fieldwork for phenotyping and preparatory laboratory work for genotyping, and we also led statistical analyses for genomic selection modelling. Most publications are linked to these genomic projects (see list below). We initiated internal projects related to the development of genomic tools in combination with wood anatomy and chemical profiling for wood identification and for the development of traceability systems. The development of adapted somatic embryogenesis protocols that allow for better integration with genomic breeding tools was also initiated.

One of our major activities was the organisation of the 2019 meeting in Lac Delage, Québec that involved resources and human resources from both forest genetics groups at the Laurentian Forestry Centre (see “Welcome” in Part 2 of these Proceedings). The way member’s activity reports are presented as well as their necessity was questioned before and during the conference. The next board of directors was mandated to review this process and suggest changes. Here, we chose an abbreviated way of reporting on key activities, unpublished experiments, and listing relevant publications, which may be taken as a suggestion for future reports.

MAJOR PROJECTS AND ACHIEVEMENTS

Spruce-Up

An ongoing Genome Canada supported large-scale genomics project (<https://spruce-up.ca/en/>). The main goal of the *Spruce-Up* Project is to produce enhanced genomics and socioeconomic knowledge for the development, validation and implementation of biomarkers and genomic selection systems to accelerate spruce breeding programs. In *Spruce-Up*, the Canadian Forest Service (CFS) provides material for spruce genome sequencing and data for economic modelling of the benefits of tree breeding (GE³LS). The tree genetics group largely supported phenotyping for drought and phenology traits, wood quality assessment, and genetic analyses of traits in white spruce (*Picea glauca*) genetic trials. Research around the use of remote

sensing methods to monitor physiological processes and other tree characteristics in genetic plantations progressed. Novel methods were developed to better characterize the drought resilience and resistance of conifers. Genomic selection modelling is progressing using advanced approaches such as multi-trait genomic selection.

FastTRAC

This is a Genome Canada supported applied partnership genomics project (<http://fasttracproject.ca/en/home/>) that ended in April 2019. The project brought together scientists, tree breeders, foresters, and economists to demonstrate and apply genomic-assisted selection at the operational scale of tree improvement programs. Genomic-assisted selection can more rapidly rate candidate trees for productivity and wood attributes to hasten the selection and reforestation of improved and adapted stock. CFS supported genotyping and phenotyping as well as the development of genomic selection models. Several reports with genomic estimated breeding values for white and Norway spruce (*Picea abies*) breeding populations were delivered to New Brunswick and Québec partners. Outcomes of the project supported the planning of next generation crosses and led to the roguing of first-generation seed orchards (JDI). They also led to the development of a genomic selection strategy for a major part of the Quebec white spruce breeding program.

Traceability for Production Systems

Biological material is at the forefront of research programs, as well as applied fields such as breeding and reforestation. While sophisticated techniques are used to produce this material, there is all too often no strict monitoring during the “production” process to ensure that the specific varieties are the expected ones. Confidence rather than evidence is often relied on when the time comes to start a new experiment or to deploy selected varieties in the field. During the last decade, genomics research has led to the development of important resources, especially in white spruce, which have created opportunities for easily developing tools to assess the conformity of the material along the production chains, such as seedling production of elite varieties. We (Univ. Laval, MFFP, and CFS) developed a simple methodology that enables the establishment of a traceability system (quality assurance control) in white spruce seedling production (from crosses to the field).

Wood Identification Project (science/policy integration project)

Since 2018, with the contribution of NRCan-CFS, Environment and Climate Change Canada (ECCC), Canada Border Services Agency, and international collaborators, Canada is developing its own capacity (methods, training, reference materials, and datasets) to identify the tree species that make up marketed wood products. The goal of this initiative is to create a Wood Identification Centre of Expertise within the Government of Canada by 2030, with the continued objectives of providing ECCC with tools to prevent the importation of illegal forest products, to contribute to international efforts to combat illegal logging and trade, and to maintain a strong reputation for sustainable and legal exports of Canadian forest products.

Populus Species and Baseline Data

The forest industry faces pressure to meet certification standards, especially with short-rotation plantations of exotic hybrids. Ongoing research provides a framework to develop safeguards that minimize gene flow from plantations to natural populations. Monitoring protocols for forest companies will help them retain their forest certification accreditation without which they risk losing or impeding market access for their products.

Special Journal Issue on Forest Genomics

N. Isabel with Jason Holliday (Virginia Tech.) and Sally Aitken (Univ. of BC) edited a special issue in *Evolutionary Applications* featuring more than a dozen papers on non-model species. Presented studies demonstrated the value of a wide range of genomic approaches that can be used to better understand the biology of forest trees, including species that are widespread and managed for timber production, and others that are threatened or endangered, or serve important ecological roles.

PROJECTS ON THE STARTING LINE

Canada – US Forest Health Initiative

Future collaboration between the CFS and the USDA, in the context of upcoming environmental changes and the increased occurrence of pest and disease that threaten native tree species. CFS forest geneticists participated in workshops and wrote (N. Isabel) large-scale project proposals aimed at enhancing the resistance of ash to the Emerald Ash Borer (*Agrilus planipennis*).

Genomic Breeding Tools for Spruce

CFS supported (P. Lenz) the development of genomic resources for red spruce (*P. rubens*) that may support the discovery of species-specific genetic markers. This species is experiencing an increasing demand in Atlantic Canada due to its' better growth than the closely related black spruce (*P. mariana*).

UNPUBLISHED WORK

Terrestrial LiDAR in Genetic Trials

We led a pilot study combining terrestrial LiDAR (a remote sensing tool) with genetic evaluation for improved phenotyping of tree form and branch characteristics. Despite a small data set (200 trees from two sites), we found indications for weak to moderate genetic control for several crown characteristics, such as the projected ground surface of the crown or its hull volume. Genetic controls are in the same range as height growth, but estimates for genetic control and correlations among traits were associated with significant errors, which was probably due to the small sample size and reduced genetic base.

LiDAR Data Analyses From Progeny Trials

Although this field of research is quickly evolving, algorithms do not seem to be developed enough to pin down fine-scale tree form attributes, such as taper, branchiness, etc., in conifers such as spruce, in an automated way and with a sufficient resolution for genetic studies. While data acquisition with drones and data treatment will evolve in the next year, aerial data collection approaches seem promising and cost-efficient if the analyses bottleneck is overcome. Nevertheless, the terrestrial LiDAR approach was perceived as too invasive. Although it delivers more precise scans, a significant number of trees must be cleared to avoid occlusion during laser scanning, which leads to very heterogeneous competition in genetic test plantations.

Improvement of Somatic Embryogenesis Laboratory Protocols

Following economic analyses and the development of approaches to include genomic tools in breeding programs, it became clear that clonal reproduction methods could play an essential role in further enhancing selection intensity for forward selection. CFS developed improved protocols that allow for a better inclusion of tissue culture in the reproduction strategy following genomic selection based breeding approaches.

MEDIA PUBLICATIONS

Virtual tour: *Forest genomics: from science to practice*: We contributed to the production of a virtual tour based on the *FastTRAC* project.

English: <https://visitesvirtuelles.partenariat.qc.ca/fasttrac/en/app/presentation>

French: <https://visitesvirtuelles.partenariat.qc.ca/fasttrac/fr/accueil>

YouTube video explaining the integration of genomic selection into tree breeding.

English: <https://youtu.be/X7DADlgWdG8>

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AAFC-STB AGROFORESTRY UNIT - TREE IMPROVEMENT SUMMARY

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Keywords: shelterbelt, agroforestry, tree improvement, *ex situ* conservation.

The Prairie Shelterbelt Program was initiated by the Government of Canada in 1901 to provide farmers with hardy trees and shrubs for shelterbelts to protect farm yards, reduce soil erosion, protect livestock, enhance biodiversity, and improve air quality. From 1901 to 2013 over 600 million tree seedlings were provided to prairie farmers protecting more than 700,000 ha of agricultural land. Since the commencement of the Prairie Shelterbelt program in 1901, significant advances have been made in the selection and improvement of tree and shrub species provided through the program. The shelterbelt tree improvement program at Indian Head, designed specifically to develop adapted, genetically superior tree and shrub species for prairie shelterbelts, has been under way since the beginning of prairie settlement in the 1880s. Since then, tree improvement and evaluation has been led by Angus McKay (1888–1903), Norman Ross (1904–1941), John Walker (1942–1946), Bill Cram (1947–1974), Gordon Howe (1975–1980), William Schroeder (1981–2015), and Raju Soolanayakanahally (2010–present). Over the years a number of people have contributed to the tree improvement program, most notable were Carl Lindquist (1953–1984), Dan Walker (1984–2011), Garth Inouye (1995–2019), Salim Silim (2002–2010), Ron Gares (2012–2014), and Chris Stefner (2011–present). Improvement efforts touched many genera and species but focused primarily on *Populus*, *Pinus*, *Picea*, *Larix*, *Fraxinus*, *Quercus*, *Celtis* and *Salix*. During the 127 years, the program encompassed species introductions and testing, plant exploration, classical breeding and selection, *ex situ* conservation, and genomics. Since its inception, the breeding program developed 15 poplar clones and improved seed strains for over 20 species. The breeding efforts of the past 127 years have changed the landscape and quality of life for thousands of prairie people. In 2013, the last trees from the Prairie Shelterbelt Program were planted following over a century of Federal government support for tree planting in western Canada. This report presents a summary of the tree breeding program.

TREE IMPROVEMENT STRATEGY

With the commitment to establishing genetically diverse tree plantings the tree improvement program concentrated on developing superior seed propagated populations. The steps followed to accomplish this are: 1) sample the native range of the species, collect seed and assess the range of genetic variation in major traits using provenance trials, 2) superior trees were selected from provenance trials, vegetatively propagated and planted in clonal banks, 3) superior trees were crossed and their progeny evaluated under a variety of site conditions, and 4) based on the performance of progeny, trees in the clone bank were rogued leaving only trees that produce progeny with the desired traits. These rogued clone banks were transformed to seed production orchards.

QUERCUS MACROCARPA

Quercus macrocarpa (bur oak) improvement aimed to improve the adaptability of *Quercus* seed populations for prairie growing conditions, study genotype-environment interactions, and develop improved seed strains for prairie agroforestry. Since 1992, the oak improvement program has assembled over 300 populations, evaluated the populations in seed source trials at locations in Manitoba (MB), Saskatchewan (SK), and Alberta (AB) and developed an improved seed strain for agroforestry planting in the Canadian Prairies. A clonal seed orchard for the production of the improved seed strain is located at Indian Head, SK. Living bur oak germplasm collections are retained at Indian Head and Birch Hills, SK and Edmonton, AB.

LARIX SIBIRICA

Larix sibirica (Siberian larch) seedlings originating from the Ural mountains in western Siberia were planted at the Indian Head Forest Nursery Station in 1908. In 1976, progeny from the 1908 plantation were planted in shelterbelts at the PFRA Shelterbelt Centre at Indian Head. In 1983, 29 superior trees were selected from these shelterbelts and planted in a clonal seed orchard. Seed from these trees were tested as accession E5100 at 12 test locations in MB and SK. Performance of the seed strain was superior to other seed strains and sources at all trial sites. Referred to as 'Lindquist', this seed strain was used in the Agriculture and Agri-Food Canada (AAFC) Prairie Shelterbelt Program. The *Larix* improvement program has assembled multiple seed sources of *Larix* species from their native ranges in Eurasia. These living collections are retained at Indian Head and Birch Hills.

FRAXINUS PENNSYLVANICA

The *Fraxinus pennsylvanica* (green ash) improvement program was initiated in 1985 when superior trees were selected from native green ash stands in SK and MB. These trees were progeny tested and the top genotypes vegetatively propagated and planted in a seed orchard. The seed strain originating from this orchard was superior to other seed strains and sources at trial locations in MB and SK. The seed strain 'Plainsman' was used in the AAFC Prairie Shelterbelt Program and is widely planted throughout the prairie provinces. In 1996, additional seed sources were obtained from the northern Great Plains states. This and other *Fraxinus* germplasm has been retained in living collections at Indian Head, Birch Hills, and Outlook, SK and Smokey Lake, AB.

POPULUS

Since 1947, the poplar improvement program has been active testing populations from breeding programs, selecting and producing new hybrids and maintaining collections of poplar species and hybrids. From its beginning, the program has bred and evaluated over 40,000 *Populus* genotypes at 40 trial locations across the prairie provinces. This breeding program has released a total of 15 cultivars. Of these the most prominent are Walker, Assiniboine, Okanese, Katepwa, CanAm and Sundancer. These cultivars constitute the majority of poplars planted in the Canadian prairies for agroforestry and plantation forestry. Living collections of *Populus deltoides* (Indian Head), *P. balsamifera* L. (Indian Head and Prince Albert, SK; Quebec City, Quebec; Fairbanks, Alaska) and *P. simonii* (Indian Head) are retained in common gardens.

SALIX

At AAFC, the *ex situ* collections and resulting common garden trials will provide opportunities for a variety of studies in population genetics, climatic adaptation, long-term phenology responses of provenances, and ecophysiology studies. In addition, the collection will also provide foundation stock for basic research and to focus on trait assisted breeding. The current research mainly uses *S. eriocephala*, a native willow, as parental stock along with other native Canadian species such as *S. discolor* and *S. interior* along with introduced species such as *S. dasyclados* and *S. viminalis*. This led to the establishment of the Agriculture Canada *Salix* collection. Traits of interest are: coppice ability, height and biomass, growth form (compact, vertical growth), wood characterization (cellulose, hemicellulose, lignin), cold hardiness, salinity tolerance, and hyper accumulation of heavy metals on roots.

PINUS SYLVESTRIS

Provenance tests of Russian seed sources of *Pinus sylvestris* (Scots pine) were established in 1962 at the Agroforestry Development Centre, Indian Head. Data from these trials indicated that the 'balcania' ecotype from Voronezh, Province of Orel and Smolensk, as well as the 'eniseensis' ecotype from Central Siberia and the 'altaica' ecotype from southern Siberia were best adapted to the Canadian prairies. Plus trees from these populations were used in a breeding program to develop, hardy, fast growing trees with minimal winter browning and long needle retention. Full-sib progeny from crosses between selected trees were tested and the best performing parents vegetatively propagated and planted in a clonal seed orchard. Progeny from this seed orchard were extensively tested across the prairie provinces and proved to be superior to other seed strains. Referred to 'Prairie Green' Scots pine, this improved seed strain was used in the Agriculture and Agri-Food Canada Prairie Shelterbelt Program.

PINUS PONDEROSA

Provenance tests of northern Great Plains seed sources of *Pinus ponderosa* (ponderosa pine) were planted at Indian Head in 1969, 1984, and 1988. Results from these trials indicated that trees originating from Valentine and Ainsworth, Nebraska and Rosebud, South Dakota were well adapted to the Canadian prairies. Progeny testing of selected trees from these specific sources was completed and outstanding individual trees with superior growth and minimal winter browning selected. These trees were planted in a seed orchard for the production of an improved seed strain for the Canadian prairies. Living collections of *Pinus ponderosa* seed sources are retained at Indian Head.

PICEA PUNGENS

In 1959, vigorous *Picea pungens* (Colorado spruce) trees were selected from 1911 plantings on the Indian Head Forest Nursery Station. The selections were based on blue needle colour and overall vigour. These trees were crossed to identify the best parental combinations to generate a high percentage (> 90%) of progeny with silver-blue needle colour. In addition to having silver-blue needle colour, progeny from these trees have proven to be well adapted to southern prairie conditions withstanding drought and exposed treeless environments. The best performing parents were vegetatively propagated and planted in a seed orchard. This improved seed strain has been widely planted throughout the prairie provinces.

CELTIS OCCIDENTALIS

In 1990, staff from AAFC collected and propagated seed sources from native *Celtis occidentalis* (hackberry) stands in MB, North Dakota, and South Dakota. Seed source trials were established in MB and SK in 1993 and 1994. The trials are designed to determine which sources were best adapted to the prairies. Both trial sites were evaluated after 20 years and data showed large variability in adaptation of seed sources. One seed source originating from North Dakota produced high quality progeny. This source is a reliable seed stain for hackberry plantings in the Canadian prairies.

GENETIC RESOURCE COLLECTIONS

A major component of AAFC tree improvement was conservation of woody genetic resources. This included sampling native populations and establishment of common gardens. These collections facilitate access to genetic resources for breeding and the study of genetic diversity. The collections provided for *ex situ* conservation of native woody plant populations which supported AAFC's actions in biodiversity. The gene pool of collections was conserved in common gardens or gene banks established within the native range of the species. The vegetative collections include 756 populations and 24,500 individual genotypes of the following species: *Prunus virginiana* var. *melanocarpa*, *Crataegus rotundifolia*, *Shepherdia argentea*, *Hippophae rhamnoides*, *Symphoricarpos occidentalis*, *Quercus macrocarpa*, *Fraxinus pennsylvanica* var. *subintegerrima*, *Populus deltoides* var. *occidentalis*, *Populus balsamifera*, *Prunus nigra*, and *Prunus americana*. The majority of these living collections have been retained, most are on private property and receive little to no maintenance so long term viability or access is uncertain. In 2015, seed representing improved seed strains from the AAFC improvement program as well as seed collections for *Crataegus rotundifolia*, *Prunus pennsylvanica*, *Prunus virginiana*, *Rosa acicularis*, *Rosa woodsii* and *Symphoricarpos occidentalis* were transferred to the National Tree Seed Centre at Fredericton, New Brunswick.

LONG TERM GENETIC TESTS

The AAFC-STB Agroforestry Development Centre has established over 200 genetic trials in the prairie region. Genera included in the tests are *Pinus*, *Picea*, *Larix*, *Juniperous*, *Acer*, *Quercus*, *Populus*, *Salix*, *Prunus*, *Hippophae*, *Celtis*, *Symphoricarpos*, *Rosa*, *Shepherdia*, and *Fraxinus*. These tests were evaluated every five years for survival, growth, adaptability, and pest resistance. Information from the tests describes genetic variability within genera and is used to recommend new species and/or provide data to support release of new clones or seed strains. Some trials have been in place since the early 1960s. In 2014 all trials were surveyed and the majority were alive and in fair to good condition.

CONCLUSION

Tree improvement is an important activity and the sustainability of prairie tree plantings depends on our ability to maintain the biological and genetic diversity that is needed for healthy landscapes. It is important, especially with native plants, to work with the greatest degree of diversity possible allowing us to maintain healthy populations that have the genetics to withstand the movement of disease through a population of plants. This requires a continued commitment to the study of plant communities with less emphasis on individual specimens.

TREE IMPROVEMENT IN ALBERTA – CHALLENGES, OPPORTUNITIES, AND HIGHLIGHTED ACHIEVEMENTS

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Keywords: breeding, seed orchard, white spruce, *Picea glauca*, lodgepole pine, *Pinus contorta*, balsam poplar, *Populus balsamifera*, ecophysiology, quantitative genetics, forest policy, silviculture, growth and yield, wood density.

INTRODUCTION

For this activity report, I will provide a summary of a selection of research projects being undertaken in my Tree Improvement Lab, since I joined the University of Alberta in 2014 with my Industrial Research Chair (IRC) in Tree Improvement. The goal of this Chair is to fill knowledge gaps in both hardwood and softwood tree improvement programs needed to directly support policy decisions related to parental selection for orchards, clonal deployment standards, and integration of genetic gain into operational growth and yield models in Alberta. Specifically, with the industrial partners, the aims of the program highlighted in this report were to investigate hybrid vigour and ecophysiological responses in balsam poplar (*Populus balsamifera*), explore trade-offs between wood density and growth, enhance conelet bud and seed production in lodgepole pine (*Pinus contorta* var. *latifolia*), and incorporate genetic gain into growth and yield models. In addition, the IRC underwent a comprehensive assessment of how to value tree improvement in Alberta, to help Canadian mills and local communities meet their future wood fibre requirements. We also published findings of a greenhouse experiment that investigated the interactions between drought and genetics on the ecophysiology of lodgepole pine. Armed with new knowledge, the IRC program is providing industry and government with the science needed to make sound economic and policy decisions. Additional projects associated with realized gain trials have also been undertaken in the lab. Additional information can be found at <https://people.ales.ualberta.ca/barbthomas/>.

A second major program I lead is the “Resilient Forests (RES-FOR): Climate, Pests & Policy – Genomic Applications” grant, which began in 2015 and is a Genome Canada Large Scale Applied Research Project. This collaborative, interdisciplinary project, has brought together 13 academics, four universities and eight end-users, and aims to provide new information on tree improvement program selections for two commercial species in Alberta, lodgepole pine and white spruce (*Picea glauca*), using predictive models linking phenotype and genotype through genomic selection. Furthermore, we are expanding the phenotypic measurements being incorporated into the models beyond just height and diameter (volume), to include additional traits such as wood quality (density and microfibril angle), drought resistance, ecophysiological responses, insect resistance, and metabolomics linked to performance. In addition to the biological sciences, 50% of the project is focused on an economic analysis of tree improvement and genomic selection with incorporation of guiding work on the social acceptance of the use of this new technology in forestry. These two aspects are helping us understand how to both deliver out outcomes to the end-users but also for our end-users to be able to evaluate the costs and benefits of the investment options. This project integrates genomics, phenomics, chemical ecology, ecophysiology, metabolomics, social science, and economics. All publications to date are in the

realm of economics paving the way for application of this new technology.

HIGHLIGHTED PROJECTS

Investigation of Hybrid Vigour of Balsam Poplar (*Populus balsamifera* L.) – Hu and Thomas

In this project, led by PhD Candidate Bobby Hu, we tested the hypothesis that within species breeding of disparate populations of balsam poplar will lead to the expression of hybrid vigour. We explored the potential underlying mechanisms through both field and greenhouse assessments. Research questions addressed included: 1) is the length of the growing season linked to increased growth, 2) what role do endogenous hormones play in physiological and growth performance, and 3) what are the effects of site origin on growth performance and epigenetic responses of progeny to drought stress? In September 2009, three field trials (two in AB, Field AB1 and AB2, and one in Quebec (QC), Field QC) were established in conjunction with Alberta-Pacific Forest Industries Inc. (Al-Pac, where Thomas led the research program at that time) and Mr. Pierre Périnet (Ministry of Forestry, QC). Five male parents from each province, five female parents from QC, and four female parents from AB were used for breeding, for both within region and between region crosses. Based on the preliminary analysis of 6-year height and diameter from the AB field sites only, the AB x QC crosses ranked first for growth and were therefore selected for further study.

In order to test the role of endogenous hormones including links to physiological and growth performance in balsam poplar produced from disparate populations, a greenhouse study was undertaken and the trees were grown from selected families and progeny from the Ab x QC crosses, under near-optimal growing conditions. The stem tissue was analyzed for gibberellic acid (GA), indole 3-acetic acid (IAA), and abscisic acid (ABA) content in order to examine whether there was a causal relationship between hormone concentration in the elongating stem (internodes) tissue and growth rate of the vegetatively propagated progeny from these selected families (Hu and Thomas 2019). Field trials were also measured for both bud-burst and bud-set in 2017 and 2018 to determine if the length of growing season was linked to increased growth. Our results showed that progeny from AB x QC had the earliest bud burst and the latest bud set which resulted in a longer growing season which corresponded to greater growth, and is consistent with previous work on poplar bud phenology (Yu et al. 2001). In spring 2018, a second greenhouse study to test epigenetic responses was carried out to examine the effect of site origin on progeny (cuttings) performance under an abiotic drought stress treatment. The results confirmed that the same progeny grown in different locations show different behaviour under well-watered and drought conditions in a controlled, common environment indicating drought response of a given poplar genotype can be shaped by the history of that clone.

Trade-offs Between Wood Density and Growth in White Spruce (*Picea glauca*) – Matheson and Thomas

This project was undertaken by Robert Matheson, a MSc student, who defended his thesis Spring 2019. There were three objectives for this project, including: 1) assessing trade-offs between wood density and growth rate in selected superior families of white spruce, 2) comparing the wood density and growth rate of progeny from these superior families to their wild parents, and 3) linking drought tolerance to wood density and growth performance in the selected families.

Data were collected from three separate white spruce Controlled Parentage Programs (D1, H, and I) (GoA 2016) using a combination of a Resistograph Series 6 drilling resistance device (Rinntech), Pilodyn penetration depth (Hylec Controls), and using the displacement method to calculate wood density from 5 mm wood cores. Both Resistograph and Pilodyn provides a relative estimate of wood density in standing trees. In addition, the Resistograph device also provides an accurate measurement of stem diameter. Wood cores were extracted using a 5 mm increment borer for the purposes of assessing wood density using a volumetric

method and for the direct observation of the physical ring structure (ring width and early wood:late wood proportion). In total, approximately 3,500 trees were measured using Resistograph, 1,000 were measured using Pilodyn, and 500 cores were extracted across the three programs and ten progeny test sites during Summer 2017. The three programs selected for study represented four different industrial partners, as well as the Government of Alberta. Thus far, trade-offs between wood density and radial growth for the Region H Controlled Parentage Program (GoA 2016) were analyzed. The analysis showed that although there was a weak-moderately negative and significant correlation between wood density and radial growth at the phenotypic level, there was only a very weak and non-significant correlation between these traits at the genetic level. A similar analysis is planned for the D1 and I regions (GoA 2016), which will also incorporate comparisons of the selected families to their wild parents. A report detailing the results of this analysis is planned to be completed for the Fall 2019 meeting with our industry partners, fulfilling the first two objectives of this project. We plan to publish the results of this study, as well produce a paper detailing the technique for obtaining, processing, and analyzing Resistograph data in a way that maximizes the statistical power. The results of this project have the potential to influence selection decisions, as there is evidence of a positive correlation between wood density and drought resistance (Hacke et al. 2001). Specifically, Alberta is expected to experience greater levels of water stress under current climate change scenarios (Gray and Hamann 2015), which could place greater emphasis on selecting trees based on their ability to survive and thrive in drought conditions, rather than simply selecting for superior growth rates under current weather regimes. Robert is now the Tree Improvement Forester for Hinton Wood Products.

Enhanced Conelet Bud and Seed Production in Lodgepole Pine – Bockstette and Thomas

Lodgepole pine orchards in Alberta are under producing seed based on industrial objectives and orchard design capacity. To begin tackling this problem, we began with the traditional approach of hormone treatments and this project started with GA_{4/7} injections (Pharis, et al. 1987; Ross and Greenwood 1979; Kong et al. 2018) of thirty-four (32%) selected clones of a possible 110 clones in the B2 high elevation lodgepole pine seed orchard located at the Huallen seed orchard facility. The B2 orchard has failed to meet target production of seed since its inception while remaining a critical orchard for the mountain pine beetle (*Dendroctonus ponderosae*) - infested areas of AB. Trees were selected based on: 1) the number of available ramets equaling 12 or greater and 2) a minimum age of 12 years with planting in 2003 or earlier. Three ramets of each clone were treated on one of three treatment dates (June 30th, July 20th, Aug 6–7th, 2015) with three control ramets for a total of 12 trees per clone in most cases. Application rates were determined based on stump diameter above the graft union. The development of conelets, both treated and untreated, was monitored through repeated counting of conelets on three marked branches per tree between 2015–2017. In addition, the total number of mature cones produced by each tree included in this study was assessed each fall, with cone harvests in 2015 and 2016 representing untreated control yields and the final harvest in 2017 the yield after GA_{4/7} treatment application dates in summer 2015. Overall, we found that GA_{4/7} stem injections promoted female conelets in 40% of genotypes included in this study. For the 10 genotypes that responded, we found that the latitude of their provenance was positively correlated with later effective application time. Of the remaining 15 genotypes, five were hypersensitive to exogenous GA_{4/7} showing needle discolouration and loss, and 10 genotypes showed no response. In general, stem-injected GA_{4/7} did not affect the number of seeds per cone while two genotypes showed a reduced seed yield and one genotype showed increased seed yield per cone. Seed weights were not affected by the stem-injected GA_{4/7}, while the July application date resulted in higher germination rates compared to control trees. The findings from this study were recently published (Bockstette and Thomas 2019).

During this study, it also became obvious that a significant fraction of conelets emerging each spring did not stay on the branches to full maturity and that this would and was likely having the most significant impact on seed yields. In 2016, for example, more than 70% of newly emerged conelets appeared to die and fall off within a few weeks without an immediately obvious reason. Given the severity of this problem and at the

urging of our industry partners we continued monitoring conelet abortion through 2018 with an additional focus on potential underlying causes for this phenomenon. Initial findings from this work showed that conelet abortion seemed to be influenced by several factors including genotype, location within the orchard, and climatic variables. However, the exact underlying cause(s) remain unclear. In order to elucidate the underlying mechanisms and develop mechanisms for early detection and mitigation of early conelet abortion, Drs. Thomas and Bockstette, with input from our industry partners, developed and submitted a Natural Sciences and Engineering Research Council of Canada Collaborative Research Development grant proposal titled “Investigation of underlying causes for low seed yields in Alberta lodgepole pine seed orchards” that will allow us to address these questions. This more intensive investigation began summer 2019 looking at detail into the role of site conditions (nutrient and water availability, soil compaction), rootstock effects, genotype, pollen availability, and pollination success on conelet abortion. We will also test non-destructive ways to detect trees likely to suffer high conelet abortion through remote sensing technology, developing mitigation strategies such as targeted fertilization to promote conelet retention.

Growth and Yield Modeling in Lodgepole Pine and White Spruce – MGM vs. GYPSY – Thomas and Luo

This project is being conducted by PhD student Dawei Luo (started in Oct. 2017) using the serial tree height and diameter data of all progeny trials from nine white spruce breeding programs (Gray et al. 2016a) and six lodgepole pine (Gray et al. 2016b) breeding programs across Alberta (GoFA 2016). The preliminary results comparing two different equations, the commonly used Lambeth’s (1980) equation and the new Alberta specific equation (Rweyongeza 2016), show that both equations work well for prediction of age-age correlations at early ages for height of white spruce and lodgepole pine. Height-DBH (diameter breast height) curves across ages were generated. We found that improved white spruce and lodgepole pine have a larger DBH than wild trees at a given height. Therefore, we expect that gains in volume are likely underestimated through current methods and both height and DBH should be considered for estimating gains in volume.

In August 2018, to consider performance of improved conifers in mixedwood stands, 16 field sites were selected in Forest Management Units (FMUs) managed by Al-Pac, including two blocks of improved white spruce and two blocks of unimproved white spruce in each of the four selected FMUs. In each block, 36 white spruce were selected. Annual height growth and diameter growth of the subject white spruce trees and the competition around them were measured.

The next step of the project includes: 1) creating a ‘hybrid progeny test dataset’ to complete the age-age correlation and apply the adjusted age-age correlation equations into the existing growth and yield models in Alberta, 2) estimate the effect of moving seedlots based on updated growth and yield models, and 3) evaluate the inter-specific competition effect on improved and unimproved white spruce in mixedwood stands of northern Alberta. The results from this project can offer our industrial partners a better tool for predicting the product of improved white spruce and lodgepole pine in pure stands. In addition, it will also offer a reference for predicting growth of improved white spruce in mixedwood stands.

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**FOREST GENETICS AND TREE IMPROVEMENT ACTIVITIES FOR THE
ALBERTA TREE IMPROVEMENT AND SEED CENTRE
2017 – 2019**

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Keywords: whitebark pine, limber pine, climate change adaptation, lodgepole pine, jack pine, seed germination.

Forest genetics and tree improvement in Alberta began in 1975 focused on applied research to support collection and use of wild seed, tree breeding and seed production, seed biology and technology, conservation of genetic resources, and contribution to science and education. The earliest work was focused on provenance trials for spruces, pines, and tamarack; superior parent selection and establishment of seedling seed orchards for white spruce (*Picea glauca*) and lodgepole pine (*Pinus contorta* var. *latifolia*); and delineation of breeding regions. Forest genetics and tree improvement activities have since evolved into a dynamic program delivered by the Government of Alberta, private forest companies, and government-industry cooperatives. In collaboration with the University of Alberta and other academic and research institutions in and outside Alberta, the Alberta forest genetics and tree improvement program has made a significant contribution to the training of forest geneticists, tree breeders, and biologists engaged in forestry-related research in and outside Alberta.

This report provides a brief summary of the Alberta tree improvement program 45 years after its inception. The Alberta Tree Improvement and Seed Centre (ATISC) activity report for the period between June 2017 and May 2019 includes recovery of whitebark (*Pinus albicaulis*) and limber pine (*P. flexilis*), climate change adaptation provenance trials for lodgepole pine and jack pine (*P. banksiana*), and research in seed biology and technology. It also includes recent staff changes at ATISC.

GENE CONSERVATION AND RECOVERY OF ENDANGERED PINE SPECIES

Alberta Gene Conservation Plan

Gene conservation strategies for native species have been published online (ISBN 978-1-4601-4133-5) to guide implementation over the next decade. The 2018 conservation plan is a product of an extensive review and revision of the previous plan that was published in 2009. It includes new *in situ* and *ex situ* plans developed after identifying gaps and priorities, and takes into consideration our growing understanding of the pattern of genetic variation of major species in Alberta.

Whitebark and Limber Pine Recovery

Alberta continued to implement a provincial species recovery plan for whitebark and limber pine, which have been seriously affected by white pine blister rust (*Chronartium ribicola*) and mountain pine beetle (*Dendroctonus ponderosae*). To date, 228 and 59 plus trees of limber pine and whitebark pine, respectively, have been identified that are putatively resistant to white pine blister rust outside the National Parks. Of these, 162 limber pine and 22 whitebark pine trees are being screened for resistance with the first results expected in 2022. In 2018, seed was collected from 101 limber pine and 14 whitebark plus pine trees. We provided seed for 1,700 whitebark pine and 101 limber pine seedlings to provincial park and Parks Canada authorities for planting in habitats that have been decimated by white pine blister rust and the 2018 wildfire. These plantings, over 25 ha, will have a long term monitoring program.

A silviculture trial to release whitebark pine by removing competing vegetation at different spacing was completed in 2018. It treated 30 hectares in a replicated controlled design including 12 permanent sample plots using standard provincial protocols. In 2018, the Alberta Wildfire Management Branch identified many high value stands with monitoring plots and protected them from wildfire.

In 2016 and 2017, respectively, Alberta established one each of a series of whitebark and limber pine provenance trials. The whitebark pine trial was donated by the BC Ministry of Forests, Lands and Natural Resource Operations, whereas the limber pine trial was donated by the University of British Columbia and the USDA Forest Service, Intermountain Region. These trials will provide knowledge on the genecology of these endangered species and enables development of species-specific seed transfer guidelines to facilitate restoration and recovery.

In September 2017, the Alberta Government and Parks Canada hosted an international Whitebark Pine Ecosystem Foundation science and management workshop and field tour in Jasper, Alberta. The goal of the workshop was to share information on current research, policy, and restoration projects. It was attended by 91 attendees from governments, academia, industry, students, and independent individuals.

More information on whitebark and limber pine recovery is available in the Nutcracker Notes 31: 18–19, 35: 19, and 37: 20 accessible through the Whitebark Pine Ecosystem Foundation website, and the Tree Seed Working Group News Bulletin 65: 11–14 and 66:12.

CLIMATE CHANGE ADAPTATION TRIALS FOR LODGEPOLE AND JACK PINE

In spring of 2019, the Alberta Government in collaboration with forest companies involved in tree breeding established a new series of field trials for lodgepole pine, jack pine, and their putative hybrids. These trials are part of the ongoing efforts by the Alberta Government and its partners to generate data that will enable the province to develop better seed transfer guidelines for climate change adaptation. The series was established on five sites (Table 1) and contains 288 seedlots planted on all five sites. These seedlots are a combination of bulk wild populations from Alberta and British Columbia, and orchard bulk seedlots from Alberta and British Columbia lodgepole pine and jack pine tree breeding programs.

Table 1. Location and climatic description of new lodgepole and jack pine climate change adaptation trials in Alberta

LOCATION	LAT (°N)	LONG (°W)	ELEV (m)	MAT (°C)	MWMT (°C)	MCMT (°C)	TD	MAP (mm)	MSP (mm)	NDD	GDD	FFP
Machesis Lake	58.37	116.57	310	-0.8	16.6	-21.4	38.1	389	242	2465	1351	96
Virginia Hills	54.47	115.85	1127	1.1	13.9	-12.7	26.6	636	434	1502	1017	95
Muskeg Grande Cache	53.89	118.72	1505	0.2	11.4	-11.7	23.1	621	369	1420	639	38
Brooks	50.55	111.83	746	4.1	18.4	-12.5	30.8	333	216	1233	1737	113
Blairmore	49.73	114.47	1796	1.3	13.0	-10.0	23.0	759	291	1213	819	70

MAT – mean annual temperature; MWMT and MCMT – mean temperature for the warmest and coldest months, respectively; TD – continentality (MWMT minus MCMT); MAP – mean annual precipitation; NDD and GDD – degree days below 0°C and above 5°C, respectively; FFP – frost-free period.

Collectively, wild populations included in this series of field trials originated from 46°N to 65°N and 91 m to 2,056 m above sea level.

After one growing season of free growth after germination, 47 populations were selected to span the entire latitudinal and elevation range of all tested wild populations. Height of five randomly selected seedlings were measured in each population and averaged. The same measurements for the 13 bulk orchard seedlots from Alberta and British Columbia pine breeding programs were completed. Figure 1 shows that even at a free growth stage in the greenhouse, when seedlings have not been exposed to any treatment to simulate a response to a change in the environment, a gentle altitudinal cline exists among populations.

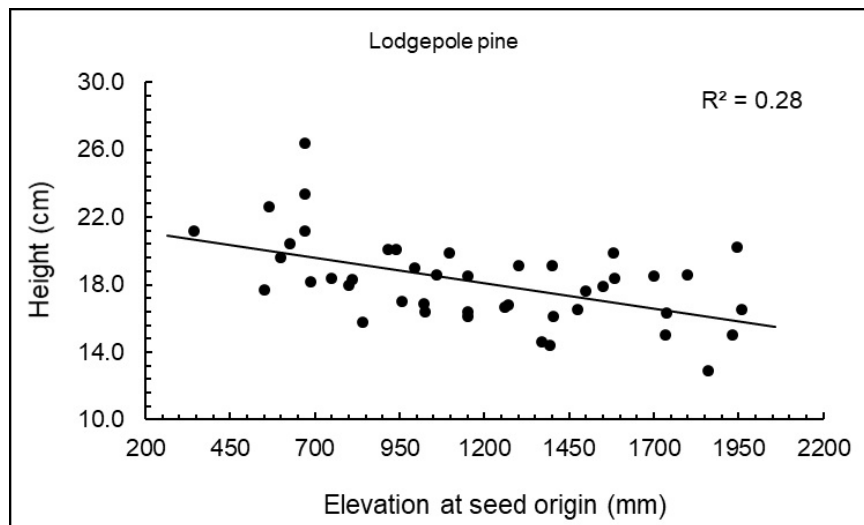


Figure 1. Post-germination free growth height of 44 wild lodgepole pine populations selected to span the range of tested population.

Figure 2 shows height of different types of seedlots from Alberta and British Columbia to illustrate the existence of regional variation among wild populations and breeding programs. These seedlots are wild lodgepole pine from Alberta (AB PL), wild jack pine from Alberta (AB PJ), putative lodgepole-jack pine hybrids from Alberta (AB PX), wild lodgepole pine from British Columbia (BC WD), orchard seedlots from Alberta lodgepole (A, B1, B2, C, J, K1) and jack (P1) pine breeding programs, and orchard seedlots from

British Columbia lodgepole pine breeding programs (BC BV, BC PG, BC NE, BC CP, BC TO). Notice height differences between orchard and wild seedlings in BC populations, which is not reflected between wild and orchard populations in Alberta.

It should be noted that the number of seedlings measured for each population was very small and the sixty selected populations are only a fraction of the 288 populations in the trials. Thus, these figures are for demonstration purpose only and do not suggest that the 288 populations will respond the same way when exposed to variation in seasonal weather and long-term temperature and precipitation conditions, and photoperiod in the field.

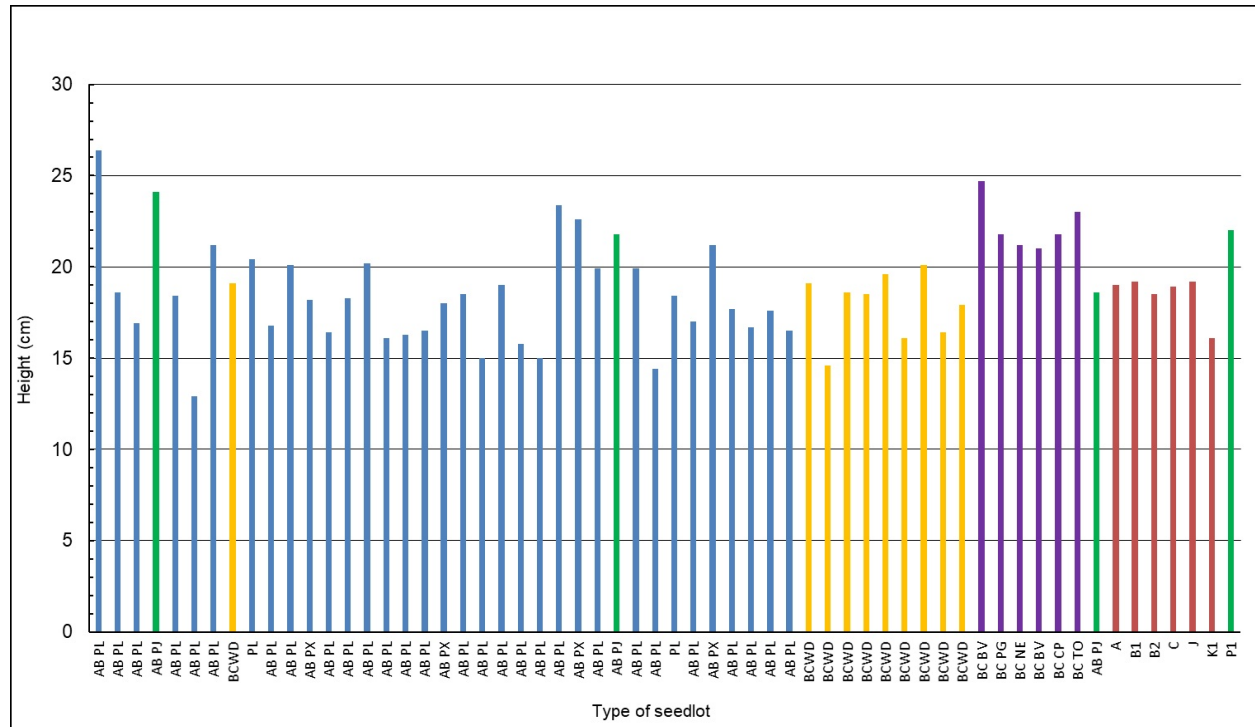


Figure 2. First growing season height (free growth) of selected wild and orchard populations of lodgepole and jack pine from Alberta and British Columbia.

ORGANIZATION AND ADMINISTRATION OF TREE IMPROVEMENT AND MANAGEMENT OF FOREST GENETIC RESOURCES IN ALBERTA

As part of this report, a brief description of the organization and administration of tree improvement in Alberta is provided as part of reporting and documentation on the management of forest genetic resources in Canada.

The Alberta tree improvement program commenced in 1975 with the establishment of conifer provenance trials, breeding regions, and progeny trials. To date, the program has 21 breeding programs for conifers and 3 for poplars. White spruce and lodgepole pine constitute more than 80% of trees planted in Alberta annually. Consequently, the two species form a bulk of the Alberta tree improvement activities for both the Alberta Government and private forest companies. Research in forest genetics both in government and the University of Alberta are also centered on white spruce and lodgepole pine. There are three types of ownership of tree breeding programs in Alberta as follows:

- 1) Programs that are completely owned and operated by the Alberta Government. There are four white spruce programs in the boreal forest as a major species, and one program for each of black spruce (*Picea mariana*), Douglas-fir (*Pseudotsuga menziesii*), and western larch (*Larix occidentalis*) as minor species.
- 2) Programs completely owned and operated by private forest companies. There are three programs for white spruce, five for lodgepole pine, two for black spruce, two for aspen (*Populus tremuloides*), and one for balsam poplar (*Populus balsamifera*). A majority of these programs are owned by tree improvement cooperatives of forest companies.
- 3) Programs jointly owned and operated by cooperatives composed of the Alberta Government and forest companies. There are two programs for white spruce, one for lodgepole pine and one for jack pine.

All three categories of tree breeding programs produce seed or vegetative propagules for reforestation on public land. Consequently, the Alberta Government regulates activities of all tree breeding programs. This ensures that all materials used for reforestation on public land are of known source, genetically adapted to planting areas, and meet a provincially mandated minimum genetic diversity measured by the effective population size. All seed is registered and stored with the government to ensure identity tracking and deployment to appropriate locations. The *Alberta Forest Genetic Resource Management and Conservation Standards* (FGRMS) is a system of rules which regulates sourcing, development, and use of forest genetic materials on public land. Likewise, prediction and verification of genetic gain is implemented through the standards. The FGRMS are publicly available by searching the name of the document.

The main goal of tree breeding in Alberta is increasing wood fibre production through selection and breeding for fast growth and reduction of wood loss through damage by insects and diseases. Thus, tolerance to common insects such as white pine weevil in spruce and terminal weevil (*Pissoides terminalis*) in lodgepole pine, and diseases especially western gall rust (*Endocronartium harknessii*) in lodgepole and jack pine are considered in the selection and breeding for growth rate. Maintenance of wood mechanical properties, especially wood density, is required for all breeding programs. In the past 15 years, Alberta has been increasingly integrating climate change adaptation in tree improvement. The Tree Species Adaptation Risk Management project is such an example (see reports on [Emissions Reduction Alberta](#) website).

In the past 15 years, the Alberta Forest Genetic Resources Council ([AFGRC](#)) has been instrumental in articulating a balanced approach to tree breeding to increase wood fibre production while maintaining genetic diversity and gene conservation on public land. The Council is a multi-sectoral body with members from Alberta Government, forest companies, University of Alberta, Canadian Forest Service, forest nurseries serving both the forestry and energy sector, and Forest Growth Organization of Western Canada. The role of the council is to provide a forum for discussing challenges of and solutions for managing forest genetic resources on public land while maintaining a vibrant forestry and energy industrial sectors, and provide appropriate advice to the Alberta Government. Research in forest genetics and related fields such as climate change adaptation, gene conservation, and recovery of endangered species are part of the Council's priorities.

SEED BIOLOGY AND TECHNOLOGY

The seed biology and technology program at ATISC manages Alberta's long-term conservation and research seed collections. This seed bank also provides the majority of research tree seed for provincial tree improvement program activities and academic forest genetic research. The seed lab research endeavours to further Alberta's knowledge of seed physiology in order to advise practical methods for industry seed handling and use.

Due to popular demand, ATISC held its 9th and 10th edition of our Seed Conservation Course in the spring of 2019. Over 100 participants coming from five provinces across Canada have attended to date. The course covers all aspects of applied seed science including collection, handling, and storage through to germination and viability monitoring programs.

Seed Testing Standards and Technical Notes Series

The 2017 harvest year marked the first implementation of Alberta's new 2016 Seed Testing Standards. There were a few questions and practicalities that were ironed out and the Standards are being upheld. At the request of industry seed owners, in spring 2018 ATISC held an aspen seed collection and handling seminar in Edmonton. The spring 2018 aspen harvest was a bumper crop and handling procedures were improved by all parties involved. Seed samples will go into ATISC's viability monitoring program. A follow up document produced from the seminar sparked the production of an ATISC Tech Notes series, aimed at relaying seed and propagation research and applications to the public. To date, there are 15 titles planned and the first 5 regarding the endangered 5-needle pines should be available in fall 2019.

There were concerns about a drop in seed production from one of Alberta's southern lodgepole pine orchards in 2017, so a seed abortion trial was conducted over the summer of 2018. The resulting report showed that the low seed crop in 2017 was most likely due to changing climate conditions at the site, including a few years of early snow melt followed by severe drought. Seed numbers per cone increased in 2018 and it is projected that with the changes to site management implemented in 2018, seed numbers should be back close to normal in the 2019 harvest.

A quality control trial was conducted using cones from 2 of Alberta's pine orchards by sending cones to two different extraction and testing facilities. ATISC then ran moisture tests, germination, and longevity tests to identify differences in test results and handling methods between the facilities. The outcome has provided data to work with the facilities to recognize potential problems and improve overall seed production for Alberta.

Reclamation Shrub Seed Research

For many of the reclamation species now being stored at ATISC for use in oilsands and oil and gas reclamation work, little is known regarding correct seed handling or germination methods. It is essential to address these issues to improve seed quality and empower seed owners with more knowledgeable control over their seed and reclamation plans.

ATISC developed a project in 2014 that included 14 woody shrub species identified as having propagation issues and used in northwest Alberta oil sands and oil and gas reclamation projects. The project is in three sections: tetrazolium (TZ) quality evaluation methods, practical germination protocols, and seed storage longevity. An update on the work was presented at the Northern Alberta Institute of Technology Centre for Boreal Research's Native Plants Seminar in November 2018. The first TZ section was completed in 2017 and factorial germination trials for six species ran during 2018, using seed generously donated from industry. ATISC also began separate hazel (*Corylus* spp.) germination and storage behaviour research in 2013 and has now completed three rounds of trials that are awaiting a full written report.

STAFF CHANGES AT ATISC

During the 2017–2019 reporting period, Katherine Spencer moved from the ATISC to British Columbia where she is currently the Skimikin Seed Orchard Manager. While at ATISC, Katherine did excellent work in the Mountain Pine Beetle program and later as a Tree Physiologist for the government and government-industry cooperative tree breeding programs. John Quinn retired after a long and excellent career with the Alberta Public Service. Most of John's career was with ATISC as a Seed Orchard Manager and forester overseeing establishment, management, and measurement of field trials; establishment and maintenance of seed orchards; seed collection; establishment and management of clonal banks; and superior parent tree selections. Dr. Dasvinder Kambo joined ATISC as a Tree Physiologist. Dasvinder is from Ontario but he is not new to western Canada where he has previously spent cold winters for his research in forest ecology in the Yukon Territory.

ACKNOWLEDGEMENTS

The authors of this report acknowledge and thank all staff of the Alberta Tree Improvement and Seed Centre for their professionalism, dedication and effort that have contributed to the success of the Alberta tree improvement program through plant propagation, field and laboratory work, data management, planning, and administration. They include Jeannette Lupaschuck, Lori Siemens, Eleanor Morin, Karen Wood, Clarissa Mazur, Pearl Gutknecht, Pat Franchuk, Raine Dekinder, and Shane Turko. We thank Tyler Stone (Manning, AB), Steve Maychak and Brianne Olson (Brooks, AB), and Doug Hankinson (Wandering River, AB) who attended to our seed orchards outside Smoky Lake. Special thank you to Erica Samis, Caroline Whitehouse, Devon Belanger, and David Tellier in the Forest Health and Adaptation Section, Forest Management Branch in Edmonton for their continuous support of the tree improvement program through administration, field work, technical assistance in orchard cone insects, and GIS. We thank Dr. Tod Ramsfield of the Northern Forestry Centre, Canadian Forest Service in Edmonton for his support on forest diseases in our field trials, seed orchards, and clonal banks.

PUBLICATIONS

- Benowicz, A.; Krakowski, J.; Rweyongeza, D. 2019. Growth and survival of Siberian larch in Alberta at the species, population and family level. Canadian Journal of Forest Research. <https://doi.org/10.1139/cjfr-2019-0014>.
- Krakowski, J. 2017. One piece of the puzzle: 5-needle pine *ex situ* conservation in Alberta. Canadian Forest Genetics Association, Tree Seed Working Group News Bulletin 65: 11–14.
- Sebastian-Azcona J.; Hamann, A.; Hacke, U.G.; Rweyongeza, D. 2018. Survival, growth and cold hardiness tradeoffs in white spruce populations: Implications for assisted migration. Forest Ecology and Management 433: 544 – 552. <https://doi.org/10.1016/j.foreco.2018.10.046>.

COADAPTREE: HEALTHY TREES FOR FUTURE CLIMATES

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Typically when replanting, foresters use local tree seed for reforestation. Local populations are generally thought to be the best choice as they have, over long periods of time, adapted to the climate conditions of the site. However, with a rapidly changing climate, it is expected that local populations will be quickly mismatched – potentially within their lifespans, resulting in a widespread maladaptation to both future climate and predicted changes in forest pests and pathogens. The aim of CoAdapTree is to develop strategies and recommendations, such as climate based seed transfer and assisted migration that will help us grow healthy forests that are better adapted to future conditions. The CoAdapTree Project also aims to develop genomic tools and strategies for improved tree breeding, not only for warmer or drier climate conditions but also for resistance to pathogens.

Building on the findings of the previous project AdapTree (2011–2015) which revealed a genetic basis for cold-adaptation in lodgepole pine (*Pinus contorta*) and interior spruce (*Picea engelmannii* x *glauca*), the CoAdapTree project (2016–2020) examines the patterns and extent of parallel adaptation along climatic gradients for Douglas-fir (*Pseudotsuga menziesii*), western larch (*Larix occidentalis*), and jack pine (*Pinus banksiana*). We also study Dothistroma needle blight (*Dothistroma septosporum*) and Swiss needle cast (*Phaeocryptopus gaeumannii*), important diseases of lodgepole pine and Douglas-fir, which are predicted to have an increased impact as climates warm. We study variability in both pathogen and host and search for candidate genes for resistance or tolerance, in order to include them in a SNP array. The project includes a study of the societal dimensions of climate adaptation.

This Genome Canada funded, large scale, applied genomics project runs from October 2016 to September 2020. There are 16 additional sponsors and several seed donors. All in all, some 35 people are working on this project, many in other labs and other universities. For details, as well as a list of publications, please visit our website <http://coadaptree.forestry.ubc.ca/>

LANDSCAPE GENOMICS OF DOUGLAS-FIR: UNDERSTANDING ITS ADAPTIVE POTENTIAL FOR FUTURE CLIMATIC CONDITIONS

Rafael Candido Ribeiro (PhD student)

Douglas-fir is an ecologically and economically important conifer in its natural range in western North America, and also in other parts of the world where it was introduced for wood supply. Based on projected climatic changes and species climatic niche models, Douglas-fir may have its habitat expanded in some regions while drastically contracted in others. It is unknown which populations may persist or expand under new conditions in the near future, especially if novel climates and other climatic and adaptive genetic uncertainties are taken into account. Assisted gene flow (AGF) strategies have the potential to mitigate the effects of adaptational lags by moving adaptive alleles across populations and subsequently, on a broader scale, reducing the negative impact of climate change on species natural ranges.

Given the incomplete understanding of the adaptation of Douglas-fir to future climates, the general goal of this project is to investigate the evolutionary potential of this species to adapt to extreme cold and drought conditions, and additionally, describe the distribution of phenotypes and genotypes underlying these adaptations throughout the species' natural range. I will integrate: 1) phenotypic data from three controlled

common garden experiments (87 different seed sources), 2) climatic data from each of the seed sources, and 3) genomic data from targeted sequence capture (DNA) sequences. My results will be used to better inform AGF among Douglas-fir populations.

PHENOTYPIC AND GENOMIC PATTERNS OF CLIMATE ADAPTATION IN WESTERN LARCH

Beth Roskilly (PhD student)

Shifting climates are disrupting historical patterns of local adaptation in tree populations, introducing a pressing need to understand the risks posed by climate change and mitigation strategies such as assisted gene flow. Climate niche modeling projects that areas of future suitable climate for western larch will stretch north of its contemporary distribution, making it a desirable candidate for assisted migration trials. I am studying local adaptation to climate in western larch populations across its current natural range by combining phenotypic data on traits related to phenology, cold, and drought tolerance from natural and selectively-bred populations in common garden experiments with genomic data (exome capture) from a long-term provenance trial. We will use these data to test associations between phenotypic and genomic variation among populations with climate and to assess vulnerabilities related to climate change and inform assisted migration strategies as a part of the CoAdapTree project.

CENTRE FOR FOREST CONSERVATION GENETICS

**Sally Aitken, Tongli Wang, Ian McLachlan, Joane Elleouet, Vincent Hanlon,
Colin Mahoney, Jon Degner and Iain Reid**

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The following projects at the Centre for Forest Conservation Genetics were active during 2017–2019:
<https://cfcg.forestry.ubc.ca/projects/>

EVALUATING GENOME-WIDE EFFECTS OF SELECTIVE BREEDING ON ADAPTIVE DIVERSITY IN REFORESTATION SEEDLOTS FOR FUTURE CLIMATES Ian McLachlan (PhD 2017)

Climate change is predicted to generate climatic envelope shifts for tree species and cause locally adapted provenances to become disconnected from their current climatic optima. It is predicted that short-term evolutionary adaptive responses of locally adapted tree populations will be insufficient to match these shifts in local climatic optima, resulting in an adaptive lag and reduced timber production. The use of locally sourced seedlots for selective breeding programs creates the possibility that reforestation seedlots will also suffer an adaptive lag and experience lower productivity. However, we do not know how well selectively bred seedlots are adapted to their local climatic optima and what degree of adaptive lag they might experience. This limits our ability to evaluate how assisted migration strategies may be used to safely mitigate decreases in forest productivity due to climate change.

AdapTree (2011–2015), a large scale genomics project, aimed to elucidate the basis of adaptive molecular genetic variation in lodgepole pine (*Pinus contorta*) and interior spruce (*Picea glauca* x *engelmannii*). I compared reforestation seedlots from natural stands and selective breeding programs to investigate how selective breeding impacts upon adaptive genomic diversity and divergence. For each species, seedling common gardens containing ~3000 individuals were established to provide phenotypic data on several climatically and silviculturally relevant traits, and genotypes for a suite of >1,500 adaptive SNPs (DNA sequence variations). By making carefully selected phenotypic and population genomic comparisons between seedlot types, my research determined whether selective breeding causes adaptive deviations from populations under natural selection regimes. This allowed me to assess how well selectively bred reforestation seedlots match their current and future climatic optima. The findings allowed an evaluation of the current provincial seedlot diversity standards and provided vital information to guide the development of assisted migration policies for selectively bred seedlots that strive to maintain forest productivity in BC and Alberta.

MacLachlan, I.R.; Yeaman, S.; Aitken, S.N. 2017. Growth gains from selective breeding in a spruce hybrid zone do not compromise local adaptation to climate. *Evolutionary Applications*. doi: 10.1111/eva.12525.

MacLachlan, I.R.; Wang, T.; Hamann, A.; Smets, P.; Aitken, S.N. 2017. Selective breeding of lodgepole pine increases growth and maintains climatic adaptation. *Forest Ecology and Management* 391: 404–416.

TRAJECTORIES OF CLIMATE CHANGE IN BRITISH COLUMBIA: INVESTIGATING CLIMATE VARIABILITY, DIFFERENTIATION, AND NOVELTY USING THE BIOGEOCLIMATIC ECOSYSTEM CLASSIFICATION

Colin Mahony (PhD 2018)

The Biogeoclimatic Ecosystem Classification (BEC) is a widely-used knowledge base for forest management in British Columbia. Climate change represents both an opportunity and a threat for the BEC system. The BEC climatic classification is a powerful tool for understanding and adapting to climate change. However, much work is required to adapt BEC to a changing climate.

The broad objectives of this project were to: 1) use ClimateBC and other newly available climate data to better understand the BEC climate classification and 2) use the BEC system to understand climate change in BC's forests. This project built on past CFCG climate change research by incorporating historical climate variability into climate envelope models of BEC climate units. This approach allowed us to pursue the following research questions: 1) How does the historical climatic variability within BEC climate units compare to the climatic differences between BEC climate units? 2) How does projected climate change compare to historical climate variability in various regions of the province? 3) Do existing BEC climate units represent viable analogs for projected future climatic conditions, or are novel (no-analog) climates emerging? We investigated these questions on elevational and latitudinal transects in several regions of BC and the province as a whole.

Mahony, C.R.; Cannon, A.J. 2018. Wetter summers can intensify departures from natural variability in a warming climate. *Nature Communications* 9: 783. <http://doi:10.1038/s41467-018-03132-z>.

Mahony, C.R.; Cannon, A.J.; Wang, T.; Aitken, S.N. 2017. A closer look at novel climates: new methods and insights at continental to landscape scales. *Global Change Biology* 23 (9): 3934–3955.

RANGE EXPANSION AND ADAPTATION OF SITKA SPRUCE

Jo Elleouet (PhD 2018)

Sitka spruce (*Picea sitchensis*) has a long and narrow distribution that spans the Pacific coast of North America from California to Alaska. In spite of a quick post-glacial colonization and a young and still expanding northern population, this species shows pronounced clinal variation in climate-related traits along its entire range. Moreover, there is strong evidence for both local adaptation and phenotypic plasticity for these adaptive traits across the range. The paradox between recent colonization history and apparently high level of adaptation raises several interesting questions about the processes that potentially influence adaptation in Sitka spruce. This research provides a better understanding of the mechanisms and extent of adaptation to climate in natural populations through addressing some of the following topics.

First, the mode and history of colonization may have an influence on the adaptive potential of the species. To address this issue, a study of the population genetic structure using molecular markers can be used to infer long-term processes of range expansion. This approach can be coupled with a more localized study of populations at the current edges of the range to infer short-term processes of range expansion.

It has been shown in other spruce species that rapid adaptation of recently established populations can be enhanced by a mechanism of epigenetic memory during embryogenesis. Testing this hypothesis in Sitka spruce could help deciphering the genetic and epigenetic contribution to adaptation, and can strongly influence predictions about the potential and speed of adaptation in a climate change context.

Another key factor influencing adaptation in natural populations is migration and, more generally, the level of gene flow. It is possible to study the effect of gene flow by comparing the levels of adaptation in isolated and continuous populations.

Elleouet, J.S.; Aitken, S.N. 2018. Exploring Approximate Bayesian Computation for inferring recent demographic history with genomic markers in non-model species. *Molecular Ecology Resources* 18: 525–540. doi: 10.1111/1755-0998.12758.

SOMATIC MUTATION IN SITKA SPRUCE

Vincent Hanlon (PhD 2019)

In evolution, a distinction is commonly drawn between mutations that occur in the body of an organism (somatic mutations) and mutations that occur in reproductive tissue (germline mutations). This is because in many animals, only the latter can be inherited by offspring. But this distinction is blurred in plants, since the same cells that build stems and branches, i.e., cells in apical meristems, also produce pollen and ovules. This means that some somatic mutations in plants can be inherited.

The inheritance of somatic mutations may be particularly important for the evolution of trees. Somatic mutations are predicted to accumulate either during DNA replication or due to sources of DNA damage, such as UV light, that are relatively constant through time. When the apical meristems of large trees must undergo many cell divisions (and thus many rounds of DNA replication) for height growth, and when old trees are exposed to time-dependent sources of DNA damage for decades or centuries, trees are predicted to accumulate many somatic mutations.

We studied an exceptionally tall population of old growth Sitka spruce (*Picea sitchensis*) in the Carmanah Valley, Vancouver Island to estimate the rate at which somatic mutations accumulate. We sequenced DNA from paired tissue samples taken from the top and bottom of 20 trees. Genetic differences between two samples from a tree are somatic mutations that happened during the tree's lifetime. The somatic mutation rate we calculated is very high per generation, but very low per year. That is, mutations accumulate more slowly in trees than in other species, but their lifetimes can be so long that they produce more mutations in the end.

Most new mutations are expected to be deleterious, or harmful. This means that for tree populations, a large boost to the per-generation mutation rate because of somatic mutations is expected to increase the frequency of harmful genetic variants. This should make trees less well-adapted to local conditions, for example. But more rarely, some new mutations are expected to be beneficial, meaning that trees should also obtain an unusual large number of new genetic variants that could facilitate adaptation. If natural selection works efficiently to separate harmful genetic variants from beneficial ones and increase the frequency of the latter, then a high per-generation somatic mutation rate could help trees overcome the evolutionary delays incurred by their long generation times and adapt to new or fast-changing conditions.

Hanlon, V.C.T.; Otto, S.P.; Aitken, S.N. 2019. Somatic mutations substantially increase the per generation mutation rate in the conifer *Picea sitchensis*. *Evolution Letters* 3(4): 348–358. <https://doi.org/10.1002/evl3.121>.

EXPLORING GENOME POROSITY IN THE INTERIOR SPRUCE HYBRID ZONE

Jon Degner (PhD candidate)

Interspecific hybridization is an important source of genetic variation for many plant species, playing prominent roles in adaptation and speciation. White spruce (*Picea glauca*) and Engelmann spruce (*P. engelmannii*) are closely related North American conifers that extensively hybridize over large areas in British Columbia and Alberta where their ranges overlap, forming a stable hybrid zone. The assortment of advanced-generation hybrids and backcrosses are collectively referred to as interior spruce. Recent research suggests that the interior spruce hybrid zone is ancient and has been maintained by hybrids possessing high fitness in environments intermediate to the parent species. While a candidate SNP study found disproportionately high Engelmann spruce ancestry in hybrids within British Columbia, a comprehensive genomic analysis of variation in ancestry across the entirety of the hybrid zone has yet to be performed. Additionally, recent advances in genomic software now allow the identification of alleles with excessive or deficient ancestry in hybrids. This opens up the possibility of identifying loci that may be responsible for maintaining species boundaries between white and Engelmann spruce despite extensive hybridization, as well as identifying alleles that are present across many genomic and geographic backgrounds which may be facilitating hybrid vigour in intermediate environments.

The *AdapTree* project has generated an extensive genomic dataset covering thousands of genic and regulatory regions in hundreds of hybrid individuals throughout the hybrid zone. This dataset was utilized to answer several standing questions regarding the genomics of hybridization in the interior spruce hybrid zone: 1) How freely do alleles move between species via their hybrids, i.e., how porous is the interior spruce genome? 2) Are species boundaries maintained by a few genomic regions of low porosity? 3) Are alleles which exhibit particularly high or low porosity associated with phenotypic and environmental clines across the hybrid zone, i.e., is there evidence of adaptive introgression? 4) Are non-porous genes enriched for functional categories associated with reproductive isolation?

WHITEBARK PINE DISEASE RESISTANCE FOR CONSERVATION

Iain Reid (M.Sc. Student)

Whitebark pine (*Pinus albicaulis*) is listed as endangered in Canada and has been proposed for endangered listing in the United States mainly due to the combined impacts of white pine blister rust (*Cronartium ribicola*), mountain pine beetle (*Dendroctonus ponderosae*), fire suppression, and climate change. White pine blister rust represents the most widespread and direct threat to whitebark pine. Mechanisms of resistance in whitebark pine are variable, and further study is needed to determine the frequency and types of resistance. No complete resistance (HR) has been detected in whitebark pine so far, but partial resistance has. Screening of seed stock for rust resistance is already occurring at the Dorena Genetic Resource Centre, Coeur D'Alene Nursery and Kalamalka Forestry Centre, where field collected seed is being grown, seedlings are control inoculated with rust spores, and identification of more rust resistant parent trees is occurring. Results from rust resistance trials can serve to find parent trees from which to collect seed for restoration planting.

A trial from approximately 500 families and 46 populations across the species range was established by Cartwright, Ukrainetz, and Murray (BC Ministry of FLNRORD), at Skimikin nursery near Salmon Arm, BC, with a nearby *Ribes* garden providing natural inoculation. Series 1 seedlings (age 5) are ready for phenotyping for blister rust. Objectives for this study are to: 1) contribute to early-stage phenotyping efforts to identify more blister rust resistant or tolerant whitebark pine progeny and locations of their parent trees, 2) examine if proximity to *Ribes* plants affects likelihood of infection by white pine blister rust in a nursery setting, and 3) determine the relationships between environmental variables for provenance location and blister rust symptoms.

EVALUATION OF CONSERVATION STATUS OF NATIVE TREE SPECIES IN BRITISH COLUMBIA

Tongli Wang

The conservation of forest genetic resources is essential to maintain the capacity of forest trees and the forest sector to adapt to climate change. British Columbia (BC) spans a wide range of climates, and supports exceptionally high species richness and ecosystem diversity. The maintenance of natural levels of genetic diversity of BC's native tree species is the main goal of the BC Forest Genetic Council. In BC, the conservation of forest tree species is primarily achieved through *in situ* protection in protected areas, complimented by *ex situ* (seed storage) protection. An assessment of the protection status of BC's tree species is critical to help prioritize efforts towards establishing new protected areas and to direct seed collection and storage activities for conservation purposes.

An initial assessment was conducted in 2005. Since then, additional protected areas have been established; the BEC system, the framework of the initial assessment, has gone through substantial changes from version 4 to 10. In addition, major improvements were made to the ecological plot dataset. Thus, a reassessment of conservation genetic status is seen as imperative. The reassessment is based on a gap analysis using an updated protected area database, the latest BEC system (ver. 10), and the improved ecological plot dataset considering both *in situ* and *ex situ* protection. A report summarizing this assessment is to be released in 2019.

ClimateBC/NA – A TOOL TO GENERATE SCALE-FREE CLIMATE DATA SUPPORTING GENECOLOGY AND LANDSCAPE GENOMICS

Tongli Wang

High quality climate data are essential to conducting genecology and landscape genomics studies. Although a large volume of climate data have become available in recent years, these datasets are in grid format at various spatial resolutions. The climate models developed at the Centre are scale-free and location specific with higher accuracy. The models cover BC and North America. These models integrate paleo, historical, and future climate data into a single package, and generates a large number of biologically relevant climate variables. These models have over 1,300 subscribers and have been cited over 1,500 times. They have become essential tools for climate and climate change related studies and applications. More information is available at: <http://cfcg.forestry.ubc.ca/projects/climate-data/climatebcwna/>.

**BRITISH COLUMBIA MINISTRY OF FORESTS, LANDS AND NATURAL
RESOURCE OPERATIONS**

**Charlie Cartwright, Lise Van Der Merve, John Russell, Michael Stoehr, Nick Ukrainetz,
Trevor Doerkson, Marie Vance, Ward Strong and Alvin Yanchuk**

**Forest Improvement and Research Management Branch
Ministry of Forests, Lands and Natural Resource Operations and Rural Development
Victoria, BC**

OVERVIEW OF THE GENETIC SECTION
(Alvin Yanchuk and Michael Stoehr)

About two years ago, Tree Improvement Branch was renamed to Forest Improvement and Research Management (FIRM) Branch. While tree breeding, genetic conservation, seed transfer research, along with the Ministry's seed orchard program still operates within this new Branch, the Provincial Research Program (i.e., any research activities in the other disciplines in forest research), are now coordinated by FIRM. So, business as usual for us with a new name!

Sadly, a few very important people in our program passed away over the last two years. The work of Dr. John Russell on cedars, as many of you know, had a big impact on our program, and around the world. Right now, we are trying our best to keep his incredible programs ongoing. The loss of two recent retirees, Jim Corrigan, seed orchard pest specialist and John Ogg, propagation specialist at the Cowichan Lake Research Station, has also been felt by all of us in forest genetics in BC.

Barry Jaquish recently retired, but still is working part-time on emeritus status. Barry's contribution to forest genetics and tree breeding, particularly with interior Douglas-fir (*Pseudotsuga menziesii* var. *glauca*), western larch (*Larix occidentalis*), and interior spruce (*Picea glauca* x *engelmannii*) has been nothing less than spectacular in what was accomplished with those species over his 35+ year career. Barry's experience will be quite valuable to our program, as he mentors the new staff at the Kalamalka Research Station as Emeritus Scientist. Speaking of that, we have been lucky recently to have been able to hire some new scientists, and you will hear about them in this submission and we hope over the years at CFGA meetings (i.e., Jong, Leong, Jon Degner, Marie Vance, Lise Van Der Merwe, Justin Whitehill, and Omnia Gamal).

Ponderosa Pine (Marie Vance)

There is one active seed orchard for ponderosa pine (*Pinus ponderosa*) which was created based on information and selections from a provenance test which included material from the species' range in BC and northwestern US. The orchard population reflects the species variation in BC and deployment of orchard seed will be restricted to an area that reflects the current realized niche of the species. The fundamental niche of the species is expected to increase with climate change and a new breeding program has been proposed for the province. Open-pollinated seed from wild stands in BC and from USDA orchards in Idaho, Montana, Oregon and Washington is currently being collected for progeny testing.

Interior Western Redcedar (Marie Vance)

Fifteen provenance tests of western redcedar (*Thuja plicata*) were established between 2009 and 2014. Early data are currently being analyzed to assess GxE across the BC portion of the species range. Two clonebanks were established with scions from 500+ parents included in provenance tests. A new breeding program has been proposed to meet current and projected seed needs under climate change. Due to naturally high rates of selfing, an OP strategy is not being considered. Polymix and selfing strategies are currently being debated.

Red Alder (Alvin Yanchuk)

Interest in studying the genetics of red alder (*Alnus rubra*) has a long history in the Pacific Northwest because it grows very fast in relation to conifers, has many soil remediation properties, and has good wood properties. While planting numbers are still low (< 100,000/yr) there is still interest in planting it in mixtures with conifers. One set of progeny tests was established in 1995, and the selections from this set of trials were used for our current red alder seed orchard (genetic worth for growth ~30%). The next phase of field trials has been established in 2 series, starting in 2014, by Dr. Chang-yi Xie. These were seen as necessary because 1) elevational transfer was in question (all the other trials were established at lower elevations), 2) to further evaluate the superiority of the older selections, and 3) increase the base population for the northern and southern zones. This population is comprised of 210 OP families from 24 populations ranging from Oregon up to the Prince Rupert area established on 13 test sites, across the two series. Age 3 measurements have been made, and finally selections for climate-based seed transfer, and a new orchard will be made in 2022.

Bigleaf Maple (Alvin Yanchuk)

Studies on bigleaf maple (BLM) (*Acer macrophyllum*) genetics were largely nursery investigations in the 1900's. Chang-yi Xie started comprehensive field-based studies utilizing 562 open-pollinated families collected from 43 populations across the range of BLM. Three test sites were established on Vancouver Island and the lower mainland, and 10-year height, diameter, and form were recently measured. Selections will be made this winter for a small breeding population/clone bank and seed orchard. While outplanting of BLM is currently small, the increased emphasis on plantation mixtures with hardwoods and conifers will undoubtedly increase, especially with improved growing stock of BLM.

Coastal Douglas-fir (Michael Stoehr and Jon Degner)

In 2018, we made pre-selections in four third-generation full-sib progeny tests of coastal Douglas-fir (*Pseudotsuga menziesii* var. *menziesii*), based on heights at age 9. Based on these measurements, we selected and grafted the top trees speculating that they will still be the best (or at least in the top 10%) after final selections are made in 2020, which will be based on fall 2019 measurements. This is beneficial as those genotypes can be deployed into the orchard two years ahead of schedule. In the spring of 2019, we established the first four progeny tests for our 4th generation breeding cycle. According to our climate-based seed transfer rules, the test sites are predicted to be suitable for coastal Douglas-fir for the next 80 years, and include one test in the interior of BC. Early survival has been good, given the excellent growing conditions in 2019. As part of our routine work in the spring, we made controlled crosses in our breeding population for future testing.

In 2018, we started a project with the remote sensing team at the University of British Columbia (UBC) (under the leadership of N. Coops) to derive LiDAR based parameters for individual trees and at the plot level in our realized gain trials. These trials are now 24 years old and future ground-based measurements will be difficult

owing to tight spacing in some of the treatments. Preliminary results indicate that LiDAR-based height measurements are very accurate at the plot-level and reasonably accurate for single-tree estimates, but the crown shape parameters and branch size estimates need more refinement.

Work to screen for Swiss needle cast (SNC) (*Phaeocryptopus gaeumannii*) is ongoing. In 2018, we ran a pilot study at two progeny test sites and are moving forward with full-site assessments at both sites. In summer 2019, after harmonizing our protocol with US groups doing similar work, we assessed one site with respect to crown appearance, branch needle retention, and stomatal occlusion by the fruiting bodies (Pseudothecia) of SNC. We are attempting to combine all observations to derive parental breeding values that reflect SNC tolerance. The second site will be assessed in 2020.

In an older progeny test series, we are assessing drought resistance and post-drought response using increment cores. These cores are being further analysed for wood quality parameters (with a subset going for extensive testing, e.g., microfibril angle, moment of elasticity) to refine our wood quality breeding values and field methodology for wood quality testing.

Clonal archiving of our selections is ongoing and will be for years to come, as grafting incompatibility is still a problem with Douglas-fir, even with the use of grafting-compatible root stock. The incompatibility often causes mortality several years after the selections have been deployed in orchards or clone banks, which is extremely frustrating from both an operational and archival standpoint. We are currently developing and testing new rootstocks in the hope that we can identify grafting-compatible rootstock from advanced-generation parents which will be able to match the increased growth of trees from our advanced breeding cycles.

Coast-Interior Transition (CIT) and Coastal-High Elevation (HE) Douglas-fir Zone

Climate-based seed transfer rules allow for our coast-interior transition and high elevation breeding zones to be combined and planted with seedlings of the same genetic background. We are currently planning a new series of progeny tests for this combined zone and have made controlled crosses including parents from the coast-interior transition and high elevation seed orchards, as well as some parents from the interior Douglas-fir program. Both zones are extremely difficult to manage as summers are very hot and dry, causing regeneration failure and requiring replants, often across several years. In our new progeny tests in these challenging ecosystems, we are looking for parent trees with offspring that have high survival rates, possibly sacrificing some volume gain at rotation. Seeds to establish these tests will be sown in January 2020.

Western Redcedar (the late John Russell, Lise Van Der Merwe, Omnia Gamel and Alvin Yanchuk)

Tree breeding for western redcedar continues to involve the development of three overlapping breeding populations from first-generation selections selected for: 1) volume growth and cedar leaf blight (*Didymascella thujina*) (three pathogens have been recently discovered as causing the 'blight'), 2) heartwood durability, and 3) deer browse resistance. Breeding for first-generation polycross testing involved ~1,000 parents for the Maritime Low Seed Planning Unit (SPU) and is complete (15-year data have been captured across the seven annual series of tests established on 46 sites). Parental breeding values for volume at rotation and cedar leaf blight resistance are currently being estimated from all parents and rogued seed orchards are currently producing seed with a genetic worth up to 24% for volume at rotation (with partial resistance to cedar leaf blight). Advanced generation breeding is currently ongoing using assortative mating with partial diallels.

Heartwood durability The original 350 BC parent trees selected in the early 1970s (also represented in the first three series of polycross testing described above) were assessed for heartwood durable chemicals using wood cores from grafted ramets established in Cowichan Lake Research Station (CLRS) clonebanks and industry seed orchards. Fifty selections based on tropolone and lignan concentrations were cloned and established in an advanced generation breeding orchard and advanced generation breeding is currently ongoing using assortative mating with partial diallels. In 2015, Dr. Russell instigated a genomic selection (GS) project through his collaboration with Dr. J. Bohlmann at UBC and Dr. Matias Kirst at the University of Florida, and we will be using GS to select for heartwood compounds, as this trait takes about 30 years to assess. Further work on the S5 inbred lines that Dr Russell created is being investigated at UBC, using SNP markers and the draft genome for one S5 individual, to look at the genetic and phenotypic effects of inbreeding. Drs Omnia Gamal and Justin Whitehill have been recently hired to help with the genomic analyses and more elaborate phenotyping for forest health traits.

Deer browse resistance Initial selections for a deer browse resistant population were made from both a family/population study (within-family forward selections) and the CLRS clonebank (parental backward selections) based on high needle monoterpene concentration and families with low deer browse in field trials. These selections were bred in an advanced generation population using assortative mating with partial diallels. Early selection for foliage monoterpenes has resulted in approximately 100 forward selections for high needle monoterpene concentration. Breeding in the F2 population is currently ongoing and more phenotyping techniques are being developed for physical traits that deter deer browsing.

Yellow Cypress (the late John Russell and Lise Van Der Merwe)

Yellow cypress (*Callitropsis nootkatensis*) is a major component of high elevation coastal BC forests and genetic management of this valuable species involves gene conservation, genecology, and tree breeding. Fifteen-year measurements were completed for the yellow cypress genecology trials, which comprise approximately 50 populations established on 10 sites throughout BC. Analyses indicate the lack of a correlation between seed-origin climatic descriptors and mean provenance performance as seen in the 15-year data. Current liberal seed transfer guidelines reflect this random provenance genetic variation.

Yellow cypress propagates vegetatively in nature and, in addition, cone crops are usually infrequent and seed viability and germination, historically poor. Tree improvement has focussed on a clonal strategy. Twelve-year data from over 20 trials (Western Forest Products Inc. and BC Forest Service) have been collected and clonal genetic values for approximately 5,000 clones have been estimated and elite clones, based on volume and form, have been established in operational hedge orchards. The advanced generation is currently being bred using assortative mating. Research on improving seed production efficiencies in clonal trials established in native yellow cypress ecosystems is ongoing.

Interior spruce (Trevor Doerksen)

Current interior spruce seed orchards target 7 deployment zones and contain backwards selections based on first-cycle open-pollinated, half-sib tests with growth breeding values updated from second-cycle full-sib tests where available. The spruce breeding program is split into two, mostly separate test series: EP670 and EP819. EP670 contains the oldest three breeding sub-populations in the program (Bulkley Valley, Prince George, and East Kootenay), from which forward selections have been made in second-cycle tests to form new breeding sub-populations and supply next-generation material to seed orchards. Tandem trait selection will be used to screen these growth-based forward selections for resistance to white pine/spruce weevil (*Pissodes strobi*) on test sites where natural weevil pressure is high and/or using artificially infested, short-term progeny trials. A third-cycle crossing scheme for the oldest of these three sub-populations is planned to begin in 2020.

In the EP819 series, second-cycle progeny tests are young (Thompson Okanagan, age 6) or are just being established (Nelson low 2019, Nelson high 2020). The Nelson breeding sub-population tests were established both within and outside their geographic zone in anticipation of wider deployment. From age 10 onwards, these tests will be evaluated for growth and weevil resistance traits and forward selections will be made to form the next breeding population(s) and supply parents to seed orchards. The Peace River (Fort Nelson) breeding sub-population is the least advanced, with a crossing design for second-cycle tests still in development. This zone is ecologically similar to adjacent zones in Alberta, with linking families mutually evaluated in first-cycle tests in one another's jurisdictions. If beneficial to both parties, a similar exchange of material may continue for second-cycle testing.

Wood quality will be considered as a non-growth trait in future evaluations. Screening for resistance to spruce weevil is considered important and will continue, using information from a combination of artificially-infested, short-term trials and naturally-infested, field-based progeny tests where available.

Interior Douglas-fir (Trevor Doerksen)

Current interior Douglas-fir (*Pseudotsuga menziesii* var. *glauca*) seed orchards target six deployment zones and contain backwards selections based on first-cycle open-pollinated, half-sib progeny tests. Crossing plans for each breeding sub-population are largely complete with second-cycle progeny testing planned to begin in 2021, and continuing each subsequent year until each sub-population has been tested. Testing will occur both within and outside current geographic zones, leveraging GxE analysis of first-cycle tests to delineate climate-based deployment zones. These second-cycle tests will be used to make forward selections based on breeding values for growth starting at age 10 and secondarily for early wood quality (acoustic velocity and/or relative density) to, at minimum, prevent quality from deteriorating. These forward selections will be used to form the next breeding population and supply seed orchards with next generation material. Non-growth traits under consideration for evaluation are linking non-destructive wood quality measures to end-use lumber value, developing screening protocols for resistance to *Armillaria ostoyae* root rot, and drought/cold tolerance.

Western larch (Trevor Doerksen)

Current western larch (*Larix occidentalis*) seed orchards target two deployment zones and contain backwards selections based on information from first-cycle open-pollinated, half-sib progeny tests. Second-cycle progeny tests were established in 2017 and 2018 for the NE and EK breeding sub-populations, both within and outside their geographic zones using projected climate information. These second-cycle tests will be used to make forward selections based on breeding values for growth starting at age 10, which will supply the next generation of western larch orchards. First- and second-cycle tests will be used to update delineation of climatic deployment zones based on GxE analysis for growth. Non-growth traits that may be considered in future evaluations are wood quality, resistance to *Armillaria ostoyae* root rot, and drought/cold tolerance.

Whitebark Pine (Ward Strong and Charlie Cartwright)

We completed our seventh year of controlled inoculations for white pine blister rust (*Chronartium ribicola*) screening. To date, 149 families have been screened, comprising 6,608 seedlings. About 25 families have been selected from the earliest inoculations (2013–2015). Thirteen of these have had scion collected and 234 grafts were made. We also have 64 families of US selections that have been grafted (552 grafts). These grafts and a few forward selections will be used to start a seed orchard in the near future.

We are now collecting scions during cone harvest, to reduce winter scion collection costs, and capture all parent material, not just resistant selections. Starting in 2018, we have collected 58 parents and made 1081 grafts. We are experimenting with graft timing of this fall-collected scion. Fall grafting has lower take (62%) than spring-grafted (92%), both of which are lower than winter-collected and spring-grafted (97%). Hot grafting of July-collected scion (3 families, either fire-threatened or mountain pine beetle (*Dendroctonus ponderosae*) attacked parents) rescued this genetic material, though graft success was low (31%).

A series of field trials was sown in 2013 using almost range-wide seed sources, (comprised of a total 220 wind-pollinated families), and out planted on six field sites in 2015. The test sites represent the diverse habitats where whitebark pine occurs in BC. Height and blister rust data are being collected for age 5 years in the field. A second series of trials with 250 more families was sown in 2015 and out-planted to a further 6 test sites in 2017. Survival data for these tests are now in hand. The purposes of the field trials, past identifying rust resistant parent trees, are to look at adaptation across the BC range in order to derive climate based seed transfer guidelines, quantify genotype by environment interaction for rust resistance, (potentially delineating rust hazard zones), and durability of that trait through multiple decades.

Farm field trials using the same almost 500 test families planted in the proximity of plants of white pine blister rust's alternate host (*Ribes* spp.) has shown strong family and seed source effects which will allow us to make further selections in the near future.

Western Hemlock and True Firs (Charlie Cartwright)

The forest genetics program for western hemlock (*Tsuga heterophylla*) in BC is focused on wrapping up activities. Efforts are underway to assure that valuable genotypes from tests to date are persevered occasioning over 200 grafts being made in the past year and reorganization of the hemlock seed banks. Calculations of the final new breeding values are in process to allow seed orchards to provide best gains achievable for investments made. As well, measurements of six hemlock genecology trials has allowed for the calculation of climate based seed transfer guidelines based on a total of over 32 such trials from across the range in the province. Finally, realized gain trials measurements were made to confirm figures from single-tree plot tests. The newest of these trials include natural regeneration as one of the genetic treatments so that economic superiority of that approach can be verified relative to planting high gain seedlings.

For true firs, the genecology tests for grand fir (*Abies grandis*) have been analyzed to produce climate based seed transfer guidelines and data are being collected so that the same analysis can be done for both Pacific silver fir (*A. amabilis*) and subalpine fir (*A. lasiocarpa*). Ten subalpine fir and 12 Pacific fir genecology trials were maintained, tagged, and measured recently. As well, trees in a subalpine fir provenance trial, heavily infested with balsam woolly adelgid (*Adelges piceae*), were scored for severity of infection with the hope of identifying less susceptible seed sources.

Lodgepole Pine (Nicholas Ukrainetz)

The lodgepole pine (*Pinus contorta* var. *latifolia*) breeding program has progressed from open-pollinated (first-cycle) progeny testing to full seed production in several seed planning zones. Five zones were identified as high priority for advanced generation breeding. Information from open-pollinated testing was used to rank parents for growth and wood density. Top parents were selected for second-generation (F1) breeding and were crossed to produce a growth and a wood density breed which was deployed on three sites per breeding zone. The highest priority trait continues to be volume at rotation, however, three rust pathogens have been identified for resistance breeding: western gall rust (*Endocronartium harknessii*), comandra blister rust (*Cronartium comandrae*), and dothistroma needle blight (*Dothistroma pini*). We have completed forward

selections from three of the five breeding zones based on age 10 growth data and are in the process of a final measurement and maintenance at age 15. We are developing a protocol to screen families for resistance to dothistroma needle blight and continue to monitor field sites for infection rates for comandra blister rust and western gall rust. The breeding program was reorganized into four breeding populations based on the analysis of a multi-environment trial dataset composed of over 40 test sites and 300,000 trees. The analysis used a factor analytic procedure to model the additive genetic (co)variance among sites and Type B genetic correlations which were used in combination with climate modelling to create the four zones. Breeding values are being calculated for growth and resistance to western gall rust, comandra blister rust, and dothistroma needle blight.

Western White Pine (Nicholas Ukrainetz)

The western white pine (*Pinus monticola*) breeding program is split into two breeding populations servicing coastal and interior regions of the province. The primary focus of the breeding program is blister rust (*Cronartium ribicola*) resistance and secondary priorities include maintaining adaptation to local biotic and abiotic factors, and enhancing growth. The program began with controlled inoculation trials of seedlings grown from seed collected from wild trees that had no active blister rust infection. Seedlings were monitored for infection for several years then selected for seed production in seed orchards. The coastal program began F1 crossing and deployed four series of progeny tests which are now serving as a source of material for seed orchards. Infection data from these trials have helped to accurately rank parent trees for resistance to blister rust and growth. Approximately 120 forward selections have been made from progeny tests for future breeding and orchard production. The interior program acquired 50 trees from the Idaho breeding program which tested well and have formed a strong genetic base. Controlled crosses were created among the Idaho parents and the progeny screened in controlled inoculation trials. The focus of the interior program now is on F1 breeding among resistant parents and the establishment of progeny field trials to assess field level resistance. Mature realized gain trials indicate strong resistance from orchard populations. A fifth series of progeny tests was deployed on four sites in Maritime, Submaritime, and Interior Continental regions with controlled-crosses among trees from the northwestern United States, coastal BC, and Idaho. This series will provide information about genotype-by-environment interactions for growth and resistance which will provide information for making recommendations about moving material between coastal and interior regions. Breeding values have been calculated based on infection data from F1 field trials and used to rank parents for future breeding and seed orchards.

Interior Hardwoods (Nicholas Ukrainetz)

Testing and selection of hybrid poplar in northern environments is ongoing. A clonal test at Red Rock was used to characterize several controlled crosses among individuals of *Populus trichocarpa*, *P. deltoides*, *P. maximowiczii*, and *P. nigra*. Several clones were identified with superior growth characteristics and tolerance to northern climates and these were selected to create a stool bed which will be available for operational use and further research. An extensive genecology and open-pollinated progeny testing program was established for paper birch (*Betula papyrifera*). There was significant genetic variation for volume and several forward selections have been made and grafted into two seed orchards for operational seed production. Forward selections from existing trials are being considered.

CLIMATE CHANGE AND ADAPTATION (Greg O'Neill)

Assisted Migration Adaptation Trial

The Assisted Migration Adaptation Trial (AMAT) (<http://www.for.gov.bc.ca/hre/forgen/interior/AMAT.htm>) is a long-term multi-species field trial intended to provide a better understanding of tree species' climate adaptation. The trial contains 48 seed sources (mostly orchard seedlots) from 15 species native to western North America planted at 48 test sites in BC, Alberta (AB), Yukon (YT), and neighbouring US states. Twelve test sites were established annually, beginning in spring 2009. Growth and health assessments are being conducted every 5 years; age-10 assessments began in summer 2018 and will conclude in fall 2021. Relationships of seedlot growth and health with plantation climate will be developed enabling identification of the seed sources most likely to be best adapted to current and future climates. The information will be used to revise BC's species and seed source selection guidelines, helping to ensure maximum health and productivity of BC's planted forests well into the future.

Interior spruce climate change/genecology trial

A large interior spruce climate change/genecology field trial established by Barry Jaquish and Greg O'Neill has provided valuable information for the development of BC's new seedlot selection program "Climate Based Seed Transfer" (CBST). The trial consists of 128 seedlots (99 wildstand and 29 orchard) from BC, AB, and neighbouring states and territories tested at 17 locations in BC, AB, and YT. Age-10 growth was assessed in 2013. Data from the trial were used in a publication (O'Neill et al. 2014) that supported the consolidation of BC's 3 systems of seed transfer (i.e., separate systems for orchard, wildstand, and superior provenance seed types) into a single system of seed transfer for all seed types. Trial results were also used to develop transfer functions for interior spruce used in CBST. The trial will be re-assessed in 2020 and results used to refine CBST.

Climate Based Seed Transfer (CBST)

CBST is a seed source selection and deployment system for BC (O'Neill et al. 2017) that was implemented in April 2018 following changes to the Chief Forester Standards for Seed Use. The new system results in better matching of seed with plantations because it is based on climate rather than geography. It also facilitates comprehensive assisted migration for all species in all parts of the province to ensure that future plantations will be optimally adapted for the duration of the plantation. Currently, users may use either the earlier geographic based system or CBST; however, the geographic based system will soon be deleted, likely within 2–3 years. The system was developed by a team of scientists and policy analysts from the BC government and UBC, with review from numerous scientists, stakeholders, and policy analysts. A description of the new system was published (O'Neill et al 2017).

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BRITISH COLUMBIA PROVINCIAL TREE SEED CENTRE 2017–2019 REPORT

Dave Kolotelo

**Provincial Tree Seed Centre
Ministry of Forests, Land and Natural Resource Operations and Rural Development
Surrey, BC**

The Tree Seed Working Group continues to provide extension on seed science and technology through its annual Newsbulletin and its biennial workshop. Since the last CFGA meeting in Edmonton, 2017 we have produced Newsbulletin editions 65, 66, and 67. Newsbulletins can be found at this new web address <http://www2.gov.bc.ca/gov/content/industry/forestry/managing-our-forest-resources/tree-seed/tree-seed-centre/cone-seed-improvement-program/tree-seed-working-group>. The workshop in Lac Delage had the theme of “To reaffirm the importance of cone and seed service activities and identify knowledge gaps” and the workshop presentations can be found here: <https://www2.gov.bc.ca/gov/content/industry/forestry/managing-our-forest-resources/tree-seed/events/tree-seed-workshop>.

The year 2018 is when the BC Tree Seed Centre (TSC) celebrated its 60th anniversary as a provincial facility. We hosted a two-day workshop called “Connections Through Seed” that covered a wide variety of cone and seed related topics. The presentations from that workshop can be found here: <https://www2.gov.bc.ca/gov/content/industry/forestry/managing-our-forest-resources/tree-seed/events/connections>. The meeting was dedicated to Heather Rooke who had been a ‘conehead’ for 41 years with about half of that as our Manager. Heather sadly passed away shortly after retiring. In recognition of our stewardship mandate we also hosted a small hands-on whitebark pine (*Pinus albicaulis*) workshop at our facility (<https://www2.gov.bc.ca/gov/content/industry/forestry/managing-our-forest-resources/tree-seed/events/whitebark>).

In 2018 we had a bumper cone crop for most of our commercial tree species and we organized a cone collection / seed planning-climate based seed transfer workshop that occurred at four different sites in BC. Presentations are available here: <https://www2.gov.bc.ca/gov/content/industry/forestry/managing-our-forest-resources/tree-seed/seed-planning-use/cone-collection-workshop>. I was invited to speak at the BC Forest Nursery Association meeting in 2017, the BC Seed Orchard Association meeting in 2018, and the Inland Empire Tree Improvement Cooperative meeting in 2019.

Genetic conservation has focussed on expanding our seed bank with collections of non-commercial tree species. These seed bank data also contributed to a provincial report on the conservation status of our native species in BC. Our 2018 bumper cone crop also included an endangered species, whitebark pine, with most collections being on a single-tree basis to facilitate parent tree blister rust (*Chronartium ribicola*) screening. A great deal of time was involved in this species in terms of extending information, managing the provincial source for this seed, and meeting the quickly growing demand for seedling production. Other technical activities included updating our sowing request moisture content recommendations and initiating work on moving our seed fungal assays to a molecular basis. On most days I feel mostly like an extension specialist and fire fighter by providing seed science and technology extension as well as expert advice on the ‘problems’ that arise in various operational settings.

I continued to participate in several committees: ISTA Forest Tree and Shrub Committee, Genetic Conservation Technical Advisory Committee (TAC), Coastal and Interior TAC, and ongoing whitebark pine initiatives. I provided facility tours, supervised our Testing group, and filled in as Acting Manager when required. We had almost a full overhaul of our testing staff and other TSC positions, so hiring and human resource management have been very demanding during the past two years.

PROCEEDINGS
OF THE
THIRTY-SIXTH MEETING
OF THE
**CANADIAN FOREST GENETICS
ASSOCIATION**

PART 2

Symposium

Joint conference of the Canadian Forest Genetics Association,
GE³LS Workshop, and Poplar and Willow Council of Canada

Lac Delage, Québec
August 19–23, 2019

EDITORS

M. Deslauriers, P. Lenz, D.A. McPhee and J.D. Simpson

COMPTES RENDUS
DU
TRENTÉ-SIXIÈME CONGRÈS
DE
**L'ASSOCIATION CANADIENNE
DE GÉNÉTIQUE FORESTIÈRE**

2^e PARTIE

Colloque

Conférence conjointe de l'Association canadienne de génétique forestière,
du Groupe sur les GE³LS et du Conseil canadien des peupliers et des saules

Lac Delage, Québec
19 au 23 août 2019

ÉDITEURS

M. Deslauriers, P. Lenz, D.A. McPhee et J.D. Simpson

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WELCOME

We wish you a warm welcome to the 36th meeting of the Canadian Forest Genetics Association! With the Manoir du Lac Delage, we have chosen a convention place just a bit outside of the busy city of Québec. The proximity of nature, and the calmness and serenity of the place, make it an ideal location to foster exchanges around our chosen theme:

Applied forest genetics – Where do we want to be in 2049?

Environmental and economic changes present important challenges to the forestry sector and society in general. There is no doubt that forest genetics (from the breeding and production of improved planting material to the conservation and better adaptation of tree species) will be part of an integrated solution to address those challenges. The different fields of forest genetics have a long-standing research history but many institutions are facing challenges to maintain acquired knowledge and resources. On the other hand, new decision support tools have been developed in the recent decade thanks to progress in biotechnology and research initiatives such as large-scale Canadian forest genomics projects. Derived products using novel measuring technologies will further accelerate the creation of resilient and renewable forest resources, improve the detection and monitoring of pests and diseases, and make our predictions of the impact of climate change on our forest landscapes much more accurate.

Seeing all these tools at our disposal, and considering the current environmental and socio-economic issues, shouldn't we establish a priority list to better prepare ourselves to meet future challenges? How can GE³LS (genomics and its ethical, environmental, economic, legal and social aspects) research help us do so?

For this conference, we aim at using the multidisciplinary nature of our CFGA meetings to develop a common vision of forest genetics research in the near future. Starting off with the Tree Seed Workshop and a satellite meeting of the Canadian Poplar and Willow Council, each section of the general meeting is then supported by a selected set of keynote speakers. We have placed several GE³LS presentations throughout the conference program to discover recent achievements made in this field and to attempt a better integration with traditional forest genetics research. A set of interactive questionnaires and discussions will help us to extract main opinions and start describing a common vision for the future.

With great enthusiasm, an entire team was helping to prepare our CFGA conference – many thanks to all of them!! We have received important financial contributions from a number of partners, which allowed us to support six invited students from the country's forestry faculties. Important logistical support and organization time were provided by Natural Resources Canada through the Canadian Wood Fibre Centre and the Laurentian Forestry Centre. The Ministère des Forêts, de la Faune et des Parcs (Quebec Ministry for Forests, Wildlife and Parks) made very valuable contributions, especially with the organisation of the conference field trip; and our colleagues from Laval University supported us particularly in setting up the scientific program.

Altogether, we wish you a great and inspiring conference! Nathalie, Patrick and a team of very motivated organizers that are committed to making the event a successful CFGA meeting!

MOT DE BIENVENUE

Nous sommes très heureux de vous accueillir à la 36^e conférence de l'Association canadienne de génétique forestière! Avec le Manoir du Lac Delage comme centre de conférence, nous avons choisi un lieu de villégiature situé à l'extérieur de la ville bourdonnante de Québec. Nul doute que la nature environnante et la quiétude des lieux créeront un espace propice aux conversations et aux échanges autour du thème retenu pour la conférence :

Génétique forestière appliquée – où voulons-nous être en 2049?

Les changements environnementaux et économiques présentent des enjeux importants pour l'industrie forestière et pour notre société en général. Sans contredit, la génétique forestière dans toutes ses déclinaisons (de l'amélioration génétique des essences forestières à la conservation des espèces en passant par l'adaptation) fera partie des solutions intégrées pour faire face à ces enjeux. Les différents domaines de la génétique se basent sur une longue tradition de recherche. Or, plusieurs institutions font face à des problèmes de rétention des ressources et de l'expertise acquise. D'ores et déjà, de nouveaux outils d'appui à la prise de décisions ont été mis en place grâce aux progrès en biotechnologie et aux grands projets canadiens de génomique forestière. D'autres produits développés utilisant de nouvelles approches de mesurage et d'évaluation permettront d'accélérer la création de ressources résilientes et renouvelables, d'améliorer la détection et la surveillance des maladies et des insectes, tout en contribuant à une meilleure prédiction des impacts des changements climatiques sur les forêts.

Compte tenu des outils à notre disposition ainsi que des enjeux environnementaux et socio-économiques actuels, devrions-nous aussi établir une liste de priorité afin de mieux nous préparer pour l'avenir? Comment la recherche GE3LS (génomique et ses aspects éthiques, environnementaux, économiques, légaux et sociaux) pourrait-elle nous appuyer dans cette démarche?

Pour cette rencontre, nous aimerions nous servir du caractère multidisciplinaire de la conférence de l'ACGF afin de développer une vision commune de la recherche en génétique forestière pour l'avenir. Le congrès débutera avec le groupe de travail des semences forestières et une rencontre du Conseil canadien des peupliers et des saules. Dans le programme général, des conférenciers invités viendront appuyer les différentes thématiques abordées au cours de la semaine. Finalement, les présentations du groupe des GE³LS durant la semaine mettront en évidence les réalisations dans ce domaine et leur meilleure intégration avec la recherche en génétique forestière plus traditionnelle. Une vision commune pour l'avenir pourra découler des questions interactives et des discussions qui vous seront proposées durant la semaine avec beaucoup d'enthousiasme, toute une équipe nous a épaulées à préparer la conférence – un grand merci à tous !! Nous avons reçu des contributions financières de plusieurs partenaires ce qui nous a permis d'inviter six étudiants des facultés forestières du pays. Ressources naturelles Canada avec le Centre canadien sur la fibre de bois et le Centre de foresterie des Laurentides étaient responsables de la coordination logistique de l'événement. Le Ministère des Forêts, de la Faune et des Parcs a apporté une aide précieuse, spécifiquement pour l'organisation de la journée terrain; et nos collègues de l'Université Laval ont, entre autres, contribué au volet scientifique.

Tous ensemble, nous vous souhaitons une conférence divertissante et enrichissante. Nathalie, Patrick et une équipe déterminée à faire de cette réunion de l'ACGF un franc succès !

INVITED SYMPOSIA PAPER ABSTRACTS

FROM READING TO WRITING GENOMES TO UNDERSTAND AND TAME EVOLUTION

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Over the past centuries, natural populations have been producing genetic diversity that allows us to relate genes to phenotypes. Our ability to read this information has been accelerating spectacularly over the last decades. Ideally, geneticists would also like to write genomes such that they can experimentally test hypotheses they derived from the association of genotypes to phenotypes. Writing genomes may also eventually enable the design of organisms from scratch so they can provide specific technological or ecological services. Recent genome editing technologies have been developed to make this possible. It is now possible to design and write genotypes that have never and may never exist in natural populations. This presentation showed and discussed how a geneticist's dream has come true. Recent work on the manipulation of the yeast genome and how it is helping us to better understand evolution as it happens at the cellular level was also discussed.

**TREES, TRUST AND GENOMICS:
LEVERAGING SOCIAL SCIENCE INSIGHTS IN THE PURSUIT OF CLIMATE
RESILIENT FORESTS**

Shannon Hagerman

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From the potential of increased global reforestation efforts, to the role of existing stands as biodiversity refugia, forests are increasingly looked upon as both mitigation and adaptation solutions to climate change. This intensified focus on forests has coincided with consideration of the use of new biotechnologies including genomics-based assisted migration of tree species. While the development of this and other forest biotechnologies has primarily been a disciplinary pursuit, the past decade has seen increased recognition of the need to also assess a suite of social aspects including those related to trust, risk perception, and governance. Attention to these and other insights from the environmental social sciences matter tremendously to enhancing an understanding of the application of new technologies in forests. For example, a failure to evaluate how the risks and benefits are differentially perceived (and experienced) across groups and scales of governance in operationalizing new technologies may lead to the development of myopic and overly optimistic policy solutions that ignore or conceal difficult societal tradeoffs implied by such interventions in the complex social-ecological spaces in which they are deployed. In Canada, where the majority of forest lands are publicly managed, and often on unceded Indigenous territories, these are critical topics that cannot be ignored. The talk aimed to demonstrate some of the contributions of the environmental social sciences to enhancing an understanding of the potential application of new biotechnologies for forests, and to spark broader interdisciplinary engagement with these critical topics in the pursuit of developing holistic solutions to the forest-related challenges facing society in the decades to come.

CONNECTING GENOTYPE WITH PHENOTYPE: IT TAKES A VILLAGE

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Discovering the genetic basis of complex traits has long been the lofty goal of geneticists. Breakthrough advances in genomic technologies continue to revolutionize the toolkit that researchers can exploit to identify genotype-phenotype relationships. The maturation of these genomic technologies, together with decreasing costs of developing genomic resources, are making it increasingly feasible to undertake these investigations for complex traits in non-model species, including forest trees. However, these genomic technologies constitute only one part of the puzzle. Drawing from lessons learned from model and agronomic species, forest geneticists are conducting progressively larger and more sophisticated experiments designed to provide higher-precision phenotypic data for greater numbers of individuals. Successful realization of these large-scale experiments requires a team approach. Collaborations that bring together researchers from diverse disciplines are opening doors to innovative ways in which to connect genotype with phenotype. The terabytes of data resulting from these large collaborative efforts necessitate close cooperation and collaboration with computational specialists to process, curate, analyze, and archive these datasets. Examples were given of ongoing collaborative projects in which we aimed to identify genotype-phenotype relationships using different approaches. These projects are predicated on unique genetic and genomic resources, and would not have been possible only a few short years ago. In turn, these projects provide a foundation for future endeavours in which new technological, analytical and computational advances will make it increasingly practicable to discover and validate the networks of genes and variants that underlie complex traits in forest tree species.

TRANSFORMATION OF FOREST TREE BREEDING IN NEW ZEALAND THROUGH GENOMICS, PROPAGATION AND REMOTE SENSING

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New Zealand is an export-oriented open economy and as such it has to stay competitive in global markets. Forestry is the third biggest export industry. The need to remain globally relevant and competitive brings significant pressure on forest growers, resulting in the need to rapidly improve and confidently deploy genetically improved planting stock. In order to fulfil this need, Scion has worked with the forestry industry to initiate the transformation of breeding programs for major exotic species using genomics and field-based phenotyping.

While Douglas-fir (*Pseudotsuga menziesii*) and *Eucalyptus nitens* breeding programs have benefited from previously developed marker arrays, no genomics resources were available for *Pinus radiata*. Scion has since developed an exome capture based genotyping panel in partnership with the New Zealand Radiata Pine Breeding Company. Currently, genomic models have been developed for wood quality, disease resistance, and productivity across all major planted exotic species.

In parallel, we have been working on improvement of individual-tree phenotyping and propagation systems. Testing early LiDAR acquisitions we have determined that individual-tree height can be accurately estimated for use in tree breeding. Future developments will focus on phenotyping a full suite of quantitative traits representing growth, stem form, and health conditions. Current tissue culture systems for radiata pine and Douglas-fir are dependent on petri-plate based technologies. We are therefore working on improving the multiplication, throughput, and resilience of tissue culture plants using bioreactors.

Combining breeding with remote sensing will mean that instead of a single point measurement (e.g., DBH), direct and quantitative measurements can be taken (e.g., stem volume). Genomics will speed the delivery of selections through speeding the breeding cycle itself. Adding tissue culture automation will facilitate the direct and rapid multiplication of the best material for deployment in the forest. The combination of all these technologies will reduce the breeding and deployment cycle significantly and has the potential to double forest productivity.

* Presenter

ON THE STARTING LINE TOWARDS 2049

**A GENOMIC-INFORMED DECISION SUPPORT SYSTEM
FOR RISK ASSESSMENT AND MITIGATION OF FOREST INVASIVE ALIEN
SPECIES IN CANADA**

**Valentine Lafond*, Federico Lingua, Stefanie Lumnitz, Gregory Paradis,
Vivek Srivastava and Verena C. Griess**

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With over 347 million ha of forested area, Canada contains 9% of the world's forests, 24% of the world's boreal forests, and is one of the world's largest forest products exporters. Canada's forests and forest sector are vulnerable to forest invasive alien species (FIAS), with surveillance and mitigation efforts being particularly challenging given the large area of forest lands in the country. Decision Support Systems (DSS) can greatly facilitate invasion risk assessment and management. Hereby, the development and use of DSS is often limited by a lack of knowledge on FIAS ecology, especially regarding "invasiveness traits" (e.g., dispersal capacity). New opportunities arise from the use of genomics tools, which allow deriving such information from intercepted FIAS, thus allowing the integration of genomics informed data into DSS.

We developed a model-based DSS framework for FIAS risk assessment and mitigation in Canada that allows one to pipeline FIAS trait information derived from genomics and project potential impacts of FIAS invasions on forest ecosystem services (e.g., timber production, recreation). We illustrated its implementation and use for Asian Gypsy Moth (AGM) (*Lymantria dispar asiatica*) invasions in British Columbia, using genomics-derived information on flight capacity from intercepted AGMs. The DSS provides stakeholders with essential information facilitating the identification and prioritization of areas at risk, estimation of potential socio-economic impacts of FIAS invasion, and comparison and selection of mitigation scenarios.

* Presenter

AGRI-ENVIRONMENTAL SOLUTIONS TO PREVENT AND MITIGATE HARMFUL ALGAL BLOOMS: MEASURING AND PLANNING ECOSYSTEM SERVICES IN THE SHORT AND LONG TERM

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The ATRAPP (Algal Blooms, Treatment, Risk Assessment, Prediction and Prevention Through Genomics) project aims to provide a better understanding of cyanobacteria, from their identification to their modes of propagation, and will propose solutions for the strategic management of harmful proliferation episodes. The project will, among other things, define new biomarkers, create a combined chemistry and genomics toolbox to determine the risks of toxicity, and facilitate the prevention and treatment of harmful episodes. The purpose of the G³ELS activity associate to the project is to integrate the socio-economic evaluation of the proposed solutions in the short and long term, in order to obtain an optimal cost of sharing strategies within the communities affected by episodes of algal blooms. The first short-term goal is the assessment of socio-economic benefits to better detect and predict episodes of blooms. This objective helps to select agri-environmental practices (e.g., tree planting in riparian buffers) that provide the most beneficial impacts and will be targeted in the cost-sharing analysis. The cost-benefit analysis of treatment options will also provide the necessary information for water treatment services and help decide on investments to improve treatment. A second long-term goal is to provide a cost sharing model (e.g., payments for ecosystem services program) in order to support agricultural transformation. The results will provide an overview of the governance and financial support strategies that are effective and sustainable.

IMPLEMENTING GENOMIC SELECTION IN SPRUCE ADVANCED BREEDING PROGRAMS: THE *FastTRAC* PROJECT

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With progress made in the development of spruce genomic resources from previous Genome Canada projects Arborea and SMarTForests, the timing was right for major forestry organizations to collaborate in moving genomic selection (GS) from successful proof of concept toward application at the operational scale. Through the *FastTRAC* project, scientists and tree breeders from seven Canadian organizations gathered to carry out this large-scale implementation of genomics in tree breeding. The objectives were: 1) to move GS at the operational level for the white spruce (*Picea glauca*) and Norway spruce (*P. abies*) advanced breeding programs of three major end-users (Ministère des Forêts, de la Faune et des Parcs du Québec, J.D. Irving, Limited, and New Brunswick Tree Improvement Council) and 2) to demonstrate the economic benefits of using GS. Target traits were growth, wood quality, and pest resistance. Highly reliable SNP genotyping chips were developed and used to genotype many thousand pedigree trees and selection candidates from partners' breeding populations. The GS models provided prediction accuracies of up to 90%. In particular, high accuracy GS models were developed for Norway spruce resistance to white pine weevil (*Pissodes strobi*), as well as multi-trait GS implicating gains for weevil resistance, height growth, and wood stiffness. By genotyping thousands of candidates, the genomic-estimated breeding and genotypic values were used by breeders to rogue seed orchards, practice forward selection, identify superior genotypes for assortative mating, and recommend the best somatic embryogenesis (SE) lines for reforestation. Cost of using GS was marginal compared to other breeding and plantation forestry costs. Compared to conventional breeding, cost-benefit analyses showed that forward GS coupled with SE resulted in the greatest benefits, followed by GS with top grafting. A pipeline was developed for delivering genomic-estimated values within 6 months from DNA extraction from very young aged material, thus reducing by around 20 years the breeding cycle for spruce mature-stage traits.

ADAPTIVE CAPACITY

QUANTIFYING THE ADAPTIVE CAPACITY OF TREE SPECIES TO CLIMATE CHANGE

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Recent evidence indicates that the migration rate of tree species will not be sufficient to follow their suitable niche under climate change scenarios. Accordingly, research interests now focus on the adaptive capacity of tree populations, i.e., their capacity to persist in place and cope with the environmental change expected with the future climate. We propose an approach to quantify the adaptive capacity of Canadian tree species based on four axes of adaptation: 1) individual adaptation through phenotypic plasticity, 2) population genetic diversity, 3) the rate of genetic recombination as influenced by gene flow and reproductive capacity, and 4) the potential of recombination beyond populations through hybridization. In the first part of this presentation, we presented the results from a meta-analysis that sought to quantify these four axes and we discussed the current limitations and the way forward. In the second part of the presentation, we presented an ongoing project that aims at measuring the adaptive capacity of 15 different tree species from the Haut St-Laurent Region in Quebec. Our ultimate goal is to compute the adaptive capacity at the forest community level and to compare this capacity between forests having experienced different management regimes: 1) old growth natural forests, 2) forests managed for sugar maple syrup production, and 3) young naturally regenerating forests.

* Presenter

ADAPTING SEED TRANSFER GUIDELINES TO THE CHANGING CLIMATE OF NORTHEAST ONTARIO

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As with many jurisdictions, Ontario's provincial system of seed zones was constructed such that each zone served for both seed procurement and deployment. These climate-based seed zones retain their seed procurement function. But, under a rapidly changing climate, seed deployment becomes geographically disparate from seed procurement. The challenge is to project geographic displacement of suitable habitat, which is unique to individual species, to support informed seed deployment.

Range-wide climate niche models derived using Random Forest procedures together with ecological genetic models derived from disparate provenance tests provided the foundation for identifying putative suitable habitat at mid-century as well as geographic shifts in seed zones for eastern white pine (*Pinus strobus*) (Joyce and Rehfeldt 2013) and black spruce (*Picea mariana*) (Joyce and Rehfeldt 2017). While ecological genetic models are insightful, the paucity of high quality provenance test data constrains development for most species. So, a generic seed transfer protocol was needed. Fortunately, the variable, Degree-Days-Above-5° C (DD5), has proven to be a strong predictor of growth potential (an adaptive attribute) in eastern Canada. Coupling species-specific climate niche models with projected shifts in DD5 at mid-century provide the context for testing and refining seed deployment. Jack pine (*Pinus banksiana*), white spruce (*Picea glauca*), and red spruce (*P. rubens*) were used to illustrate seed transfer guidelines for Northeast Ontario.

Joyce, D.G.; Rehfeldt, G.E. 2013. Climatic niche, ecological genetics, and impact of climate change on eastern white pine (*Pinus strobus* L.): Guidelines for land managers. *Forest Ecology and Management* 295: 173–192.

Joyce, D.G.; Rehfeldt, G.E. 2017. Management strategies for black spruce (*Picea mariana* (Mill.) B.S.P.) in the face of climate change: climatic niche, clines, climatotypes, and seed transfer. *Forestry: An international journal of forest research*. 90(4): 594–610. [doi:10.1093/forestry/cpx018](https://doi.org/10.1093/forestry/cpx018).

RELATIONSHIP BETWEEN INTROGRESSION PROPORTION AND GENETIC DIVERSITY IN NATURAL SEED STANDS OF SEVEN MEXICAN PINE SPECIES

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Hybridization is an evolutionary key force, since interspecific gene transfer can introduce more new genetic material than is directly generated by mutations. In general, hybrids are unfit in relation to their ancestors, especially because of reproductive barriers. However, especially between geographic races or closely related species, there are hybrids which tend to outgrow their parents in vegetative vigor or robustness. For parapatrically distributed species and species with weak isolation barriers, such as many Mexican pine species, genome-wide introgression can result in higher genetic diversity and, therefore, can facilitate the increase of evolutionary resilience of populations. Thus, hybridization and introgression may support a quicker recovery or avoid negative impacts on population decline. Moreover, hybridization can boost local adaptation chances, both facilitating evolutionary innovation and promoting conditions in which mutation and gene flow among conspecifics produce local adaptation. However, there is a lack of studies on the association of hybridization with genetic diversity in tree species. In this study, therefore, we analyzed the relationship between the proportion of introgression and genetic diversity in 83 natural seed stands (2,905 individuals) of seven pine species (*Pinus arizonica*, *P. cembroides*, *P. durangensis*, *P. engelmannii*, *P. herrerae*, *P. leiophylla*, and *P. teocote*), which are widely spread in the Sierra Madre Occidental, Mexico. By using 376 amplified fragment length polymorphisms (AFLP) and the software STRUCTURE and NewHybrids, we estimated the hybrid proportions and measured genetic diversities for each stand. We detected both significant positive and negative moderate associations between the proportion of introgression and genetic diversity.

* Presenter

COMMUNITY-LEVEL MODELLING PREDICTS VULNERABLE CONIFER POPULATIONS UNDER PROJECTED FUTURE CLIMATES

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Greenhouse gas emission and global warming are likely to cause rapid climate change within the natural range of conifer trees over the next few decades, thus bringing uncertainty to their adaptation to the environment. Here, we used community-level modelling methods to associate genetic variation with environmental variables. The fitted models were used to predict adaptive genetic variation of conifer trees within their natural range under current and projected future climate conditions. In the case of loblolly pine (*Pinus taeda*), genetic variation within the range changed from east to west, which presented evidence of isolation by distance. A heat-related variable, maximum temperature of the warmest month, was found to be the most important predictor in determining adaptive genetic variation in loblolly pine populations, particularly in the western and middle parts of the range. Loblolly pine trees in the northeastern part of the range were predicted to be most likely impacted by climate change since their genomic vulnerability, the mismatch between genetic variation and environmental variables, showed the greatest values. Loblolly pine trees in the northern part of the range, both west and east of the Mississippi River, might also be endangered by changing climates. Studies on genomic vulnerability of lodgepole pine (*Pinus contorta*) and interior spruce (*Picea glauca*, *Picea engelmannii*, and their hybrids) were presented. These studies provide new perspectives on local adaption of conifer trees to changing climates, and the results can be used to target particular populations while developing adaptive forest management guidelines.

* Presenter

GENETIC FEATURES UNDERLYING LOCAL ADAPTATION TO DROUGHT IN WHITE SPRUCE

**Claire Depardieu^{*,1,2}, Martin Girardin², Simon Nadeau², Sébastien Gérardi¹,
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A rapidly warming climate may affect water availability for boreal conifer species. There is therefore an urgent need for assessing their adaptive capacity in order to better predict forest vulnerability and resilience under drier climates. In this study, we used a dendroecological approach in combination with a provenance-family common garden to determine the level of climate sensitivity in white spruce (*Picea glauca*). We detected a clear signal of local genetic adaptation to drought, with provenances originating from drier locations showing a higher resilience than those from wetter locations. Based on these results, we further dissected the genetic features underlying white spruce local adaptation to drought by combining genotype-environment association (GEA) and genotype-phenotype association (GPA) analyses. A set of 281 genes associated with either a climate variable or a phenotypic trait was identified. The interlinked phenotype-genotype-environment network revealed ten target genes related to local adaptation to drought. Overall, our findings represent a significant step forward in the characterization of the genomic basis of drought resilience in conifers and provide a valuable resource for breeders to establish resilient boreal forests able to face new climate scenarios.

* Presenter

UNDERSTANDING THE ADAPTIVE CAPACITY OF FOREST TREE SPECIES FOR CLIMATE CHANGE: QUAKING ASPEN, A KEYSTONE NORTH AMERICAN TREE SPECIES

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Climate change is accelerating and causing more climate extremes, such as severe drought episodes, that will have negative consequences on many North American forest tree species. We therefore need to develop tools to assess tree species' adaptive capacity and guide future sustainable management. The ecologically important *Populus tremuloides* (quaking aspen) is a species of choice for studying the genetic basis of adaptation due to its wide distribution, from northern Quebec to Mexico, in varying altitudes and climatic ranges, e.g., different precipitation regimes. However, a recent decline of quaking aspen cover observed in central Canada is thought to be a result of increased drought periods due to climate change. This suggests that quaking aspen stands in Quebec could follow in the future. My project aims to elucidate the genetic makeup of quaking aspen across North America in order to identify populations with highest adaptive potential to projected climate change. I will describe genetic diversity and population structure and identify adaptive genetic variants using a genomics approach. Moreover, I will perform germination and growth experiments to assess the fitness and adaptive variation of southern populations (from Utah and Mexico) in Quebec conditions. These results will help improve climate-modelling predictions on the impact of climate change on forest productivity and biodiversity.

* Presenter

CHALLENGES

OVERVIEW OF THE PRODUCTION SYSTEM OF FOREST SEED AND TREE SEEDLINGS IN QUEBEC

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In Quebec, seed and seedling production is managed provincially, as it is for research and development on tree improvement. The general directorate for the production of seeds and seedlings, Direction générale de la production de semences et de plants forestiers, is responsible for producing all the seeds and seedlings that are needed for reforestation. Around 350 million seeds are required each year, 85% of which are genetically improved. To produce plants, it takes efficient, resistant, tested, certified seeds. A process that is more complex than it looks which is provincially supervised by the Seed Division – Expertise and Coordination Directorate (Direction de l'expertise et de la coordination) is within the general directorate for the production of seeds and seedlings. Approximately 130 million seedlings are delivered each year, mainly conifers in containers. The seedlings needed for reforestation are produced by 19 nurseries; 6 public and 13 private. The presentation illustrated the main workings of the supply of forest seeds and seedlings in Quebec and the future challenges which are anticipated.

* Presenter

**WITHER THE SOCIAL?
WHY SOCIAL ASSESSMENTS MATTER FOR THE DEVELOPMENT OF
NEW BREEDING TECHNIQUES IN FORESTRY**

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Social analysis of new breeding technologies (NBT) is crucial at early innovation stages, and must extend beyond considerations of economic feasibility, cost-benefit analysis, market acceptability, and risk. Key lessons emerging from previous contentious agricultural biotechnology applications in Canada and the UK will be summarized and applied to emerging NBT such as genomic selection. What past controversies teach us is that failure to address the social aspects of technology, including, how harms and benefits are distributed, who owns and controls technology, how nature is represented, and which groups are authorized to govern and which are excluded, can spark public controversy and contribute to subsequent regulatory challenges. Recognizing and overcoming potential roadblocks to the realization of social analysis of NBT is essential, particularly for research and development that relies on public funding, and for breeding applications that take place on public land.

* Presenter

**FOREST TREE BREEDING IN SWEDEN –
DEVELOP GENETICALLY IMPROVED PLANT MATERIAL ADAPTED TO THE
FUTURE CLIMATE AND TO MEET THE NEEDS FOR FOREST RAW MATERIAL**

Charlotte Bengtsson

Skogforsk, the Forestry Research Institute of Sweden, Uppsala, Sweden

The objective of the Swedish long-term breeding programs for Norway spruce (*Picea abies*), Scots pine (*Pinus sylvestris*), Birch (*Betula* spp.), lodgepole pine (*Pinus contorta*), and larch (*Larix* spp.) is to improve commercially important tree characteristics like adaptation, productivity, and wood quality; to adapt to climate change; and to maintain genetic diversity without compromising future selection response.

Genetic tests in Sweden and in Finland have demonstrated about 10% gain in volume production per ha over a rotation period with seedlings originating from untested first-generation seed orchards compared to unimproved seedlots. Differences in quality traits are positive but smaller.

The predicted gain in volume production from the second round of Norway spruce seed orchards established during the 1980s varies from 10% (untested plus trees) to 25% (intense selection from tested plus trees). Genetic thinning of seed orchards can increase the gain further. The gain in volume production from the second round of seed orchards established using a mix of untested and tested parent trees is estimated to be in the range of 12–25%.

In the now established third round of seed orchards, based on the best tested plus trees, a gain of some 25% is anticipated. Even higher genetic gains are associated with the use of clonal reforestation material. Plantations established with rooted cuttings of selected clones or bulk propagation of rooted cuttings from selected full-sib families are nowadays used only on a small scale. Clonal forestry based on somatic embryogenesis (SE) has a potential to become a valuable tool for intensive wood production, but is not yet implemented operationally.

SWETREE – PART OF A FOREST BIOTECHNOLOGY INNOVATION SYSTEM

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One of the major opportunities for the future is the sustainable growth of high value forest raw material facilitating new uses and replacement of non-renewable products. SweTree Technologies is a plant and forest biotechnology company providing science based technologies to improve the performance properties of plants, wood, and fiber for the industry. A key strength of SweTree is the integrated environment with academia and industry partners, where scientific findings in a collaborative effort travels from the university, through SweTree to applications in the customer community.

In breeding, SweTree develops trait gene technologies applied to customer's elite germplasm. SweTree has a technology platform for GM Eucalyptus and a large trait gene portfolio including genes improving yield, yield protection, and wood quality. In somatic embryogenesis (SE), SweTree is developing automated solutions for large-scale production of SE derived plants. The SE technology is currently being set up for major Swedish forest owners for Norway spruce (*Picea abies*) operations.

Arevo, one of the SweTree spin-offs, is paving the way for new types of fertilizers, with characteristics differing from traditional fertilizers. Nitrogen availability is a key factor for plant growth. Traditionally, mineral nitrogen (ammonium and nitrate) were considered the only nitrogen sources for plant growth but recent research has shown that plants can access a range of organic nitrogen compounds as well. Within the large group of organic nitrogen compounds, basic amino acids, and in particular arginine, displays optimal characteristics as nitrogen fertilizer; high retention in soil and rapid uptake by plant roots. Arevo has developed a series of fertilizer products based on arginine.

Currently, the adoption of the arginine-based, controlled-release granular fertilizer in the Nordic forestry market has been rapid and the technology will be a key component in the transformation of forest regeneration in the Nordic countries, comprising enhanced efficiency of operations and improved seedling survival and growth.

* Presenter

VARIATION IN SEED AND CONE TRAITS IN A CLONAL SEED ORCHARD OF RED PINE (*Pinus koraiensis* Sieb. et Zucc.) IN NE CHINA

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In a red pine (*Pinus koraiensis*) clonal seed orchard, established in 1974, with a total number of 76 clones, cone and seed traits were studied in 2008 and 2018. The cone traits studied in 2008 included cone length, cone width, and number of seed per cone, while seed traits included seed length and width. In 2018, in addition to the traits studied in 2008, cone weight, number of scales, thousand seed weight per cone, seed weight, seed kernel and seed coat thickness were measured. Results showed that most variation in cone traits except cone length and cone width in 2018 was mainly due to inter-ramet variation within a clone and inter-cone variation within a ramet, while inter-clone variation was small. Similarly, genetic control of seed traits was weak with most variation being accounted for by intra-clone variation, which was contributed by inter-ramet, inter-cone, and within-cone similarly in magnitude. The estimated broad-sense heritabilities were low, less than 0.10, for all traits other than cone width and length in 2018 (both were under strong genetic control with high heritability estimates), but their heritability estimates based on clonal means were moderate, around 0.45 for cone and 0.35 for seed traits, suggesting clonal selection could still be effective in improving these traits. Genetic correlations between cone traits or between seed traits were moderate to strong in 2018. Some strong genetic correlations between cone traits and between seed traits and between years were also observed. The implications of these results to manage this seed orchard were discussed. Overall, while genetic selection will be effective, cultural management may be more effective in improving cone and seed traits of the seed orchard. The limited genetic variation in cone/seed traits indicated that it should not be the only selection criterion when roguing the orchard or selecting clones for a new seed orchard.

* Presenter

THE BACK UP PLAN

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The National Tree seed Centre (NTSC) was established in 1967 to address the demand for seed of known origin and quality for provenance testing. With Canada's, ratification of the Convention on Biological Diversity (CBD) in 1992, the NTSC's mission shifted to one that safeguards Canada's forest genetic resources in the face of climate change and other threats by acquiring, evaluating, preserving, and providing a national collection of forest genetic resources. How is this being conducted? Where does the NTSC stand in its efforts? What are the challenges to addressing the research and conservation needs of the country? What constitutes the forest genetic resources of Canada's forests? Who are the collaborators and research partners needed to ensure the NTSC is getting it right? These questions and more were presented, addressed, and discussed as the NTSC aims to be 'The Backup Plan' for Canada's Forest Genetic Resources.

BUTTERNUT: WHERE DO WE GO FROM HERE?

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The butternut canker, caused by the fungal pathogen *Ophiognomonia clavigignenti-juglandacearum*, has rapidly spread across the range in the US and Canada since first reported in 1967. Surveys in the US show an infection rate of over 90% in some areas and similar infection rates have been found in Canada. In New Brunswick (NB), surveys conducted in 2014–2017 showed that the canker was present throughout the range of butternut (*Juglans cinerea*) despite being first identified on the western border of NB/Maine 20 years ago. Recent studies assessing butternut's resistance/tolerance to canker have shown that there is most likely no genetic basis for resistance. However, NB butternut trees, asymptomatic for canker disease, are still found in areas with high canker incidence. Genetic diversity analysis of NB butternut shows that diversity is unique as compared to that found in the US. To conserve this diversity, the Canadian Forest Service has developed and implemented an *ex situ* cryo-storage program primarily for NB populations. The absence of evidence for canker resistance/tolerance in the species is resulting in researchers assessing alternative approaches to conserve the species. The health status and genetic diversity of NB butternut as well as the butternut *ex situ* program were discussed.

* Presenter

STATE-OF-KNOWLEDGE

SOCIAL ASPECTS OF FOREST GENOMICS: HINDSIGHT ON 15 YEARS OF RESEARCH

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The state of Canada's forest health and productivity is a critical factor determining the competitiveness of the forest industry. Genomic technologies have significant potential to expand the range of management options for managing future forests. For example, the application of genomic selection could lead to more consistency in tree form and properties, higher growth rates, resistance to insects or diseases, and improved wood properties for specific high-value applications. Since social acceptance is vital to the success of a wider scale implementation of genomics tools, we also examined the related barriers and opportunities. After 15 years of research, and by using different methodologies like economic analysis, survey and inquiry, we obtained various outputs: cost-effectiveness analysis, assessment of social acceptance, typology of policy instruments, diagram of the policy community related to the implementation of genomics tools, and forest stakeholders' perceptions of intensive silviculture. We now have a better understanding of the perceptions of decision makers towards the use of genomics as a sustainable forest management tool and the possible management compromise that could help implement intensive silviculture strategies in the context of integrated land management.

* Presenter

OPTIMUM-CONTRIBUTION SELECTION IN FOREST TREE BREEDING – TOOLS FOR PRACTITIONERS

Tim J. Mullin

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Tree breeders must often consider conservation of gene diversity, while at the same time attempting to maximize response to selection. The challenge of optimizing selection applies to both assembly of breeding populations as well as establishment of seed orchards. The optimum selection tool “OPSEL” uses state-of-the-art mathematical optimization approaches such as Second-Order Cone Programming and Mixed-Integer Linear Programming to optimize selection for various tree breeding applications, with a constraint on gene diversity. The tool can optimize selection on estimated breeding values (EBVs) from a list of many thousands of candidates and their pedigree, often in a matter of a few seconds. After optimizing selected gene contributions to a breeding population, the practitioner still faces the daunting task of preparing mating plans that represent unequal contributions from selected parents, while avoiding excessive relatedness between parents that might give rise to inbreeding depression in test progeny. To generate such plans for more than a few parents using pencil and paper is hugely difficult and prone to error. A generalized tool “XDesign” accepts a list of selected candidates, their pedigree, EBVs, and the desired frequency of use in the mating plan. The user can specify if mating is to be positive-assortative or random, and can specify a threshold on the maximum acceptable coancestry between parents for a given cross. The program prepares a crossing list, giving the parents to be crossed, their mid-parent EBV, and the coancestry between parents in each cross. OPSEL and XDesign are freely available for non-commercial purposes under general licenses.

HOW DO TREE BREEDING AND SILVICULTURE AFFECT GROWTH, STEM QUALITY AND WOOD QUALITY OF COASTAL DOUGLAS-FIR?

Miriam Isaac-Renton^{*,1} and Michael Stoehr²

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Since faster tree growth can be associated with lower wood strength and stiffness, selection for volume gain in tree improvement programs may inadvertently lead to reduced wood quality. At the same time, silvicultural practices may also affect wood and stem quality. It is critical to evaluate the impact of silviculture and recurrent selection on tree growth, wood quality, and stem quality to maintain value and validate growth and yield models that set sustainable harvest rates.

Here, we aimed to determine: 1) if productivity of genetically superior seed sources materializes as expected, 2) if superior crosses show declines in wood and stem quality relative to unimproved controls, and, if so, 3) whether silvicultural prescriptions involving higher planting densities can offset quality losses. We analyzed growth, wood quality, and stem quality traits of over 18,000 advanced generation trees from a 20-year realized gain trial for coastal Douglas-fir (*Pseudotsuga menziesii* var. *menziesii*). We tested three genetic entry levels grown under four initial planting densities on five sites in coastal British Columbia.

Improved seed sources exceeded expectations in terms of volume gain and stem quality, although there were minor reductions in wood density and stiffness proxy measures. These losses in wood quality were minimized under higher operational planting densities, which also appear to be the most suitable silvicultural compromise among traits. Since 15 million improved coastal Douglas-fir seedlings are planted annually in western Canada, there is high potential to increase productivity across the landscape while also maintaining value.

* Presenter

GENOTYPIC VARIATION, HERITABILITY AND GROWTH STABILITY OF CLONES IN A LARGE HYBRID POPLAR TRIAL IN NORTHERN ALBERTA

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Productivity, wood density, and disease resistance of poplar clones under specific climatic conditions are important traits in selecting for cultivation at an industrial scale. In our study, we focused on using hybrids from the *Aigeiros* and *Tacamahaca* sections in a large clonal trial (1978 clones within 63 families) to improve economically important traits for plantations in northern Alberta. The specific objectives were to: 1) quantify the clonal variation in growth and disease resistance, 2) calculate the broad sense heritability (H^2) of these traits, and 3) assess the clonal stability of performance across time in the context of further clonal selection. Genetic parameters for diameter at breast height (DBH) and height (H) were compared at ages 3, 8, and 10 years. The assessment of *Septoria musiva* stem canker symptoms was carried out twice (ages 8 and 10) by visual observation and wood density of selected families was assessed indirectly using drilling resistance at age 10. Growth parameters were under moderate to strong genetic control (H^2 for DBH was 0.37 to 0.64 and for H was 0.46 to 0.65 at age 3 and 8, respectively) while the genetic component of wood density and resistance to *Septoria* stem canker only explained a small part of the overall phenotypic variance. The age-age genetic correlations for growth traits indicated weak positive correlations between age 3 and 8 (0.59 for H and 0.45 for DBH) and stronger clonal stability between age 8 and 10 (0.86 for H and 0.92 for DBH). Our results showed that there were changes in clonal performance between ages 3 and 8(10), which implies that age 8 may be more reliable for selection. Moreover, susceptibility to *Septoria* stem canker appears to be associated more with environmental conditions than under direct genetic control.

* Presenter

TIME EFFECT ON HEIGHT AND DIAMETER GROWTH AND ITS IMPACT ON SELECTION

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The long breeding cycle and harvest rotation of forest trees has led to the development of indirect selection methods for rotation-age merchantable volume (target trait), which involve the use of juvenile height measurements to select parents for future breeding cycles. To validate this approach, we measured height (HT) and diameter at breast height (DBH) in three *Larix laricina* and one *Pinus banksiana* progeny trials at various ages (juvenile, mature, or rotation). We fitted four individual-tree linear mixed models to investigate indirect genetic effects and spatial autocorrelation, and used the best model for each trait to predict individual breeding values (PIBs). Scatter plot of PIBs for mature DBH (MDBH) and juvenile height (JHT) showed four growth profiles: (+PIBMDBH, +PIBJHT), (-PIBMDBH, +PIBJHT), (-PIBMDBH, -PIBJHT), and (+PIBMDBH, -PIBJHT). To further explore these results, we felled 40 study trees of *L. laricina* and measured dendrochronological variables. Results suggested that trees producing more merchantable volume could be infused into advance-generation breeding populations.

^{*} Presenter

**OPERATIONAL BREEDING
AND
PREDICTIVE TOOLS**

GENOMIC SELECTION - FROM PROOF OF CONCEPT TO APPLICATION: WESTERN REDCEDAR BREEDING PROGRAM

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Western red cedar (WRC) (*Thuja plicata*), a major ecological and commercial conifer species in British Columbia (BC), is renowned for its natural wood durability. The current WRC breeding strategy, however, requires the use of lengthy traditional approaches for measuring phenotypes, resulting in a long breeding cycle (~25 years). Genomic Selection (GS) has created a paradigm shift in animal and crop breeding by improving the speed and accuracy of selection but has not been applied yet in conifers due to lack of advanced testing and validation. WRC's unique biology, including long-distance linkage disequilibrium and precocious reproduction makes it an ideal species to evaluate the application of GS in conifers. Exome capture was used to genotype 45 parents and 1,520 first-generation offspring (18 years old), representing 26 polycross families collected from three sites in BC. Initial genotyping produced 1,300 SNPs that were used in parentage assignment to convert these 26 families to ~ 408 full-sib families and to identify pedigree errors. GS prediction models were fitted for the traits growth, foliar monoterpenes, and heartwood thujaplicins and lignans. The models were validated using a ten-fold cross validation and the prediction accuracy ranged between 0.86 and 0.89, depending on the attribute. Moreover, across-generations, -environments, -time validation, and effect of relatedness were assessed. Currently we are using > 50K SNPs from genic and intergenic regions, working on the independent validation of the models developed using different full-sib offspring populations. The initial results are promising and suggest that GS can be successfully applied to reduce the WRC breeding cycle from 25 to 2 years by predicting late-age expressed phenotypes at the seedling stage, for early selection.

* Presenter

ELITE BREEDING AND EARLY PARENTAL SELECTION OF WHITE SPRUCE USING MOLECULAR TOOLS AND MIXED MODELS

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In Alberta, the Region G1 white spruce (*Picea glauca*) Controlled Parentage Program (CCP) was initiated in 1977 using backward selections (choosing parents with the best height performance following progeny testing) to produce open-pollinated seeds for different forestry companies in the province. In order to increase gain for height and volume of this species, this CPP requires elite material for a second-generation orchard. Therefore, using new methodologies for parental selection at an early stage, understanding of inbreeding breakdown in improved progenies produced from this orchard facility, and determining reliable estimates of pollen contamination are being studied in this orchard. To meet those needs, four projects are in progress: 1) production and analysis of elite seedlots from controlled crosses using the best 18 genotypes (based on their % height breeding values at rotation), 2) comparisons of gibberellic acid (GA) gene expression and enzymatic content in trees coming from wild stands, open-pollinated orchards, and controlled crosses, 3) assessment of the inbreeding effect of progeny coming from wild stands, open-pollinated orchards, and controlled crosses, and 4) genotyping white spruce bulk seedlots from different years using SNP panels to calculate pollen contamination. For those experiments, different phenotypic (e.g., height and diameter), physiological (e.g., photosynthesis, biomass, and GA hormone level), and molecular (e.g., GA gene expression and genotyping) traits will be compared among elite, open-pollinated, and wild progenies. Genetic models will be used to fit and analyze all the data. It is expected the results will enable the selection of white spruce elite parents based on growth performance and GA levels and thus the establishment of a second-generation breeding population for maximum gains in a shorter timeframe than using traditional breeding methods.

* Presenter

COMPLEX TRAIT PREDICTION BY SIMULTANEOUSLY CONSIDERING GENOMIC RELATIONSHIP, FUNCTIONAL KNOWLEDGE AND ENVIRONMENTAL VARIABILITY

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Conifers have acquired a series of unique characteristics over their evolutionary history including their mega-size genomes but with a significantly lower number of protein-coding regions in comparison. Getting sufficient genetic markers to capture the marker-QTL relationship, while accurately estimating genetic parameters, requires a substantial amount of genotyping effort. Further with the dynamics of genome structural changes responding to environmental variability, known as genotype by environment interaction (GxE), conifer genomes possess a great challenge for genomic prediction in this rapidly changing climate. Accuracy and stability of prediction models are the result of simultaneously accounting for Mendelian sampling terms, linkage disequilibrium between markers with QTLs, as well as their relative response across environments (GxE). In this presentation, we reported a multivariate Bayesian weighted kernel approach that concurrently considers genome-wide association and genetic heterogeneity among populations for a multi-environment prediction. Our results showed that the Bayesian framework provided improved predictability when the genomic background was modeled, the gain in predictability most evident in the traits with low multi-environment heritability. Considering functional knowledge of SNPs in kernel function is also reckoned, as our weighted kernels resulted in a 10–21% improvement in predictability. Accurate and stable prediction is crucial for the implementation of genomics-assisted tree improvement. Based on our study, prediction models capable of comprehending genetic heterogeneity among breeding families, as well as the imperfect genetic correlation of trait performance across environments, would facilitate the practical use of genomic prediction in tree breeding programs.

* Presenter

INCORPORATING GENETIC GAIN INTO GROWTH AND YIELD PROJECTION MODELS FOR ALBERTA'S WHITE SPRUCE AND LODGEPOLE PINE TREE IMPROVEMENT PROGRAMS

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Tree improvement is considered an effective method to address the shrinking forest land-base in Alberta resulting from land conversion, creation of reserves, and climate change as well as the impacts of fire and insects. It is of great necessity to quantify the potential harvest from deployed improved trees. However, the growth and yield models currently used in Alberta were originally developed from growth measurements and projections of wild trees, and therefore, there is no widely accepted method to incorporate genetic gain in volume from tree improvement. Furthermore, there is also an important challenge associated with acceptance of an appropriate age-age correlation when selecting trees at a young age and projecting their anticipated increase in volume at rotation. Since white spruce (*Picea glauca*) and lodgepole pine (*Pinus contorta*) are the most important commercial tree species and account for 80% of the reforestation in Alberta, they are the focus of this study. This presentation described an approach to incorporate genetic gain for volume into growth and yield models in Alberta based on progeny and provenance trials of white spruce and lodgepole pine.

* Presenter

A CUMULATIVE-EFFECTS MODELLING FRAMEWORK LINKING IMPROVED FOREST GROWING STOCK TO CANADIAN BIOECONOMY VALUE STREAMS

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The UBC-FRM Bioeconomy Lab focuses on the development of decision support tools for productive and resilient forests that are linked to supply chain management/logistic tools for the allocation of fibre to manufacturing sectors. The forest fibre decision model was developed through multivariate mapping for the forestry sector which includes an assessment of the current state of the forest and a projection of the forest stock through time. The major research areas we have emphasized are: 1) incorporate genetic gain and reduction of losses into modelling tools, 2) determine adaptive capacity of improved stock in the environmentally sensitive to drought vulnerable area, 3) identify where, when, what, and how much improved genetic stock can be planted through a modelling tool, and 4) link the fibre cascade model with the forest sector model to identify economic value of harvested logs from forests transformed into various products. Our current plans are to develop a cumulative effects framework by further developing models (e.g., Fibre Cascade Model, Q3 Model) that link improved forest growing stock for the forests of Canada and connect genome impacts to potential bioeconomy value streams and emerging global markets.

* Presenter

GENOMIC PREDICTION ENABLES FORWARD SELECTION IN A WHITE SPRUCE POLYCROSS MATING DESIGN

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Polycross mating designs have been conventionally used for evaluation of general combining ability (GCA) in breeding strategies that were mainly based on backward selection. The possibility to use genetic markers for reconstruction of full pedigree and more so to obtain genomic-estimated breeding values based on marker data, allows for a broader use of polycross tests, especially in forward selection schemes. In the current study, we evaluated the accuracy of genomic prediction in a white spruce (*Picea glauca*) polycross trial repeated in three environments in Quebec. Phenotypes for growth and wood quality from 856 trees were associated to a panel of 4,092 markers. Precision of genomic predictions was compared to predictions obtained based on the known (maternal) pedigree only or the reconstructed full pedigree following paternity assignments using genetic markers. Genetic parameter estimates such as heritabilities and type-B correlations were rather comparable among the tested methods, with slightly higher estimates of heritability obtained for pedigree-based models compared with genomic selection models. However, genomic predictions of phenotypes and breeding values were more accurate than predictions based on the pedigree or the reconstructed pedigree. Considering the operational advantages of polycross mating designs in terms of easier handling of crosses and lower associated costs for test establishment, we believe that this crossing scheme offers great opportunities for operational application of forward genomic selection. This is especially true for spruces, considering the continued development of clonal reproduction techniques such as somatic embryogenesis.

* Presenter

INTER- AND INTRA-GENERATION GENOMIC PREDICTIONS FOR DOUGLAS-FIR GROWTH IN UNOBSERVED ENVIRONMENTS

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Conifers are prime candidates for genomic selection (GS) due to their long breeding cycles. Previous studies have shown much-reduced prediction accuracies (PA) of breeding values in unobserved environments, which may impede its adoption. The impact of explicit environmental heterogeneity modeling, including genotype-by-environment (G×E) interaction effects using environmental covariates (EC) in a reaction-norm genomic prediction model, was tested using single-step GBLUP (ssGBLUP). A three-generation coastal Douglas-fir (*Pseudotsuga menziesii* var. *menziesii*) experimental population with 14 genetic trials (n = 13,615) permitted estimation of intra- and inter-generation PA in unobserved environments using SNPs derived from exome capture. Intra- and inter-generation PAs ranged from 0.447–0.640 and 0.317–0.538, respectively. The inclusion of ECs in the prediction models explained up to 23% of the phenotypic variation for the fully specified model and resulted in the best model fit. Modeling G×E effects in the training population increased PA up to and over the base model for inter- and intra-generations, respectively. GS-PA can be substantially improved using ECs to explain environmental heterogeneity and G×E effects. The ssGBLUP methodology allows historical genetic trials containing non-genotyped samples to contribute to genomic prediction, effectively boosting training population size which is a critical step. Further pheno- and enviro-typing developments may improve GS-PA.

* Presenter

CONNECTING GENOTYPE WITH PHENOTYPE

**GENOMICS AND BIOLOGY OF SPRUCE RESISTANCE AGAINST
THE WEEVIL *Pissodes strobi***

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The spruce weevil (*Pissodes strobi*) is a major pest of naturally regenerating and planted conifer forests in North America. Weevil-host interactions occur in two major phases of the insect life cycle, defined here as the Exo- and Endo-Phases. In the Exo-Phase (outside the host), mobility of adult weevils is not restricted by host defenses allowing insects to make host choices. In the Endo-Phase (inside the host) mobility and development from eggs to young adults is restricted by host tissues and defenses without the option of host choice. The Exo-Phase is critical for the weevil to identify a suitable host, but it is in the Endo-Phase where damage to the living host is done. Genetic resistance to weevil exists in several spruce species throughout the endemic range of the pest. Resistance is exerted through a complex synergism of constitutive and induced, chemical and physical defenses that comprise the spruce defense syndrome. We reviewed spruce defense systems that disrupt the weevil life cycle and mechanisms by which resistant trees thwart weevil attack. We highlighted the development of genomic approaches targeted to specific traits to facilitate the rapid identification of elite weevil resistant spruce genotypes. Knowledge of the spruce defense system supports the development of pest management and forest health strategies in spruce breeding programs.

* Presenter

RESISTANCE MECHANISMS AGAINST *Didymascella thujina* IN *Thuja plicata*

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Didymascella thujina (cedar leaf blight, CLB) is one of the most devastating foliar diseases of *Thuja plicata* (western red cedar, Cw). The pathogen was responsible for diebacks in North America last century and can be a concern in nurseries and young Cw plantations. Genetic variability in resistance against CLB has been reported in Cw populations and is a key trait in the Cw genetic improvement program in British Columbia. However, resistance mechanisms against the pathogen in Cw have been little studied. Between 2012 and 2015, a series of studies were carried out on full-sib seedlings and clones of Cw with contrasting resistance to CLB in order to elucidate resistance mechanisms at the histological, chemical, and gene expression levels. The analyses revealed that resistant seedlings had significantly thicker cuticles and significantly higher concentrations of sabinene and α -thujene. Both resistant and susceptible seedlings showed a significant accumulation of foliar aluminum as the disease progressed. At the genetic level, resistant seedlings had significantly higher expression levels of various disease resistance protein transcripts. Resistant clones had a significantly higher expression of transcripts of bark storage proteins and dirigent proteins. Overall, the data collected suggest the existence of age-related resistance in the pathosystem, as well as a strong genetic component to the resistance that may involve disease resistance proteins, bark storage proteins, dirigent proteins, and proteins related to terpene synthesis.

* Presenter

**BREEDING FOR SWISS NEEDLE CAST TOLERANCE:
Nothophaeocryptopus gaeumannii IN COASTAL DOUGLAS-FIR**

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With changing climates, there is increasing concern in western Canada regarding the impact of Swiss Needle Cast (*Nothophaeocryptopus gaeumannii*), a native fungus causing premature needle loss in Douglas-fir (*Pseudotsuga menziesii*). Low needle retention is associated with growth losses up to 30–50% in an otherwise productive and valuable timber tree species. While historically of lower concern, epidemics in the southern range of coastal Douglas-fir as well as modelling suggest higher disease risk in the coming decades in coastal British Columbia. To address this risk, we: 1) screened an advanced-generation breeding population for variation in disease resistance or tolerance, 2) evaluates heritability of tolerance, and 3) understood the molecular basis of disease response to facilitate marker-assisted selection in subsequent breeding cycles using RNA-seq. We evaluated signs of the pathogen itself (fungal fruiting bodies occluding stomata) as well as symptom severity (needle retention) on two climatically different sites over three years, allowing us to disentangle the effects of genotype and environment. There were differences in needle retention and fruiting body counts among families, sites and years. In addition to this variability, tolerance to the disease appears to be under moderate genetic control. Preliminary results were presented, and implications discussed.

* Presenter

INFERENCE ON POPULATION GENETICS OF THE INVASIVE INSECT ASIAN LONGHORNED BEETLE THROUGH NGS TECHNOLOGY

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Asian longhorned beetle (ALB), *Anoplophora glabripennis*, native to China and South Korea, has successfully spread and established in North America and Europe. ALB is a wood-boring insect with a wide range of hosts, mainly poplars, willows, maples, and elms and poses a significant threat to forest ecosystems. It is widely distributed both in its native and its invasive range, counting as one of the major devastating pests worldwide. In this study, we used NGS technology (Genotyping-by-sequencing) to generate restriction enzyme reduced ALB genomes from population collections throughout its native range. We analysed neutral genetic variants (SNPs) across the genome to examine genetic diversity and population structure of ALB. The results showed clear ALB population differences between China and South Korea. Remarkably, Korean ALB's heterozygosity is significantly lower. For Chinese ALB populations, we found different levels of population structure. ALB in NW China and N China appear to be genetically clustered together, while ALB populations in NE China differ genetically from those in E China. Moreover, populations in E China exhibit a strong latitudinal gradient pointing at great adaptive capacity in this region. These preliminary results provide improved insights into the recent history of human-mediated dispersal of ALB and local adaptation within its native range, and will foster future studies on the invasive pathways of ALB worldwide.

* Presenter

GENOME-WIDE ASSOCIATION STUDIES TO UNRAVEL THE GENETIC ARCHITECTURE OF QUANTITATIVE PHENOTYPIC TRAITS IN POPLARS

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How variation in phenotypic traits can be explained by variation at the genetic level is a fundamental question for accelerated tree breeding. Molecular breeding uses genetic information to select individuals in breeding programs. Therefore, it is necessary to identify genetic variants that are associated with phenotypic trait variation of interest beforehand. In this project, we sought to discover the genetic architecture underpinning quantitative phenotypic trait variation in North American poplars. For this purpose, we used common (frequency in a population > 5%) and rare (frequency < 5%) genetic variants to perform genome-wide association (GWA). Rare variants are not often used in GWA but hold great potential in explaining a significant part of the observed heritability in phenotypic trait variation. First, we used a dataset of 1,039 re-sequenced poplars to identify small genetic variants (single base; insertion/deletion) across individual genomes using two different variant calling software for comparison. We then evaluated population structure of the studied population to prevent false positive discovery during genetic association tests. Finally, we performed GWA tests to associate rare and common variants to phenotypic variation related to wood properties. We used 900 individuals with both genetic and phenotypic data to associate these previously identified genetic variants to wood property measurements. Our results will help better understand the genetic architecture of phenotypic trait variation in poplars. This GWA project focused on small genetic variants only, but another recent study highlighted the importance of gene copy number variations in poplar adaptation over wide geographical ranges.

* Presenter

CHARACTERIZING THE GENETIC INFLUENCE ON WOOD DENSITY VARIATION IN WHITE SPRUCE

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Conifer breeding programs are more and more considering wood quality as a selection criterion to improve end-use properties. Wood density is among the key traits as it is related to mechanical strength and dimensional stability. Variation in density within a piece of wood may lead to deformation during transformation and heterogeneous machining properties. In the present study, we aimed at disentangling age, genetic, and environmental influences on the pith-to-bark variation of wood density. We analysed wood density profiles from a 16-year-old genetic trial repeated in two contrasting environments in Québec. A total of 2,365 trees belonging to 97 full-sib families was sampled for this study. We fitted exponential functions to describe the pith to bark inter-annual variation of wood density. The optim function in R was used to iteratively search for the best combination of parameters in each disk. The density trend due to development differed significantly in the two environments. Preliminary results showed some intrafamily variation. Genetic control of mean ring width and mean wood density was low to moderate and moderate to strong, respectively. Parameters describing the density variation trend were however under somewhat weaker genetic control indicating an important environmental component. The results of this study will allow us to characterize the homogeneity of the average density of wood between the two study sites and to determine the heritability of this homogeneity. Thus, the most homogeneous families will be identified for reforestation and the variables to consider in breeding of growing trees with less variable wood will also be identified.

* Presenter

NEW DEVELOPMENTS

EVALUATING NEW GENOME-BASED PATHWAYS TO FOREST BIOPRODUCT DEVELOPMENT

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The SYNBIOMICS project is developing biocatalysts that upgrade the three wood fractions produced by pulp mills. Numerous pathways exist for new bioproduct development. Assessing these pathways and comparing different product options can be extremely challenging. Three unique bioproducts, including modified cellulose and lignin outputs achieved through the application of optimized biocatalysts developed through the SYNBIOMICS project, were discussed. Biomass availability and suitability for product delivery is determined by examining current fibre streams within the forest products sector. Two mill case studies were utilized to quantify the availability of cellulosic fibre, lignin, and residual streams. An initial review of techno-economic and life cycle assessment of selected bioproducts products was provided and bottlenecks in potential production were identified. The presentation delivered a methodology for early assessment of bioproduct potential, allowing industry and government to screen candidates for future bioproduct development to support Canada's bioeconomy.

* Presenter

THE DELEAVES DRONE, A DEVICE FOR EFFICIENT TREE CANOPY SAMPLING

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Sampling the canopy of a tree is useful for many disciplines: biodiversity conservation, propagation, genetic diversity analysis, monitoring of plant health, precision forestry, etc. For example, the youngest leaves, which are in the upper third canopy of a tree, contain nutrients related to the growth of the preceding year. Such samples are precious for species identification, chemical analysis in the context of fertilization, and can also be used for monitoring insects and disease as well as for artificial propagation. However, the current sampling techniques all have common limitations, which is their lack of reach and their usage complexity. Without cutting a tree, the access to branches located at more than 10 m high is time-consuming, expensive, and sometimes impossible. In some situations, the topography simply doesn't grant access to the sample (canyon, watercourse, etc.). Consequently, there is a need to remotely reach these samples in an efficient way. We presented a new device named DeLeaves which can be used for efficient canopy sampling using a drone. To date, this tool was able to remotely collect branches from more than 100 trees located out of sight from various species, at an average altitude of 15 m and in about 5 minutes per sample. The DeLeaves was tested in complex environments such as isolated regions in Vietnam as well as in deciduous forests with various maturity levels in the southeast of Canada.

* Presenter

PRIMING AND PELLETING OF BOREAL SEED FOR FOREST RECLAMATION

Jean-Marie Sobze

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In Alberta, forest fragmentation from resource extraction has increased and industrial reclamation is in a dynamic state. This arises from a substantial change in the regulatory expectations (standards) to return the land to “equivalent land capability”. This evolutionary step requires industry to establish a fully functioning plant community of herbaceous, low shrubs, tall shrubs and trees.

The current practice in forest reclamation is to grow seedlings and hire crews to out-plant nursery stock (plugs) on well sites. While this method is reliable, nursery stock and labour make this a high-cost endeavour.

Direct broadcast seeding is an alternative approach that is rarely practiced as part of re-vegetation programs due to uncertainty resulting from failures in previous trials. The weaknesses of broadcast seeding are due to: 1) poor seed/soil contact from lightweight seeds, 2) loss of seed due to predation and sun, 3) potential seed dormancy, and 4) seed susceptibility to wind drift during aerial deployment.

The objective of this project was to assess germination and emergence of priority boreal native species in response to a combination of seed priming and pelleting treatments. Our assumption was that coupling priming and pelleting would improve or facilitate direct broadcast seeding through dormancy breaking, an increase in the seed size, and seed protection.

While priming and pelleting is practiced in the agricultural sector, there is negligible knowledge and practice on priming and pelleting for native boreal species. This presentation shared greenhouse results and early outcomes of field trials using pelleted native boreal seeds.

EFFECT OF METAFFOUNDERS IN FOREST TREE GENETIC EVALUATION

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Forest tree breeding programs are still in the very early stages of domestication due to the biological constraints that affect forest trees, such as late expression of economically important traits and delayed onset of sexual maturity. Therefore, the impact of evolutionary processes such as natural selection, random drift, and migration of wild populations will still be reflected in the phenotypic expression of traits in breeding program populations and modelling of these processes should be included in the genetic evaluation system. The New Zealand coastal Douglas-fir (*Pseudotsuga menziesii* var. *menziesii*) breeding population is based on a provenance/progeny test that includes samples from a geographically broad area, covering both Oregon and California, and is thus a suitable candidate to explore the impact of modelling provenance effects on genetic evaluation. We modelled provenance effects through several scenarios that manipulated genetic groups and found that modelling different metafounders (genetic groups) for the maternal and paternal sides of the pedigree resulted in the best model fit and breeding values with the smallest standard errors. These findings were further explored in a single-step genomic evaluation, with modelling of relatedness between defined metafounders through genomic information obtained from descendants included in the breeding population.

* Presenter

GENOME SEQUENCING IN BARK BEETLES

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Bark beetles (Coleoptera: Scolytinae) pose a significant threat to many conifer species in Canada. In the six years since the first genome of a forest insect was sequenced (the mountain pine beetle, *Dendroctonus ponderosae*), the costs, sequencing technologies, and assembly and analysis methods have changed significantly. These improvements have permitted the genome assembly of several additional forest insect pests and substantial resources now exist for several endemic and invasive forest insects. Recent genome projects in *D. ponderosae*, *D. rufipennis* (spruce beetle), *D. pseudotsugae* (Douglas-fir beetle), and *Dryocoetes confusus* (western balsam bark beetle) were discussed and how they will facilitate a greater understanding of the mechanisms underlying adaptation of forest insect pests to their different hosts and environments.

* Presenter

GENOME ASSEMBLIES AND ANNOTATIONS OF ENGELMANN, SITKA, WHITE AND INTERIOR SPRUCE

**Lauren Coombe^{*,1}, Kristina Gagalova¹, René L. Warren¹, Stewart A. Hammond¹,
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With widespread distribution in diverse forest ecosystems across the Canadian landscape, spruces are a major source of wood and fiber. Under climate change, they are increasingly affected by adverse conditions such as drought and forest pests. Characterizing the genomes of different spruce species should hasten research into their local adaptation, which can in turn inform spruce breeding programs and applications in forest health. As part of the Spruce-Up Project, we have sequenced, assembled, and annotated the massive 20 Gb genomes of four *Picea* spp. native to Canada: Sitka spruce (*P. sitchensis*), white spruce (*P. glauca*), Engelmann spruce (*P. engelmannii*), and interior spruce (*P. engelmannii* x *glauca*). The latter was represented by an elite genotype from the British Columbia interior spruce breeding program with trihybrid composition from the three former taxa. To assemble the highly repetitive spruce genomes, we utilized a combination of Illumina short reads, linked and long reads, and made use of various scalable bioinformatics tools developed in our group, including assembly (ABYSS), correction (Tigmint), and scaffolding (ARCS) utilities. We improved the contiguity of our previously published white spruce and interior spruce nuclear genome assemblies (NG50 = 131 and 121 kb, respectively), and produced initial assemblies of the Sitka spruce and Engelmann spruce nuclear genomes. Complete organellar genome sequences were also obtained and annotated. In assessing the completeness of our assemblies in the genic space, we found that all assemblies have over 41% complete BUSCOs (Benchmarking Universal Single-Copy Orthologs), and comprise over 27K high-quality genes, as annotated by the Maker pipeline. These genomic resources will facilitate the mapping of polymorphisms and functional investigations at the genome-wide level, expanding our knowledge on the evolution of adaptive divergence in conifers.

* Presenter

POSTERS ABSTRACTS

GROUND-BEETLE (COLEOPTERA: CARABIDAE) DIVERSITY AND BUNDANCE IN FORESTRY AFFECTED AREAS OF ALEZA LAKE RESEARCH FOREST

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Forestry drives not only the economy, but the ecological turnover in many parts of the world, including British Columbia. Much research has been done on the regeneration of forest ecosystems within forestry-affected areas. Carabids are a family of beetle that are well known biodiversity indicators. They have been used to extrapolate overall health and maturity of forest sites in boreal regions of Europe. In this study, I looked at the Intermediate Disturbance Hypothesis (IDH) within a northern Canadian boreal forest by collecting Carabids at Aleza Lake Research Forest. Pitfall traps were installed in 2017 in early growth (EG) plots, historically harvested (HH) plots, and old growth (OG) plots in both a knolls and a plateau type landscape. I predicted that, with a greater number of micro-niches, the knolls area would have a higher level of biodiversity than the plateau. Also, in accordance with the IDH, I predicted that the HH sites would have a greater biodiversity than the EG and the OG sites. From this, I predicted that abundance levels would be higher within the HH areas as my samples were only identified to subfamily. My data demonstrated that the Carabinae abundance trends supported the IDH as there were more in the HH and the OG forests than in the EG forests ($df = 2$, $F = 4.4381$, $p = 0.02468$). There were more Carabinae in the knolls than the plateau, though, there was more Trechinae in the plateau than in the knolls ($df = 1$, $F = 6.9964$, $p = 0.009604$). Subfamily richness was lower in the EG forest than in the HH and the OG forests, following the IDH ($df = 2$, $F = 6.2024$, $p = 0.002961$). Further research should continue looking at the connection between Carabids and overall biodiversity within an ecosystem. There should be multiple samples collected throughout an entire season to see if there are temporal differences as well as refining the taxonomic scale to species from subfamily.

BALSAM POPLAR GENOTYPE AND ITS ASSOCIATED ROOT MICROBIOME INFLUENCE GROWTH ON ACID AND NEUTRAL MINE SOILS

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Abandoned, unreclaimed mines represent an important environmental issue since they typically remain unvegetated for decades, allowing vast amounts of exposed and contaminated soil, waste rock and tailings being spread via aeolian and water erosion. Several factors limit the revegetation of these sites, including extreme abiotic conditions (e.g., very low pH) and low availability of nutrients. The selection of tree genotypes with an associated microbiome favoring their growth under harsh conditions, such as those prevailing in mine waste environments, is a strategy that could facilitate the restoration of mining sites. Therefore, the aim of this study was to determine the importance of host genotype on their ability to revegetate a disturbed site by recruiting a specific microbiome. Two mining sites in Abitibi were selected for this study: Westwood, an old gold mine containing acid generating pyrite-rich waste rock and La Corne Mine, a former molybdenum and bismuth mine containing neutral nutrient-poor mine tailings. Eighteen genotypes of *Populus balsamifera*, from cuttings harvested at the mine sites and from a national collection of poplars, from the east, the west and the centre of Canada, were grown in these mining substrates in a greenhouse experiment. Tree growth was monitored during two growing seasons, after which the soil strongly attached to tree roots (i.e., rhizosphere) was harvested from fine roots to extract DNA and characterize bacterial and fungal communities by sequencing taxonomic markers. Several physicochemical characteristics of the bulk soil were also measured (e.g., pH, C, N, S, exchangeable cations).

* Presenter

**POPULATION GENETICS AND EPIGENETICS OF THE PLANE TREE
(*Platanus orientalis*) AND ITS EVER-GROWING NATURAL MUTATION**

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Temperate and subtropical perennial woody plants alternate between active growth and dormancy periods that are associated with favorable and unfavorable growth conditions. Despite the importance of this phenomenon, for survival and plant growth, the gene networks that are involved in the developmental pathway(s) of bud and dormancy induction are not well known. In this respect, dormancy-incapable mutations are invaluable for studying regulatory genes associated with bud and dormancy induction. To our knowledge, mutations that fail to enter dormancy under dormancy-inducing conditions are known only for *Corylus avellana* and *Prunus persica*. Herein, we reported an evergrowing mutation in the plane tree (*Platanus orientalis*) that occurs in Greece and compare its genetic and epigenetic variation to typical natural populations. We sampled and analyzed eight natural populations, six from northern Greece and two from Crete, one being that of the evergrowing mutation. Genetic variation was assessed by seven microsatellite (SSR) markers, while epigenetic variation was assessed by four combinations of MSAP epigenetic markers. Results showed that both the typical form and the evergrowing mutation share a common gene pool, however, they are well separated in multivariate space. Moreover, results provide the first evidence on the degree of coupling between the extent and the structure of epigenetic and genetic diversity in the typical form and the evergrowing mutation of *Platanus orientalis*.

* Presenter

**ARBUSCULAR MYCORRHIZAL FUNGAL COMMUNITIES IN HABITATS
IMPACTED BY IRON ORE MINING WASTE AFTER THE FUNDÃO DAM COLLAPSE
IN MINAS GERAIS STATE, BRAZIL**

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Iron ore mining activities have resulted in severe damage to water supply and biodiversity including soil microbial diversity, after the failure of Fundão Dam in November 2015 in Minas Gerais (MG), Brazil. This region has been exposed to deposition of iron ore mining waste (IOMW) and the aim of this study was to evaluate the community dynamics of arbuscular mycorrhizal fungi (AMF) and soil physico-chemical characteristics, three years after the disaster. Five habitats were selected: two undisturbed habitats, forest (UND) and pasture (PAST), and three habitats affected by IOMW under different stages of recovery (REC1, REC2) and pasture (PAST-rec). Molecular analysis of AMF communities and soil physico-chemical analyses were conducted. Soil samples were collected in triplicate in two seasons, March 2018 and September 2018. DNA was extracted and PCR-DGGE was performed using AML1-AML2 and Glo1-NS31 (Nested) primers. The bands of DGGE gel were analyzed and normalized in Bionumerics. Each band was considered as an OTU (operational taxonomic unit) and dendrograms were generated using DICE-WARD index. AMFs are dispersed in all disturbed habitats. In both sample periods, UND and PAST were grouped closely, maybe due to the absence of the IOMW. In March, REC1, REC2, and PAST habitats presented low similarity with other habitats, but a higher similarity in September (> 40%) was observed due to the plant recruitment process and increase in OTUs. The CCA showed that contaminated habitats were undergoing small changes in relation with biological and chemical factors. These changes and the increase in AMF community can be influenced by the revegetation process and the changes of soil chemical characteristics, suggesting the importance of mycorrhizal association for the ecosystem recovery and AMF distribution.

* Presenter

CO-DEVELOPMENT OF INDIGENOUS AND SCIENTIFIC KNOWLEDGE: STEP I

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Climate change (CC) is one of the major challenges that our society is facing in the twenty first century. Forests are already undergoing the repercussions of these changes. Forest management practices promoting forest resilience need to be rapidly established. One of the first steps consists of evaluating the genetic diversity and adaptability of forest tree species to CC using a genomic approach. We have chosen *Populus tremuloides* (PTS) as a case-study, since aspen is broadly distributed in North America. While the genetic makeup of PTS will be determined, another component of the project will focus on a knowledge co-development approach. Technologies and local indigenous knowledge will both be used. Indigenous peoples have used and stewarded forests for centuries, accumulating valuable knowledge, as well as accommodating and responding to environmental change over time. They are therefore primary actors in climate change solutions.

My project consists of gathering information from community members of the Innu of Essipit First Nation in order to better understand the importance of trembling aspen and other relevant species within the community's culture (e.g., white pine (*Pinus strobus*), blueberry (*Vaccinium* spp., etc.) in the CC context. Using the PTS as an example, my project is also focusing on how genomics allows development of tools to support decision making within a sustainable forest management context. PTS samples collected in 2018 and 2019 on the Essipit reserve were included in the large genetic survey and used to connect the forest genetic diversity of Essipit community to the rest of North America. The first step of the project aims to build a communication workshop in order to introduce forest genomics (tools and potential) to community members by using case studies such as the PTS example. The results obtained with PTS from Essipit will be presented to the community. Then, we will evaluate if this approach is suitable to demonstrate the benefits of genomic applications. The perceptions and apprehensions about CC and their impacts will also be discussed with community members.

* Presenter

**UNASSISTED MIGRATION WITHIN A RIPARIAN TREE SPECIES:
INFERENCES FROM THE GENETIC STRUCTURE OF *Populus deltoides***

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Global change will have major impacts on riparian ecosystems, thereby leading to greater forest vulnerability. In this study, our objective was to understand how genomic diversity of the foundation species *Populus deltoides* was shaped by its environment to gauge its adaptive capacity. We used two complementary approaches to get a full understanding of *P. deltoides* genetic diversity at both the species and whole genome ranges. We first used a low (but selected) number of SNPs from a large number of individuals that covered the entire range of the species. This allowed us to design a Sequence-capture experiment using a small (but selected) number of trees representative of the three different lineages we detected in the range sampling.

The comparison between both cpDNA and ncDNA patterns showed that gene flow between the lineages is unbalanced. We proposed that it could represent a case of “unassisted” migration within a tree species. Indeed, gene flow direction, that follows the river flow, is in line with future climate predictions.

* Presenter

UNDERSTANDING THE ADAPTIVE CAPACITY OF FOREST TREE SPECIES FOR CLIMATE CHANGE: QUAKING ASPEN, A KEYSTONE NORTH AMERICAN TREE SPECIES

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Climate change is accelerating and causing more climate extremes, such as severe drought episodes, that will have negative consequences on many North American forest tree species. We therefore need to develop tools to assess tree species' adaptive capacity and guide future sustainable management. The ecologically important *Populus tremuloides* (quaking aspen) is a species of choice for studying the genetic basis of adaptation due to its wide distribution, from northern Quebec to Mexico, in varying altitudes and climatic ranges, e.g., different precipitation regimes. However, recent decline of quaking aspen cover observed in central Canada is thought to be a result of increased drought periods due to climate change suggesting that quaking aspen stands in Quebec could follow in the future. My project aims to elucidate the genetic makeup of quaking aspen across North America in order to identify populations with highest adaptive potential to projected climate change. I will describe genetic diversity and population structure and identify adaptive genetic variants using a genomics approach. Moreover, I will perform germination and growth experiments to assess the fitness and adaptive variation of southern populations (from Utah and Mexico) in Quebec conditions. These results will help improve climate-modelling predictions on the impact of climate change on forest productivity and biodiversity.

* Prersenter

ADAPTIVE POTENTIAL OF SUGAR MAPLE FACING CLIMATE CHANGE

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Current climate disorder is a threat to global biodiversity and related ecosystem services. When climatic conditions change abruptly, as currently observed, living organisms can either adapt to their new living conditions or migrate to a more favorable habitat. This PhD project aims to study climate-related genomic adaptations in sugar maple (*Acer saccharum*), a species widely distributed in eastern North America. Since the demographic history of a species may leave genetic signals that make it difficult to detect adaptive genetic variations, we will first carry out a phylogeographic study of sugar maple from sequence capture data. Then, we will use a landscape genomics approach to study the local adaptation of sugar maple populations in Quebec. Finally, the future distribution of allelic variation will be projected under different climatic scenarios. This project will be the first large-scale study to discuss genetic adaptations in response to changing climate conditions in sugar maple. In addition, understanding the adaptability of sugar maple to climate change may be useful for decisions related to the conservation of this economically important species. This would maximize the adaptive potential and resilience of maple forests to climate change.

* Presenter

DROUGHT TOLERANCE IN DOUGLAS-FIR: ARE POPULATIONS LOCALLY ADAPTED?

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Drought is a major concern in forest management and conservation around the world as it can directly or indirectly hinder tree growth and increase tree mortality, affecting ecological processes and ecosystem services. With climate change, droughts are expected to increase in frequency and intensity. Douglas-fir (*Pseudotsuga menziesii*) is an important species in North America, both ecologically and economically. In order to investigate how tolerance of summer drought varies among populations and varieties (coastal, var. *menziesii* and interior, var. *glauca*), we established a greenhouse common garden experiment with seedlings from 88 different provenances spanning ~30° latitude, ~27° longitude, and ~2,900 m elevation. The experiment had a split-plot design with a drought treatment gradually reducing soil water content and a control treatment maintaining field capacity. Chlorophyll fluorescence (Fv/Fm), visual damage, and height were assessed five times in 160 days. Drought reduced the photosynthetic performance of seedlings, which negatively affected growth in both varieties, but the rate of response differed among provenances. There were significant differences in drought hardiness between varieties for all traits. However, within varieties, most of the variation observed was within provenances, suggesting local adaptation to drought is weak within var. *glauca* and even weaker for var. *menziesii*. Targeted exome capture and sequencing of DNA pools from each population is underway to detect candidate genes associated with the observed patterns in drought tolerance and other climate-related traits. Results from this study, which is part of the CoAdapTree Project, will be used to inform assisted gene flow strategies for reforestation.

* Presenter

SELECTION OF DROUGHT TOLERANT GENOTYPES OF WHITE SPRUCE AND LODGEPOLE PINE USING TREE RING ANALYSIS

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The productivity and sustainability of forest ecosystems relies on the correct and timely adaptation of trees to the environment where they are living. In Alberta, recent studies have shown that drought-induced forest decline suggest an increase in the maladaptation of Alberta's forests due to climate change over the last several decades. Selecting and testing drought-adapted genotypes through tree improvement programs may therefore be a useful strategy to maintain healthy forests under future climate change projections, which predict increasingly severe water deficits for western boreal and sub-boreal forests. In this study, we retrospectively analyzed drought resistance, resilience, and recovery of selected families and progeny within families, of white spruce (*Picea glauca*) and lodgepole pine (*Pinus contorta*). Using dendrochronological methods, we can detect how growth of the different genotypes has been affected by the drought events experienced in the last 30+ years at the test sites and how well the trees were able to recover from those events. Combining this information with other drought-related physiological traits we aim to determine trait combinations that confer drought tolerance and, on this basis, select well-performing genotypes and families that also show resistance or resilience to drought conditions. This study is part of the RES-FOR project, that aims to use genomic selection and metabolomic technologies for a more rapid and holistic selection of fast growing, drought tolerant, and pest resistant trees.

* Presenter

INCORPORATING PHENOLOGICAL TRAITS INTO MEASURES OF NITROGEN USE EFFICIENCY FOR CONIFERS

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Nitrogen use efficiency (NUE) is a term that describes the proficiency with which plants produce biomass as a function of available nitrogen (N). Forest soils are often N-limited, meaning that the primary productivity of forest trees and other plants may be enhanced by N fertilization. Fertilizer production is an expensive and energy-demanding process and frequent N fertilization can lead to adverse environmental effects. Consequently, alternatives to direct N fertilization are being sought in both agriculture and forestry to increase productivity on N-limited soils. The aim of this project was to identify families of white spruce (*Picea glauca*) that exhibit favorable NUE traits in unfertilized plantations. To this end, we conducted a two year field study on 10 white spruce families located in a plantation near St. Casimir, Quebec, measuring several physiological parameters important for estimating NUE. Field measurements were conducted in May (coincident with bud burst), July (active growth), and October (coincident with conclusion of bud set). Families can be distinguished on the basis of photosynthetic NUE, a classic measure of NUE, but family rankings change from bud burst to bud set. In addition to comparing family performance using conventional NUE expressions, we also used the data to explore new measures of NUE that better account for NUE traits that are influenced by the perennial, evergreen nature of white spruce. These new expressions of NUE will have applications in both tree improvement programs as well as ecological and ecophysiological studies.

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* Presenter

INVESTIGATING UNDERLYING CAUSES FOR LOW SEED YIELDS IN AB LODGEPOLE PINE ORCHARDS

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Lodgepole pine (*Pinus contorta*) is an ecologically and economically important conifer species in Western Canada. A combination of changing climate and insect outbreaks has put severe pressure on this species and led to an increased need for reforestation. However, seed orchards in British Columbia and Alberta have been struggling to meet seed yield targets and satisfy the demand for genetically improved seed. The underlying causes for this problem in each region remain largely unknown.

The Thomas Tree Improvement lab has been conducting a research program to identify and mitigate factors contributing to low seed yield in lodgepole pine seed orchards in Alberta. In the initial study we assessed the efficacy and optimal timing of a hormone treatment ($GA_{4/7}$) intended to promote female conelet development in order to ultimately increase cone and seed yields. We were able to show that the efficacy of such a treatment depends strongly on genotype and that the optimal timing varies based on the geographic origin of each parental genotype. As part of this study, we identified early abortion of female conelets as a major contributor to low seed yields. Moreover, it has become apparent that grafted lodgepole pines have considerably higher abortion rates than orchard trees that originate from seed. We are therefore embarking on a new three-year project that will examine the role of orchard location, climate, soil conditions, and grafting on conelet abortion. We will also test non-destructive means of phenotypic assessment, including drone-based remote sensing, that would allow orchard managers to identify and target trees likely to suffer high conelet abortion rates.

* Presenter

**NATURAL HYBRIDIZATION IN SEED STANDS OF SIX *PINUS* SPECIES
IN THE SIERRA MADRE OCCIDENTAL, DURANGO, MEXICO**

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In Mexico, there are high levels of variability in morphology and low levels of interspecific differentiation among Mexican pines, however, few studies have been conducted about natural hybridization of *Pinus* species in the Country's natural forests. Since Mexican pines are species with weak isolating barriers, genome-wide introgression can result in higher genetic diversity, which can facilitate the increase of evolutionary resilience of populations. The goals of this study were: 1) to determine the existence of natural hybridization between species of *P. durangensis*, *P. arizonica*, *P. engelmannii*, *P. teocote*, *P. leiophylla*, *P. lumholtzii*, and *P. cembroides* in 41 seed stands in the Sierra Madre Occidental of Durango, Mexico and 2) to check differences in survival and growth of height and diameter at ground level between putative hybrids and pure individuals under nursery conditions, after a 15-month observation period. Putative hybrids were detected in a random sampling of 1,421 adult trees using amplified fragment length polymorphism (AFLP). The correct assignment (hybrid or pure) of trees, which contributed seed for the growing experiment of 6,000 seedlings, was analyzed by 21 qualitative and quantitative morphological traits. Hybrids were found in 98 % of the seed stands of all studied tree species, except *P. cembroides*. We found significant differences in survival and growth of height and diameter at ground level between putative hybrids and pure individuals. Therefore, it is important to document the degree of hybridization of seedlots to be used for seedling production, to improve the quality control of plantations and reforestation.

* Presenter

OPERATIONAL REALIZED GAIN TRIALS - VARIATION AT ESTABLISHMENT?**Eden McPeak* and Barb R. Thomas****Department of Renewable Resources, Faculty of Agricultural, Life, and Environmental Sciences, University of Alberta, Edmonton, AB**

The importance of realized gain trials is to validate tree volumes on an area basis and to use this information in growth and yield modelling for improved seed to reduce error around predicted genetic gain that is based on progeny trial data alone. Improving growth modelling accuracy can assist in future forest planning and sustainability. In this study I assessed 10, 2-year-old paired plots of wild and improved seedlots (+elite seedlots) of lodgepole pine (*Pinus contorta* var. *latifolia*) and white spruce (*Picea glauca*) for growth, performance, and survival. To assess performance I measured gas exchange, height, root collar diameter, and survival. As well, to assess the environmental conditions at the sites I measured competition using a ceptometer, took soil pH, and used a theta moisture probe. Preliminary results show levels of light and soil moisture varied among plots, while pH was much more consistent. At this early establishment phase, growth differences may in fact favour wild lots, based primarily on wild seed collection methods. Improved lots had an average genetic worth of only 4.35%.

* Presenter

GENETICS OF SOLID WOOD PHYSICAL AND MECHANICAL PROPERTIES OF WHITE SPRUCE

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White spruce (*Picea glauca*) is a boreal conifer species that is valued by the Canadian forest industry for production of structural lumber, plywood, and pulp and paper. Genetic improvement of the species had previously focussed on enhanced growth, but it is vital to include important wood traits into selection criteria to ensure appropriate physico-mechanical properties of future fibre stock for wood supply chains. To do so, our objective was to estimate genetic parameters for physico-mechanical properties in solid wood samples and to evaluate the possibility to select superior genotypes at a relatively young age. In this research, a total of 300 trees representing 39 polycross families were sampled in 2 progeny trials from different environments in Quebec. Growth, wood density, and acoustic velocity were measured at age 20 on standing trees. Modulus of elasticity and modulus of rupture were studied both on large and small, defect-free specimens extracted at breast height. Samples were prepared and tested according to ASTM standard D143-94, 3-point bending tests. Our preliminary analyses showed considerable genetic variation among and within families. This study will provide more precise knowledge of genetic parameter estimates such as heritability or genetic correlations in a polycross trial. Furthermore, the results will help breeders to select superior individuals to help breeders to improve rotation age by including superior wood traits into white spruce tree improvement program.

* Presenter

CLONAL TESTING OF SELECTED TREES TO OPTIMIZE GENETIC GAINS

Mireille Desponts* and Josianne DeBlois

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Taking advantage of the rooting ability of black spruce (*Picea mariana*), we used hundreds of rooted cuttings to replicate trees selected in first-generation progeny trials and establish a clonal seed orchard, a breeding population, and two clonal trials for each of Quebec's breeding zones. These trials allowed us to compare, on a same site, trees selected in several progeny trials established under contrasting bioclimatic conditions. After 8 to 10 years, top-ranked clones for growth were used to establish the next generation breeding population. As a second step, we integrated improvement of wood stiffness into some of Quebec's black spruce deployment populations. At 15 years, we used pilodyn and acoustic velocity measurements on standing trees in clonal trials to predict MoEdir + pil. We ranked clones for both growth and wood stiffness to guide genetic roguing and to recommend seed harvests on top-ranked parents only, according to operational needs and the productivity the various clonal seed orchards.

* Presenter

SOMATIC EMBRYOGENESIS: AN ADVANCED TECHNOLOGY FOR REPRODUCING AND DEPLOYING ELITE WHITE SPRUCE

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Somatic embryogenesis is an *in vitro* cultivation technique that yields a large amount of somatic embryos from a single seed that will become plants genetically identical to the seed. This technique allows for the deployment of white spruce (*Picea glauca*) with significant productivity gains by producing the most productive clones in large quantities. Work is underway to identify superior clones in the laboratory and in the field to build multiclonal varieties with the desired characteristics. Simultaneously, significant advances have been made at the Saint-Modeste Forest Nursery in order to achieve operational scale-up of this technique.

* Presenter

KEYS POINTS REGARDING THE PROCESS OF IMPLEMENTING GENOMIC SELECTION INTO QUEBEC'S WHITE SPRUCE BREEDING PROGRAM

Martin Perron* and Josianne DeBlois

**¹ Direction de la recherche forestière, Ministère des Forêts, de la Faune et des Parcs,
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The key points that are used to inform and convince our managers and Assistant Deputy Minister to support the integration of genomic selection (GS) into the Quebec's white spruce (*Picea glauca*) breeding program were: 1) the results of the economic analysis for our specific project (cost-benefit, genetic and silviculture scenarios), 2) the increased confidence derived from our consultation to obtain input from many Ministère des Forêts, de la Faune et des Parcs (MFFP) key staff members for the economic analysis, 3) the fact that the scenario involving the establishment of top-grafted seed orchards increases the deployment of elite material to the entire annual seedling production, 4) the possibility of improving many traits for an investment similar to what conventional breeding requires to improve only one trait, 5) the fact that the MFFP pilot project is part of the *FastTRAC* project supported by Genome Canada and Génome Québec, 6) the many ministerial priorities that could benefit from rapid white spruce improvement (e.g., wood production, adaptation to climate change), and finally, 7) the fact that implementation is planned over 6 years. The strategy under consideration integrates genomic selection using the GBLUP method in two elite populations over a 5-year breeding cycle (2020–2024). This strategy will target short-term genetic gains (2–3 breeding cycles) for growth, wood rigidity, and resistance to abiotic and biotic stresses (e.g., drought, spruce budworm (*Choristoneura fumiferana*)). Multi-trait GS is planned based on screening of a very large number of candidates. Presently, we expect to use this same strategy for the third breeding cycle (2025–2029).

* Presenter

MULTI TRAIT GENOMIC SELECTION FOR BALANCING IMPROVEMENT OF WEEVIL RESISTANCE, GROWTH, AND WOOD QUALITY IN NORWAY SPRUCE

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Environmental changes will result in increasing pressure of pests and diseases and will challenge the production of sufficient amounts of high quality fibre from future forest plantations. Breeding approaches using genomic selection systems may offer efficient and flexible tools to face this pressure and combine multiple improvement objectives. Norway spruce (*Picea abies*) was introduced to North America more than a century ago and is valued for its superior growth compared with native spruces. Initial selection efforts focussed on growth and hardiness traits. In Canada, Norway spruce plantations can get heavily attacked by the white pine weevil (*Pissodes strobi*). In the present study, we evaluated possibilities to improve Norway spruce resistance to the native white pine weevil. Single and multi-trait genomic selection (GS) models and selection indices were developed considering the relationships between weevil resistance, intrinsic wood quality, and growth traits. Weevil resistance was genetically positively correlated with tree height, height to diameter ratio, and wood stiffness. The accuracy of the different GS models tested (GBLUP, Threshold GBLUP, Bayesian Ridge Regression, and BayesC π) was high and did not differ among those methods. Multi-trait models performed similarly to single trait models when all trees were phenotyped. However, with an increasing proportion of missing values, e.g., when weevil attack assessment could not be conducted on all trees, weevil resistance was more accurately predicted by integrating genetically correlated traits into multi-trait GS models. A genomic selection index that corresponded to the breeders' priorities achieved near maximum gains for weevil resistance, wood stiffness, and height growth, but a small decrease for DBH. The results of this study indicated that it is possible to breed for high quality, weevil resistant Norway spruce reforestation stock with integration of multi-trait genomic selection approaches.

* Presenter

FUNCTIONAL GENOMICS FOR UNDERSTANDING TRAIT EVOLUTION IN FOREST TREE-ENVIRONMENT CONTEXTS

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Genomics can provide many fascinating insights into the traces of evolution on plant genomes in the form of genetic variation that, over the millennia, proved beneficial for the plant's survival and fitness upon recurrent exposure to parasitizing organisms present within the plant's local environment. Moreover, adaptation to local climate also left respective traces of genetic variation along the genome, usually detected as strong signals in association genetics. Here, we discussed different cases of such signal detections in the context of long-lived forest tree-environment interactions that is: 1) herbivory by *Pissodes strobi* (Coleoptera) in spruce and the issue of growth and host defenses trade-offs (Porth 2018), 2) different host utilization by the polyphagous *Lymantria dispar* (Lepidoptera) on naïve vs. exposed conifer species comparing differences in hosts' inherent defensive foliage metabolites with the insect's unique enzymatic detoxification potential (Keeling 2019), and finally 3) the role of genome-wide gene copy number variations in a widely distributed North American *Populus* species that we linked to adaptive selection for resistance to disease in the south and to abiotic stress in the north of its distribution (Prunier 2019). In summary, we investigated three different systems to elucidate traits' variation that coevolved under diverse environmental circumstances.

* Presenter

A GENETIC MAP FOR SPRUCE TREE, WHY?

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For nearly 25 years, Natural Resources Canada has been continuously developing a genetic map of white spruce (*Picea glauca*). Today, this map is the most complete and informative representation of the unique and complex genome structure of the Pinaceae family (including pines, spruces, and firs) and, by extension, to all conifers. The Pinaceae, with a common ancestor that dates back more than 140 million years, have among the largest genomes on Earth and have a genome structure that changed very little over time. By ordering a majority of the expressed genes, the genetic map also participates directly in the scaffolding of the physical sequence of the spruce genome, whose hundreds of thousands of pieces (the scaffolds) would remain scattered if they could not be anchored to the genetic structure.

In addition to helping us understand the genome of conifers and their evolution, this map, combined with the replication of the mapping population on different sites, can allow us to identify genome regions involved in the transmission of various functional traits. To date, studies have been carried out on the timing of bud burst and bud set, annual growth, and metabolites associated with defence against insects. Other studies are underway, including one involving the optimization of high-throughput phenotyping methods that uses hyperspectral data collected using drones.

This poster is a synthesis of the development of the genetic map, its uniqueness and the advances that it may allow.

* Presenter

THE BLACK SPRUCE GENOME PROJECT

Ashley M. Thomson

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Black spruce (*Picea mariana*) is one of the most abundant coniferous tree species in the boreal forests of North America and is among the most sought-after tree species for pulp production in Canada. While whole-genome sequences exist for some economically important conifers (e.g., Sitka spruce (*P. sitchensis*), white spruce (*P. glauca*), loblolly pine (*Pinus taeda*)), no whole-genome assemblies for black spruce are currently available. Although the immense genome size of spruces (ca. 20 gigabase pairs) presents a challenge, advances in DNA sequencing have increased throughput making the costs of conifer whole-genome sequencing projects much less prohibitive. Furthermore, the advent of new linked-read sequencing using 10X Genomics and Illumina X technologies makes it possible to accurately map reads to repetitive sequence regions and assemble long contigs from short-read sequencing data. A project using 10X Genomics technology to reconstruct the complete genome of black spruce is currently underway. The initial results of the black spruce genome sequencing project were presented, including assembly quality metrics and preliminary gene annotation. We discussed how this new genomic resource can be used to facilitate functional genomics studies and improved breeding and suggested how the lessons learned can be applied to future conifer genome sequencing projects.

GENOME CANADA'S RES-FOR PROJECT: GENOMIC SELECTION FOR WHITE SPRUCE AND LODGEPOLE PINE – AN OVERVIEW

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Tree improvement is one of the last measures available to tackle the challenges forest practitioners face in selecting parent trees adapted to both current and future climates. Providing the genomic, economic, and social framework to understand the potential for adoption of new technologies in forestry is being undertaken in a project titled: *Resilient Forests (RES-FOR): Climate, pests and policy – genomic application*. Through the adoption of genomic selection, this project will provide new mathematical models, combined with new ways of identifying naturally resilient trees and ultimately, allow us to shorten the time it takes to complete a typical tree breeding cycle in Alberta from ~30 years to less than ~10 years. These new tools will enable the selection of a broader range of important tree traits, with a particular focus on insect resistance to both mountain pine beetle (*Dendroctonus ponderosae*) and spruce budworm (*Choristoneura fumiferana*) as well as improve wood quality and drought. Two tree improvement programs, one lodgepole pine (*Pinus contorta*) and the other white spruce (*Picea glauca*), are the focus of this study and both programs are on the cusp of moving to second-generation seed orchards. The opportunity to impact the selection of those second-generation parents is ideal. Initial results from our *RES-FOR* team and key outcomes were highlighted in areas of economics, physiology, and genomics.

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36th CFGA/ACGF MEETING**

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