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

PART 1 Minutes and Member's Reports
PART 2 Symposium

Forest Health and Productivity in Changing Environments

Forest Genetics Edmonton 2017

Santé et productivité des Forêts dans un contexte de changements environnementaux

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

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

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I Centre de foresterie de l'Atlantique.
II Titre: Santé et productivité des Forêts dans un contexte de changements environnementaux
III Titre : Comptes rendus du trente-cinquième congrès de l'Association canadienne de génétique forestière

PROCEEDINGS

OF THE

THIRTY-FIFTH MEETING

OF THE

CANADIAN FOREST GENETICS ASSOCIATION

PART 1

Minutes and members' reports

Edmonton, Alberta
June 26-29, 2017

Editors

D.A. McPhee and J.D. Simpson

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COMPTES RENDUS

DU

TRENTE-CINQUIÈME CONGRÈS

DE

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1^re PARTIE

Procès-verbaux et rapports des membres

Edmonton, Alberta
26 au 29 juin 2017

Éditeurs

D.A. McPhee et J.D. Simpson

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BUSINESS MEETING MINUTES

Thirty-fifth Business Meeting of the Canadian Forest Genetics Association[1]

University of Alberta, Edmonton, Alberta
June 27, 2017

411 Attendance

Andy Benowicz (AB)
Brad St. Clair (OR)
Brian Barber (BC)
Chris Hennigar (NB)
Christopher Keeling BC)
Deogratias Rweyongeza (AB)
Greg O'Neil (BC)
Jean Beaulieu (QC)
Jean Bousquet (QC)
Michael Stoehr (BC)
Nathalie Isabel (QC)
Patrick Lenz (QC)
Paul Charrette (ON)
Pia Smets (BC)
Sally Aitken (BC)
Shane Ford (BC)
Steve McKeand (NC)
Ward Strong (BC)

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[1] In these minutes, where names of movers and seconders of the motions may be missing (not correctly recorded) the voting process was followed as per Robert's Rules of Order. All decisions contained in these minutes were unanimously made by a show of hands.

412 Minutes of the 34th meeting

Motion:	That the minutes of the 34th Business Meeting be approved.
Moved by:	Jean Beaulieu
Seconded by:	Patrick Lenz

Carried.

413 Membership

413.1 Honorary Membership

The following name was presented:

Dale Simpson – nominated by Dave Kolotelo

Nomination for Honorary Membership requires a 60-day notice and signatures of four sponsors for consideration. The current nomination was submitted three days before the meeting with no signatures from sponsors. The motion will be tabled at the next business meeting in 2019.

413.2 Active Membership

The names of six nominees were presented:

Donnie McPhee – nominated by Dale Simpson
Chris Hennigar – nominated by Michele Fullarton
Shane Ford – nominated by Brian Barber
Ilga Porth – nominated by Jean Bousquet
Christopher Keeling – nominated by Nathalie Isabel
Janice Cooke – nominated by Nathalie Isabel

Motion:	That the nominated Active Members be duly elected.
Moved by:	Deogratias Rweyongeza
Seconded by:	Mike Stoehr

Carried.

414 Chair's Report

Organizing the 2017 CFGA-WFGA meeting

The earlier plan from the 2013 meeting in Whistler was to host the 2017 meeting at Banff National Park to attract good attendance. This was not feasible due to high projected costs, meeting coinciding with the high tourism season in Banff, Canada 150 years, and free admission in National Parks that would also inflate hotel costs. We settled for the University of Alberta, Edmonton

Meeting sponsorship

Alberta Government (Agriculture and Forestry)	$ 15,000
Alberta Innovates	$ 5,000
FastTRAC (Fast tests for rating and amelioration of conifers)	
Funding one invited speaker (Nathalie Isabel)	$ 2,500
Funding for one sponsored one student	$ 1,500
Genome Alberta	$ 1,500
Integrated DNA Technologies	$ 1,000
University of Alberta (Faculty of Science)	$ 5,000
University of Alberta (Agriculture, Food and Life Sciences):	$ 5,000
Weyerhaeuser Company Ltd	$ 5,000
West Fraser Mills (groups of forest companies)	$ 3,000

Conference attendance

91 people (85 full conference and 6 one-day registrants)

29 people participated in a post-conference field trip to the Alberta Tree Improvement and Seed Centre and Smoky Lake Forest Nursery, in Smoky Lake, Alberta

Mailing list

Opened a Google group (email: cfgacanada@googlegroups.com)

Members were encouraged to use it for sharing information, promoting discussions, sharing publications, posting job opportunities, graduate and postdoctoral positions, etc.

Deogratias Rweyongeza
Chair

Motion: That the Chair's report be accepted.
Moved by: Deogratias Rweyongeza
Seconded by: Greg O'Neil
Carried

415 Treasurer's Report

The Treasure's financial report was presented by Chris Hennigar for Michele Fullarton. The statement shows a balance of $ 17,514.10. See below.

Motion: That the financial statement be accepted as presented.
Moved by: Sally Aitken
Seconded by: Patrick Lenz
Carried.

Holdings – June 30, 2015

Cash balance	$	20,634.68
Total Holdings	**$**	**20,634.68**

Credits (June 2015-June 2017)

Interest (GIC)	$	120.00
CFGA 2015 -repayment of Seed Money	$	4,950.00
Total credits	**$**	**25,704.68**

Debits

Student awards (CFGA 2015)	$	800.00
Seed Money for CFGA 2017	$	6,000.00
Website (hosting and annual fees for domain)	$	243.36
Gary Carleton (honorarium for managing CFGA 2015 website)	$	1,000.00
BMO Rate Riser GIC	$	10,000.00
Conference account closure	$	2.40
CD Mailers/Cases and Labels	$	144.82
Total debits	**$**	**18, 190.58**

Holdings – June 30, 2017

Cash	$	7,514.10
Rate Riser GIC	$	10, 000.00
Total Holdings	$	17, 514.10

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416 Editor's Report

There was no report from the editor. The proceedings of the 34th conference and business meeting are not yet published on the CFGA website. Members will be informed what they are published.

417 Student Attendance and Awards

The CFGA education program sponsors undergraduate students from Canadian universities with accredited forestry degree programs to attend the conference. For the 2017 conference, CFGA sponsored the following students:

Barrbara Wong (MSc, University of British Columbia)
Laurel Nikiforuk (undergraduate, Forestry, University of Alberta)
Bianca Sacchi (undergraduate, Biological Sciences, University of Alberta)
Justine Laoué (PhD, Laval University)

All other universities (Lakehead, Moncton, Northern British Columbia, and New Brunswick) were unable to provide a student (undergraduate or graduate) to be sponsored for any of the following reasons:

Undergraduates may be available but already committed to summer employment,
Graduate students may be available but not interested in genetics conferences if the university has an accredited forestry degree program but does not have active forest genetics research units, or
Some universities had potential students who CFGA had sponsored at previous conferences (cannot be sponsored twice).

It was noted that even though this CFGA education program was intended for undergraduate students, many sponsored students tend to be graduate students in forest genetics. Therefore, it was decided that:

When a university cannot find an undergraduate student to accept sponsorship, the sponsorship be opened to graduate students in forest genetics.
To create a fair playing field, all graduate forest genetics students in the respective department should compete for sponsorship on merits, which may include submitting abstracts for presentation relevant to the theme of the conference, which the organizing committee will evaluate as a criterion for awarding the sponsorship.

Motion:	That the guidelines for student sponsorship be approved.
Moved by:	Pia Smets
Seconded by:	Nathalie Isabel

Carried.

For the 2017 conference, registration, flights, meals, and $100 for incidental costs were paid by CFGA for the two students from outside Edmonton. Paying for student incidental costs was a decision made locally for the 2017 conference in Edmonton because the budget allowed it; past conference organizers had discretion on this as do future conference organizers.

In addition to sponsoring students to attend the conference, CFGA administers the Carl Heimburg Award for the best student presentation and Gene Namkoong Award for the best student poster. Winners for the 2017 conference awards were:

Carl Heimburg Award, best student presentation
Ian MacLachlan, University of British Columbia (*Selective Breeding for Growth in the Interior Spruce Hybrid Zone Maintains Adaptation to Climate*).
Gene Namkoong Award, best student poster
Bianca Sacchi, University of Alberta (*In situ Quantification of Blue Stain Fungi in Jack, Lodgepole and Hybrid Pine*).

418 Tree Seed Working Group

Since the 2015 meeting in Fredericton, NB, the Tree Seed Working Group (TSWG) has produced four News Bulletins (#62 to 65) which are available online. For the 2017 conference, the tree seed workshop, that has been held separately at previous CFGA conferences, was fully integrated into the main conference plenary and concurrent sessions with Dr. Fiona Hay (International Rice Research Institute, Laguna, Philippines) as Keynote speaker. TSWG may bring back a separate workshop at future CFGA conferences.

Dale Simpson retired in March 2017 after a long and successful career with the Canadian Forest Service. Dale has made a remarkable contribution to CFGA as its Executive Secretary and Editor since 1998, and Editor of the TSWG News Bulletin since 2002. Under Dale's leadership, the Canadian Tree Improvement Association (CTIA) changed name to Canadian Forest Genetics Association (CFGA), the CFGA conference proceedings changed from two to one volume, and the TSWG News Bulletin moved from hard copies to online access. Dale was the one person who had a firm knowledge of the CFGA bylaws and business meeting procedures.

Melissa Spearing (Forest Gene Conservation Association of Ontario) is the new Editor of the TSWG News Bulletin.

Those wishing to contact Ben Wang, a retired prominent tree seed scientist, long-time member of the Canadian Forest Service, and member of the TSWG can reach him through Steve D'eon (email: sdeon@sympatico.ca).

Dave Kolotelo
Chair

419 Old Business

None

420 New Business

420.1 CFGA, WFGA and SFTIC Working Together

In recent years, members of the Canadian Forest Genetics Association (CFGA), Western Forest Genetics Association (WFGA), and Southern Forest Tree Improvement Conference (SFTIC) have expressed concerns about the continued decline in attendance at the forest genetics and tree improvement meetings/conferences, and general funding of forest genetics research. This has prompted informal discussions on increased integration of CFGA, WFGA and SFTIC activities that may range from having a single North American forest genetics association (USA, Canada and Mexico) to having a system of joint meetings/conferences while retaining local regional associations to cater for regional-specific needs and audiences.

This agenda was tabled at the 35th CFGA and WFGA business meetings in Edmonton. Dr. Steve McKeand (SFTIC) and Dr. Brad St. Clair (WFGA) attended this meeting and took active part in the discussions. It should be noted that by participating in CFGA business meeting discussions, Steve McKeand and Brad St. Clair were not officially representing SFTIC and WFGA decisions but had prior knowledge of informal discussions that have taken place within and across SFTIC and WFGA. Hence, their participation in the discussions was very helpful in setting up a roadmap to advance the discussion within and across the three organizations and come to a decision before the next meetings in 2019.

From the discussions, the following were observed.

While the idea of having a single forest genetics association for North America is possible, local associations still have value because they serve audiences with specific needs. Members want to retain these associations.

There is strong support for regularly scheduled joint conferences/meetings. The issue is how to schedule them so that regions have the opportunity to host the meeting every 2 to 3 years. This is especially critical for SFTIC where not hosting a meeting beyond 3 years would be a deal breaker. Not hosting meetings in the regions for a long time has the risk of undermining interest and coordination of activities, especially for people who cannot regularly attend international conferences outside their regions.

Alternative conference scheduling has been suggested through email discussion between some members of SFTIC and WFGA, which will provide a starting point for formal CFGA-WFGA-SFTIC discussions.

It was decided that:
Because all three associations have an already-scheduled meeting for 2019, leadership teams of the three groups should get together quickly and see if one group can host the joint meeting in 2019 (i.e., the other two drop their 2019 meetings), and then figure out scheduling of successive meetings beyond 2019. This is an action item for:

Dana Nelson (SFTIC)
Jessica Wright (WFGA)
Nathalie Isabel (CFGA)
Patrick Lenz (CFGA)

CFGA Active Members will have to vote on the decisions made jointly by the CFGA-WFGA-SFTIC leadership teams before CFGA can formally implement those decisions. There are online survey tools to facilitate this.

Motion:	To approve a procedure to engage in formal CFGA-WFGA-SFTIC discussion
Moved by:	Brian Barber
Seconded by:	Jean Bousquet

Carried.

421 Future Meetings

421.1 Location of 2019 Meeting

Quebec, subject to CFGA-WFGA-SFTIC discussions.

421.2 Location of 2021 Meeting

To be decided at the 2019 business meeting.

422 New Executive

Co-chairpersons:	Nathalie Isabel and Patrick Lenz
Treasurer:	Michele Fullarton
Editor:	Kathleen Forbes
Executive Secretary:	Michele Fullarton

423 Adjournment

Meeting adjourned.

ACTIVITY REPORTS
FROM ACTIVE MEMBERS

NEW BRUNSWICK TREE IMPROVEMENT UPDATE

Michele Fullarton and Chris Hennigar

NB Department of Energy and Resource Development
Kingsclear Provincial Forest Nursery
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, genetically improved seeds for reforestation. The Department of Energy and Resource Development (DERD) coordinates the NBTIC activities, and is responsible for the breeding and growing of test material. The Seedling Production section of DERD is currently growing 21 million seedlings annually for planting, with over 90% 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 comprising of 7 coniferous species (Fig. 1).

These orchards are meeting the reforestation demands for Crown land. Seed production in 2016 was low, just under 5 million seeds, with the majority of that collected from black spruce orchards. In 2017, indications are that there will be a large cone crop in the high value second generation white spruce orchards. The trees were injected with GA 4/7 in 2016.

TREE BREEDING, TESTING AND SELECTION

Polycrossing of second-generation black spruce and jack pine selections was completed in 2007. 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 have been uniformly deployed to breeding groups, and breeding is conducted in a positive assortative mating design. A total of 23 sub-lines have been established for black spruce and 21 for jack pine and full-sib breeding and testing is now completed. The black spruce breeding strategy is under review and will be modified 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 rogueing. 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 around the province. In 2016, the first series of second-generation white spruce full-sib progeny tests was established. These will be used for third-generation selections. In 2016, the last series of jack pine second-generation full-sib progeny tests was established. No new selections were made for any species in 2016, but we intend to make third-generation selections in 2017 in black spruce using 10 year standardized breeding values across all series.

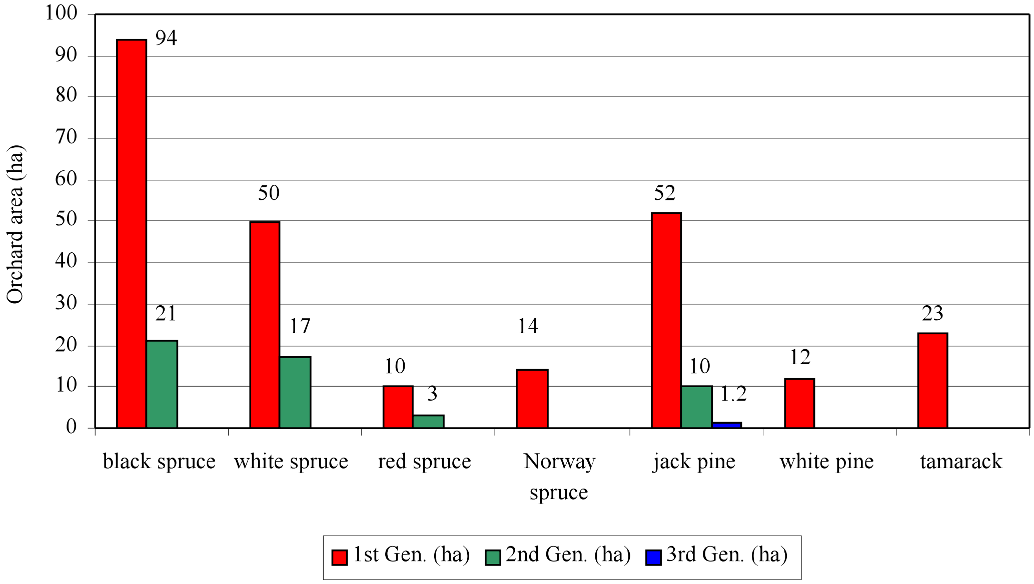

Figure 1. Orchard area broken down by species and generation.

NBTIC DATA ANALYSIS AND RESEARCH

The data analyst at DERD resigned his position at the end of 2015 to take on other employment, so there is some backlog of datasets that need analysis. A total of 10 NBTIC test series were measured in 2015, 2016, and 2017 and one series has been analyzed in order to obtain rogueing information for the second generation white spruce orchard. Analysis was done on 2 series measured in 2014. The 10-year measurements of the 2005 black spruce full-sib series, made up 56 families tested on 5 sites, were analyzed. Only 4 of the sites were used in this analysis. As these tests will be used for forward selecting the next generation breeding population, individual-tree breeding values were predicted using Best Linear Unbiased Prediction (BLUP) by targeting the average environment of 5 sites and tree height at age 10. Selecting the best 5% or 10% of trees by tree height breeding value would result in a gain of 3.2% or 2.8% in 10-year height and a gain of 8.9% or 6.5% for 10-yr volume. Due to low heritability estimates, genetic gains in this series were lower than those for 10-year height in the 2000 series (7.6 and 6.8%), 2001 series (9.2% and 8.0%), 2003 series (8.4% and 6.9%), and 2004 series (7.2 and 6.5%).

The 2008 jack pine full-sib series was measured for the first time at 7 years. As the series will be used for forward selection for the next generation breeding population, individual-tree breeding values were predicted using BLUP by targeting the average environment of 3 sites and tree height at age 7. As specific combining ability effects were stronger than additive effects, selections of particular combinations may produce slightly higher gains. If forward selection is applied to height and the plan is to select the top 5%, the predicted gain will be 3.0% for 7-year old height. This gain in 7-year height was much lower than those observed in the 2000 and 2002 full-sib progeny testing series (7.1% and 4.6%, respectively).

Jiejie Wang, a student at the University of New Brunswick, submitted her thesis for a Master of Science in Forestry degree. She examined a series of 35-year-old black spruce family tests retrospectively. There were two parts to the thesis, genetic parameters of growth and stem forking. She concluded that stem forking was primarily caused by environmental causes rather than genetic. Secondly, black spruce tree growth in New Brunswick is affected by both climatic and edaphic factors. Within the province the climate is not very diverse but height growth appeared to be better on cooler sites. The greatest gains in height growth tended to be achieved by distributing the best families to medium rich and medium moist soils.

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Fullarton, M.S. 2016. 2016 Jack pine full-sib progeny tests. NBTIC Establishment Report. No. 83, NB Dept. of Environment and Resource Development. 54 p.

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NATIONAL TREE SEED CENTRE

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The mission of the National Tree Seed Centre is to safeguard Canada's forest genetic resources 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 seed of tree and shrub species from throughout their ranges in Canada. On-going activities include collecting and processing seed; conducting tests such as germination, moisture content, and 1,000-seed weight; and setting up and evaluating research trials. This report covers activities during 2015 and 2016.

In order to expand the geographic sampling for species and to add new species to the inventory, seed is obtained by collecting, donation, and purchase. Collecting focuses on obtaining seed from natural populations thereby capturing the natural genetic variation that is present within species. Most of the collection effort focuses on collecting seed from a minimum of 15 trees in a population and keeping the collections separate by 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 seed is available for research, and Gene Conservation. During the two-year period, 63 seedlots from 14 species were collected and 383 seedlots from 39 species were donated or purchased. Of that number, a significant donation of 317 seedlots of 21 species came from Agriculture and Agri-Food Canada, Agroforestry Development Centre in Indian Head, Saskatchewan. In addition, 35 seedlots were donated from various collaborators: Melissa Spearing (private collector), Point Pelee National Park, Thousand Islands National Park, The University of Guelph Arboretum, and Yukon Department of Energy, Mines and Resources.

Almost 7,100 seedlots from 148 species exist in Seed Bank. The Gene Conservation collection also continued to grow with over 5,400 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 conservation program, led by Tannis Beardmore, for butternut (*Juglans cinerea*). Butternut is listed nationally as endangered due to butternut canker caused by an exotic disease (*Sirococcus clavignenti-juglandacearum*). Butternut seed are recalcitrant, however the embryonic axis is tolerant to desiccation and freezing.

A program, for the conservation of ash seed has been led by the Seed Centre since 2004 due to the threat imposed by emerald ash borer (*Agrilus planipennis*) that is expanding its 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 2015 that resulted in over 80 collections made by NTSC staff with a few donated from Ontario and Quebec. About 880 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. About 1,238 tests were completed during the two-year period. Testing is conducted using Petawawa Germination Boxes. Generally, 4 reps of 50 seed are tested in a box. For larger seed such as *Fraxinus* and *Acer* 25 seed per rep is tested. 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.

Operational research is an important activity. Evaluating germination test data is one aspect as discussed above. Another activity is setting up germination trials to evaluate seed treatments to determine which one promotes maximum germination. An experiment to determine optimal treatment protocols to maximize germination of pin cherry (*Prunus pennsylvanica*) seed demonstrated that 2 weeks of moist incubation followed by 20 weeks of moist chilling were sufficient. This trial was conducted to improve seed germination for nurseries growing seedlings for mine site reclamation in Alberta. Results from an experiment to promote germination of highbush cranberry (*Viburnum opulus* var. *americanum*) seed demonstrated that practically all seed that germinated did so during a second chilling treatment. The longer durations of this treatment resulted in an increase in the proportion of damaged germinants.

PUBLICATIONS AND PRESENTATIONS

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FOREST GENOMICS AND GENETICS AT UNIVERSITÉ LAVAL

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INTRODUCTION

This report summarizes our research efforts and results obtained in forest genomics and genetics over the 2015–2017 period. John MacKay left for a position at the Univ. of Oxford, and Ilga Porth from the Univ. of British Columbia (UBC) has been recruited to assume the leadership of our functional genomics program. While remaining scientist emeritus at the Canadian Wood Fibre Centre (CWFC) after his retirement from Natural Resources Canada (NRCan), Jean Beaulieu was renewed for a second mandate as invited professor at the Département des Sciences du bois et de la forêt of Univ. Laval.

The large-scale spruce genomics project SMarTForests was completed in 2015. A new Genome Canada LSARP (Large-Scale Applied Research Program) project, also supported by Génome Québec, Genome BC, and Genome Alberta, was launched at the end of 2016 (running until 2020), under the name of Spruce-Up project (Advanced spruce genomics for productive and resilient forests). It is co-led by J. Bohlmann (UBC) and J. Bousquet (Univ. Laval), and it involves many other Canadian academic scientists from Univ. Laval (N. Gélinas, J. Beaulieu, I. Porth, A. Achim, E. Bauce, B. Boyle), UBC (G. Bull, I. Birol, S. Jones, S. Mansfield), Univ. of Alberta (J. Cooke), and Univ. of Toronto (I. Ensminger). It also involves scientists from other Canadian research organizations such as NRCan (N. Isabel), CWFC (P. Lenz), Forest Products Innovations of Canada (FPInnov) (F. Robichaud), the Ministère des forêts, de la faune et des parcs du Québec - MFFPQ (M. Perron, A. Rainville), BC Forests, Land and Natural Resource Operations - BCFLNRO (B. Jaquish). Several collaborators worldwide also participate in the project, including scientists from the Max Planck Institute for Chemical Ecology (A. Hammerbacher), the Univ. of Oxford (J. Mackay) and the U.K. Forestry Commission (S. Lee). 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 shoot weevil and spruce budworm 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 glauce*), interior spruce

(*P. glauca* x *engelmannii*), and Sitka spruce (*P. sitchensis*) in Canada and in the U.K. The Univ. Laval component of the project currently implicates 1 senior research associate, 4 postdocs, 4 PhD students, 1 MSc student, and 4 research assistants, notwithstanding staff at NRCan, CWFC, MFFPQ, and FPInnov in Quebec City.

A new Genome Canada LSARP project called BioSafe (Biosurveillance of alien forest enemies) was launched at the end of 2016 (running until 2020). 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, 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, M. Boyland), FPInnov (A. Uzunovic), the Canadian Food Inspection Agency (CFIA) (G. Bilodeau, 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 participle in the project, including scientists from the Beijing Forestry Univ. (J. Shin), the *Phytophthora* Genome Consortium (B. Tyler), the USDA (M. Keena, 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 threaths 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 studied pests are the Asian longhorned beetle, the Asian gypsy moth, 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.

The Genome Canada large-scale applied project *FastTRAC* – Fast Tests for Rating and Amelioration of Conifers, was launched in spring 2015 under the Genomics Applied Partnership Program (GAPP) of Genome Canada. It also receives additional support from Génome Québec, 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 has been co-led by J. Bousquet from Univ. Laval and G. Smith from FPI-CWFC, and it is involving scientists and practitioners from Univ. Laval (J. Beaulieu), FPI-CWFC (P. Lenz, F. Robichaud, and Y.-S. Park), MFFPQ (M. Campagna, M. Perron, A. Rainville and M.-J. Mottet), JDI (G. Adams, A. McCarthy, and Shona Millican), NRCan (N. Isabel and K. Klimaszewska) and NBTIC (M. Fullarton). Its goal is to bring GS to the operational scale for eastern white spruce and Norway spruce advanced breeding programs in Quebec and New Brunswick. Growth, wood density, and resistance to white pine weevil (*Pissodes strobi*) (aka Norway spruce shoot weevil) attacks are the targeted traits of deploying GS predictive systems.

Under the leadership of J. Bousquet, the Canada Senior Research Chair in Forest Genomics, which was established in 2001, has been successfully renewed for a third mandate of seven years until 2022. It was the first Canada chair to have been successfully renewed for a third period since the inception of the program.

Under the European Union Framework Program and the leadership of several European research organizations and M.T. Cervera (INIA, Spain), the ProCoGen (Promoting Conifer Genomics) large-scale project has completed its activities at the onset of 2016, where J. Bousquet and N. Isabel (RNCan) were involved in collaborative research on conifer genome mapping.

During the past two years, the group has included N. Pavy (ongoing) as senior research associate and several postdoctoral researchers: L. Benomar (ongoing), G. de Lafontaine (now at Univ. of Illinois), J. Godbout (ongoing at NRCan with N. Isabel), B. Hornoy (now consultant in R&D), P. Lenz (now at CWFC), and J. Prunier (ongoing). Several MSc and PhD students have also been supervised including S. Carles (now at MFFPQ), B. Cinget (now at Parks Canada), M. Lamara (ongoing), J. Laoué (ongoing), G. Otis-Prud'Homme (ongoing), A. Sahli (now at Wellcome Trust Centre for Human Genetics), J. Stival Sena (now at NRCan), I. Villeneuve (now at PrairieTech Propagation, Alberta), and E. Warren (now consultant in conservation biology).

PHYLOGEOGRAPHY, GENETIC DIVERSITY, HYBRID ZONES

J. Bousquet

Our ongoing work of the Phylogeographical Atlas of Conifers has been progressing with a number of additional studies completed. The range-wide phylogeographical study of the cosmopolitan balsam fir (*Abies balsamea*) using newly discovered cpDNA and mtDNA markers has revealed new glacial refugia in central North America and has confirmed controversial refugia on the northeastern coast of North America (Cinget et al. 2015a). Contrary to other largely distributed boreal conifers, there was a large congruence between cpDNA and mtDNA geographical structures in spite of different transmission of chloroplast and mitochondrial genomes in the Pinaceae (respectively paternally and maternally), indicating limited cpDNA gene flow in balsam fir compared to other boreal conifers such as jack pine (*Pinus banksiana*), white spruce or black spruce (*Picea mariana*). Reduced pollen gene flow could be due to the morphology of *Abies* large pollen grains and/or more likely, recurrent spruce budworm epidemics that afflict the demography of the species with high mortality rates.

The range-wide phylogeography of tamarack (*Larix laricina*) has also been investigated using newly discovered cpDNA and mtDNA markers, revealing geographic patterns largely congruent with that of other widespread boreal conifers, with well-delineated eastern and central glacial lineages (Warren et al. 2016). Higher population differentiation was noted in the Prairies, indicating a demographic signature of historically more competitive environment, likely due to eastern larch postglacial colonization postceding that of pines and spruces in the region.

The cpDNA diversity and population structure of endangered mountain spruces such as *Picea mexicana* in the Sierra Madre of northern Mexico and *Picea rubens* in the Appalachian Mountains of eastern North America have also been investigated with J.P. Jaramillo-Correa (Univ. Automomous of Mexico - UNAM) and the late Tom Ledig (Univ. of California at Davis) and member of the North American Forest Commission), who unfortunately passed away in May 2015, and who devoted much of his fruitful professional life to the conservation genetics of endangered tree species. The genetic data revealed the signature of population declines for both species, with a quite ancient and severe bottleneck for the endemic *P. mexicana* dating back to the last interglacial, and a less severe and likely more recent bottleneck for *P. rubens* (Jaramillo-Correa et al. 2015).

The study of conifer hybrid zones has been pursued to better understand their evolutionary trajectory and implications for differential adaptation and speciation in trees. The zone of contact between *A. balsamea* and subalpine fir *A. lasiocarpa* in western Alberta has been investigated by using newly discovered species-specific paternally inherited cpDNA markers and maternally inherited mtDNA markers (Cinget et al. 2015b). The results indicated limited introgression outside the zone of contact and the stability of the zone for the greater part of the Holocene since the first postglacial contact. This is in contrast to the zone of contact between lodgepole pine (*Pinus contorta* var. *latifolia*) and *Pinus banksiana*, currently in the same area in western Alberta, which was previously shown to have extended much further to the east during the middle Holocene, using species-specific mtDNA and cpDNA markers (Godbout et al. 2012).

The patterns of introgression in eastern North America between *P. mariana* and *P. rubens* have been investigated using gene SNPs spread along the 12 spruce chromosomes (De Lafontaine et al. 2015). While most of the loci were selectively neutral, some permeable loci were more subject to introgression, indicative of ancestral polymorphism along with balancing selection. A smaller set of loci spread over 10 chromosomes was found to reflect impermeable regions, thus indicative of species boundaries and ongoing divergent selection and speciation. These heterogeneous patterns of introgression along the genome indicate a young and incomplete speciation process between these progenitor-derivative species (Perron et al. 2000). A preferential direction of introgression (from the progenitor black spruce to the derivative red spruce) was also observed. Contrary to the most common pattern observed in annual plants, this asymmetric pattern of introgression was not linked to directional selection or other exogenous factors (De Lafontaine et al. 2017).

GENOME MAPPING AND SEQUENCING

J. Bousquet

Through the SMarTForests project and in collaboration with UBC scientists, we have made several updates and improvements to the white spruce genome assembly, which is the most contiguous one produced for a spruce species (Warren et al. 2015). Improvements have been achieved by sequencing a second white spruce genotype from eastern Canada (tree used for gene mapping from NRCan, N. Isabel), and using it to further resolve the structure of the white spruce genome and developing custom bioinformatics solutions for species with giga-bp genomes. The overall assembly was much improved but it remained highly fragmented. Efforts to further improve the genome assembly are currently deployed using innovative long-fragment library construction and improved bioinformatic methods currently developed under the Spruce-Up project. The same team has also released and published the chloroplast and mitochondrial genome sequences of white spruce (Jackman et al. 2016). The plastid genome was contiguous with a length of 123 kb, and 114 genes could be identified. The mitochondrial genome could be assembled in about 17 gene-containing scaffolds representing altogether a genome size of 5.9 Mb, which was much larger than expected. A total of 106 genes could be identified.

Through the SMarTForests and Spruce-Up projects, we have also recently released a most extended (5X) gene linkage map of the white spruce genome, with nearly 9000 expressed genes mapped, and representing the most advanced gene map for a conifer to date (Pavy et al. 2017). The work involved the close collaboration of scientists from NRCan (team of N. Isabel) and their pedigree material. The map is also the most precise ever produced for a conifer given the 2000 progeny used for mapping. Several structural features were discovered and the map was found to be in large synteny with an existing less extensive pine gene map, which indicates the slow evolution of the genome macro-structure in the Pinaceae. Under the Spruce-Up project, the map will be most useful to help assemble large genome sequence scaffolds, improve overall genome sequence contiguity and help map more precisely quantitative trait loci (QTL) related to resilience to biotic and abiotic stresses.

POPULATION GENOMICS AND PHYLOGENOMICS
J. Bousquet

As part of the SMarTForests project, association genetics studies at the genomic level have been pursued with a few notable results. First, using relaxed statistical criteria in a discovery mode and scanning SNPs from several thousand genes, a large number of associations were found between wood traits and gene SNPs in white spruce. Given the number of associations discovered, co-expression networks could be identified implicating expression in xylem and expression hubs centering around a few key transcription factors (Lamara et al. 2015). This work was conducted in collaboration with J. Mackay (now at the Univ. of Oxford).

In addition, environmental association studies were conducted in eastern white spruce on a large set of populations spanning more than 10 degrees of latitude and nearly 20 degrees of longitude in eastern Canada. Using stringent statistical criteria and a combination of different methods, a few dozen genes could be identified that were significantly related to temperature or precipitation variation, out of 11,000 SNPs from nearly 8000 genes tested (Hornoy et al. 2015). Notably, most significant associations implicated temperature rather than precipitation, reinforcing the idea that eastern white spruce may have more limited adaptive variation for precipitation, and that it would be best adapted to mesic site conditions throughout the geographical area sampled.

Work conducted in collaboration with J. Mackay (Univ. of Oxford) also aimed at detecting gene copy number variation (CNV), which is a different type of genetic variation than SNPs and which appears to be quite abundant in the white spruce genome (Sahli et al. 2017). Possible relationships with genetic adaptation are currently being investigated.

Also as part of the SMarTForests project and our ongoing collaboration with Univ. of Oxford (J. Mackay), we have also been investigating candidate genes for resistance to drought stress in white spruce (Stival Sena et al. 2017). By analyzing the dehydrin gene family, which contains dozens of members in white spruce alone and which has been previoulsy shown to be among the genes with highest rate of nonsynonymous substitutions (Pavy et al. 2013), we found a rapidly expanding clade specific to the genus *Picea*, which could provide higher adaptation potential in temporally and spatially heterogenous environments. Phylogenetic patterns were also correlated with amino acid motif structures and gene expression patterns, where different family members showed differential tissue preferential expression and contrasted patterns of inducibilty under drought stress.

FUNCTIONAL GENOMICS
I. Porth

Research under this theme span**s** the following areas: functional genomics of wood formation (poplar) and functional genomics of insect resistance (spruce). The following paragraphs involve work mainly conducted while I. Porth was at UBC but also some completed since her arrival at Univ. Laval. More importantly, information is provided about the current and future directions of functional genomics work. The general aim is to enhance our understanding regarding diversity and the genetic architecture of complex traits. A better understanding of the molecular basis of forest tree growth and development is also sought, in order to lead toward the selection of more stress resilient trees with enhanced biomass productivity and advantageous cell wall chemistry (Porth et al. 2015a, b; Muchero et al. 2015; McKown et al. 2017).

Knowledge about trait interrelations is also investigated, as it can help to foresee the expected response to selection for one trait relative to another (Porth et al. 2013a, b). Gene-based master regulons that underlie a large extent of phenotypic trait variation and involve multiple traits are termed pleiotropic. When such genes are knocked out, this can have detrimental effects on plant development. We previously employed forward genetics approaches such as Quantitative Trait Locus (QTL) mapping (Porth et al. 2011, 2012) and genome-wide association studies (GWAS) (Porth et al. 2013c, McKown et al. 2014) to discover such genes. In spruce, we identified a significant interrelation between the tree's inherent growth rate and constitutive resistance to herbivory. Here, intricate gene interaction networks determining the mainly positive and some negative gene-based relationships, respectively, between growth, development and pest resistance have been uncovered (Porth et al. 2017 in prep.). In poplar, we uncovered functional pleiotropy on a gene-by-gene basis by employing GWAS (Porth et al. 2014). Genes that associated with different phenotypic traits that themselves are functionally unrelated were considered pleiotropic *sensu lato* (McKown et al. 2014; Porth et al. 2015b). This is because trait characteristics that are genetically correlated are constrained in their ability to evolve independently. Thus, studying naturally-occurring mutations in the natural environment enhanced our understanding regarding genetic pleiotropy in normal gene functions.

We are also currently pursuing the systematic investigation of the gene space for allelic variants to better understand the evolution of complex trait (cell wall related) regulation across distant plant genera using population sequencing data and association genetics. I. Porth is also expanding opportunities for gene functional studies at Univ. Laval through her NSERC Discovery grant and Spruce-Up project collaborations, which is currently undertaken by one PhD student (J. Laoué) in close collaboration with J. Bousquet (Univ. Laval), and N. Isabel and A. Séguin (NRCan).

In a study conducted in collaboration with INRA Bordeaux, France and completed at Univ. Laval, we investigated the theme of species maintenance under interspecific gene flow. We have shown that European white oaks, section *Erythrobalanus*, *Q. petraea/Q. robur* known for being under intensive interspecific genetic exchange, exhibited limited gene-flow for beta-tubulin based on the two common alleles, which might be due to selection acting either directly on the locus or due to hitchhiking effects from closely linked sites under selection (Scotti-Saintagne et al. 2004; Porth et al. 2016a). We found significant associations between genotypic variation at this locus and leaf dimensions as well as leaf structure patterns, after having accounted for species and stand effects. The gene locus exhibited significant species differentiation and was linked to morphological discriminant traits. We concluded that the locus likely contributes to species divergence of putatively adaptive nature within the European white oak complex.

GENOMIC SELECTION

J. Bousquet and J. Beaulieu

Under the SMarTForests project, our proof-of-concept genomic selection (GS) work on eastern white spruce (Beaulieu et al. 2014a, b) has been extended to a MFFPQ advanced-breeding population of *Picea mariana*, which is the most reforested conifer in Québec. First, a genotyping chip of about 5000 informative gene SNPs was developed from innovative exome capture and sequencing approaches (Pavy et al. 2016). By developing and applying a robust bioinformatic pipeline for clustering gene sequences and filtering SNPs, about 100,000 high-confidence SNPs representative of about 15,000 genes were identified, with exceptionally high true-positive rate of predicted SNPs (96%) as validated by genotyping. In collaboration with MFFPQ (M. Desponts), the chip was then used to genotype mature trees from a large number of full-sib families replicated on two sites. In collaboration with CWFC (P. Lenz), several factors affecting the accuracy of GS models were tested and it was found that relatedness and long-range linkage disequilibrium were the main drivers of GS model accuracy (Lenz et al. 2017). As for white spruce full-sib families (Beaulieu et al. 2014a), model accuracies were high for both growth and wood traits, and the genetic gain per year was found to be two to three times higher than that obtained through conventional selection. Given the propensity of black spruce for vegetative propagation through somatic embryogenesis and cuttings, a forward selection scheme appears to be the most productive. Strategies for deploying GS in the context of multi-varietal forestry have been further outlined and discussed (Park et al. 2016).

Current work under the *FastTRAC* project aimed at implementing GS models built for white spruce (Beaulieu et al. 2014a) at the operational level of advanced breeding programs in Québec and the Maritimes. *FastTRAC* is also targeting Norway spruce, which is used in reforestation in Eastern Canada, and for which we recently constructed a gene SNP catalog from exome capture and sequencing, built a genotyping chip and developed GS models for weevil resistance and wood quality in this species. This white spruce and Norway spruce work is implicating scientists from end-users MFFPQ (M.-J. Mottet, A. Rainville), JDI (G. Adams, A. McCartney, S. Millican), and NBTIC (M. Fullarton), as well as scientists from CWFC (P. Lenz), NRCan (N. Isabel), IBIS (B. Boyle, J. Laroche), FPInnov (F. Robichaud), and research associates S. Nadeau, S. Blais and postdoc C. Deng. Preliminary results indicate that high accuracy of GS prediction is also achievable for weevil resistance in Norway spruce, provided that trees for which prediction of breeding values are sought are genetically related to those used to develop the GS models.

Regarding the Spruce-Up project and its GS component, the focus of new GS model development will be for white spruce advanced multi-trait selection implicating resilience traits such as spruce budworm resistance, nutrient use efficiency, drought tolerance, and wood traits related to crown morphology, wood homogeneity and stiffness, as well as carbon sequestration.

On a related applied matter and with funding from Fonds de recherche du Québec sur la nature et les technologies (FRQ-NT), we have been collaborating with MFFPQ (L. Tremblay and A. Rainville) on a project led by NRCan (N. Isabel and J. Godbout) on the development of an operational traceability system based on a SNP genotyping assay for the large-scale production of elite seedlings from the MFFOQ white spruce advanced-breeding program. The system is based on a small number of highly informative SNPs drawn from the large white spruce gene SNP registry (Pavy et al. 2013), in order to retrace pedigree information at all steps of production from crosses to vegetative propagation through somatic embryogenesis, cryoconservation and production of cuttings and seedlings. Illegitimate material was discovered at a low rate, and most of it originated from the upstream step involving crosses among selected parents, and where pollen contamination was detected (Godbout et al. 2017).

GENOMICS AND ECONOMICS

I. Porth

We initiated studies aimed at linking forest genomics with economics and investigated the potential for implementation of genomic tools at the operational scale in tree breeding programs. Based on a first economic assessment study conducted while I. Porth was at UBC (Porth et al. 2015c) and implicating a total of 36 forest genomics projects (USA, Canada), we identified the research priorities and potential economic implications of each project. To achieve this objective, a robust typology of forest sector genomics research relevant to Canadian applications was developped, with each initiative being categorized for its application potential (commercial, non-commercial). By considering silvicultural and genetic gains for productivity, insect resistance, and wood quality traits, modeling and economic analyses were developed. At Univ. Laval, and in collaboration with economists from UBC, we applied our findings to conduct an economic assessment of an independent set of 7 forest genomics research projects in Canada, including value judgements on the potential of commercialization and research application (Porth et al. 2016b). The outcome of the work allowed us to (1) categorize the projects by type including the description of the economic frameworks, (2) undertake an economic assessment of each of these projects, using qualitative and quantitative (if available) information and (3) provide advice and a value judgement on the necessary micro-level economic conditions for application and commercial success.

Current socio-economical assessment work under the Genome Canada Spruce-Up and *FastTRAC* projects aims at providing cost/benefit analyses for using biomarkers or genomic selection systems aimed at improving more rapidly various traits related to better resilience to abiotic and biotic stresses, as well as higher productivity and wood quality. Also, Spruce-Up will be looking at the conditions for social acceptance of intensive forestry and deployment of improved spruces under diverse socio-political conditions and jurisdictions in Canada.

QUANTITATIVE GENETICS AND CLIMATE CHANGE RESEARCH

J. Beaulieu

Through a project funded by FRQ-NT and in collaboration with MFFPQ colleagues (M.S. Lamhamedi and A. Rainville), we have pursued our research program on the potential impact of climate change on boreal tree species and the need to resort to assisted migration as an adaptive strategy. Climate-related variations in functional traits of boreal tree species can result both from physiological acclimation and genetic adaptation of local populations to their biophysical environment. To improve our understanding and prediction of the physiological and growth responses of populations to climate change, we studied the role of climate of seed origin in determining variations in functional traits and its implications for tree improvement programs for white spruce.

From 2015 to 2017, our research mainly focused on variation in morpho-physiological traits of seedlings from eight seed sources (six first- and two second-generation seed orchards) studied first in greenhouse, and then in nursery and on plantation sites (Benomar et al. 2015, 2016; Villeneuve et al. 2016). Genetic tests including the eight seed sources were established at three sites on each of three latitudinal transects.

Height and total dry mass (TDM) of 3-year-old seedlings raised in the greenhouse were positively correlated with photosynthetic capacity, stomatal conductance and mesophyll conductance. Total dry mass was strongly correlated with the latitude of seed source origin and associated climate variables.

Morpho-physiological traits measures collected at the end of the second growing season in the nursery made it possible to cluster the seed sources into three distinct groups. Modeling growth curves of these different groups showed that the height growth of seedlings from the second-generation and southern first-generation seed orchards was significantly higher than that of those from other orchards. The final height of seedlings from the first-generation seed orchards was also significantly related to the local climatic conditions at the orchard sites, suggesting local adaptation of each seed source given that each first-generation orchard was established from mass selection among local trees. Seedling height growth measured on three sites was significantly affected by both seed source origins and planting sites, but the relative ranking of the different seed sources was maintained regardless of reforestation site.

Traits such as height at age 4, photosynthetic rate, stomatal conductance, ratio of mesophyll to stomatal conductance, water use efficiency, and photosynthetic nitrogen-use efficiency were measured at three sites along one of the three climatic gradients two years after planting. Results showed significant variation in both physiological plasticity due to the planting site and seed source variation related to local genetic adaptation. However, the amplitude of seed source variation was much less than that related to plantation sites in the area investigated. Seed sources showed similar levels of physiological plasticity. The presence of locally adapted functional traits suggests that the use of assisted migration might have advantages for optimizing seed source productivity under future local climates. However, it is only over the long term that the common garden test will provide an accurate answer about the real value of assisted migration as a means to maintain white spruce plantation productivity in eastern Canada.

In a recent review (Sáenz-Romero et al. 2016), we have presented and discussed indications that the shift in geographic location of suitable climatic habitat for North American forest tree species because of rapid climatic change will likely cause important stresses on natural tree populations. Due to the physical limits of natural migration, tree populations will be challenged to keep pace with the moving target that their suitable climatic habitat will become. We have addressed various questions such as: In order to accommodate climate change, what forest management options do we have? What would be the consequences of inaction? We have aimed at providing foresters with a framework of basic knowledge regarding the magnitude and speed of climate change and its current and potential effects on forest resources, as well as suggesting some options for active management aimed at maintaining healthy tree ecosystems in the future.

As part of a collaboration with scientists at the Univ. of Alberta (N. Erbilgin) and in anticipation of possible future outbreaks of mountain pine beetle across the central and eastern parts of the natural range of *P. banksiana*, we determined the genetic and environmental bases of variation in foliar monoterpenes across the range of jack pine (Taft et al. 2015). Natural stands were sampled and three widespread chemotypes were identified, which presence was partly correlated to climatic variation among sampling sites. When sampling from common-garden studies with trees from various provenances, the three chemotypes could be observed but there was no obvious relationship with the geographic origins of trees or their phylogeographic lineages. Thus, a large part of the variation observed was the result of acclimation rather than local genetic adaptation.

WOOD QUALITY AND BIOMASS

J. Beaulieu

Over the last two years, we carried out a methodological study on white spruce wood density using computed tomography (CT) scanning, and conducted a few other studies aimed at evaluating growth and biomass of poplar and willow plantations, and biomass from young hardwood stands on marginal sites.

CT scanning technology was used to collect millions of three-dimensional data on eight white spruce wood disks (Beaulieu et al. 2016). The collected data were converted to wood density estimates using a calibration equation. Virtual wood cores of three sizes (diameters of 1 voxel, which is the smallest volumetric unit on which a CT number is computed, 5 mm, and 12 mm) were extracted in four orthogonal directions from pith to bark. This made the assessment of the effects of direction and core size on the wood density estimates possible. The averaged values and radial patterns of wood density as estimated from CT scanning data were found to be typical of the values and patterns reported for white spruce tree species in the literature, especially in relation to the year of growth because the experimental trees varied in age. This study showed that the application of CT scanning technology in wood science would allow the digital extraction of three-dimensional data subsets to perform wood density estimation, radial pattern analysis, and hypothesis testing, and that the results would be valuable complements to those obtained with other technologies such as X-ray densitometry.

Short-term growth and morphological responses to nitrogen availability and plant density in hybrid poplars and willows were studied in a greenhouse experiment (Mamashita et al. 2015) with the collaboration of various research organizations (T. Mamashita, G. Larocque, A. Mosseler, J. Major and D. Sidders of NRCan; B.R. Thomas of Univ. of Alberta; A. DesRochers of UQAT). The aim was to identify main characteristics leading to superior growth under increased plant competition with low or high nitrogen (N) availability. Hence, seven hybrid poplar and five willow clones were grown under greenhouse conditions for 13 weeks at three spacings (20 x 20, 35 x 35, and 60 x 60 cm) and two N levels (20 and 200 mg kg^{-1}). Positive relationships were found between leaf area and above-ground biomass per tree for both more and less productive clones. More productive clones had greater leaf area (+102%), leaf area per unit plant biomass (+12%) and lower root-to-shoot ratios (-27%) compared to less productive clones. Results also suggest that an addition of N could help mitigate negative effects of tree competition.

Short-rotation intensive culture for bioenergy production is at its pre-commercial stage in Canada. To be economically viable, these types of plantations need an accurate examination of actual yields, which requires precise and efficient estimation methods. In a study made in collaboration with scientists of about 10 Canadian research organizations (Lupi et al. 2015), and based on data collected on 10 poplar and six willow clones in six trials installed in three provinces Québec, Ontario and Alberta, it was possible to develop allometric equations for these clones and estimate the biomass produced. Plant allometric equations were developed using a stem selection approach, which allowed reducing the number of stems to be measured by up to 81% in coppiced plantations relative to traditional stem equations. Stratified random sampling (based on the position inside the plantation) made it possible to reduce the sample size as compared to simple random sampling, but only at higher levels of precision.

We also developed allometric equations for small-diameter woody species growing on mixed forest marginal lands, which are potential sources of biomass for bioenergy (Lupi et al. 2017). Eleven species of trees and shrubs were sampled from sites located in eastern Canada, Québec. Derived equations generally performed better than equations from the literature. Fixed-area plots and line-intersect sampling methods using both random or systematic selection of sampling units were compared to determine which method required the lowest number of measurements to estimate stand biomass for the same precision. The fixed-area plots method was successfully used to estimate relatively accurate oven-dry biomass per hectare. Results indicated that potentially harvestable woody biomass (oven dry basis) varied between 33-41 and 12-13 t ha^{-1} for the most and least productive marginal sites, respectively. Based on the results obtained, we recommended using fixes-area plots with 100 m^2 plots to estimate small-diameter woody biomass on marginal lands with dense vegetation.

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

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This report summarizes the progress made by the Canadian Forest Service (CFS), Canadian Wood Fibre Centre (CWFC), and Laurentian Forestry Centre (LFC) in forest genomics for the 2015–2017 period. Our research activities have mainly focused on spruce species. This work was made possible through grants obtained from the Genomics R&D Initiative Funds, a major initiative funded by Genome Canada to develop molecular breeding in softwood trees. Moreover, the development of a traceability system in white spruce (*Picea glauca*) and a study of cambium phenology in black spruce (*Picea mariana*) were completed, thanks to funding from the Fonds québécois de recherche sur la nature et les technologies (FQRNT) to respectively J. MacKay, J. Bousquet, N. Isabel, L. Tremblay, and S. Rossi, A. Deslauriers, M. Desponts and H. Morin.

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It is important to emphasize the retirement of three researchers working in forest tree biology: Jean Beaulieu (forest tree breeding and genomics) in 2014, Krystyna Klimaszewska (somatic embryogenesis and tissue culture) and Bob Rutledge (biotechnology and genomics) in 2015. The tissue culture activities of the LFC laboratory are currently carried out by Caroline Levasseur, Cathy Overton, and Nathalie Isabel. However, with the additional retirement of Yill-Sung Park (somatic embryogenesis and tree breeding) from the Atlantic Forestry Centre, NRCan research capacities have diminished significantly in the field of tissue culture and vegetative reproduction and its application to tree breeding.

TREE GENOMICS

White Spruce, Black Spruce and Norway Spruce

During the last 2 years, a grant was obtained from the GRDI (Genome R&D Initiative) to finish and advance projects related to gene and quantitative trait loci (QTL) mapping as well as to the development of genomic selection tools for spruce breeding programs in eastern Canada. This grant was also used as co-funding for two major research activities. The first one is the FastTRAC (Fast Tests for Rating and Amelioration of Conifers) project, supported by Genome Canada, and co-led by the CWFC and Université Laval. It aims to introduce the genomic selection of growth and wood traits into breeding programs managed by the MFFPQ (Ministère des Forêts, de la Faune et des Parcs du Québec), NBTIC (New Brunswick Tree Improvement Council), and JDI (J.D. Irving, Limited). The second initiative is the Spruce-Up Project, recently funded by Genome Canada, Genome Quebec, Genome BC, and Genome Alberta, for developing molecular breeding in softwood trees. This project is co-led by J. Bousquet (Université Laval) and J. Bohlmann (University of British Columbia, UBC). Nathalie Isabel and Patrick Lenz are co-principal investigators in this project.

Genomics of wood traits Gene association studies, in conjunction with gene expression networks, were conducted in white spruce in order to identify gene complexes linked to different wood traits: density, stiffness, microfibril angle and ring width (Lamara et al. 2016). The association of 229–292 genes per wood traits was made and the majority of those genes were also found in a xylem preferential co-expression group in an independent experiment, thus highlighting their importance in wood formation. A network analysis revealed several known MYB and NAC regulators as network hubs. A major link between the gene PgNAC8, wood stiffness, and microfibril angle was identified, underlying that the integration of association experiments and co-expression networks can enhance our understanding of complex wood traits.

Genomic selection in black spruce Genomic selection (GS) models were built for a subpopulation of the MFFPQ breeding program in order to test genomic selection in black spruce (Lenz et al. 2017). The study relied on 734 25-year-old trees belonging to 34 full-sib families derived from 27 parents; the trees were established on two contrasting sites. Genomic profiles were obtained from 4993 single nucleotide polymorphisms (SNPs) representative of as many gene loci distributed among the 12 linkage groups common to spruce. Very high accuracy of predicted genomic breeding values was reported for all traits investigated: height and diameter growth as well as wood density and cellulose microfibril angle. In addition, models were also accurate across sites, indicating little genotype x environment interaction in the area investigated. The significant loss of accuracy when half-sibs were used for model building instead of full-sibs highlights the major role of relatedness in GS modeling. About 500 to 1000 markers were sufficient to obtain GS model accuracy that is almost equivalent to that obtained with all markers, whether they were well spread across the genome or came from a single linkage group, further confirming the involvement of relatedness and potential long-range linkage disequilibrium (LD) in the highly accurate estimates obtained. Only slightly higher model accuracy was obtained when using marker subsets that were identified to carry large effects, indicating a minor role for short-range LD in this experiment. This study by Lenz et al. (2017) supports the integration of GS models in advanced-generation tree breeding programs, given that high genomic prediction accuracy was obtained with a relatively small number of markers due to high relatedness and family structure in the population. A much larger gain per unit of time could be obtained by GS at an early age than by conventional breeding approaches with long breeding cycles in boreal spruces.

Genomic breeding tools Co-led by the CWFC and Université Laval, the FastTRAC project started in 2015 and aims to introduce GS in spruce breeding programs of the MFFPQ, NBTIC, and JDI. Massive efforts in phenotyping and genotyping were undertaken in the last years to make model building possible as well as genomic predictions of breeding values in breeding populations of Norway spruce (*Picea abies*) and white spruce and in white spruce somatic lines. The phenotypes analysed were height and diameter growth as well as wood density, cellulose microfibril angle, and acoustic velocity. The latter three traits are related to mechanical use of wood. Trees were genotyped for 5308 high-quality SNP markers (white spruce) and more than 3950 markers were used for Norway spruce modeling. For the latter species, markers came from a newly developed SNP database (> 68k quality genes) using the gene-capture approach and a new analysis pipeline at Université Laval. In total, almost 1000 Norway spruce trees from Quebec were analysed for model building and validation; an additional 150 trees were sampled in JCI's related program for prediction purposes. Current modeling efforts include wood stiffness and weevil resistance in the analyses of Norway spruce. The first results indicate a positive correlation between weevil resistance and mechanical wood quality. A major issue was the non-homogeneous rate of attack among test sites, leading to significant genotype x environment interaction for growth traits. Quantitative genetic analyses are currently underway in 1739 white spruce trees from New Brunswick and 2340 trees from Quebec using the pedigree relationship matrix (ABLUP) and the realized genetic relationship matrix (GBLUP). Different genomic selection models are currently being run to evaluate the ridge regression and Bayes C algorithms in our data sets. The first results show rather high model precision and correlations above 0.8 between estimated genomic breeding values and *true* breeding values. This leads us to expect significant genetic gain based on marker selection at a young age.

Knowledge exchange activities As part of the knowledge exchange activities linked to the FastTRAC project, a video on genomic selection was produced by FPInnovations and Partenariat Innovation Forêt (PIF); https://www.youtube.com/watch?v=WxHcIVS79QI&feature=youtu.be . Several stakeholders, including representatives of the MFFPQ, CFS, CWFC, and Université Laval, contributed to the making of the video. In recent years, knowledge exchange activities began with a group of potential end-users of the FastTRAC technology, which includes the provinces of British Columbia and Alberta. A special workshop held during the 35th CFGA conference allowed for more discussions and for the presentation of options for including GS into conifer breeding programs.

A reference genetic map for conifers and QTL mapping Over the last decade, extensive genetic and genomic resources have been developed for white spruce, which has one of the largest plant genomes (20 Gbp). Draft genome sequences of white spruce and other conifers have recently been produced, but dense genetic maps are needed to comprehend genome macrostructure, delineate the regions involved QTLs, complement functional genomic investigations, and assist with the assembly of fragmented genomic sequences. In Pavy et al. (2017), a greatly expanded white spruce composite linkage map was generated from a set of 1976 full-sib progenies, with the positioning of 8793 expressed genes. QTLs involved in the timing of budburst and budset as well as clusters of co-expressed genes putatively involved in abiotic stress responses were also identified and located. A high level of synteny was found between spruce and pine genetic maps, which should facilitate the transfer of structural information within the Pinaceae family. This gene linkage map shall assist the large-scale assembly of the next-generation white spruce genome sequence and provide a reference resource for the conifer genomics community. In addition, a reciprocal transplant experiment (2000 genotypes replicated 10 times and genotyped for thousands of SNPs using SMarTForests) was established on four different sites along latitudinal and altitudinal gradients. In the new project, Spruce-Up, we started to evaluate new traits that are essential to climate adaptation and to resistance mechanisms against forest pests, such as the accumulation of phenolic compounds. This project will lead to the development of new phenotyping tools for the large-scale characterization of new traits useful for tree breeding.

Precision phenotyping for drought resistance Understanding the genotype-phenotype-environment connection is central to predicting tree responses to changes in their environment. However, phenotyping represents a major bottleneck for genomic studies. Several projects have been undertaken to develop new classes of traits to study climate sensitivity throughout a tree's lifespan or precision phenotyping to evaluate tree resilience during extreme events.

High-throughput precision phenotyping Through the Spruce-Up and Genome Ontario projects (led by I. Ensminger, University of Toronto), new phenotyping methods are currently under investigation. Over the next few years, we will develop high-throughput phenotyping methods using spectral data acquired by drones in order to establish quantitative relationships with drought resistance and nutrient use efficiency (in collaboration with Janice Cooke, University of Alberta). The experiments are being conducted in controlled cross progeny tests of the MFFPQ breeding program as well as in a biparental family.

Tree-rings to determine past climatic constraints Local adaptation in tree species has been documented through a long history of common garden experiments and, more recently, using association genetics, in which functional traits (height, phenology) are used as proxies for fitness. However, the ability to identify potential causal genes responsible for adaptation to climate requires the evaluation of traits that precisely reflect how and when climate exerts selective constraints. In collaboration with colleagues from the LFC (Martin Girardin) and CWFC (Isabelle Duchesne), we proposed an interdisciplinary approach that combines dendroecology, which provides a new class of phenotypes, with association genetics. In a paper recently submitted by Housset et al. (2017), we illustrated this approach by investigating the climatic sensitivity embedded in the annual rings of 233 eastern white pine (*Pinus strobus*) trees growing in a common garden experiment representing 38 populations from the species' entire range. We found that populations' interannual variability in growth was particularly affected by punctual and extreme climatic events, such as summer droughts and fall or spring frosts. Combining dendroecology with association genetics will allow us to assess tree vulnerability to past climate at fine temporal scales and provide avenues for future genomic studies on functional adaptation in forest trees.

Phenology of bud and cambium under a changing climate Bud and cambial phenology represents the adaptation of species to the local environment, which allows the growing season to be maximized while minimizing the risk of frost for developing tissues. The temporal relationship between apical and radial meristems can help understand tree growth as a whole process. In a study by Perrin et al. (2017), carried out in collaboration with Sergio Rossi, Annie Deslauriers, and Hubert Morin (Université du Québec à Chicoutimi) and Mireille Desponts (MFFPQ), we compared cambial phenology in black spruce provenances classified as early and late bud flushing. The different phases of cambial phenology were assessed using wood microcores sampled weekly from April to October in 2014 and 2015 from 61 trees growing in a provenance trial in Quebec. Trees showing early bud flush also exhibited early reactivation of xylem differentiation, but no significant difference in the period of xylem formation and total growth was observed between flushing classes.

Phenological changes are expected to occur with ongoing global warming, which could create mismatches in growth patterns among sympatric species or create synchrony with insect herbivores. We performed different sets of experiments in a comparative assessment of the timing of budbreak among seven conifer species of eastern Canada by evaluating seedling development in growth chambers under different temperatures (16, 20, and 24°C). In general, warmer conditions advanced budbreak, with the greatest effects being observed at the lower temperatures. The observed nonlinear responses of the timing of budbreak to warming suggest that the most important changes in bud phenology should be expected at the lowest temperatures (Rossi and Isabel 2017). Finally, we investigated the effects of asymmetric experimental warming on spruce phenology by testing the hypothesis that daytime warming is more effective in advancing budbreak than nighttime warming. Budbreak was monitored daily in black spruce seedlings belonging to 20 provenances from eastern Canada subjected to daytime and nighttime warming in growth chambers at temperatures varying between 8 and 16°C. Our observations conducted under controlled conditions allowed us to experimentally demonstrate that budbreak can advance under nighttime warming, but to a lesser extent than under daytime warming. Prediction models using daily timescales could neglect the diverging influence of asymmetric warming and should be recalibrated for higher temporal resolutions (Rossi and Isabel 2016).

Traceability method In collaboration with the Direction générale de la production de semences et des plants forestiers du MFFPQ (Laurence Tremblay and André Rainville) and Université Laval (John Mackay and Jean Bousquet), Godbout et al. (accepted) worked on developing a traceability system in order to monitor the production of white spruce elite varieties via somatic embryogenesis (SE) at the St-Modeste provincial nursery. In order to detect human errors both upstream and downstream of the production process, this project had two main objectives: 1) to develop methods that make it possible to trace the origin of the plants produced and 2) to generate a unique genetic fingerprint that could be used to differentiate each embryogenic cell line and make its genetic monitoring possible. Such a system had to rely on a minimum number of low-cost DNA markers and be easy to use by non-specialists. An efficient marker selection process was operationalized by testing different classification methods on simulated data sets. These data sets were generated using in-house bioinformatics tools that simulated crosses involved in the breeding program for which genotypes from thousands of SNP markers were already available. The rate of misidentification was estimated and various sources of mishandling or contamination were identified. The method can be applied to other production systems, such as breeding and aquaculture, for which genomic resources are already available.

POPULATION GENOMICS

Eastern White Pine and Western White Pine

Genetic-environment associations (GEA) In this study, we attempted to disentangle the effects of local adaptation and isolation by environment (IBE) from those of isolation by distance (IBD) and isolation by colonization from glacial refugia (IBC) using range-wide samples in two white pine species. To do so, SNPs from 168 genes, including 52 candidate genes for growth and phenology, were genotyped in 133 and 61 populations of eastern white pine and western white pine, respectively. For eastern white pine, climate did not significantly explain among-population variation when controlling for IBD and IBC in redundancy analyses (RDAs). However, 26 SNPs were significantly associated with climate in single-locus GEA analyses (Bayenv2 and LFMM), thus suggesting that local adaptation took place in the presence of high gene flow. For western white pine (*Pinus monticola*), we found no evidence of IBE using RDAs and weaker signatures of local adaptation using GEA and F_{ST} outlier tests, which is consistent with adaptation via phenotypic plasticity. In both species, the majority of the explained among-population variation (69 to 96%) could not be partitioned between the effects of IBE, IBD and IBC. GEA methods can account differently for this confounded variation, and this could explain the small overlap of SNPs detected between Bayenv2 and LFMM. This study, conducted in collaboration with K. Ritland and S. Aitken (University of British Columbia), illustrates the inherent difficulty of taking into account neutral structures in natural populations and the importance of sampling designs that maximize climatic variation, while minimizing collinearity between climatic gradients and neutral structure. This work was reported in Nadeau et al. (2016).

Poplars and Aspens

Population genetics of poplars In one study by Meirmans et al., we investigated the influence of hybridization between balsam poplar (*Populus balsamifera*) and black cottonwood (*P. trichocarpa*) on population structure and adaptation in balsam poplar. Hybridization between species is known to greatly affect their genetic diversity and, therefore, their evolution. Also, within species, there may be genetic clusters between which gene flow is limited, which may impact natural selection. However, few studies have looked simultaneously at the influence of among-species and within-species gene flow. To do this, we sampled over 1500 individuals from across these two species' ranges, and genotyped them using a combination of 93 nuclear and 17 cpDNA SNPs. We found that hybridization was mostly limited to the contact zone where the species' distributions overlapped. Within balsam poplar, we found multiple levels of population structure. Interestingly, the border between the eastern and central clusters was very sharp, while the border between the central and western clusters was diffuse. Outlier analysis revealed that three loci associated with the sharp border were also associated with climate. We hypothesize that the observed clusters derive from three Pleistocene refugia. Between the central and western clusters, postglacial long-distance gene flow led to the diffusion of their border. In the eastern cluster, we hypothesize that endogenous genomic barriers developed, leading to the sharp border and a spurious climate association. We conclude that the influence of hybridization on the large-scale genetic structure of balsam poplar is limited, and that it was mostly shaped by historical factors.

A similar study was also undertaken in eastern cottonwood (*P. deltoides*). This species is a foundation species that is an important component of riparian habitats in North America. It occurs over a wide natural range: from the southeastern Gulf of Mexico region in the U.S. to southern Canada. The objective of this study was to understand how eastern cottonwood genomic diversity is distributed across its natural range in order to assess its adaptive capacity in the perspective of current global warming. Genomic diversity was compared to a set of abiotic (climatic and edaphic) and biotic (corresponds to the genomic diversity of a natural fungus pathogen) variables. Key results showed three distinct lineages for eastern cottonwood, two of them corresponding to the delineation of the two subspecies while the third one was located at the northeastern margin of the species' natural range. The distribution of these lineages was strongly associated to both abiotic and biotic variations. The comparison between the chloroplast and nuclear DNA patterns showed that gene flow between the three lineages is unbalanced and appears to have been shaped by ocean watersheds. Such disequilibrium may favour the genetically richer *deltoides* subspecies and disadvantage the poorer *monilifera* subspecies that could not benefit from the arrival of novel alleles to its local gene pool. Indeed, those "pre-adapted" and new incoming alleles may help populations facing changing conditions cope with maladaptation. A manuscript by Godbout et al. is in preparation.

Tree-microbiome interactions In collaboration with Brad Pinno (Northern Forestry Centre) and Armand Séguin (LFC), a project was undertaken to gain a better understanding of the ability of different reclamation strategies used in the Athabasca oil sands mining sites to restore them to a state of functional ecosystems. In a paper by Stefani et al., we used a host-microbiota approach to characterize the above- and belowground diversity in reclaimed sites made up of upland forest floor-mineral mix (FFMM) and low-lying peat-mineral mix (PMM). An in-depth analysis of the above- and belowground genetic diversity was performed in sites under reclamation and in mature aspen (*P. tremuloides*) stands and recently naturally disturbed sites (3-year-old burned aspen stands). The objective of this study was to investigate the genetic diversity of trembling aspen that naturally recolonizes these novel environments and their associated belowground microbiota. Aspen genotyping showed that trees mostly originated from sexual reproduction on reclaimed sites with soil covers. In contrast, most individuals in mature and burned stands sampled near the reclamation sites as a benchmark for natural disturbance originated from vegetative reproduction. Nonetheless, aspens in FFMM and PMM stands were not genetically different from those in mature and burned stands. DNA metabarcoding of bacteria and fungi in root and soil samples revealed that the diversity of the belowground microbiota associated with aspen and the relative abundance of putative symbiotic taxa in PMM were significantly lower than in FFMM and naturally disturbed sites. Despite the genetic diversity and origin of trembling aspens being similar between FFMM and PMM, trees were not associated with the same belowground microbiota and long-term monitoring is suggested to better understand these novel ecosystems.

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FOREST GENETICS AND TREE IMPROVEMENT ACTIVITIES FOR ALBERTA TREE IMPROVEMENT AND SEED CENTRE

2015 – 2017

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This report covers operational and applied research activities in forest genetics, tree improvement, gene conservation and seed biology and technology by the Alberta Tree Improvement and Seed Centre (ATISC) for the period between August 2015 and May 2017. The main focus of ATISC activities continued to be tree improvement dominated by white spruce (*Picea glauca*) and lodgepole pine (*Pinus contorta* var. *latifolia*) within Alberta government programs and government-industry cooperative programs. Our research in climate change adaptation through genetics also focused mainly on white spruce, lodgepole, and jack pine (*P. banksiana*) is intended to address long-term sustainability of the Alberta forestry industry and ecosystem health. Recovery of whitebark (*P. albicaulis*) and limber pine (*P. flexilis*)constitutes a greater part of forest gene conservation in Alberta through selection, testing and *ex situ* conservation of blister rust tolerant genotypes; development of seed handling and germination methods for whitebark and limber pine; adoption of efficient field working tools; and facilitating planting of putative whitebark and limber pine blister rust trees in Alberta national parks by Parks Canada. Restoration of forest ecosystems on sites disturbed by energy development using forest trees and shrubs has been integrated into provincial rules that govern seed transfer to maintain genetic adaptation. Consequently, ATISC will be registering, storing and approving seed transfer for shrubs. To facilitate this, ATISC is conducting applied research to develop seed germination and storage protocols for shrubs commonly used in Alberta reclamation projects.

GENE CONSERVATION AND ENDANGERED SPECIES RECOVERY

Alberta is revising its *in situ* gene conservation plan for better alignment with the taxonomy, updates the status of all native tree species by natural subregions based on improved species distribution inventory data, and revisits the criteria for ranking. The provincial *ex situ* gene conservation plan summarizing the status and gaps of provincial *ex situ* genetic resources is under review for publication online as a complement to the *in situ* plan.

The implementation of species recovery plans for whitebark pine and limber pine received substantial support from the governments of Alberta and British Columbia, University of British Columbia, University of Alberta, Athabasca University, Kings University College, USDA Forest Service, Canadian Forest Service, Parks Canada, and Crown Managers Partnership. In 2015 staff from Parks Canada and Alberta government were trained on the species' biology, operational recovery objectives, methods of identifying blister rust, selecting plus trees, collecting cones, and documentation. Eighty five limber pine trees phenotypically selected for putative blister rust resistance were identified. Because there were few cones on selected trees, one whitebark pine population with 60 parent trees in *ex situ* collections was assessed for health and 8 putative blister rust resistant tree identified. Screening results from 10 unselected trees from this population revealed that all parents were in the lowest resistance quartile, supporting the need for stringent phenotypic selection as part of seed collection for *ex situ* gene conservation. The USDA Forest Service, Coeur D'Alene Forest Nursery did this 7-year resistance screening. In addition, seed from 100 limber pine trees was sent to USDA Forest Service, Dorena Genetic Resource Center for rust resistance screening. Likewise, seed from 17 whitebark pine plus trees was sent to Kalamalka Forestry Centre in Vernon, BC for screening as a support by the British Columbia government.

As part of species recovery effort, the Alberta Tree Improvement and Seed Centre donated seed from putative blister rust resistant trees to Parks Canada. Subsequently, the Whitebark Pine Ecosystem Foundation produced 2500 seedlings from this seed, which will be planted in the Castle-Waterton Lake National Park region in the fall of 2018. Mycorrhizal samples from two species symbiotic with whitebark pine were collected to support research and seedling inoculations led by Athabasca University. One of two range-wide limber pine provenance trials including 32 populations and 143 families was established near the northern limit of the species in Alberta, designed by Dr. Anna Schoettle, USDA Forest Service.

We developed two mobile apps (one for citizen scientists and one for field crews) that greatly expedited field data collection and data management. Both apps have ESRI platforms that enable real-time remote data management through ArcGIS Online (Survey123 and Collector). We also developed an ESRI Story Map for public information. Educational material produced as part of the species recovery effort include brochures, magnets, stickers, bookmarks, interpretive signs, a web page, and a blog.

CONE ABORTION IN LODGEPOLE PINE SEED ORCHARDS

Cone production in some of Alberta lodgepole pine seed orchards has been lower than expected for the orchard age and tree size. Earlier observations suggested that cone abortion was a likely cause. To confirm this, cone survival in two cone crop years was monitored for orchards in Edson (central Alberta), Grande Prairie and Manning (northern Alberta). Each orchard is linked to a separate tree breeding program and, therefore, parental clones differ among these seed orchards. For the orchard in the Manning area (most northern orchard location), the rate of cone abortion differed between years. In the 2014–15 survey (cones pollinated in 2014), the abortion rate was 45%. The biggest drop in the number of living cones occurred in mid-July of the first growing season. In the 2015–16 survey (cones pollinated in 2015), the abortion rate was 68%. The biggest drop in the number of live cones occurred in late June of the first growing season. There were large differences in abortion rates among clones in both years. Synchrony between the timing of pollen shed and seed cone receptivity was good in both years. In addition, the amount of pollen averaged over the receptive period was similar in both years. This suggests that inadequate pollination is an unlikely cause of cone abortion in this orchard. Because the orchard in Manning is located on farmland outside the main natural range of lodgepole pine, environmental factors may be suspects of cone abortion. Therefore, a more concerted study may be needed to establish cone abortion trends in relation to weather and compare cone abortion in seed orchards and natural stands. A collaborative project between the forest companies, Alberta Tree Improvement and Seed Centre, and the University of Alberta is underway to address the issue of low seed production in pine orchards.

POLLEN CONTAMINATION IN WHITE SPRUCE SEED ORCHARDS

High pollen contamination rate (89%) was found in one mast crop collected in a white spruce orchard at the Alberta Tree Improvement and Seed Centre in Smoky Lake. The rate was determined using pollen traps, a standard method employed in Alberta. The contamination rate was re-evaluated using chloroplast DNA markers. Complete five-locus cpDNA markers were obtained from buds of all white spruce clones in one orchard, wild white spruce trees growing in the orchard vicinity, and from seeds collected in the mast year. Close to 46% of seeds were pollinated with the outside pollen with unique haplotypes. However, only 55% of outside pollen was different from the orchard pollen. After correcting for the probability that the outside pollen grain has a haplotype unique to the outside pollen, the contamination rate based on the markers came to 84%. Should determination of pollen contamination based on DNA markers be attempted again in the future, it is recommended that different, more polymorphic markers are used.

CLIMATE CHANGE ADAPTATION

The Alberta Tree Improvement and Seed Centre, University of Alberta and forest companies undertaking tree improvement in Alberta completed the implementation of the Tree Species Adaptation Risk Management Project. This project is designed to integrate climate change adaptation in tree improvement and was funded by the Climate Change and Emissions Management Corporation (CCEMC), which is the precursor of the Emissions Reduction Alberta (ERA) of the Alberta government. Results for white spruce breeding programs are published in DOI 10.1007/s11295-016-0983-1 and those of lodgepole pine in http://dx.doi.org/10.1016/j.foreco.2016.06.041. Alberta is currently looking at options to integrate climate change adaptation into seed transfer rules based in these results. To address data limitations identified by this project, the Alberta government, University of Alberta, and forest companies are working together to establish new series of white spruce and lodgepole-jack pine provenance trials. The white spruce trials will be established in 2018 with about 300 seedlots replicated on five test sites. An equally large series for a combination of lodgepole pine, jack pine and their putative hybrids will be established in 2019. Both series bridge the data gaps in sampling of tree populations and test site environment. The pine trials will include 20 populations from British Columbia, carefully selected to cover the entire range of *Pinus contorta* var. *latifolia* in BC. Emphasis has been given to population sampling to optimally cover the entire natural ranges of the species in Alberta including areas without active reforestation. Test sites were chosen to include drier and much higher elevation areas not covered by existing provenance and progeny trials.

EXPANDED USE OF GENETICALLY IMPROVED SEED

In an attempt to improve forest productivity and support tree breeding in the province, the Alberta government has issued a directive mandating the use of genetically improved seed for reforestation whenever available. On average, genetically improved seed makes up 15% of the current conifer reforestation in Alberta depending on the age of the breeding program and associated seed orchards. It is expected that this directive will increase forest productivity on managed forest land base compensating for loss of productivity in areas that may be negatively impacted by climate change, forestry areas deleted due to mining and energy development and other land uses. It will also encourage forest companies to continue investing in tree breeding. To qualify and be sold by the producer as genetically improved seed, the seedlot must have a minimum of 2% genetic worth for height growth at a specified rotation age. Seed producers (owners) set their own seed price.

SEED BIOLOGY AND TECHNOLOGY

The seed biology and technology program at ATISC manages Alberta’s long-term conservation and research seed collections including Alberta’s two endangered tree species, whitebark and limber pine. This seed bank also provides the majority of research tree seed for provincial tree improvement program activities and academic forest genetic research. Our seed lab research endeavours to further Alberta’s knowledge of seed physiology in order to advise practical methods for industry seed/cone handling and use.

Operational Changes

This season our biggest operational change came from using some of the results from our limber pine cone maturation trial 3 years ago. Since both limber and whitebark pine are extremely short-lived in seed storage, we used an *ex situ* method on immature whitebark pine cones collected by Parks Canada and sent to ATISC for seed storage. This first use showed a marked visual improvement in seed quality, which we hope to quantify in the future.

Seed Conservation Course

This spring the Alberta Tree Improvement & Seed Centre offered its 8th edition of our Seed Conservation Course. It is a free 2-day course with over 70 participants to date from all over Alberta and BC. Topics covered included seed moisture, assessment and collection, seed handling, chemical viability testing, seed storage behaviour and longevity, and germination and dormancy problem solving. Feedback was again very positive and attendees this year covered mainly forestry and private tree/native plant nursery sectors.

New Seed Testing Standards

Alberta has been regularly storing non-tree seed used in reclamation since 2010, reflecting a significant increase in reclamation on Alberta public land. Changes to the Alberta Forest Genetic Resources and Conservation Standards (FGRMS) in 2016 now include regulations for seed collection, storage, and deployment of woody shrub species. The accompanying new Alberta Seed Testing Standards came into effect in December 2016 with many changes and updates which reflect the requirements of these new species, including the addition of water activity methods and limits to measure seed moisture.

Reclamation Seed Research

For many of the reclamation species now being collected and stored at ATISC, little is known regarding correct seed handling or germination methods often resulting in greenhouse emergence of < 50%. Not only does this make it difficult and expensive to produce plants and maintain high genetic diversity for resilient populations but it also makes quality control nearly impossible. Since some of these species have collection or handling requirements that are different from our economically important tree species, it is essential to address these issues and be able to provide feedback to seed collectors and handlers, eventually improving seed quality and empowering seed owners with more knowledgeable control over their seed and reclamation plans.

ATISC began research on non-tree seeds four years ago starting with hazels (*Corylus* spp.), which have been proven by ATISC to be orthodox with some results presented at the 2016 NAIT Boreal Research Institute Native Plants Seminar. The project has now grown into a 3-stage multi-year process for 14 species: developing chemical viability testing methods (TZ or TEZ), carrying out germination trials with results that combine high genetic diversity with practical and economical methods, and finally conducting comparative longevity tests on each species to determine the approximate lifespans of these seeds in cold storage. These three stages must be completed in sequence and the majority of TZ work is now complete, with germination trials started this past winter. In addition to providing information to seed owners, the results will provide the underlying knowledge required to begin provenance trials and other research in shrub genetics in Alberta.

PUBLICATIONS

Gray, L.K.; Hamann, A.; John, S.; Rweyongeza, D.; Barnhardt, L.; Thomas, B.R. 2016. Climate Change risk management in tree improvement programs: selection and movement of genotypes. Tree Genetics and Genomes 12: 23. DOI 10.1007/s11295-016-0983-1.

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Rweyongeza, D.M. 2016. A new approach to prediction of the age-age correlation for use in tree breeding. Annals of Forest Science 73: 1099–1111. doi:10.1007/s13595-016-0570-5.

CONE AND SEED IMPROVEMENT

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The Tree Seed Working Group (TSWG) continues to provide extension on seed science and technology through its "biannual" News Bulletin and its biennial workshop. Since the last CFGA meeting in Fredericton (2015) we have produced News Bulletin editions 62, 63, and 64. All TSWG News Bulletins 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 BC Tree Seed Centre helped organize and hosted the BC Seed Orchard Association in June, 2016. The program booklet and presentations from this meeting, as well as information from other past meetings, can be found here: http://www.fgcouncil.bc.ca/bcsoa/past-meetings.html.

Research and development continued in the areas of seed extraction efficiency, priority processing methodology, genetic conservation, and implementation of water activity as a tool for evaluating our genetic conservation samples. We were fortunate to receive capital funding that allowed us to obtain a 4-probe water activity meter. This greatly helped in decreasing the backlog of genetic conservation samples which we had not yet freezer stored. Genetic conservation has focused on expanding our seed bank with collections of native non-commercial tree species. I completed a stratification trial with whitebark pine and my current recommendation is a 3-day soak followed by 56-days of warm stratification (20°C) and then 112-days of cold stratification (2-5°C).

I was fortunate to be sponsored to attend an International Seed Testing Association (ISTA) Method Validation course in Zurich Switzerland in the fall of 2016. It was a great learning experience as well as a great opportunity to meet many people involved in seed science and technology worldwide. I was also able to combine this with a trip to Finland to spend a few days touring research, seed orchard, seed processing and nursery facilities. Truly an awesome experience!

I continue to participate in several committees: ISTA Forest Tree and Shrub Committee; Genetic Conservation Technical Advisory Committee (TAC); Coastal and Interior TAC. I provide facility tours, supervise our Testing group and continue to assist with advice, extension and fire fighting activities with regards to cone and seed science and technology topics.

PROCEEDINGS

OF THE

THIRTY-FIFTH MEETING

OF THE

CANADIAN FOREST GENETICS ASSOCIATION

PART 2

Symposium

Joint conference of the Canadian Forest Genetics Association and
Western Forest Genetics Association

Edmonton, Alberta
June 26–29, 2017

Editors

A. Hamann, D.A. McPhee and J.D. Simpson

COMPTES RENDUS

DU

TRENTE-CINQUIÈME CONGRÈS

DE

L'ASSOCIATION CANADIENNE DE GÉNÉTIQUE FORESTIÈRE

2^e PARTIE

Colloque

Conference conjointe de l'Association canadienne de génétique forestière et de la Western Forest Genetics Association

Edmonton, Alberta
26–29 juin 2017

Rédacteurs

A. Hamann, D.A. McPhee et J.D. Simpson

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THE APPLICATION OF GENOME-WIDE INFORMATION TO TREE BREEDING: WHAT IS COMING NEXT?

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Almost three decades have passed since the first quantitative trait loci were identified in tree mapping populations, but the wide application of genomic information to forest breeding programs has hardly ever materialized. Difficulties in uncovering the majority of loci that control complex traits and high costs of genotyping technology kept these approaches in check. Recently, new developments in genome-wide prediction methods and the dramatic reduction in the cost of genome services have created a renewed interest in these approaches. Still, it remains unclear if current advances will be sufficient to unleash the wide use of genomics in tree breeding, or if they will once again remain the domain of academics. Here I briefly reviewed the current application of genome-wide information to tree breeding and the outcomes of numerous pilot studies already completed or under way. While the preliminary results from these studies are exciting, they may not be sufficient to entice most tree breeders to incorporate genomic technology, unless decreasing costs and added value and efficiencies can be created. Thus, I focused largely on what are likely to be the next major leaps in the use of genome-wide information in tree breeding, including the application of prediction models to guide the establishment of the most productive crosses based on specific combining ability, the use of methods that pool progeny to generate accurate predictive models at a fraction of current costs, and the application of low-density, ultra-low cost and high throughput methods of genotyping based on sequencing.

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BRITISH COLUMBIA'S FOREST GENETICS PROGRAM: THE TOP 10 REASONS FOR SUCCESS

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Tree Improvement in British Columbia has a long history of industry-government-academic cooperation dating back to 1959 with the formation of the Plus Tree Board. Since 1998, conservation, tree breeding, genecology, seed production, and related activities have been coordinated under the auspices of the Forest Genetics Council of British Columbia (FGC), a multi-stakeholder advisory body appointed by the Provincial Chief Forester. SelectSeed Co. Ltd, established in 1999, helps FGC achieve its goal of increasing future timber supply by producing select seed (via contracts with 5 independent companies) and selling it to government programs and forest tenure holders. The presentation outlined FGC's current strategies, goals and accomplishments, and highlighted several initiatives underway in response to climate change, forest health issues, and other challenges. The presentation also featured a Top 10 list of reasons for BC's forest genetics program's success.

FURTHER INFORMATION

Forest Genetics Council of BC website: http://www.fgcouncil.bc.ca

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ASSESSING TREES' ADAPTIVE CAPACITY TO ENVIRONMENTAL CONSTRAINTS: FROM GENOMIC APPROACHES TO THE DEVELOPMENT OF INNOVATIVE PHENOTYPING TOOLS

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Understanding climate change impacts at various scales, from trees to landscapes, and providing suitable responses are critical priorities for forest managers and policymakers. Predicting tree responses to changes in their local environment is a key to decision-making in tree breeding, forest resource management, carbon accounting models, and biodiversity conservation practices. However, making genotype-phenotype-environment connection is central to these predictions.

Over the last decade, extensive genomic resources have been developed by Genome Canada's projects and major achievements have been made. For instance, the white spruce genome has been sequenced, and genomic selection for wood properties is being transferred to end-users. However, the prediction of tree responses to future climate remains challenging. The possibility of identifying putative causal genes responsible for adaptation to climate requires the evaluation of quantitative traits that precisely reflect how and when climate exerts selective constraints on trees. The list of traits reflecting tree adaptation to climate that could be efficiently assessed is limited and their evaluation is labor-intensive. Indeed, the evaluation of classical traits usually consists in taking punctual measurements that only represent a snapshot of a tree's life. This presentation will summarize different approaches we initiated to establish connections between adaptive traits (e.g. timing of budburst, tree ring-derived traits) and genotypes, and the results we have obtained so far in spruce and pine. Future research directions will be discussed.

FURTHER INFORMATION

http://www.genomiqueforestiere.chaire.ulaval.ca

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CONFRONTING EMERGING PATHOGENS: A GENOMICS EMPOWERED APPROACH TO PROTECTING FOREST HEALTH

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Invasive microbes, causing diseases such as sudden oak death (*Phytophthora ramorum*) and chestnut blight (*Cryphonectria parasitica*), negatively impact forest health, affecting ecosystems and economies around the world. Approaches for managing introduced diseases typically rely on breeding programs that can take decades to identify and deploy resistant plants. To demonstrate how this process can be accelerated to rapidly identify host genes associated with resistance to emerging pathogens, we challenged ca. 1000 re-sequenced *Populus trichocarpa* genotypes with *Sphaerulina musiva*, an invasive fungal pathogen in western North America. We used genome-wide association mapping to identify three loci associated with resistance and one locus associated with susceptibility to *S. musiva.* Whole transcriptome analysis supported these results with consistent patterns of differential expression with the mapping results. A population-wide characterization of these loci found a disproportionately high number of detrimental mutations in the genes encoding resistance receptors compared to the highly conserved susceptibility locus. Functional characterization of these loci is currently underway. The approach used herein demonstrates the power of population-wide re-sequencing of undomesticated, non-model plant species to rapidly identify loci that could be used to help mitigate long-term impacts of emerging diseases in native ecosystems.

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WHAT DO WE KNOW ABOUT THE GENETICS OF SEED LONGEVITY?

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The availability of high quality seeds, with high and vigourous germination, is essential for the production of healthy, high-yielding plants, be that an arable crop, a horticultural crop, a forest species, or any other useful plant species. Seed quality is inextricably linked with seed longevity, since it is the detrimental effects of seed ageing that lead to declines in seed vigour and germination. Seed longevity depends on the conditions under which seeds are stored, most importantly, moisture content and temperature. But it is also a highly plastic trait that varies depending on pre- and post-harvest factors such as climate during seed development, moisture content at harvest and post-harvest drying regime. It also varies greatly between species, if seeds are stored under the same, standardized conditions. For different seedlots within a species, it was originally thought that variation in longevity would correlate with the initial viability of the seeds and that all seedlots of a species would age (lose viability) at the same rate. However, we are now starting to understand that the rate of ageing can also vary between different seedlots within a species. This presentation presented our current understanding of the genetic basis of variation in seed longevity.

FURTHER INFORMATION

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RESPONDING TO THE INFLUENCE OF PESTS IN FORESTRY GENETICS, SEED PRODUCTION, AND DEPLOYMENT OF IMPROVED MATERIAL

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Pests (insects and diseases) influence our tree improvement activities in many ways, from tree breeding through seed deployment. This presentation explored how we understand and respond to the constraints pests place on our seed-related activities. For genetic improvement of forest trees, we are screening for genetic resistance to pests, with the objective of creating pest-resistant genotypes for inclusion in seed orchard programs. Active screening programs include white pine blister rust (*Cronartium ribicola*), spruce leader weevils (*Pissodes strobi*), gall rust (*Endocronartium harknessii*), Comandra rust (*Cronartium comandrae*), spruce budworm (*Choristoneura fumiferana*), and Dothistroma. Regarding seed production, our research program over the years has made tremendous gains in managing seed orchard pests, which can dramatically limit seed yield. Pests addressed have included the Western conifer seedbug (*Leptoglossus occidentalis*), the fir coneworm (*Dioryctria abietivorella*), spruce gall adelgids (*Adelges abietis*), and cone midges (*Contarinia oregonensis*). We also conducted trials for registration of new pesticides. Seed deployment is one means of addressing climate change, in conjunction with a switch to climate-based seed transfer. This process is informed through trials like the AMAT, the Assisted Migration and Adaptation Trial. By examining pest issues associated with AMAT, we can get a heads-up on what pests are likely to be a problem in future climates, and adjust our seed deployment accordingly. Finally, threatened or endangered tree species are often at risk because of insects and diseases. Screening for pest resistance, then establishing seed orchards of resistant material, offers an avenue to repopulate species at risk with durable genetic material. We are currently screening whitebark pine (*Pinus albicaulis*) for white pine blister rust resistance. Early selections have been made and will be established in seed orchards within a few years.

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TREE BREEDING IN THE SOUTHERN US: GENETIC GAIN EQUALS PRODUCTIVITY AND PROFITABILITY FOR LANDOWNERS

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Tree improvement is logistically complex, time-consuming, and expensive. The NCSU Cooperative Tree Improvement Program continuously seeks innovative ways to accelerate breeding while reducing costs in our loblolly pine (*Pinus taeda*) breeding program. For the fourth-cycle breeding strategy, we have implemented the MateSelect algorithm to balance diversity and genetic gain. To reduce the progeny testing effort and increase progeny testing efficiency, the program has been implementing alpha cyclic incomplete block row-column designs. The presentation summarized some of the operational and research innovations, including the incorporation of genomic data into our fourth-cycle strategy.

The conduit from the breeding program to the deployment program is via seed orchards and nurseries. Seed orchard managers have reaped tremendous benefits from three cycles of breeding and have established the best selections into advanced-generation seed orchards. The vast majority of seedlings sold by nurseries are specific families derived from these orchards. About 84% of loblolly pine plantations are now established with open-pollinated families, 8% with full-sib families, 2% with clonal varieties, and the remainder with mixtures of seedlings from seed collected from seed orchards. Landowners now have a wide range of options when choosing the loblolly pine genetics to plant on each hectare being regenerated. Many landowners elect to plant the highest quality genetics available, and the return on their investment is substantial. On a regional basis, when the genetic gain per year is increased to any extent, the financial impacts are worth hundreds of millions of dollars. Details of the economic analyses were presented.

FURTHER INFORMATION

For information on the Cooperative, visit http://treeimprovement.org/

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THE GENOMIC BASIS OF ADAPTIVE AND PLASTIC RESPONSES TO CLIMATE IN CONIFERS

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Conifers display extensive evidence of local adaptation, with divergence among populations in a range of phenotypes, from budset to cold injury tolerance. They can also respond plastically to a wide range of climatic stresses, which can result in repatterning of gene expression. Here, we used comparative genomic approaches to study how both gene expression and adaptive differentiation respond to climate in lodgepole pine (*Pinus contorta*) and interior spruce (*Picea engelmanii*, *Picea glauca*, and their hybrids). We compared RNAseq expression profiles under 7 different environmental treatments and characterized genes that respond similarly vs. differently in their expression. We also explored the genetic basis of adaptive differences among populations using exome capture and phenotype- and environment-association analyses. We found 47 genes with strong signatures of convergent adaptation to climate in both species, despite 140 million years of independent evolution. Interestingly, the genes that are involved in convergent adaptation are also more likely to have conserved gene expression profiles. We are now expanding this study to explore climate adaptation in Douglas-fir (*Pseodotsuga menziesii*), western larch (*Larix occidentalis*), and jack pine (*Pinus banksiana*), as well as to study the basis of resistance to *Dothistroma* in lodgepole pine, and Swiss needle cast (*Phaeocryptopus gaeumannii*) in Douglas-fir.

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GENOMICS AND TREE IMPROVEMENT

SINGLE-STEP GENOMIC EVALUATION OF SIMPLE AND COMPLEX PEDIGREES

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Maximizing genetic gain at minimal cost is a major goal of tree improvement programs. Observed genetic gain depends primarily on the accuracy and precision of the estimated genetic parameters obtained from progeny trials. Thus, the quality of these parameters is contingent on the accuracy of the individual-tree field performance records and their genealogical relationships. The use of genomic marker information can improve estimates of relatedness over the expected values by quantifying an actual proportion of alleles shared by individuals, however, the cost of genotyping every individual is still prohibitive in large forest tree improvement programs. Here, we investigated the use of a blended relationship matrix (***H***: HBLUP) (Legarra et al. 2009, Misztal et al. 2009, Christensen and Lund 2010) and compared it to traditional ABLUP analysis (Henderson 1984) implemented in ASReml-R (Butler et al. 2007). The blended HBLUP method reflects the realized genomic relationship information (***G***) of a subset of genotyped individuals to the full traditional average numerator matrix (***A***) making it possible to combine both genotyped and non-genotyped individuals in a single analysis. Thus, the requirement for genotyping the full breeding population is unnecessary.

We investigated this approach using 22-year tree height and X-ray wood density from a white spruce (*Picea glauca*) progeny trial representing 214 unrelated open-pollinated (OP) families growing in a single progeny test site in Quebec (Beaulieu et al. 2014a). We also investigated the approach utilizing age 11 height from a Douglas-fir (*Pseudotsuga menziesii*) breeding population with a more complex pedigree structure.

Genomic based evaluations and pedigree based evaluations were assessed on the basis of model fit, accuracy and precision of genetic parameter estimates, breeding value rank changes, and cross-validation prediction accuracy of breeding values. The results showed that the HBLUP method considerably improved the accuracy and precision of breeding value estimates over traditional ABLUP analysis by accounting for Mendelian sampling variation. Further, the genomic information helped in reducing the heritability bias commonly observed in OP progeny trials as it revealed hidden relatedness, inbreeding, as well as possible pedigree errors.

FURTHER INFORMATION

Ratcliffe, B.; Gamal El-Dien, O.; Cappa, E.P.; Porth, I.; Klapste, J.; Chen, C.; El-Kassaby, Y. 2017. Single-Step BLUP with Varying Genotyping Effort in Open-Pollinated *Picea glauca*. G3: Genes, Genomes, Genetics (https://doi.org/10.1534/g3.116.037895)

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GENOMIC SELECTION MODELLING FOR WEEVIL RESISTANCE, WOOD QUALITY AND GROWTH TRAITS IN A NON-NATIVE TREE SPECIES, NORWAY SPRUCE (*Picea abies*)

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White pine weevil (*Pissodes strobi*) is a major damaging agent in Norway spruce (*Picea abies*) plantations in eastern Canada. It causes leader dieback, which in turn impacts stem straightness and growth of afflicted trees. Previous work identified resistant progeny and moderate to high genetic control of weevil resistance. To provide proof of concept for genomic selection (GS) applied to insect resistance, and investigate links between weevil resistance and wood traits in Norway spruce, we conducted a GS study involving 952 trees (belonging to 39 full-sib families from 34 parents) tested in three contrasting environments in Quebec. Wood density, cellulose microfibril angle, acoustic velocity as a proxy for wood stiffness, and growth were measured from age 5 to 15 years. Cumulative weevil attack was also recorded at 4 regular time points from age 6 to 15. Genotyping data were obtained for 3934 validated SNPs representative of as many gene loci using a newly developed Illumina Infinium iSelect array. SNPs were identified from *de novo* exome capture and sequencing. Wood density ($h^2 = 0.32$), acoustic velocity ($h^2 = 0.24$), and weevil resistance ($h^2 = 0.28$) were found to be under moderate genetic control, while growth traits had lower heritability estimates. Genotype-by-environment interactions were found to be small for wood traits and weevil resistance, but larger for growth traits. GS models including those for weevil resistance led to high accuracy estimates reaching 0.75 to 0.94. The accuracy of GS models was largely comparable with the conventional pedigree-based ABLUP models. Positive genetic correlations were found between wood traits, height growth, and weevil resistance. Thus, positive responses are expected for growth and wood traits when selecting for weevil resistant trees, whether using the conventional or GS approach.

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PEDIGREE-BASED AND GENOMIC PREDICTIONS OF NORWAY SPRUCE PERFORMANCE IN MULTICLONAL FORESTRY IN NEW BRUNSWICK

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Conventional tree improvement is slow, especially for traits that can only be assessed at a mature stage. Genomic selection (GS) has been successful in animal species, and it is now more frequently studied and implemented in other species of economic value including in forestry. Because GS allows predicting breeding values using only genotypic information, it offers the possibility to considerably hasten breeding cycles and to stack traits for which accurate predictions of genetic values are obtained. This is especially important in the context of multiclonal forestry such as is practiced in New Brunswick (NB). Multiclonal forestry which is made possible through the use of somatic embryogenesis and cuttings requires families and lines with substantial genetic values and stable performances over sites and breeding zones.

Norway spruce (*Picea abies*) is a non-native coniferous species used extensively in reforestation programs in NB, with 2–4 million seedlings planted per year. It has high genetic variation in growth, wood, and weevil resistance traits. Here we used Norway spruce as an example to evaluate the additive and non-additive genetic effects, and the genetic parameters of economically important traits, and test the feasibility of GS across breeding zones. Four NB trials were phenotyped for obtaining solid reference breeding values for genomic selection modeling. Moreover, we assessed for white pine weevil (*Pissodes strobi*) attacks and genotyped 952 trees of 39 full-sib families from Quebec and 141 clones from NB using 3,934 single-nucleotide polymorphisms (SNPs) developed from the *FastTRAC* project. In the light of possible genotype-by-environment effects, the accuracy of prediction and amplitude of genetic gains obtained within and among tests were estimated and compared.

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DEVELOPMENT OF A HIGH-DENSITY AFFYMETRIX AXIOM GENOTYPING ARRAY FOR GENOMIC SELECTION IN DOUGLAS-FIR

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We designed and tested a high-density Axiom genotyping array for Douglas-fir. We designed SNP assays for 55,776 potential SNPs that were discovered from transcriptome sequencing projects described by Muller et al. (2012) and Howe et al. (2013). Because the SNPs were derived from transcriptome sequences, the array targets SNPs in the expressed genes of the Douglas-fir genome. We tested the array on ~2,300 related and unrelated Coastal Douglas-fir trees (*Pseudotsuga menziesii* var. *menziesii*) from Oregon and Washington, and found that as many as ~26K SNPs could be reliably genotyped and were polymorphic, depending on the desired call rate. We worked with Affymetrix bioinformaticists to develop protocols to 'rescue' SNPs that did not pass the default Affymetrix quality control criteria (e.g., 97% call rate). Lowering the call rate threshold from 97% to 60% using the custom R scripts increased the number of successful SNPs from 16,177 to 24,192 in one population and from 18,932 to 25,881 in another. We used a subset of 395 unrelated trees to calculate SNP population genetic statistics. Over a range of call rate thresholds (97% to 60%), the median call rate for SNPs in Hardy-Weinberg equilibrium ranged from 99.2% to 99.8%, and the median minor allele frequency ranged from 0.198 to 0.233. Based on a small number of samples, the successful SNPs also work well on Interior Douglas-fir (*P. menziesii* var. *glauca)*. The Axiom genotyping array will serve as an excellent foundation for studying the population genomics of Douglas-fir and for implementing genomic selection. We are currently using the array to test genomic selection in a third-generation breeding program for Coastal Douglas-fir.

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MANAGING CLIMATE CHANGE

REFORESTATION FOR AN UNCERTAIN FUTURE: DO WE REALLY NEED TO WORRY ABOUT CLIMATE CHANGE?

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Populations of native plants are genetically different from one another and are adapted to different climatic conditions. Therefore, natural resource managers must match the climatic adaptability of their plant materials to the climatic conditions of their planting sites. For forest trees this has typically been done using geographically defined seed zones or seed transfer rules that specify a geographic or climatic distance beyond which populations should not be moved. However, these recommendations assume that climates are stable over the long-term, an assumption that is unlikely given climate change. Because forest tree populations are generally considered to be locally adapted, climate change will likely lead to declines in health and productivity of native ecosystems. In this presentation we use the Seedlot Selection Tool, a new web-based, user-friendly mapping program, to address two questions: 1) Assuming local adaptation, are native populations adapted to current and future climates? and 2) If not, how far do we need to go to find populations adapted to a planting site? Using several examples, we concluded that now and in the near-term (next decade or two), native populations are approximately adapted to their local climates, although better-adapted populations might be found at lower elevations or further south. By the mid- to late-century, however, native populations are at a high risk of maladaptation to projected climates, and adapted populations are generally found far away and to the south. In some cases, no analogous climates exist in the future. This presentation demonstrates the utility of the Seedlot Selection Tool for exploring different assumptions about climate variables important for adaptation, how they might change in the future, and acceptable levels of risk of users.

FURTHER INFORMATION

https://seedlotselectiontool.org/sst/

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SELECTIVE BREEDING FOR GROWTH IN THE INTERIOR SPRUCE HYBRID ZONE MAINTAINS ADAPTATION TO CLIMATE

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Hybrid zones contain extensive standing genetic variation that facilitates rapid adaptive responses to selection. The *P. glauca* x *P. engelmannii* hybrid zone in western Canada is the focus of tree breeding programs that produce ~90 million reforestation seedlings annually and support a multi-billion dollar forest industry. Understanding the direct and indirect effects of selective breeding on adaptive variation is necessary in order to implement assisted gene flow polices in Alberta and British Columbia (BC) that match these seedlings with future climates. We decomposed relationships among hybrid ancestry, adaptive traits, and climate to understand the implications of selective breeding for assisted gene flow strategies. The effects of selection on associations among hybrid index, adaptive traits in a seedling common garden (n ~ 2400), and provenance climates were assessed. Hybrid index differences between natural and selected seedlings within breeding zones were small in Alberta (average +2%), but larger and more variable in BC (average -7 %, range -24% to +1%), slightly favoring *P. glauca* ancestry. The average height growth gain of selected seedlings over natural seedlings within breeding zones was 36% (range 12% to 86%). Clines in growth with temperature-related variables were strong, but differed little between selected and natural populations. Selected seedling hybrid index and growth trait associations with evapotranspiration-related climate variables were more than two times stronger than in natural seedlings, indicating possible pre-adaptation to moisture-limited future climates. Preliminary genotype – phenotype association analyses suggest that in selected seedlings allele frequency shifts at candidate adaptive SNPs are detectable but small. Associations among cold hardiness, hybrid ancestry and cold-related traits dominated signals of adaptation that were preserved in breeding populations. Strong hybrid ancestry – phenotype – climate associations suggest that assisted gene flow will be necessary to match interior spruce breeding populations with shifting future climates. Absence of negative correlated selection responses among traits and maintenance of cold adaptation in selected seedlings suggests breeding populations can be safely redeployed using assisted gene flow prescriptions similar to those of natural populations.

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PROVISIONAL CLIMATE-BASED SEED ZONES FOR MEXICO: GUIDING REFORESTATION UNDER OBSERVED AND PROJECTED CLIMATE CHANGE

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Seed zones for forest tree species are a widely used tool in reforestation programs to ensure that seedlings are well adapted to their planting environments. Ideally, seed zone delineations reflect genetic population differentiation in adaptive traits as inferred from provenance and progeny trials, although if these are not available, other approaches may be used. This is the case in Mexico, where seed zones have been delineated based on physiographic regions. These zones, however, may include too much climatic variation, exposing planting stock to risks of maladaptation. Here we developed climate-based seed zones with two variables that have generally been shown to often be associated with tree growth and genetic population differentiation. Ten bands of the variable mean coldest month temperature were overlaid on seven bands of a variable representing aridity, resulting in 63 provisional climate-based seed zones for Mexico for seed collection and deployment of the corresponding planting stock. The approach has the advantage that adjusting seed zones and seed movement guidelines for responding to climate change is relatively straight forward. Over the last three decades temperature has increased by about 0.7°C and several regions of Mexico have also seen pronounced shifts toward drier conditions. The observed trends largely conform with climate change predictions for Mexico as well. Using medium-term ensemble model projections for the 2050s, we recommend moving seed sources from warm, dry locations towards currently wetter and cooler planting sites to compensate for climate change that has already occurred and is expected to continue for the next decades. Our transfer recommendations using climate-based seed zones can be implemented within the existing framework of physiogeographic regions, which often span large climate gradients.

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CLIMATE CHANGE RISK MANAGEMENT IN TREE IMPROVEMENT PROGRAMS: SELECTION AND MOVEMENT OF WHITE SPRUCE AND LODGEPOLE PINE GENOTYPES IN ALBERTA

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Concern of the impact of climate change in forestry has prompted tree improvement programs and regulatory agencies to integrate climate change adaptation in the production and use of tree seed. Long-term genetic transplant experiments in the form of provenance and progeny trials provide an opportunity to gain insight into the environmental tolerances of planting stock. Additionally, these trials allow tree improvement programs to identify genotypes especially sensitive to observed and projected climate change, so that these genotypes can be removed from seed orchards and breeding populations.

Building on 35 years of tree improvement research for white spruce (*Picea glauca*) and lodgepole pine (*Pinus contorta*) in Alberta, we analyzed data from 80 genetic tests established by industry and government agencies. We showed how the risk of planting maladapted trees can be minimized by moving planting stock to new areas, or by eliminating genotypes from breeding programs that are sensitive to anticipated future climate environments. Transfers that outperformed local sources consistently originated from locations with higher temperatures, suggesting north or northwest transfers for spruce and movement to higher elevations for lodgepole pine. Adaptation to cold appears to be a prevalent driver for genetic population differentiation in both species. Therefore, care should be taken in avoiding seed movements too far north and up in elevation to colder environments to avoid frost damage to planting stock. A number of transfers among breeding regions were identified that ensure productivity gains under recent climate conditions and moderate warming, associated with minimal risks.

FURTHER INFORMATION

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GENETIC ADAPTATION
TO CLIMATE EXTREMES

DROUGHT SENSITIVITY OF NORWAY SPRUCE AT THE SPECIES' WARMEST FRINGE: QUANTITATIVE AND MOLECULAR ANALYSIS REVEALS HIGH GENETIC VARIATION WITHIN AND AMONG PROVENANCES

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Norway spruce (*Picea abies*) is by far the most important timber species in Europe, but due to its sensitivity to drought periods combined with increasing bark beetle populations its outstanding role in future forests is strongly scrutinized. Predictions of the species' future distribution and plantation areas indicate significant reductions with subsequent consequences for the European forest and wood sector. So far, genetic variation and local adaptations at the warm edge of the Norway spruce range have rarely been addressed. In the present study, we analyzed drought response of Norway spruce in a drought-prone environment at the fringe of its natural range. Based on a 30-year-old provenance experiment we tested for genetic variation among seed provenances and estimated the degree of genetic determination of drought reaction across consecutively occurring strong drought events. Moreover, we report the first association analysis done in Norway spruce merging drought reaction, wood, and climate-related traits. We observed significant genetic variation among provenances originating from the species' Alpine, Central, and Southeastern European range. Moreover, genetic variation within provenances varied significantly and revealed significant degrees of genetic determination of drought response of up to 0.44. Also, varying phenotypic correlations between drought response and wood traits suggest differences in selection intensity within the original populations. Phenotypic correlations between drought, ring width, and density are also reflected by a single SNP that is significantly associated to drought resistance, minimum density, ring width, and earlywood width. Overall, 27 SNPs were identified to be responsible for 45 significant genetic associations for drought and wood property traits, explaining between 11% and 37% of the trait variation. The present study is a step towards a better understanding of drought reaction in Norway spruce as a basis for future breeding and genetic conservation measures at the species' warmest fringe.

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CHARACTERIZING DROUGHT TOLERANT LODGEPOLE PINE POPULATIONS FOR PLANTING UNDER CLIMATE CHANGE

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Characterizing and identifying drought-tolerant seed sources for reforestation could decrease risks of forest maladaptation under climate change. To study drought tolerance of populations of a wide-ranging conifer in western North America, lodgepole pine (*Pinus contorta*), we analyzed annual growth, stable isotope, and functional wood anatomical data of tree rings obtained from a large provenance trial. Within this trial, long-distance seed transfer simulates climate change, while planting sites in southern British Columbia also captured a drought event occurring in 2002 and 2003. We found that northern populations showed poor growth, lower water use efficiency, and limited stomatal plasticity. Therefore, these populations may be most at risk under drought and climate change. In contrast, populations from British Columbia's central and southern interior regions showed better growth, higher water use efficiency and a stronger stomatal response to changing environmental conditions. While seed sources from more southerly areas in the United States were relatively drought tolerant, this tolerance may be better explained by wood anatomy rather than stomatal conductance. Implications of these results to assisted migration were discussed.

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RECORDS OF COLD ADAPTATION IN TREE RINGS: SEED TRANSFER LIMITS UNDER WARMING CLIMATES

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Damage from late and early frosts may limit the success of assisted migration prescriptions to address climate change. As planting stock is moved higher in elevation and northward in latitude, these seedlings may be temporarily more susceptible to frost and cold as the future climate optimums materialize. We addressed this concern by analyzing 20 provenances of lodgepole pine (*Pinus contorta*) from four major climatic regions: the boreal North, the Central Interior of British Columbia (BC), the Southern Interior of BC, and the United States. Frost tolerance of these populations is compared using natural frost events recorded in the natural archive of tree rings. Two proxies were used: blue rings and frost rings. Blue rings occur when low temperatures prevent completion of the lignification process. These un-lignified cells can be highlighted by staining with Safranin and Astrablue. Frost rings occur when the cambial cells are killed by freezing. This causes discontinuation of radial cell rows and a zone of irregularly shaped tracheids. The occurrence of blue and frost rings differed significantly among populations. Provenances from the boreal North showed the least cold damage, followed by sub-boreal populations from the Central Interior of BC, and then followed by the populations from the Southern Interior of BC and the United States. Blue rings occurred in years with short growing seasons and low temperatures. Frost rings in the latewood were linked to cold temperatures in fall whereas frost rings in the earlywood were associated with unusually warm springs, followed by a cold spell. We showed that frost risks need to be considered when implementing assisted migration and we introduced blue and frost ring proxies to screen for frost tolerance in genetic trials.

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WHAT CAN WE LEARN FROM TREE-RING STRUCTURE ON CLIMATE ADAPTATIONS? A CASE STUDY FROM IUFRO - SPRUCE PROVENANCE TRIALS

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Current climate change involves growth reaction of forest trees that can be interpreted as a proxy of their adaptation to environmental conditions. Climate-induced changes in growth rate were manifested not only in ring width but also in intra-annual tree-ring structure. We hypothesized that the tendency to form intra-annual density fluctuation (IADF) is provenance dependent. In order to test our hypothesis we determined IADF frequency for Norway spruce (*Picea abies*) populations tested in the IUFRO 1972 provenance trails. As a climatic factor triggering IADF frequency, we applied standardized precipitation evapotranspiration index (SPEI) and Palmer drought severity index (PDSI) from the global gridded SPEI dataset. We used nuclear microsatellite variation (SSR markers) to define genetic diversity between provenances. Based on the generalized linear mixed model (GzLMM) we confirmed significance of the trees' origin as well as genotype x environment interaction (G x E), for different IADFs type. Principal component analysis (PCA) allowed as to designate groups of provenances with a common growth pattern. However, the phenotype-based PCA was not related to genetic distance (Fst) based principal coordinate analysis (PCoA). This may be related to the neutral nature of the SSR markers used in the analysis. For climate-growth relationship studies, we created three groups of provenances (N, E, S). In the case of IADF located in earlywood (E and Eplus type), SPEI proved to be a more sensitive indicator of provenance-specific climate adaptation. Our findings lead us to assume that a populations' adaptive capacity depends on "climate shift" which means differences between site climate and provenance origin climate.

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FOREST PESTS

AND

DISEASES RESISTANCE

GENETIC CONTROL OF THE NATURAL RESISTANCE OF *Picea glauca* AGAINST *Choristoneura fumiferana*

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Choristoneura fumiferana, spruce budworm (SBW), is the most damaging native defoliator in North America. In the province of Quebec alone, more than 6.3 million ha have been damaged from 2006 to 2015, during the current SBW epidemics. Recently, a constitutive resistance mechanism was identified in white spruce (*Picea glauca*). It is linked to the accumulation of the phenolic compounds piceol and pungenol in the needles, which results from overexpression of the Pgβglu-1 gene, and negatively affects the survival rate and development of SBW larvae. These compounds are classified as acetophenones and their abundance is highly variable among genotypes, leading to contrasted levels of susceptibility and resistance. In the present study, we analyzed 870 trees belonging to different white spruce full-sib and clonal trials from seven locations in the provinces of Quebec and New Brunswick. We aimed at: 1) characterizing the phenotypic variation of the Pgβglu-1 gene expression and the piceol and pungenol contents, 2) understanding their genetic control and inter-trait relationships, and 3) evaluating the potential trade-offs between the resistance mechanism and tree growth. Piceol and pungenol accumulation were 2% and 1.3% of foliar dry weight on average, respectively, and ranged among individuals from non-detected to relatively high concentrations. Individual-tree heritability of piceol, pungenol, and Pgβglu-1 gene expression was estimated to be moderate (0.55, 0.50, and 0.58, respectively). Slightly higher broad sense heritability estimates were obtained for acetophenones (0.66 and 0.60 respectively), indicating that additivity plays a major role in resistance. Positive, albeit small, genetic correlations were found between the resistance traits and growth (from 0.14 to 0.30), suggesting that this constitutive resistance does not compromise growth in white spruce. Our findings show our understanding of the evolvability of resistance traits against defoliators and imply that considerable gains could be expected from genetic selection.

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DIFFERENCES IN PINE RESISTANCE TO *Dothistroma* NEEDLE BLIGHT IN ALBERTA AT THE SPECIES, PROVENANCE AND FAMILY LEVELS

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Dothistroma needle blight caused by *Dothistroma septosporum* is a serious disease of pine in many regions around the world. Until recently the disease was not known to occur or cause damage in Alberta pine forests. However, in 2012–15 heavy Dothistroma infections were found in several locations in central Alberta. The infected locations included two genetic test sites: Calling Lake (CL) and Whitecourt Mountain (WM). CL is a provenance test of lodgepole pine (*Pinus contorta*), jack pine (*P. banksiana*), and their hybrids while WM is a lodgepole pine progeny/provenance test. At the time of infection trees in CL and WM were 30- and 15-years old, respectively. The CL provenance test includes 36 wide-range collections: 21 of pure lodgepole pine form Alberta (18) and British Columbia (3), six pure jack pine and nine hybrid seedlots. On average, 24 trees per provenance were alive at age 30. The WM progeny-provenance test includes 67 seedlots: 46 single family open pollinated collections and 21 provenance collections from Alberta and British Columbia. On average, 19 trees per seedlot were alive at age 15. The severity of the disease was assessed quantitatively by estimating the percent of healthy foliage on each tree. Between the two sites a total of 2,142 trees were assessed. The mean percent of healthy foliage was 35% at CL and 52% at WM. Lodgepole pine was found to be much more susceptible than jack pine (19% vs 64% healthy foliage) with their hybrids showing intermediate levels of resistance. Large differences among the lodgepole provenances were found at both test sites. Likewise, the open pollinated families at WM showed different levels of resistance with breeding values ranging from 34% to 92% healthy foliage. There were seven common provenances present at CL and WM. The ranking of these provenances was stable across the two sites (r = 0.93).

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ADAPTIVE VARIATION IN LODGEPOLE AND JACK PINE POPULATION RESPONSES TO MOUNTAIN PINE BEETLE FUNGAL ASSOCIATES AND ABIOTIC STRESSES

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Mountain pine beetle (MPB) (*Dendroctonus ponderosae*) is a historic component of pine forests in the central and southern interior of British Columbia. However, in recent years MPB populations have expanded north- and eastward, threatening pine forests naive to attack from this pest. This study investigates adaptive variation in lodgepole pine (*Pinus contorta*), the ancestral host, and jack pine (*P. banksiana*), a naive host, across east-west gradients in Canadian pine populations for traits that influence host quality to MPB. Characterizing the susceptibility of naive pine populations is important for predicting the impact MPB will have as it expands beyond its historic range. Lodgepole pine is distributed throughout western North America, moving eastward to transition to jack pine, whose distribution range extends from Alberta to the Maritime provinces. Using population genomics, we have redefined the large hybrid zone that occurs between these two species in Alberta and discovered introgression and patterns of diversity that suggest genetic variation is linked to variation in environmental factors along the east-west gradient. We hypothesized that genetic variation along this gradient in lodgepole and jack pine also corresponds to a gradient in susceptibility to MPB fungal associates (*Grosmannia clavigera*), and that traits affecting tree defence capacity, such as drought tolerance, differ across these same gradients. To test these hypotheses we conducted a large-scale phenotypic screening of seedlings from 18 pine provenances from across Canada for response to *G. clavigera* infection and to drought. We measured lesion length at 1 and 2 weeks after infection with *G. clavigera* and photosynthetic capacity at 1, 3, 5, and 11 weeks of drought conditions in 756 and 816 trees, respectively, from the 18 populations. We observed wide variation between the populations in phenotypic response to our biotic and abiotic treatments. We are currently preparing to conduct a genome-wide association study to identify genomic regions that underlie this variation. The results of this work contribute to our understanding of how genetic variation in pine contributes to differences in host quality and, by combining these results with our population genetic work, will identify whether population genomics can identify spatial patterns of differential pine susceptibility to mountain pine beetle in novel habitats.

FURTHER INFORMATION

Project website: http://tria-net.srv.ualberta.ca/

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GENETIC APPROACHES TO IDENTIFYING WESTERN GALL RUST RESISTANCE IN LODGEPOLE PINE

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Western gall rust (WGR), caused by *Endocronartium harknessii*, is a damaging autoecious fungal rust of hard pines, including lodgepole pine (*Pinus contorta* var. *latifolia*) and jack pine (*P. banksiana*). Infection generally occurs in the spring and early summer on immature and elongating shoot stems, usually of younger trees, where damp and humid conditions contribute to the success of infection. Once infected, gall formation (comprising symptoms such as discolouration, cankers, and woody swellings) on both stems and branches of infected trees can be observed within 1–2 growing seasons. Galls generally result in stunted growth and deformities in stem architecture, with a portion of the infected trees dying. Quantitative resistance to *E. harknessii* has been reported for both of these species, with jack pine showing relatively greater resistance compared to lodgepole pine. In the province of Alberta, tree improvement programs that target resistance to pests and pathogens are considered a priority. This project aims to use phenotypic, transcriptomic, and quantitative genomic based techniques to: 1) identify phenotypic responses of pine to *E. harknessii* infection that definitively lead to gall formation, 2) identify genes through RNA-Seq that are differentially expressed in the early phases of infection, and may contribute to pathogen resistance, and 3) use genomic selection to identify marker systems associated with resistance to *E. harknessii*. Through the use of these genomic approaches, we hope to identify markers that can be developed and used in lodgepole pine breeding programs in Alberta.

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SEED BIOLOGY AND MANAGEMENT

RESIN VESICLES IN CONIFER SEEDS: MORPHOLOGY AND ALLELOPATHIC EFFECTS.

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Conifer seeds of many species of fir, hemlock, and cedar contain resin vesicles in their seed coat. Although there is limited information on the morphology and chemical ecology of these vesicles, their damage during seed processing can negatively impact germination success. We examined the resin vesicle morphology of intact dry seeds of western redcedar (*Thuja plicata*), eastern white-cedar (*Thuja occidentalis*), amabilis fir (*Abies amabilis*), balsam fir (*A. balsamea*), grand fir (*A. grandis*), and subalpine fir (*A. lasiocarpa*) by ^{1}H magnetic resonance imaging to characterize the volume, shape, and quantity of resin vesicles. Germination assays confirmed that resin vesicle damage prior to stratification can significantly reduce germination success, but for some species this damage had a negligible or positive effect on germination success. Extracts of these resin vesicles from some of these *Abies* and *Thuja* species inhibited the germination of *Arabidopsis* Col-0 seeds in a dose-dependent manner, but the germination of *Arabidopsis ab*scisic acid-*i*nsensitive (*abi3-6*) seeds was unaffected.

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REFERENCE SEEDLOT MONITORING PROGRAM: WHAT HAVE WE LEARNED IN 36 YEARS?

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The Alberta Tree Improvement and Seed Centre has had a research based reference seedlot monitoring program since 1981. The criteria for inclusion in the program, when it started, was arbitrary and included 80 collections of both single-tree and multiple-tree seedlots from 13 species, with 5 species which either did not have adequate germination protocols during testing and/or did not include enough seedlots to provide any confident results. In addition, many seedlots spanned the switch from 2°C to -18°C storage during the early years of the program. However, data for the remaining 8 species were analysed in 2013 and yielded interesting trends, which provided the focus for an overhaul of the program going forward. Most seedlots were retired in order to focus on species that had previously been left out or where trends were unclear, as well as phasing out single-tree collections in favour of bulk collections to provide a better overall picture of each species that would be more useful to researchers and industry. The testing intervals are also now larger and specific to each species now that we have some longevity information. Results provided thus far were discussed.

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CHALLENGES IN A HIGH ELEVATION PINE SEED ORCHARD IN ALBERTA

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Seed orchard production is fundamental to the success of any tree improvement program. In an orchard designed to produce seed for an area of 1,106,686 ha and an elevation operating range of 1200–1600 m, production targets have never been met. With a target yield of approximately 6.6 million seeds/year, the crop has never reached 20% of its target in the last decade of production. To address this shortfall, in the summer of 2015, 34 of 110 clones were selected for treatment with gibberellic acid ($GA_{4/7}$) with a total of 284 trees being treated (~3 ramets/clone x three injection dates) with three control trees per clone. The three injection dates selected were June 30th, July 20th, and August 6/7th.

Two key results were obtained: 1) six of the 34 clones showed sensitivity to GA regardless of the rate of application, which was based on stem diameter, and 2) female conelet production increased significantly in the spring of 2016 for the first two treatment dates.

In the fall of 2015 and 2016 all cones were counted on the treatment and control trees for the 34 clones and five cones per tree were randomly selected to further investigate the seed yield per cone. All cones collected to date represent 'untreated' yields and the 'GA treatment' harvest will be completed in the fall of 2017. Results were presented on clonal sensitivity to GA, seed and cone yields per clone, conelet development through GA treatments and conelet abortion rates measured on three branches per ramet in the spring and fall of 2016.

FURTHER INFORMATION

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BREEDING NEEM TREE (*Azadirachta indica*) FOR MULTIPLE USES

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The neem tree (*Azadirachta indica*) is an important multipurpose species with enormous potential especially for protection of environment and developing sustainable agriculture and forestry. Individual neem trees exhibit great variation in morphological and chemical makeup. Rural people can easily obtain economic benefits through production of seeds, leaves, and firewood within a short period of time from improved genetic material. Neem can be bred for higher fruit yield with higher amounts of bio-active compounds (limonoids) as well as desired agronomic characters. Higher fruit yield usually related with the production of high amount of biochemical compounds. These compounds are very valuable for producing medicine, pesticides, fungicides, nematicides, cosmetics, animal feed, and organic manure. Agronomic traits such as timber quality, fuel wood, agro-forestry species, shelterbelts, avenue trees, and drought and disease resistance are useful for selection breeding. In this presentation, yield parameters such as provenance variation, cline, physiological, and isozymes variation were reviewed. It is necessary to popularize the cultivation of neem by improved genetic materials to benefits and economic advantages on marginal, degraded, and wastelands through social forestry and commercial plantations. Conservation of the genetic resources of this species is essential for the improvement of its genetic quality and adaptability in ex situ and in situ conditions. Genetic conservation and long term breeding plans were also presented.

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CONSERVATION OF GENETIC RESOURCES

LIFEGENMON: LIFE FOR EUROPEAN FOREST GENETIC MONITORING SYSTEM

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Management and conservation of forest genetic resources need to consider all processes which might affect their genetic variability, especially those influencing the ability of a population to reproduce and regenerate in heterogeneous environments under increasing threats from climate change and other direct and indirect effects of human related activities. The information on actual genetic variation through time can be obtained through genetic monitoring, which serves as an early warning system of a species response to environmental changes at a long-term temporal scale. By genetic monitoring, temporal changes in population genetic variation can be measured by appropriate parameters, contributing to biological conservation. Within the LIFEGENMON (LIFE ENV/SI/000148) project, six partners are testing the suitability of a set of indicators and verifiers for genetic monitoring. For this forest genetic monitoring (FGM), sites for European beech (*Fagus sylvatica*) and silver fir (*Abies alba*) were established in Germany, Slovenia, and Greece. FGM guidelines for these two and five additional species, of different biology, will be developed. A Manual for FGM and a Decision Support System are to be discussed in all transect countries between Germany and Greece, depending on the needs of policy makers and forestry practitioners in the region and wider. The problems encountered within the first three years of the six-year project were presented, as well as approaches for establishment of regional common action plans. Issues related to the identification of FGM objectives and strategies, identification of communication systems with key stakeholders and policy makers regarding FGM, and formation of future action plans to establish a discussion line with policy makers on development and implementation of the FGM system were discussed.

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FOREST GENETIC MONITORING (FGM) APPLIED: FIRST RESULTS FROM TWO FGM SITES IN GREECE

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Recent literature suggests that species demography and genetic diversity have been affected both by climatic oscillations and anthropogenically induced stresses, in a way that future adaptation may be questionable. Moreover, the pace of contemporary environmental change puts a great challenge on forest tree populations and their ability to adapt, taking into account their life history characteristics. As genetic variation is the key component which enables species to adapt sufficiently to new conditions, securing gene conservation in situ is of paramount importance. Tracking and quantifying temporal changes in conserved populations' genetic variation and structure, "forest genetic monitoring (FGM)", can serve as an early warning mechanism for changes that on higher levels (species/ecosystems/landscape) could only be seen later on. FGM baseline data are being developed for two keystone species *Abies borisii-regis* and *Fagus sylvatica* in Greece, as part of a larger network that involves FGM sites in Slovenia and Germany as well, through the European project LIFEGENMON (duration 2014–2020). FGM entails: 1) demographic assessments (age, height, DBH, % filled seeds, % germination, regeneration abundance) and 2) genetic analyses, involving two cohorts, mature trees, and regeneration, which has been carried out by multiplex PCR of 11 fluorescent SSR primers. Initial FGM results were presented and discussed in light of the second assessment that will be carried out by the end of the project. The temporal progression of demographic and genetic diversity values is the main integral part of FGM and is expected to enhance forest genetic resource conservation and assist forest management, leading to the development of a comprehensive FGM strategy.

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LIFEGENMON website: http://www.lifegenmon.si/

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ADAPTIVE CAPACITY AND CLIMATE REFUGIA FOR INTERIOR *Pinus albicaulis*

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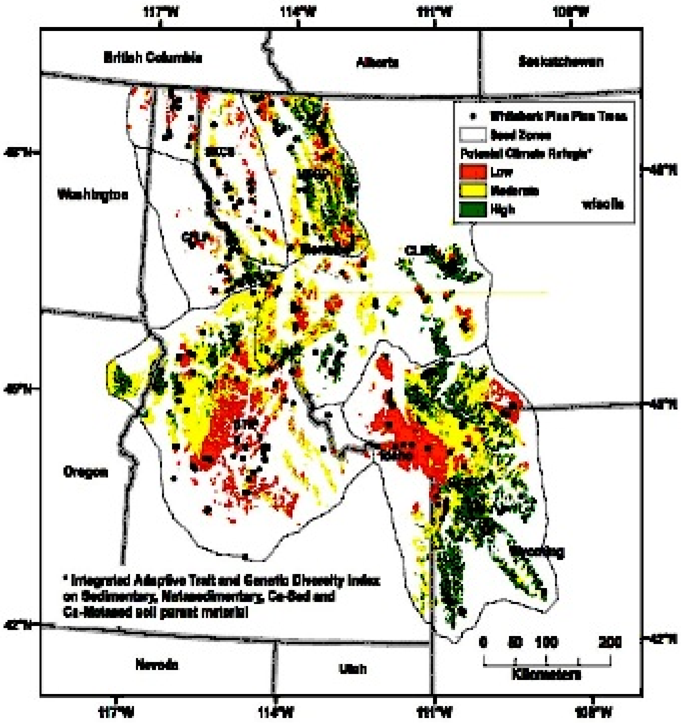
Refugia have long been studied from the paleontological record to better understand how populations persist during periods of unfavorable or rapid environmental change. These concepts are now being applied to contemporary plant populations to identify potential areas buffered from climate change. Here we characterize the adaptive capacity of several key traits impacting this species' ability to survive in the context of associated physical and climatic parameters favoring the long-term persistence of interior *Pinus albicaulis*. Spatially explicit layers of white pine blister rust (*Cronartium ribicola)* resistance, drought tolerance, late winter cold hardiness, and genetic diversity are integrated to identify buffered locations that possess desirable genetic attributes. A filter for suitable substrates is subsequently applied, as plant populations are known to retract to limestone, ultramafic, and podosols during rapid environmental change. Model validation includes downscaled future climatic grids and two representative concentration pathways (RCP 4.5 and 8.5) for areas experiencing ≤ 1° C change in mean annual temperature and ≤ 10% change in precipitation in the form of snowpack. Wilderness areas are widely held as germplasm repositories for plant populations. While an average of 85% of present day *P. albicaulis* occurs in designated wilderness, our results indicated less than one-third of projected climate refugia are located within the boundaries of these unmanaged areas. These findings have far-reaching implications for prioritizing areas for conservation and active restoration if *P. albicaulis* is expected to provide a valuable food source for dependent wildlife and continue to function as both a foundation and keystone species.



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ASSESSING RANGE-WIDE GENETIC DIVERSITY AND STRUCTURE IN SUBALPINE LARCH (*Larix lyallii*)

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Subalpine larch (*Larix lyallii*) is a deciduous conifer that only grows at timberline in the Cascade Range and Rocky Mountains of the Pacific Northwest. Predicted climate change could further reduce available habitat by increasing the frequency of late-summer drought events and/or by encouraging the upward migration of more competitive timberline species. To cope with its changing environment, subalpine larch will be required to adapt in situ or face maladaptation and eventual decline. Unfortunately this species may not be particularly adaptable. Demographic factors such as a relatively long generation time (average 500 years) and late arrival at sexual maturity (100 – 200 years) will slow adaptation. Low levels of genetic diversity could further limit the magnitude of a potentially adaptive response to selection. To assess the amount of genetic variation within populations and the structure of that variation across the landscape, 62 populations distributed across the species' natural range were sampled. Individuals were genotyped using single nucleotide polymorphisms (SNPs) identified via restriction enzyme associated DNA sequencing (RADseq). Subalpine larch has low genetic diversity, most likely due to a northward post-Pleistocene range expansion via successive founder events. Elucidating patterns of genetic diversity in this species will allow for the identification of genetically unique populations that should be prioritized for future conservation efforts.

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ECOLOGICAL GENETICS AND GENOMICS

DO LONG-TERM PROVENANCE TRIALS AND RAPID GENOMIC APPROACHES PAINT THE SAME PICTURE OF CLIMATE ADAPTATION?

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Provenance trials provide valuable information on variation among populations in long-term survival and growth and the extent of local adaptation to climate for designing assisted gene flow. However, they are expensive to establish and can take decades to deliver good information. Existing provenance trials often do not sample a wide enough range of populations or include sufficiently warm environments to approximate future conditions. As an alternative to provenance trials, the AdapTree Project used genomic tools and short-term common garden experiments (Liepe et al. 2016) to evaluate the patterns and strength of local adaptation in lodgepole pine (*Pinus contorta*) and interior spruce (*Picea glauca, P. engelmannii* and their hybrids) by analyzing hundreds of natural populations across Alberta and British Columbia. Custom ~50K SNP arrays were developed for both lodgepole pine and interior spruce based on candidate genes and SNPs from sequence capture (Suren et al. 2016). These were used to genotype thousands of trees per species and to analyze genotype-environment associations with climatic and geographic variables. Climatic drivers of local adaptation identified from genomic associations were compared to 20-year provenance trial results for lodgepole pine and 10-year results for interior spruce. The strength and relative importance of different temperature and moisture variables for local adaptation were highly correlated between provenance trial and genomic analyses. Lodgepole pine is predominantly locally adapted to the severity and timing of low temperatures, while interior spruce is adapted to both low temperatures and precipitation that falls as snow. Results indicated that genomic approaches can rapidly characterize climate adaptation patterns in widespread tree species.

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LACK OF THERMAL ACCLIMATION OF NEEDLE RESPIRATION AND PHOTOSYNTHESIS OF TWO WHITE SPRUCE SEED SOURCES TESTED ALONG A REGIONAL CLIMATIC GRADIENT

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Knowledge about the thermal acclimation potential of physiological processes of boreal tree species is important to: 1) determine the ability to adapt to predicted global warming, 2) assist reforestation decisions under a changing climate, and 3) reduce the uncertainty regarding forest ecosystem-climate change feedback on a global carbon cycle. In the present study, we measured the temperature responses of net photosynthesis (A_n), its biochemical and biophysical limitations, and dark respiration (R_d) in needles of two white spruce (*Picea glauca*) seed sources (from south and north of the commercial forest zone) growing on nine sites along a regional climatic gradient of 5.5°C in Quebec. The aim of this work was to examine the extent of thermal acclimation of A_n and R_d in response to latitudinal and seasonal variations in growing conditions. The average optimum temperature (T_{opt}) for A_n was 19±1.2°C and was similar among plantation sites. Maximum potential electron transport rate (J_{max}) peaked at 28°C and maximum carboxylation capacity (V_{cmax}) at 32°C. A_n was nevertheless limited by V_{cmax}. A_n varied significantly among sites and was quadratically related to mean July temperature (MJT). The rate of change in R_d, due to an increase of 10°C (Q_{10}), did not show any significant relationship with site temperature and averaged 1.5±0.1. Thermal responses of the two seed sources to latitudinal and seasonal variations under natural site conditions were similar. Our results showed a lack of evidence for respiration and photosynthetic thermal acclimation, which may constrain the growth of white spruce in warm conditions at current atmospheric CO_2 concentration.

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IDENTIFYING ADAPTIVE VARIATION IN LODGEPOLE AND JACK PINE: OUTLIER DETECTION ACROSS METHODS AND LANDSCAPES

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Lodgepole pine (*Pinus contorta*) and jack pine (*P. banksiana*) are two economically and ecologically important tree species that hybridize in western Canada in an area of recent mountain pine beetle (*Dendroctonus ponderosae*) range expansion. To better understand the potential response of these forests to mountain pine beetle outbreak we aim to identify genetic regions that have adaptive potential. Results of empirical and simulation studies using large scale genomic data suggest cumulative information from different outlier tests, followed by validation using additional populations as a means to identify good adaptive candidates. Adopting this approach, we aimed to validate 16 loci that were previously identified as candidates in lodgepole and jack pine (Cullingham et al. 2014). Over 800 individuals were typed at 87 SNP loci (including the 16 candidates) from 58 locations across the species ranges. We used both frequency (ARLEQUIN, BAYESCAN, LFMM) and correlation based (BAYENV) methods to identify candidate loci similar to our previous analysis. We were able to validate eight of the 16 candidate loci, however, only three of these loci were identified across multiple methods. The identification of the three candidates using a different pool of samples suggests these loci have signals consistent with adaptive markers. Annotation of these loci suggests they may play a role in tree response to pathogens. To further validate these loci, we will continue exploration using in-depth, gene-level analyses including phenotypic information.

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EXOME GENOTYPING AND ASSOCIATION GENETICS OF QUANTITATIVE TRAITS IN CLONALLY TESTED LOBLOLLY PINE POPULATIONS (*Pinus taeda* L.)

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Loblolly pine (*Pinus taeda*) is one of the most widely planted and commercially important forest tree species in the USA and worldwide. However, whole genome resequencing in loblolly pine is hampered by its size and complexity. Additionally, the genetics underlying quantitative traits of loblolly pine remains to be discovered. As a valid and more feasible alternative, entire exome sequencing was hence employed to identify gene-associated single nucleotide polymorphisms (SNPs) and to genotype the 375 tress in a clonally tested loblolly pine population. Adaptive and growth traits were also measured and analyzed on this population. The exome capture efficiency was high. We found that linkage disequilibrium (LD) decayed very rapidly within this population. Two main distinct clusters, representing western and eastern parts of the loblolly pine range, were demonstrated by the population structure analysis using unlinked SNPs. Over 2.8 million SNP markers were used to test for single locus associations, SNP-SNP interactions, and correlation of individual heterozygosity with phenotypic traits. Genetic correlations between traits as well as geographical variation exist within this population. A total of 36 SNP-trait associations and 11 SNP-SNP interactions were found for quantitative traits. Non-additive effects imposed by dominance and epistasis compose a large fraction of the genetic variance for the quantitative traits. Candidate genes that underlie these traits have a wide spectrum of functions. The multiple effects that influence the performance of loblolly pines identified in this study provide great resources for understanding the genetic control of complex traits, and have potential value for breeding through maker assisted selection and genomic selection.

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OPERATIONAL TREE IMPROVEMENT

REALIZED GAIN TRIALS IN COASTAL DOUGLAS-FIR: 20-YEAR RESULTS

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Estimated and predicted genetic gain estimates can be verified and confirmed through the use of realized genetic gain trials. Realized gain trials usually are area-based test plantations with trees of estimated genetic quality growing together in large blocks to forecast yield improvements over unselected (unimproved) trees. In coastal Douglas-fir (*Pseudotsuga menziesii* var. *menziesii*), one of the most important timber species in British Columbia, there are realized gain trials on 5 sites of varying site quality. Each test site has trees with an expected genetic gain of 18% (expressed as tree volume at rotation age), 10% gain, and 0% gain, planted in 12x12 tree square blocks at four different planting spacings (densities). These three genetic gain classes are referred to as top cross (TC), mid-gain (MG), and control (CON). In general, TC trees produced the highest volume with MG trees being intermediate at age 20 across all spacings and sites. Mortality was highest at the tightest spacing as inter-tree competition started to express itself. Forecasting the results to expected gains at age 60 showed that estimated gains will be achieved, if not exceeded. These tests are also a valuable asset to conduct studies in forest health, wood property evaluations, and remote sensing (Lidar) verifications.

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A TALE OF TWO SERIES:
LATITUDINAL EFFECTS ON ASPEN GROWTH IN ALBERTA

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Two aspen (*Populus tremuloides*) clone trial series were established on the same three sites in northwestern Alberta in 2002, using a similar field design. The test sites were located near Manning at 56.8°N, Grovedale at 55.1°N, and Drayton Valley at 53.4°N. Two different sets of source-identified clones were vegetatively propagated in separate nurseries and tested on the same three sites. Clonal materials were collected over a latitudinal range of six degrees from 53.0°N to 59.0°N in northern Alberta and northeastern British Columbia. A total of 79 clones was tested in the G814 series and 39 clones in the G813 series, but not all clones were represented on all sites. The presentation examined the effect of latitudinal transfer on growth and genetic parameters.Variance component analysis was used to partition environmental and genetic contributions to total phenotypic variation. Mixed model analyses were used to calculate broad-sense heritability and type B correlations. While there were clear provenance differences in aspen growth response in relation to latitudinal transfer, there was also a very large amount of clonal variation within populations. Volume gains in the order of 30 to 40% are achievable from clone selection within populations. Broad-sense heritabilities at age 11 or 12 years averaged around 0.5, but much larger percentage gains are possible for volume (39%) than for height (10.5%), given the higher variance levels in this trait. Almost all of the top selections originate to the south of the test sites. These two clone trial series can be viewed as replicate experiments. While they tell a similar story, their differences are attributable to the different populations sampled, nursery effects, and possible differences in response to latitudinal transfer.

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IS HYBRID VIGOUR POSSIBLE IN NATIVE BALSAM POPLAR BREEDING?

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Poplars (*Populus*) are the most widespread deciduous trees in Canada's boreal forest, covering a total of 13.1% of the boreal region, and are second only to spruce (47.3%) in total area covered. Hybrid poplars occur both naturally and artificially and result from crossing two (or more) distinct species or two individuals within one species with desirable characteristics. Hybrid vigour, typically achieved through controlled crossing of two species, or pure genetic lines of the same species, has long been exploited in agriculture and in some tree species including *Populus*. When two or more species are crossed to produce hybrid progeny, some of them can be expected to yield growth performance far superior than either parent (i.e., hybrid vigour/heterosis).

In this project, we tested the hypothesis that within-species breeding of widely spaced populations of balsam poplar (*Populus balsamifera*) will lead to the expression of hybrid vigour. We explored the potential underlying mechanisms through both field and greenhouse assessments. In September 2009, three field trials (two in Alberta (AB) (Field 7 and 23) and one in Quebec (QC) (Field QC)) were established in conjunction with Alberta-Pacific Forest Industries Inc. (Al-Pac) and Mr. Pierre Périnet (Ministry of Forestry, Quebec). Five male parents from each province with five female parents from Quebec and four female parents from Alberta were used for breeding, both for within region and between region crosses. Preliminary analysis of 6-year height and diameter from the Alberta field sites only, indicated differences in family performance among the different cross-types. In addition, the preliminary results showed that AB x QC crosses ranked first for height and DBH and exhibited later bud-burst. Clones were selected, based on growth performance in the field trials, for a greenhouse trial carried out in summer 2016. Trees were grown in a randomized complete block design under near-optimal greenhouse conditions from May 2016 to August 2016. Diameter and height growth were measured biweekly and photosynthesis three times during the growing season. In late June, internode tissue samples were collected from 2–3 trees from each cross and each parent for hormone analysis (gibberellic acids, indole-3-acetic acid, and abscisic acid.These hormones will tell us if enhanced growth (hybrid vigour) is correlated with hormone levels and linked to photosynthetic performance.

Overall, the above approaches will determine the potential of using disparate, native populations of balsam poplar to produce superior progeny with enhanced stem growth traits. Future use of this material on Crown land for reforestation or reclamation may require additional field testing to meet policy regulations.

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TREE IMPROVEMENT IN CANADA – PAST, PRESENT AND FUTURE

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Canada has a long history of tree improvement starting with shelterbelt species in the prairies in the early 20th century leading to high yielding breeding programs for economically important tree species today. This review summarized the past, present, and anticipated future state of tree improvement by province and highlighted objectives, management, and productivity associated with these programs. We also attempted to connect breeders and researchers across Canada in order to facilitate inter-provincial collaborations on important issues in forestry and reforestation such as climate change, forest health, seed transfer and research.

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ADAPTATION TO CLIMATE

SEED TREK: THE NEXT GENERATION

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A well designed seedlot selection system is central to the maintenance of healthy and productive forest plantations, particularly in an era of rapidly changing climates. Opportunities for improving the effectiveness and efficiency of seedlot selection in British Columbia are provided by new technologies, analysis techniques, and genetic data. We proposed a climate-based system of seed transfer that is expected to better match seedlots to planting sites using new transfer functions to identify biogeoclimatic ecosystem classification subzone variants where each seedlot is anticipated to grow well. The system also: 1) facilitates the use of assisted migration to reduce climate change impacts to forests, 2) allows for wider seedlot deployability and flexibility, 3) increases ease of use, 4) simplifies system updating, 5) quantifies adaptation of seed source options to improve seed source deployment, and 6) integrates with other natural resource management decision support tools.

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CAN CLIMATE NICHE MODEL PREDICT AMONG-POPULATION VARIATION IN FOREST TREES?

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Climate niche models, also called bioclimate envelope models, have been widely used to define climate niches (or bioclimate envelopes) and project their shifts in future climates for tree species or forest ecotypes. However, knowing the climate niche at a species level is often not adequate for the development of forest management strategies for adaptation to climate change. Provenance trial-based population response functions and transfer functions have been used to consider among-population variation existing within many forest tree species. The limiting factor is the lack of provenance trials for many tree species. Can climate niche models help? To explore such a possibility, we used lodgepole pine (*Pinus contorta*), a model species for genecology studies, to examine a spectrum of climate niche models and related their output to growth potential observed and the output of population-based response functions. We have found that some of our results are encouraging, but it is critical to select the right model and to optimize the modeling process.

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PROTECTING LOCALLY ADAPTED GENETIC DIVERSITY OF ALBERTA'S NATIVE TREE SPECIES

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Genetic diversity is the basis of biodiversity, and the adequate availability of diverse genetic resources can help species adapt to ecosystem change such as climate change. The protection of genetic resources is therefore an important aspect of biodiversity conservation. One of the most widely used methods for protecting species and their genetic diversity is the use of in situ reserves, but such reserve systems are not necessarily designed to capture genetic diversity of species. We conducted a conservation gap analysis for the province of Alberta, in which we useed ecological sub-regions as proxy for genetic population differentiation of native tree species to assess the effectiveness of the current reserve system. The analysis was based on synthesizing forest inventory data, forest inventory plot data, high resolution satellite data, and species distribution modeling to infer missing data. Overall, approximately 14.7% of Alberta's trees are currently located within protected areas. However, all but one species have one or more genetic populations that are currently considered inadequately protected. The long-term conservation goal will be to reduce the number of unprotected populations for each species, by identifying potential areas for new reserves that may address these conservation gaps. In the design of new reserves, priority will be placed on species with low representation, high vulnerability to ecosystem change, or high numbers of unprotected genetic populations.

FURTHER INFORMATION

Project website: https://sites.ualberta.ca/~sekely/

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WATER USE EFFICIENCY MEDIATED THE PHOTOSYNTHESIS ABILITY OF TWO PINE SPECIES AND THEIR HYBRIDS IN RESPONSE TO WATER AVAILABILITY

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In Alberta, drought stress is a factor compromising the growth potential and survival in lodgepole pine (*Pinus contorta* var. *latifolia*). Hence, understanding its genetic variation in drought resistance in the region and matching it to environmental conditions at the seed source is of paramount importance. Furthermore, lodgepole and jack pine (*Pinus banksiana;* a more drought resistant species) hybridize in Central Alberta, and the effects of introgression in drought resistance traits are unknown. A main mechanism of drought resistance in pine species relys on rapid stomatal closure in response to water scarcity. However, this strategy severely reduces gas exchange and carbon fixation hindering the production of photosyntates for other functions. Therefore, trade-offs between fast stomatal closure and growth or defense production are expected. To minimize such trade-offs pines require a highly efficient and dynamic hydraulic system that can rapidly adjust to water availability, and genetic variation is expected both among and within species in Alberta. Six lodgepole, five jack, and six hybrid (lodgepole x jack) half-sib families were selected based on a latitudinal gradient in Alberta and subjected in a greenhouse experiment to three contrasting treatments of water withholding following re-watering during nine weeks. Gas exchange, growth, and monoterpene composition were monitored during the experiment. Jack pine families showed increased net photosynthesis when water was available but reduced it relatively more than lodgepole and hybrid families when water became scarce. Lodgepole and hybrid families sustained net photosynthesis under drought conditions by increasing WUE. Hybrids showed similar net photosynthesis as compared with pure lodgepole pine under drought, but were intermediate between pure pine species when water was available. Hybrid families showed promising results for selecting families with high growth potential while maintaining the ability to cope with drought.

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ADAPTATION OF WHITE SPRUCE TO CLIMATE: COLD HARDINESS AND LONG-TERM FIELD PERFORMANCE

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Under expected climate change, the health and productivity of our forests will face a great risk and human intervention might be necessary to help its adaptation. Assisted migration has been proposed as a tool to help this adaptation but a deeper knowledge of different species' adaptation to climate is needed to implement it effectively. In this study, we tried to find a relation between climate, tree physiology, and performance in the field. We worked in a 33-year-old provenance trial in central Alberta with 10 provenances from a wide range of white spruce (*Picea glauca*) distribution in Canada. We recorded height and mortality in the field and measured different anatomical, hydraulic, and cold hardiness variables trying to find a relation between climate adaptation and performance in the field. Local provenances showed the best performance in terms of height (10.8 m) and survival (95%) but we observed interesting tradeoffs between survival and growth in the more extreme regions, with northern provenances having better survival (94% but 4.9 m height) and southern provenances better growth (10.3 m but 80% survival). Survival at the site was clearly related to cold hardiness while growth was mostly related to the length of the growing season in the climate of origin. These results suggested a potential of southern provenances having increased productivity with better use of an extended growing season under climate change, but good synchrony with frost events seems to be key for good survival in the field.

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DIFFERENCES IN STABLE CARBON ISOTOPE CONTENT OF WHITE SPRUCE (*Picea glauca*) POPULATIONS IN ALBERTA

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In Alberta, white spruce (*Picea galuca*) exhibits clinal genetic variation for growth-related traits. This pattern of variation is consistent with the geography and a complicated topography, which determine the pattern of climatic variation in the province. The current challenge in forest management is guiding seed transfer to maintain adaptation and forest productivity in the interim while adapting to a changing climate for long-term forest sustainability. This prompted us to explore different options of identifying populations that are potential seed producers for reforestation in a warmer and drier climate.

We studied ^{13}C content of ten populations of white spruce originating from a large geographic area (52°33' – 59°53'N and 110°13' – 119°40'W), elevation (180 – 1341 m), and climate (degree days < 0°C = 1310 – 3004; degree days >5°C = 952 – 1382). Wood cores, extracted from selected trees of these populations on two test sites, provided samples for ^{13}C analysis during the driest year identified by the width of the growth rings and for the entire 24 years of tree life in the field. Populations differed significantly ($P < 0.05$) on individual sites and across sites. At the Hay River site near High Level, ^{13}C content was correlated more with diameter at breast height ($r = 0.54 – 0.89$) than height growth. At Hangingstone near Fort McMurray, the correlation of ^{13}C with height and diameter growth was generally low. On both sites, ^{13}C was more correlated ($r = 0.49 – 0.89$) with growing season temperatures such as degree days > 5°C, warmest month temperature and frost-free period. In conjunction with other biological and climatic indicators, this study will supplement our knowledge on how tree populations respond to environmental stresses and use this information to plan for and adapt managed forests to a changing climate.

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POSTER ABSTRACTS

GENETIC PARAMETERS OF MARITIME PINE RADIAL GROWTH DURING A SPECIFIC DROUGHT EVENT

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The main selection criteria of the French maritime pine (*Pinus pinaster*) breeding program are growth at 12 years old and stem straightness. Scenarios of climate change, forecast an increase in frequency and intensity of droughts in southwestern France where maritime pine plantations are currently established. In that context, a key issue for breeding is to be able to evaluate growth in future climatic conditions characterized by low precipitation during the growth period.

A maritime pine genetic trial was established 19 years ago on two contrasting sites (humid and dry) with half-sib families. One hundred-fifty high resolution dendrometers were installed on trees of 25 families selected to represent a large range of growth performance (based on growth data collected at 12 years old). Radial growth was measured every hour during two successive years. The two years (2015 and 2016) were characterized by contrasting climate (dry spring in 2015 and wet spring in 2016). Soil moisture and climatic data were also recorded on this trial during the same period.

Genetic analyses (estimation of genetic parameters and GxE interactions) were carried out on radial growth data related to short periods of time (few weeks) selected either for a low or high precipitation level. This methodology allowed us to estimate the genetic variability for growth in dry versus wet conditions and to identify genotypes best adapted to future climate.

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TRANSCRIPTOME OF YELLOW-CEDAR (*Callitropsis nootkatensis*) DURING SEED STRATIFICATION AND GERMINATION

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Yellow-cedar (*Callitropsis nootkatensis*) is a culturally, economically, and environmentally significant species in the North Pacific coastal rainforest between California and Alaska. Deep dormancy and poor germination rates of seeds in this species favor the costlier use of rooted cuttings for commercial propagation. To expand the sequence resources for this conifer, and to explore the expression of transcripts potentially involved in seed development, dormancy, and germination, we collected tissues for RNAseq from seeds of first year developing cones, and from dry, imbibed, stratifying, and germinating seeds. Over 252 million high-quality paired-end reads were generated, which were *de novo* assembled into 734,006 contigs (ranging from 300–43,112 nt) with an N50 of 814 nt. This assembly was explored for various gene families, pathways, and processes, including the regulon and interactome of ABI3 (ABSCISIC ACID INSENSITIVE3), a component of the abscisic acid (ABA) signal transduction pathway, which plays a major role during seed development and dormancy.

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IN THE RIGHT PLACE: HABITAT SUITABILITY MODELS FOR ENDANGERED WHITEBARK PINE AND LIMBER PINE TO SUPPORT RECOVERY AND MANAGEMENT

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High quality forest inventories delineate polygons with species presence, density, and productivity attributes, but typically focus on merchantable species and operable forest areas, with sparse data for other species and habitat types. For endangered whitebark pine (*Pinus albicaulis*) and limber pine (*P. flexilis*) , species-specific habitat mapping and modeling are urgent goals in pending federal and approved provincial recovery plans. Adapting methods developed for Waterton Lakes National Park, habitat suitability was modelled for 310 townships where empirical data were available. These townships encompass both species' Alberta ranges with the exception of National Parks which were mapped under separate initiatives. The habitat suitability models for both species were based on the following parameters: elevation, topographic position, slope, aspect and, where LiDAR data were available, canopy height. SPOT imagery was classified within areas identified as potential habitat to further refine the results. Moderate and high suitability habitat polygons were predicted for whitebark pine. Limber pine data only supported reliable predictions of high suitability habitat. Models were validated by reverse engineering and by checking presence and absence records with independent empirical data. Mesotopographic ridge model definitions and aspect had slight discrepancies in predicted suitability. Point accuracy for the species by resolution combinations averaged across townships was good, up to 87%. Field verification will be essential for due diligence, as these species are bird-dispersed, poor intraspecific competitors, and whose site specific occurrence is influenced by other factors that could not be modelled. The approach represents a significant improvement over previous mapping, providing enough accuracy and detail to support management decisions and effectively prioritize areas, regions, and some stands for recovery actions.

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PRODUCTIVITY AND ADAPTATION OF SELECTED POPLAR (*Populus* spp.) CULTIVARS UNDER CLIMATIC CONDITIONS OF POLAND

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Ten poplar cultivars used commercially in Europe in short-rotation forestry systems were tested to compare their productivity and adaptation to the climatic conditions of Poland. An additional objective was to assess the potential of selected cultivars to incorporation of carbon from atmospheric CO_2 into woody biomass. We tested the fallowing poplar cultivars: 'AF-8', 'AF-6', 'AF-2', 'Monviso', 'Albelo', 'Degrosso', 'Polargo', 'Koster', 'Fritzi Pauley', and 'NE-42'. The study was carried out on 7-year-old trees. The following variables were measured: diameter at breast high (DBH), height, survival rate, single-tree fresh and dry mass, biomass production, and the proportion of organic carbon in woody biomass.

The 'NE-42' and 'Fritzi Pauley' cultivars showed the best growth characteristics (DBH and height) and highest biomass production (from 5.7 to 9.5 t dry mass ha^{-1} yr^{-1}; and from 6.3 to 10.8 t dry mass ha^{-1} yr^{-1}, respectively). Data for the 'AF-6' and 'MON' cultivars were not analysed because of their cold-tenderness and high mortality. Of the eight cultivars analysed, 'AF-8' had the poorest growth parameters producing approximately 3 t dry mass ha^{-1} yr^{-1}. The proportion of organic carbon in woody biomass was very similar for all investigated cultivars and amounted to around 49%. For this reason, the incorporation of carbon into biomass is limited directly by yield, which in our study was the highest for the 'NE-42' and 'Fritzi Pauley' cultivars. Furthermore, our results indicated the importance of testing cultivars under local climatic conditions before planting on a commercial scale.

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WHITE SPRUCE WOOD QUALITY IN ALBERTA BREEDING REGIONS D1, H AND I

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The majority of tree improvement (TI) programs focus on the improvement of growth and yield where increased stem volume is the pursued characteristic. Unfortunately, increased volume growth rate in white spruce (*Picea glauca)* is negatively correlated with key wood quality traits, including wood density (WD), modulus of elasticity (MOE), and modulus of rupture (MOR). White spruce represents 30% of Alberta's forests and is utilized as a feedstock in the manufacturing of several important products, most notably dimensional lumber and pulp. Compromised wood quality through TI practices could lead to potential declines in white spruce utilization if wood characteristics no longer meet the needs of industry. For example, diminished loading capacity of white spruce lumber caused by a decrease in WD (and subsequently MOE and MOR) may lead to compromised quality for structural applications. Three TI programs were selected for study (D1, H, and I), each representing distinct geographic regions and forest types in Alberta over 11 progeny trials. Family breeding values for height, calculated from data provided by Alberta Agriculture and Forestry, ANC Timber, Hinton Wood Products, Millar Western Industries, West Fraser, and Weyerhaeuser Pembina, will be used to select families to be assessed for WD using a combination of increment coring, Resistograph, and Pilodyn measurements. The purpose of this study is to determine the effects and trade-offs of selecting for increased volume growth rate on wood density and to select desirable families to utilize within Alberta's TI programs. Preliminary results are expected summer 2017.

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DROUGHT TOLERANCE AND GROWTH OF POPULATIONS IN A WIDE-RANGING TREE SPECIES INDICATE CLIMATE CHANGE RISKS FOR THE BOREAL NORTH

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Choosing drought-tolerant planting stock in reforestation programs may help adapt forests to climate change. To inform such reforestation strategies, we tested lodgepole pine (*Pinus contorta* var. *latifolia*) population response to drought, and inferred potential benefits of a northward transfer of seeds from drier, southern environments. The objective was addressed by combining dendroecological growth analysis with long-term genetic field trials. Over 500 trees originating from 23 populations across western North America were destructively sampled in three experimental sites in southern British Columbia, representing a climate warming scenario. Growth after 32 years from provenances transferred southward or northward over long distances was significantly lower than growth of local populations. All populations were affected by a severe natural drought event in 2002. Provenances from the most southern locations showed the highest drought tolerance but low productivity. Local provenances were productive and drought tolerant. Provenances from the boreal north showed low productivity and poor drought tolerance on southern test sites, implying that maladaptation to drought may prevent boreal populations from taking advantage of more favorable growing conditions under projected climate change.

FURTHER INFORMATION

Montwé, D.; Isaac-Renton, M.G.; Hamann, A.; Spiecker, H. 2016. Drought tolerance and growth in populations of a wide-ranging tree species indicate climate change risks for the boreal north. Global Change Biology 22: 806–815.

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USING THE LEGACY OF PAN-CANADIAN PROVENANCE TESTS: TREE RING ANALYSES AND ASSOCIATION GENETICS FOR STUDYING SENSITIVITY TO CLIMATE

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Climate change is already impacting growth of Canadian forests and the negative effects of climate extremes are expected to increase in the near future. More insights are needed to better understand the sensitivity to climate of seed sources and to estimate their adaptive capacity in order to guide forest management and breeding strategies. To address these questions, we propose to combine dendroecology and genomic approaches, and present results from ongoing analyses in eastern white pine (*Pinus strobus*) (EWP), white spruce (*Picea glauca*) (WS), and black spruce (*P. mariana*) (BS). A comprehensive database representing increment cores from more than 2000 trees from 6 provenance trials in Quebec and Ontario (1 EWP, 3 WS, and 2 BS) is under development. To evaluate sensitivity to specific climatic constraints, the relationships between annual growth variability assessed from tree rings and climatic variables were investigated. Our first results showed contrasting adaptation strategies for the three species. In EWP, sensitivity to summer drought and to spring/autumn frost varied clinally along the mean annual temperature of provenances, indicating local adaptation. More genes were associated with these new climatic sensitivity traits than with classical growth traits (tree diameter and height), highlighting their importance for studying adaptation to climate in conifers. WS also showed among-population differentiation for growth and wood traits, but this could not be related to differential sensitivity to climate across the species eastern range. WS populations showed rather high plasticity to climate. Overall, site conditions such as site fertility and growing season length appeared to be the major driver of among site differences. BS on the other hand showed sensitivity to summer drought which was especially true for eastern seed sources. Provenance trials established by the Canadian Forest Service in the 1960s and 1970s now represent an invaluable resource for evaluating climatic sensitivity of seed sources and to study its genetic basis. Our findings will help to better mitigate risks arising from climate change and support the long-term quality and quantity of fibre production.

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ASSESSING THE INTRASPECIFIC INTERACTIONS AMONG SIX DIFFERENT PROVENANCES OF ASPEN BASED ON A STRESS GRADIENT HYPOTHESIS

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The Stress Gradient Hypothesis (SGH) is used to understand the facilitation and competition among plant communities. The basic idea of the SGH is that facilitation among plants increases under high physical stress (high temperature, drought, etc.). However, most of the research studies in the past have used SGH to understand the facilitation and competition interspecifically. Plant-plant interactions are recognized as important factors in determining the response of species communities to climate change. Here we are proposing a study to understand the intraspecific interactions among plants using SGH. This research study was conducted at Athabasca, central Alberta (54°53' N, 113°18'W) using six different aspen provenance seedlots: ABf (Alberta Foothill), BC (British Columbia), cAB (Central Alberta), MN (Minnesota), nAB (Northern Alberta), and SK (Saskatchewan). Data were collected for plant height, diameter at breast height (DBH), and root collar diameter (RCD) from 2002 to 2005 and 2008 and was correlated with mean annual temperature and rainfall. Repeated measures one-way ANOVA revealed that provenance MN yielded the highest overall plant height and DBH. However, under stress conditions, northern sources performed unexpectedly well even though the stress environments differ from their local environmental conditions. The best performers, including MN, show a disproportionate collapse in their annual growth.

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IMPROVING SEED QUALITY AND GENETIC DIVERSITY IN NATIVE BOREAL RECLAMATION SPECIES

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Alberta has been regularly storing non-tree seed used in reclamation since 2010, reflecting a significant increase of reclamation on Alberta public land. Changes to the Alberta Forest Genetic Resources and Conservation Standards (FGRMS) in 2016 now include regulations for seed collection, storage and deployment of woody shrub species.

However, for many of the reclamation species being collected, little is known regarding germination methods. Not only does this make it difficult to produce plants and maintain high genetic diversity for resilient populations but it also makes quality control nearly impossible. Since some of these species have collection or handling requirements that are different from our economically important tree species in Alberta, it is essential to address these issues and be able to provide feedback to seed collectors and handlers to improve quality and also empower seed owners with more knowledgeable control over their seed and reclamation plans.

The Alberta Tree Improvement and Seed Centre began research on non-tree seeds four years ago starting with hazels (*Corylus* spp.) and the project has developed into a 3-stage process for 14 species: developing chemical viability testing methods (TZ or TEZ), carrying out germination trials with results that combine high genetic diversity with practical and economical methods, and finally conducting comparative longevity tests on each species to determine the approximate lifespans of these seeds in cold storage. As these three stages must be completed in sequence, the project is ongoing and will require years for completion.

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IN SITU QUANTIFICATION OF BLUE STAIN FUNGI IN JACK, LODGEPOLE AND HYBRID PINE

Bianca M. Sacchi*, Chandra H. McAllister, Kate R. St. Onge and Janice E.K. Cooke

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Grosmannia clavigera is considered the most pathogenic fungal associate of the mountain pine beetle (*Dendroctonus ponderosae*). This blue stain fungus contributes to the exhaustion of tree defenses during beetle attack, and serves as a nutrient source for beetles and their offspring following attack. Lesion length has been used as both a measure of fungal pathogenicity and tree defense response. The main objective was to develop a quantitative PCR (qPCR) assay to quantify the amount of fungal DNA within the xylem of *G. clavigera*-inoculated jack (*Pinus banksiana*), lodgepole (*P. contorta* var. *latifolia*), and hybrid pine seedlings. By comparing these qPCR data to lesion lengths measured in each sample, I can determine the degree to which lesion length reflects fungal growth. The amount of fungal DNA in inoculated pine is expected to be low relative to the amount of pine DNA in each sample, necessitating a sensitive and specific method. For this qPCR assay, blocked, cleavable RNase H2 primers were designed specifically against *G. clavigera*, increasing the sensitivity and specificity of the assay relative to previously published nested PCR or qPCR approaches. RNase H2 qPCR primers were also used to quantify the lodgepole or jack pine DNA in each sample, and *G. clavigera* values were normalized against the pine values. The method is well suited to mid- to high-throughput analyses, enabling studies with hundreds of samples. By correlating fungal DNA content to the lesion length data, this study has established a better understanding of how lesion length reflects fungal growth versus tree defense, and thus offers an improved method for evaluating tree resistance to *G. clavigera*.

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DEAD OR ALIVE:
MOLECULAR ASSAYS FOR PATHOGEN DETECTION

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In order to determine if living fungi of phytosanitary concern are present in wood or to evaluate the efficacy of treatments, the method of choice is to grow microbes in petri dishes for subsequent identification. However, some fungi are difficult or impossible to grow in cultures, and thus, to validate the effectiveness of existing and emerging wood treatments, a molecular methodology that can detect living fungi and fungus-like organisms is required. RNA-based molecular diagnostic assays were developed to detect the presence of living fungi and fungi-like organisms of phytosanitary concern. Since RNA represents the transcription of genes and can therefore only be produced by living organisms, it provides a marker to determine if an organism is alive. The assays were designed to target genes that are essential to vital processes, then used to assess their presence and abundance through real-time reverse transcription polymerase chain reaction (PCR). A stability analysis was conducted by comparing the RNA to DNA ratio over treatment time. The results illustrated that for treated samples, DNA remained stable over a period of 10 days post treatment, whereas RNA could not be detected after 24 hours for *Phytophthora ramorum* or 96 hours for *Grosmannia clavigera*. Therefore, this method provides a reliable way to evaluate viability of organisms following treatments and can have profound impacts on assessing both timber and non-timber forest products of commercial value.

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FastTRAC WORKSHOP

PROOF OF CONCEPT OF GENOMIC SELECTION IN TREE BREEDING

Tree improvement practitioners have heard of advanced genetic technologies employed in Brazil and the southeastern United States. Now there is an opportunity to see a practical example of marker systems to assist tree breeding in eastern Canada. *FastTRAC* represents a "proof of concept" for genomic selection in spruce improvement programs from Eastern Canada. Real users are bringing real genetic resources to the development and use of new methods based on genomics.

FastTRAC (Fast Tests for Rating and Amelioration of Conifers) is a three-year project funded by Genome Canada, Génome Québec, and multiple partners through the Genomics Applied Partnership Program (GAPP). The project brings together scientists, tree breeders, foresters, and economists to demonstrate and apply genomic-assisted selection in eastern Canadian tree improvement programs. Project partners will use FastTRAC models to rate candidate trees for productivity and resilience attributes, thereby accelerating the selection and reforestation of improved and adapted stock.

The workshop presented the thrust of *FastTRAC*, its focus on genetic gain through genomic selection in white spruce (*Picea glauca*) and Norway spruce (*P. abies*), the commitment and roles of user-partners, the benefits to be realized, and corresponding resources required (including genetic resources). Economic and financial perspectives covered silvicultural scenarios for cost-benefit analysis, impacts on costs of production, valuation of volume and quality gains, integration of genomic selection with conventional breeding, and analysis of deployment with or without somatic embryogenesis.

The workshop was designed to encourage discussion of questions such as: What would it take to adopt this approach in other breeding programs? What is needed in the field to make use of genomics tools? What might change in approaches to field testing? What genetic resources do we have to work with? What factors might influence business decisions to adopt genomic technologies? What are the economic barriers to adoption, how could they be overcome?

AGENDA

1:00 – 1:00 PM	Welcoming remarks and workshop objectives
1:10 – 1:40 PM	The Project: The implementatiion of Genomic Selection (GS) in conventional tree breeding programs in Quebec and New Brunswick
1:40 – 2:00 PM	Discussion
	● What are the perceived technical obstacles for integration of GS in breeding programs?
	● What is needed to make operational use of genomic tools?
2:00 – 2:25 PM	Financial and economic assessment of the implementation of GS in conventional tree breeding programs
2:25 – 2:50 PM	Discussion
	● What are the perceived factors influencing business decisions to integrate genomic tools into tree breeding programs?
	● What are the perceived financial barriers to adoption?
	● How can they be overcome?
2:50 – 3:00 PM	Concluding remarks

FURTHER INFORMATION

Program website: www.fasttracproject.ca

ATTENDEES OF THE

35th CFGA/ACGF MEETING

John Acorn
University of Alberta
Alberta, Canada

Sally Aitken
University of British Columbia
British Columbia, Canada

Anthonia Anderson
Northern Pulp Forest Nursery
Nova Scotia, Canada

Phil Aravanopoulos
Aristotle University of Thessaloniki
Thessaloniki, Greece

Jaime Sebastian Azcona
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Lahcen Benomar
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Andy Benowicz
Alberta Agriculture and Forestry
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Jean Beaulieu
Université Laval
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Simon Bockstette
University of Alberta
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Jean Brouard
Isabella Point Forestry Ltd.
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Tom Byram
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Emma Derenowski
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Chen Ding
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Forest, Lands and Natural Resource Operations
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Andreas Hamann
University of Alberta
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Chris Hennigar
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