Conference Program & Abstracts

Forest Genetics 2017
Forest Health and Productivity in Changing Environments

June 26-29, 2017 in Edmonton, Alberta
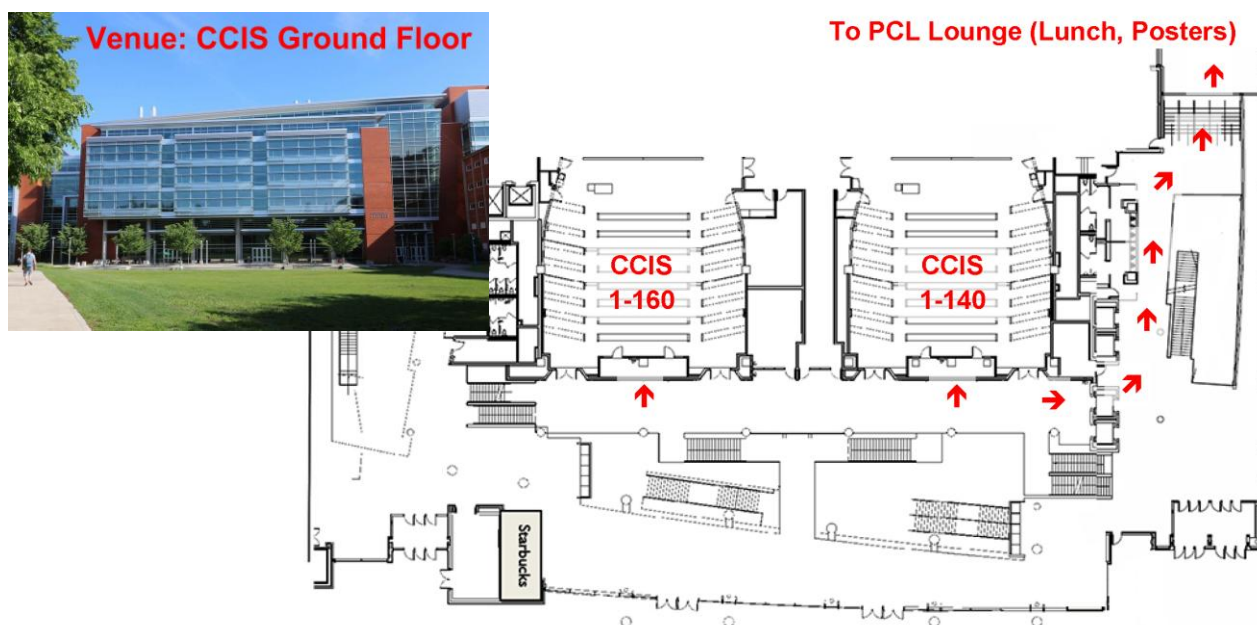
A joint meeting of WFGA & CFGA

Conference Sponsors

Program Overview

Mo (26th)	Tu (27th)	We (28th)	Th (29th)	Fr (30th)
	Breakfast (7:45 am) in PCL Lounge	Breakfast (7:45 am) in PCL Lounge	**Business Meeting WFGA and/or Breakfast**	
	Keynotes 1 & 2 Applied Genomics, Tree Improvement Policy	**Keynotes 3 & 4** Genomics of Pest and Disease Resistance	**Keynotes 7 & 8** Operational Tree Improv, Environmental Genomics	**Post-Conference Trip**
	Coffee Break	Coffee Break	Coffee Break	**Smoky Lake:** guided tours of Alberta Tree Improvement and Seed Centre and Coast to Coast Reforestation, Smoky Lake Forest Nursery, lunch included
	Concurrent Session 1A/B Genomics & Tree Improv., Managing Climate Change	**Concurrent Session 2A/B** Adaptation to Climate, Forest Pest & Diseases	**Concurrent Sessions 4A/B** Ecological Genetics, Operational Tree Improv.	
	Lunch in PCL Lounge	Lunch in PCL Lounge	BBQ Lunch (outside CCIS)	
	Activity #1 - Visit U of A Botanical Garden **Activity #2** - Tours of Lab Facilities at UofA	**Keynotes 5 & 6** Tree Seed Biology, Seed Orchard Management	**Concurrent Session 5A:** Adaptation to Climate **Session 5B:** FastTRAC Workshop	
		Coffee Break	Coffee Break	
Registration PCL Lounge (4-8pm) **Poster Session** (starting 5pm, up until Th 3pm) **Mixer** with cash bar (5-8pm)	**Business Meeting CFGA**	**Concurrent Session 3A -** Tree Seed Management **Concurrent Session 3B -** Conservation Genetics	**Wrap-up session, Awards**	
		Mixer & Banquet (5:30pm) in Faculty Club		

Venue Overview

Venue: CCIS Ground Floor

To PCL Lounge (Lunch, Posters)

CCIS 1-160

CCIS 1-140

Starbucks

Campus & Venue: http://forestgenetics2017.ca/Maps.pdf **General Area:** https://goo.gl/maps/8DG92SbDZ6E2

Forest Genetics 2017: Health and Productivity under Changing Environments. A Joint Meeting of WFGA and CFGA, University of Alberta, Edmonton, AB, June 26-29, 2017.

Monday – June 26

Monday 4–8pm Tuesday 8–11am	PCL Lounge	Registration is open, and posters can be mounted nearby
Monday 5pm – Thursday 3pm	PCL Lounge	Posters on display until Thursday afternoon
5:00 – 8:00 pm	PCL Lounge	Mixer with hors d'oeuvres and cash bar Poster session

Tuesday – June 27

7:45 – 8:30 am   Continental breakfast in PCL lounge

8:30 – 10:10 am, Rm 1-140, Welcome & Keynotes 1 & 2
Moderator: *Janice Cooke*

		Abstract on Page:
8:30 – 8:40 am	Welcome to Forest Genetics 2017 *Andreas Hamann & Deogratias Rweyongeza*	
8:40 – 8:50 am	Opening remarks by Alberta Agriculture and Forestry *Darren Tapp*	
8:50 – 9:30 am Keynote #1	**KN-1. The application of genome-wide information to tree breeding: what is coming next?** *by Matias Kirst*	13
9:30 – 10:10 am Keynote #2	**KN-2. British Columbia's forest genetics program: the top 10 reasons for success** *by Brian T. Barber*	14

10:10 – 10:30 am   Coffee Break

10:30 – 11:50 am, Rm 1-140, 1A – Genomics and tree improvement
Moderator: *Pia Smets*

		Abstract on Page:
10:30 – 10:50 am	**1A-1. Single-step genomic evaluation of simple and complex pedigrees** *by Blaise Ratcliffe, Michael Stoehr, Yousry El-Kassaby*	15
10:50 – 11:10 am	**1A-2. Genomic selection modelling for weevil resistance, wood quality and growth traits in a non-native tree species, Norway spruce (*Picea abies*)** ...	16

	by Patrick Lenz, Simon Nadeau, Marie-Josée Mottet, Martin Perron, France Gagnon, Sylvie Blais, Brian Boyle, Jérôme Laroche, Marie Deslauriers, Nathalie Isabel, Jean Beaulieu, Jean Bousquet	
11:10 – 11:30 am	**1A-3. Pedigree-based and genomic predictions of Norway spruce performance in multiclonal forestry in New Brunswick** *by Chen Ding, Patrick Lenz, Simon Nadeau, Greg Adams, Shona Millican, Marie-Josée Mottet, Jean Beaulieu, Jean Bousquet*	17
11:30 – 11:50 am	**1A-4. Development of a high-density Affymetrix Axiom genotyping array for genomic selection in Douglas-fir** *by Scott E. Kolpak, Keith Jayawickrama, Jennifer Kling, Matt Trappe, Valerie Hipkins, Terrance Ye, Stephanie Guida, Richard Cronn, Samuel A. Cushman, Susan McEvoy, and Glenn T. Howe*	18

10:30 – 11:50 am, Rm 1-160, 1B – Managing for climate change
Moderator: *Miriam Isaac-Renton*

Abstract on Page:

10:30 – 10:50 am	**1B-1. Reforestation for an uncertain future: Do we really need to worry about climate change?** *by Brad St. Clair, Glenn Howe, Dominique Bachelet*	19
10:50 – 11:10 am	**1B-2. Selective breeding for growth in the interior spruce hybrid zone maintains adaptation to climate** *by Ian R. MacLachlan, Sam Yeaman, Sally N. Aitken*	20
11:10 – 11:30 am	**1B-3. Provisional climate-based seed zones for Mexico: guiding reforestation under observed and projected climate change** *by Dante Castellanos-Acuña, Kenneth W. Vance-Borland, J Bradley St. Clair, Andreas Hamann, Javier López-Upton, Erika-Gómez-Pineda, Juan Manuel Ortega-García, Cuauhtémoc Sáenz-Romero*	21
11:30 – 11:50 am	**1B-4. Climate change risk management in tree improvement programs: selection and movement of white spruce and lodgepole pine genotypes in Alberta** *by Laura K. Gray-Steinhauer, Andreas Hamann, Sally John, Deogratias Rweyongeza, Barb R. Thomas*	22

12:00 – 1:00 pm   Lunch in PCL Lounge

1:00 – 5:00 pm   Afternoon activities (buses leave in front of PCL Lounge)

Option #1	University of Alberta Botanical Gardens	Guided tour of themed gardens (e.g. Kurimoto Japanese Garden) and exhibits featuring rare and diverse specimens from around the world. Golf cart based tour for those who prefer to walk less are available. Explore the grounds at your leisure as well as a café and gift shop. • 1:00 Meet at PCL Lounge east-exit for departure on Saskatchewan Drive: http://forestgenetics2017.ca/Maps.pdf • 1:30 pm - Group arrival • 1:45 pm - 2:30 pm - Lee Foote to walk the group to the Aga Khan location, discuss construction and future developments • 2:30 pm - 3:15 pm - Bruce Dancik to speak • 3:15 pm - 3:30 pm - Lee to lead the group through the main garden to the Native Peoples Garden • 3:30 pm - 4:00 pm - Justine to speak about the Native Peoples Garden • 4:30 pm - Group departure • 5:00 pm - Return to UofA
Option #2	University Lab Tours	This is a guided tour of the genetics research laboratories in the Biological Sciences and Renewable Resources Departments of the University of Alberta. • 1:00-1:15 pm Assemble in PCL lounge near Second Cup coffee shop, go to EAS • 1:15-1:35 pm Barb Thomas' lab • 1:45-2:10 pm Mol. Biology Service Unit, CCIS 5-047 • 2:15-2:50 pm The Metabolomics Innovation Centre • 3:00-3:30 pm Biogeochemical Analytical Service Laboratory, CCIS 2-255 • 3:30-4:15 pm LRT • 4:15-5:00 pm Delta Genomics, 10230 Jasper Ave, 4244 Enterprise Square • 5:00 pm + Refreshments

5:00 – 6:00 pm   CFGA Business Meeting, Rm 1-140
Moderator: *Deogratias Rweyongeza*

Wednesday – June 28

7:45 – 8:30 am   Continental breakfast in PCL lounge

8:30 – 10:00 am, Rm 1-140, Keynotes 3 & 4
Moderator: *Barb Thomas*

Abstract on Page:

8:30 – 9:10 am Keynote #3	**KN-3. Assessing trees' adaptive capacity to environmental constraints: from genomic approaches to the development of innovative phenotyping tools** *by Nathalie Isabel, C. Depardieu, M. Girardin, J. Housset, P. Lenz, S. Nadeau, I. Duchesne, J. Bousquet, J. Cooke, I. Ensminger*	23
9:15 – 9:55 am Keynote #4	**KN-4. Confronting emerging pathogens: A genomics empowered approach to protecting forest health** *by Jared M. LeBoldus*	24

10:00 – 10:30 am Coffee Break

10:30 – 11:50 am, Rm 1-140, 2A – Genetic adaptation to climate extremes
Moderator: *Raul de la Mata*

10:30 – 10:50 am	**2A-1. Drought sensitivity of Norway spruce at the species' warmest fringe: quantitative and molecular analysis reveals high genetic variation within and among provenances** *by Silvio Schueler, Carlos Trujillo-Moya, Jan-Peter George, Silvia Fluch, Thomas Geburek, Michael Grabner, Sandra Karanitsch-Ackerl, Heino Konrad, Konrad Mayer, Eva Maria Sehr, Elisabeth Wischnitzki*	25
10:50 – 11:10 am	**2A-2. Characterizing drought tolerant lodgepole pine populations for planting under climate change** *by Miriam Isaac-Renton, David Montwé, Andreas Hamann, Heinrich Spiecker, P. Cherubini, K. Treydte*	26
11:10 – 11:30 am	**2A-3. Records of cold adaptation in tree rings: Seed transfer limits under warming climates** *by David Montwé, Miriam Isaac-Renton, Heinrich Spiecker, Andreas Hamann*	27
11:30 – 11:50 am	**2A-4. What can we learn from tree-ring structure on climate adaptations? A case study from IUFRO-spruce provenance trials** *by Marcin Klisz, Joanna Ukalska, Marcin Koprowski, Paweł Przybylski, Radosław Puchałka, Cristina Nabais, Szymon Jastrzębowski*	28

10:30 – 11:50 am, Rm 1-160, 2B – Forest pests and disease resistance
Moderator: *Catherine Cullingham*

Abstract on Page:

10:30 – 10:50 am	**2B-1. Genetic control of the natural resistance of *Picea glauca* against *Choristoneura fumiferana*** *by Claudia Méndez-Espinoza, Isabelle Giguère, Geneviève Parent, Patrick Lenz, Éric Bauce, John MacKay*	29
10:50 – 11:10 am	**2B-2. Differences in pine resistance to *Dothistroma* needle blight in Alberta at the species, provenance and family levels** *by Andy Benowicz, Deogratias Rweyongeza, Tom Hutchison*	30
11:10 – 11:30 am	**2B-3. Adaptive variation in lodgepole and jack pine population responses to mountain pine beetle fungal associates and abiotic stresses** *by Kate R. St.Onge, Catherine. Cullingham, Rhiannon Peery, Chandra McAllister, Bianca Sacchi and Janice E.K. Cooke*	31
11:30 – 11:50 am	**2B-4. Genetic approaches to identifying western gall rust resistance in lodgepole pine** *by Chandra H. McAllister, Michael Mbenoun, Eden McPeak, Janice E.K. Cooke*	32

12:00 – 1:00 pm   Lunch in PCL Lounge

1:00 – 2:30 pm, Rm 1-140, Keynotes 5 & 6
Moderator: *Deogratias Rweyongeza*

Abstract on Page:

1:00 – 1:40 pm Keynote #5	**KN-5. What do we know about the genetics of seed longevity?** *by Fiona Hay*	33
1:45 – 2:25 pm Keynote #6	**KN-6. Responding to the influence of pests in forestry genetics, seed production, and deployment of improved material** *by Ward Strong*	34

2:30 – 3:00 pm Coffee Break

3:00 – 4:20 pm, Rm 1-140, 3A – Seed biology and management
Moderator: *Simon Bockstette*

Abstract on Page:

3:00 – 3:20 pm	**3A-1. Resin vesicles in conifer seeds: morphology and allelopathic effects** *by Christopher I. Keeling, Andrew R. Lewis, David Kolotelo and Allison R. Kermode*	35
3:20 – 3:40 pm	**3A-2. Reference seedlot monitoring program: What have we learned in 36 years?** *by Lindsay Robb*	36
3:40 – 4:00 pm	**3A-3. Challenges in a high elevation pine seed orchard in Alberta** *by Barb R. Thomas*	37
4:00 – 4:20 pm	**3A-4. Breeding neem tree (*Azadirachta indica*) for multiple uses** *by Sunil K. Kundu*	38

3:00 – 4:20 pm, Rm 1-160, 3B – Conservation of genetic resources
Moderator: *Jodie Krakowski*

Abstract on Page:

3:00 – 3:20 pm	**3B-1. LIFEGENMON: LIFE for European forest genetic monitoring system** *by Hojka Kraigher, Barbara Fussi, Filippos Aravanopoulos, Monika Konnert, Fotis Kiourtsis, Živan Veselič, Veronika Vodlan, Marjana Westergren*	39
3:20 – 3:40 pm	**3B-2. Forest genetic monitoring (FGM) applied: first results from two FGM sites in Greece** *by F.A. (Phil) Aravanopoulos, E. Avramidou, E. Malliarou, N. Tourvas, V. Kotina, I. Korompoki, I. Ganopoulos, P. Alizoti, E. Barbas, P. Bekiaroglou, P. Hasilidis, G. Roussakis, F. Kiourtsis, N. Fragiskakis*	40
3:40 – 4:00 pm	**3B-3. Adaptive capacity and climate refugia for interior *Pinus albicaulis*** *by Mary F. Mahalovich, Mark J. Kimsey*	41
4:00 – 4:20 pm	**3B-4. Assessing range-wide genetic diversity and structure in subalpine larch (*Larix lyallii*)** *by Marie Vance, Patrick von Aderkas*	42

5:30 – 10:00 pm   Banquet at Faculty Club
5:30 – 6:30 pm Mixer with hors d'oeuvres and cash bar upstairs
6:30 – 8:30 pm Dinner in main hall & Banquet speaker
8:30 – 10:00 pm Mixer with cash bar

Thursday – June 29

7:45 – 8:30 am   Continental breakfast in PCL lounge

7:45 – 8:30am   WFGA Business Meeting and breakfast in PCL lounge
Moderator: *Deogratias Rweyongeza*

8:30 – 10:00 am, Rm 1-140, Keynotes 7 & 8
Moderator: *Andreas Hamann*

		Abstract on Page:
8:30 – 9:10 am Keynote #7	**KN-7. Tree breeding in the southern US: genetic gain equals productivity and profitability for landowners** *by Steve McKeand, J.B. Jett, Trevor Walker, Austin Heine, Daniel Genung, Tori Brooks, April Meeks, Ross Whetten, and Fikret Isik*	43
9:15 – 9:55 am Keynote #8	**KN-8. The genomic basis of adaptive and plastic responses to climate in conifers** *by Sam Yeaman, K.A. Hodgins, K.E. Lotterhos, H. Suren, S. Nadeau, J.C. Degner, K.A. Nurkowski, P. Smets, T. Wang, L.K. Gray, K. Liepe, A. Hamann, J.A. Holliday, M.C. Whitlock, L.H. Rieseberg, S.N. Aitken*	44

10:00 – 10:30 am Coffee Break

10:30 – 11:50 am, Rm 1-140, 4A – Ecological genetics and genomics
Moderator: *Ian MacLachlan*

		Abstract on Page:
10:30 – 10:50 am	**4A-1. Do long-term provenance trials and rapid genomic approaches paint the same picture of climate adaptation?** *by Sally Aitken, Ian MacLachlan, Jon Degner, Jeremy Yoder, Tongli Wang, Pia Smets, Sam Yeaman, Katharina Liepe, Andreas Hamann*	45
10:50 – 11:10 am	**4A-2. Lack of thermal acclimation of needle respiration and photosynthesis of two white spruce seed sources tested along a regional climatic gradient** *by Lahcen Benomar, Mohammed S. Lamhamedi, Jean Beaulieu, André Rainville, Jean Bousquet, Steeve Pépin, Hank A. Margolis*	46
11:10 – 11:30 am	**4A-3. Identifying adaptive variation in lodgepole and jack pine: outlier detection across methods and landscapes.** *by Catherine Cullingham, Janice Cooke, David Coltman*	47
11:30 – 11:50 am	**4A-4. Exome genotyping and association genetics of quantitative traits in a clonally tested loblolly pine population (*Pinus taeda* L.)**	48

| | *Mengmeng Lu, Konstantin V. Krutovsky, C. Dana Nelson, Jason B. West, Tomasz E. Koralewski, Thomas D. Byram, Nathalie A. Reilly, Carol A. Loopstra* | |

10:30 – 11:50 am, Rm 1-160, 4B – Operational tree improvement
Moderator: *Andy Benowicz*

<div align="right">Abstract on Page:</div>

10:30 – 10:50 am	**4B-1. Realized gain trials in coastal Douglas-fir: 20-year results** *by Michael Stoehr*	49
10:50 – 11:10 am	**4B-2. A tale of two series: latitudinal effects on aspen growth in Alberta** *by Jean S. Brouard*	50
11:10 – 11:30 am	**4B-3. Is hybrid vigour possible in native balsam poplar breeding?** *by Yue (Bobby) Hu, Barb R. Thomas*	51
11:30 – 11:50 am	**4B-4. Tree improvement in Canada – past, present and future** *by Stefan G. Schreiber, Barb R. Thomas, Michael Stoehr, Andy Benowicz, William R. Schroeder, Newton Philis, Margot Downey, Pierre Perinet, Dale Simpson, Michele Fullarton, Mary Myers, David Steeves, Basil English*	52

12:00 – 1:00 pm   BBQ lunch outside - CCIS south patio

1:00 – 2:40 pm, Rm 1-140, 5A – Adaptation to climate
Moderator: *Stefan Schreiber*

<div align="right">Abstract on Page:</div>

1:00 – 1:20 pm	**5A-1. Seed Trek: the Next Generation** *by Greg O'Neill*	53
1:20 – 1:40 pm	**5A-2. Can climate niche model predict among-population variation in forest trees?** *by Tongli Wang, Greg O'Neill, Elizabeth Campbell, Sally Aitken*	54
1:40 – 2:00 pm	**5A-3. Protecting locally adapted genetic diversity of Alberta's native tree species** *by Jill Sekely, Andreas Hamann*	55
2:00 – 2:20 pm	**5A-4. Water use efficiency mediated the photosynthesis ability of two pine species and their hybrids in response to water availability** *by Raul de la Mata, Nadir Erbilgin, Barb R. Thomas*	56

2:20 – 2:40 pm	**5A-5. Adaptation of white spruce to climate: cold hardiness and long-term field performance** *by Jaime Sebastian Azcona, Uwe Hacke, Andreas Hamann*	57
2:40 – 3:00 pm	**5A-6. Differences in stable carbon isotope content of white spruce (*Picea glauca*) populations in Alberta** *by Deogratias M. Rweyongeza, Robert D. Guy*	58

1:00 – 3:00 pm, Rm 1-160, 5B – FastTRAC Workshop
Moderator: *Guy Smith*

1:00 – 3:00 pm	**Proof of Concept of Genomic Selection in Tree Breeding** *(further postings here: http://forestgenetics2017.ca/program.html, PDF here: http://forestgenetics2017.ca/files/documents/FastTRAC.pdf, and FastTRAC website here: http://fasttracproject.ca/en/home/*

3:00 – 3:20 pm   Coffee Break

3:20 – 3:40 pm   Conference wrap-up, Award announcements
Moderators: *Deogratias Rweyongeza & Andreas Hamann*

Friday – June 30, 2017

8:00 – 5:00 pm   Post-conference trip (buses leave in front of PCL Lounge)

Smoky Lake Tree Improvement Center	Guided tours of Alberta Tree Improvement and Seed Centre and Coast to Coast Reforestation Smoky Lake Forest Nursery. • 8:00 Meet at PCL Lounge exit for departure on Saskatchewan Drive: http://forestgenetics2017.ca/Maps.pdf • 8:00 – 10:00 Travel, snacks & refreshments on the bus • 10:00 – 10:15 Bus unloading and bio break • 10:15 – 12:15 Smoky Lake Forest Nursery tour • 12:15 – 1:00 Lunch • 1:00 – 3:00 Alberta Tree Improvement & Seed Centre tour • 3:00 – 5:00 Travel and snacks & refreshments on bus

List of Posters

The application of genome-wide information to tree breeding: what is coming next?

*Matias Kirst**

School of Forest Resources and Conservation, Gainesville, Florida

Abstract: 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 will briefly review 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, the 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 will focus 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.

Bio: Matias Kirst is Professor in Quantitative Genetics at the School of Forest Resources and Conservation (SFRC) in Gainesville, Florida, which he joined in 2005. In addition to his affiliation to the SFRC, he is also a member of the Plant Molecular and Cellular Biology Program (PMCB) and the University of Florida Genetics Institute (UFGI). His group in Quantitative Genomics Research is part of the Forest Genomics Laboratory. Research is focused in three areas: (1) Fundamental Genomic Research in the genetic regulation of gene expression and gene expression networks; (2) Applied Genomic Research for the discovery of genes, metabolic and regulatory networks that control variation in wood quality, growth and other important traits for the forestry and agronomic industry; and (3) Technology and genomic tool development.

*) Corresponding author's email: mkirst@ufl.edu

British Columbia's forest genetics program: the top 10 reasons for success

Brian T. Barber, BSF, MA, RPF*

CEO, Select Seed Co. Ltd.
Program Manager, Forest Genetics Council of BC

Abstract: Tree Improvement in BC has a long history 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. Brian's presentation will outline FGC's current strategies, goals and accomplishments, and highlight several initiatives underway in response to climate change, forest health issues, and other challenges. His presentation will also feature a Top 10 list of reasons for BC's forest genetics program's success.

Bio: Brian is Program Manager, Forest Genetics Council of BC (FGC), and CEO, SelectSeed Co. Ltd., which is wholly owned by the FGC. Prior to starting his new role in Nov. 2016 (replacing Jack Woods), Brian worked for the BC Public Service for 25 years. During the previous nine years, he served as Director, Tree Improvement Branch, BC Ministry of Forests Lands and Natural Resource Operations, and Co-chair, FGC. Brian obtained his Bachelor of Science from UBC Forestry in 1987. In October of the same year, he was attacked by a black bear while conducting silviculture surveys north of Prince George. Following some 'repairs', he worked in Japan and cycled through SE Asia, Australia and New Zealand with his future wife. In 1992, they moved to Victoria to raise their family and resume his forestry career. In 2007, he earned a Masters of Arts in Environment and Management from Royal Roads University. His thesis was on policy barriers and opportunities for adapting BC's forests to climate change. He is an active member of the Association of BC Forest Professionals, Canadian Institute of Forestry, and several community groups.

Further information:

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

*) Corresponding author's email: bbarber.fgc@shaw.ca

Single-step genomic evaluation of simple and complex pedigrees

Blaise Ratcliffe*, Michael Stoehr, Yousry El-Kassaby

The University of British Columbia, Dept. of Forest Science

Abstract: 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 are 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, Canada (Beaulieu et al. 2014a). We also investigated the approach utilizing a Douglas-fir (*Pseudotsuga menziesii*) breeding population with more complex pedigree structure for age 11 tree height.

Genomic based evaluations and pedigree based evaluations were assessed on the basis 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 EP, Porth I, Klapste J, Chen C, and El-Kassaby Y. Single-Step BLUP with Varying Genotyping Effort in Open-Pollinated *Picea glauca*. G3: Genes, Genomes, Genetics (https://doi.org/10.1534/g3.116.037895)

*) Corresponding author's email: b.ratcliffe@gmail.com

Genomic selection modelling for weevil resistance, wood quality and growth traits in a non-native tree species, Norway spruce (*Picea abies*)

Patrick Lenz[1,3],*, Simon Nadeau[1], Marie-Josée Mottet[2], Martin Perron[2], France Gagnon[3], Sylvie Blais[3], Brian Boyle[4], Jérôme Laroche[4], Marie Deslauriers[1], Nathalie Isabel[3,5], Jean Beaulieu[1,3], Jean Bousquet[3,4]

[1]) Canadian Wood Fibre Centre, Natural Resources Canada
[2]) Ministère des Forêts, de la Faune et des Parcs du Québec
[3]) Canada Research Chair in Forest Genomics, Université Laval
[4]) Institute for Systems and Integrative Biology, Université Laval
[5]) Canadian Forest Service, Natural Resources Canada

Abstract: White pine weevil is a major damaging agent in Norway spruce 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 a 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 implicating 952 trees (belonging to 39 full-sib families from 34 parents) tested in three contrasting environments in Québec. Wood density, cellulose microfibril angle, acoustic velocity as a proxy for wood stiffness, and growth were measured from age 5 to 15. Cumulative weevil attack was also recorded at 4 regular time points from age 6 to 15. Genotyping data was 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.

*) Corresponding author's email: patrick.lenz@canada.ca

Pedigree-based and genomic predictions of Norway spruce performance in multiclonal forestry in New Brunswick

Chen Ding[1,2,], Patrick Lenz[2,3], Simon Nadeau[3], Greg Adams[4], Shona Millican[4], Marie-Josée Mottet[5], Jean Beaulieu[2,3], Jean Bousquet[2]*

[1]) Natural Resources Canada, Canadian Wood Fibre Centre, 1350 Regent Street, P.O. Box 4000, Fredericton, NB, E3B 5P7, Canada
[2]) Canada Research Chair in Forest Genomics, Institute for Systems and Integrative Biology, Université Laval, Québec, QC, G1V 0A6, Canada
[3]) Natural Resources Canada, Canadian Wood Fibre Centre, 1055 Du P.E.P.S. Street, P.O. Box 10380, Québec, QC G1V 4C7, Canada
[4]) JD Irving, Limited, Sussex Tree Nursery, 181 Aiton Road, Sussex, NB, E4G 2V5, Canada
[5]) Ministère des Forêts, de la Faune et des Parcs du Québec, Direction de la recherche forestière, 2700 rue Einstein, Québec, QC, G1P 3W8, Canada

Abstract: 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 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* (L.) Karst.] 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 modelling. Moreover, we assessed for white pine weevil attacks and genotyped 952 trees of 39 full-sib families from Quebec (Qc) 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.

*) Corresponding author's email: chen.ding@canada.ca

Development of a high-density Affymetrix Axiom genotyping array for genomic selection in Douglas-fir

Scott E. Kolpak[1],*, Keith Jayawickrama[1], Jennifer Kling[1],
Matt Trappe[1], Valerie Hipkins[2], Terrance Ye[1], Stephanie Guida[3],
Richard Cronn[4], Samuel A. Cushman[5], Susan McEvoy[1], and Glenn T. Howe[1],†

[1]) Department of Forest Ecosystems and Society, Oregon State University, Corvallis, OR, USA
[2]) USDA Forest Service, National Forest Genetics Laboratory, Placerville, CA, USA
[3]) National Center for Genome Resources, Santa Fe, NM, USA
[4]) USDA Forest Service, Pacific Northwest Research Station, Corvallis, OR, USA
[5]) USDA Forest Service, Rocky Mountain Research Station, Flagstaff, AZ, USA

Abstract: 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 three-generation breeding program for Coastal Douglas-fir.

Further information:

Howe, G.T., Yu, J.B., Knaus, B., Cronn, R., Kolpak, S., Dolan, P., Lorenz, W.W., and Dean, J.F.D. 2013. A SNP resource for Douglas-fir: de novo transcriptome assembly and SNP detection and validation. BMC Genomics 14.

Muller, T., Ensminger, I., and Schmid, K.J. 2012. A catalogue of putative unique transcripts from Douglas-fir (*Pseudotsuga menziesii*) based on 454 transcriptome sequencing of genetically diverse, drought stressed seedlings. BMC Genomics 13.

*) Presenter
†) Corresponding author's email: glenn.howe@oregonstate.edu

Reforestation for an uncertain future: Do we really need to worry about climate change?

Brad St. Clair[1],*, Glenn Howe[2], Dominique Bachelet[3]

[1]) USDA Forest Service, Pacific Northwest Research Station, Corvallis, OR, USA
[2]) Oregon State University, Corvallis, OR, USA
[3]) Conservation Biology Institute, Corvallis, OR, USA

Abstract: 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 conclude 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/

*) Corresponding author's email: bstclair@fs.fed.us

Selective breeding for growth in the interior spruce hybrid zone maintains adaptation to climate

Ian R. MacLachlan[1],*, Sam Yeaman[2], and Sally N. Aitken[1],†

[1]) Dept. of Forest and Conservation Sciences, University of British Columbia, 3041 – 2424 Main Mall, Vancouver, BC, Canada, V6T 1Z4

[2]) Dept. of Biological Sciences, University of Calgary, 507 Campus Drive N.W., Calgary, AB, Canada, T2N 1N4

Abstract: 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 to implement assisted gene flow polices in Alberta and British Columbia 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 ($n \sim 2400$), 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 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.

*) Presenter
†) Corresponding author's email: sally.aitken@ubc.ca

Provisional climate-based seed zones for Mexico: guiding reforestation under observed and projected climate change

Dante Castellanos-Acuña[1],*, Kenneth W. Vance-Borland[2], J Bradley St. Clair[3], Andreas Hamann[1], Javier López-Upton[4], Erika-Gómez-Pineda[5], Juan Manuel Ortega-García[6], Cuauhtémoc Sáenz-Romero[5]

[1]) University of Alberta, Department of Renewable Resources, Edmonton, Alberta, T6G 2H1, Canada
[2]) The Conservation Planning Institute. 8285 NW Wynoochee Dr, Corvallis OR 97330-2878, USA
[3]) USDA Forest Service, Pacific Northwest Research Station, 3200 SW Jefferson Way, Corvallis, Oregon 97330 USA
[4]) Postgrado en Ciencias Forestales, Colegio de Postgraduados, Carretera México-Texcoco km 36.5, Montecillo, Texcoco, Edo. de México 56230, México
[5]) Universidad Michoacana de San Nicolás de Hidalgo, Instituto de Investigaciones Agropecuarias y Forestales. Av. San Juanito Itzícuaro s/n, Col. Nueva Esperanza, Morelia Michoacán 58337, México
[6]) Facultad de Biología, UMSNH, Avenida Francisco J. Múgica s/n, Ciudad Universitaria, Morelia Michoacán 58330, México

Abstract: 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 develop 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 are 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.

*) Corresponding author's email: dcastell@ualberta.ca

Climate change risk management in tree improvement programs: selection and movement of white spruce and lodgepole pine genotypes in Alberta.

Laura K. Gray-Steinhauer[1],*, Andreas Hamann[1], Sally John[2], Deogratias Rweyongeza[3], and Barb R. Thomas[4]

[1] Department of Renewable Resources, University of Alberta, 751 General Services Building, Edmonton AB, Canada, T5H 4R1
[2] Isabella Point Forestry Ltd., 331 Roland Road, Salt Spring Island, BC V8K 1V1, Canada
[3] Alberta Agriculture and Forestry, Forest Management Branch, 9920-108 Street, Edmonton, AB T5K 2M4, Canada
[4] Department of Renewable Resources, University of Alberta, 442 Earth Sciences Building, Edmonton, AB T6G 2E3, Canada

Abstract: The 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 opportunity to gain insight into the environmental tolerances of planting stock. Additionally these trials allow tree improvement programs to identify genotypes especially sensible 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 and lodgepole pine in Alberta, we analyzed data from 80 genetic tests established by industry and government agencies. We show 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 up in elevation 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:

Gray, L.K., Hamann, A., John, S., Rweyongeza, D., Barnhardt, L. and Thomas, B.R. 2016. Climate change risk management in tree improvement programs: selection and movement of genotypes. *Tree Genetics & Genomes* **12**: article 23.
Gray, L. K., Rweyongeza, D., Hamann, A., John, S. and Thomas, B.R. 2016. Developing management strategies for tree improvement programs under climate change: insights gained from long-term field trials with lodgepole pine. *Forest Ecology and Management* **377**: 128–138

*) Corresponding author's email: lkgray@ualberta.ca

Assessing trees' adaptive capacity to environmental constraints: from genomic approaches to the development of innovative phenotyping tools

Nathalie Isabel*, Claire Depardieu, Martin Girardin, Johann Housset, Patrick Lenz, Simon Nadeau, Isabelle Duchesne, Jean Bousquet, Janice Cooke, Ingo Ensminger

Natural Resources Canada, Canadian Forest Service, Laurentian Forestry Centre

Abstract: 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.

Bio: Nathalie received her B.Sc. in Forestry from Université Laval in 1988. She completed her Ph.D. in Forest Sciences in 1995 at the same university. She has been a research scientist with Natural Resources Canada (Canadian Forest Service, Québec region) since 1996. She is Adjunct Professor of the Canada Research Chair in Forest Genomics at Université Laval. Her research revolves around the development of knowledge and genomics tools to better understand forest tree adaptation to climate. Over the last decade, she has been involved in successive Genome Canada projects mainly focusing on spruce species. She is also interested in translational research to foster forest certification and social acceptance of forest management practices.

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

*) Corresponding author's e-mail: nathalie.isabel@canada.ca

Confronting emerging pathogens: A genomics empowered approach to protecting forest health

*Jared M. LeBoldus**

Oregon State University, Department of Botany and Plant Pathology & Forest Engineering and Resources Management, Corvallis, OR 97331, USA

Abstract: Invasive microbes, causing diseases such as sudden oak death and chestnut blight, 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.

Bio: Dr LeBoldus is an Assistant Professor in Forest Pathology and researches the genetics of host-pathogen interactions in forest trees. His current projects focus on using genomic tools to understand the relationship between genes in the host and pathogen, how they impact virulence and pathogenicity, and how this information may be scaled to elucidate landscape level patterns of pest and disease occurrence. Dr. LeBoldus received a B.Sc. (2003) in Forest Science from the University of British Columbia. He received his M.Sc. (2006) and Ph.D. (2010) from the University of Alberta.

*) Corresponding author's email: lebolduj@oregonstate.edu

Drought sensitivity of Norway spruce at the species' warmest fringe: quantitative and molecular analysis reveals high genetic variation within and among provenances.

Silvio Schueler[1],*, Carlos Trujillo-Moya[1], Jan-Peter George[1], Silvia Fluch[2], Thomas Geburek[1], Michael Grabner[3], Sandra Karanitsch-Ackerl[3], Heino Konrad[1], Konrad Mayer[3], Eva Maria Sehr[2], Elisabeth Wischnitzki[2]

[1]) Federal Research and Training Centre for Forests, Natural Hazards and Landscapes (BFW), Seckendorff-Gudent-Weg 8, 1131 Vienna, Austria
[2]) Center for Health &Environment Department, AIT Austrian Institute of Technology GmbH, Konrad-Lorenz-Strasse 24, 3430 Tulln, Austria
[3]) University of Natural Resources and Life Sciences (BOKU)-Institute of Wood Technology and Renewable Resources, Konrad-Lorenz-Strasse 24, 3430 Tulln an der Donau, Austria

Abstract: Norway spruce 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, the 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 test for genetic variation among seed provenances and estimate the degree of genetic determination of the 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 basis for future breeding and genetic conservation measures at the species warmest fringe.

*) Corresponding author's email: silvio.schueler@bfw.gv.at

Characterizing drought tolerant lodgepole pine populations for planting under climate change

Miriam Isaac-Renton[1],*, D. Montwé[1], A. Hamann[1], H. Spiecker[2], P. Cherubini[3], K. Treydte[3]

[1]) University of Alberta, Department of Renewable Resources
[2]) University of Freiburg, Chair of Forest Growth and Dendroecology
[3]) Swiss Federal Institute for Forest, Snow and Landscape Research - WSL

Abstract: 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 will be discussed.

*) Corresponding author's email: isaacren@ualberta.ca

Records of cold adaptation in tree rings: Seed transfer limits under warming climates

David Montwé[1,], Miriam Isaac-Renton[1], Heinrich Spiecker[2] & Andreas Hamann[1]*

[1]) University of Alberta, Department of Renewable Resources
[2]) University of Freiburg, Chair of Forest Growth and Dendroecology

Abstract: 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 address this concern by analyzing 20 provenances of lodgepole pine 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 are 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 show that frost risks need to be considered when implementing assisted migration and we introduce blue and frost ring proxies to screen for frost tolerance in genetic trials.

*) Corresponding author's email: david.montwe@ualberta.ca

What can we learn from tree-ring structure on climate adaptations?
A Case study from IUFRO-spruce provenance trials

Marcin Klisz[1,], Joanna Ukalska[2], Marcin Koprowski[3], Paweł Przybylski[1], Radosław Puchałka[3], Cristina Nabais[4], Szymon Jastrzębowski[1]*

[1]) Forest Research Institute in Poland Department of Silviculture and Genetics, Poland
[2]) Warsaw University of Life Sciences, Faculty of Applied Informatics and Mathematics, Department of Econometrics and Statistics, Biometry Division, Poland
[3]) Nicolaus Copernicus University, Faculty of Biology and Environmental Protection, Department Ecology and Biogeography, Torun, Poland
[4]) Department of Life Sciences, Centre for Functional Ecology, University of Coimbra, Coimbra, Portugal

Abstract: The current climate change involve growth reaction of forest trees that we can be interpreted as a proxy of theirs 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 hypothesize that the tendency to form intra-annual density fluctuation (IADF) is provenance dependent. In order to test our hypothesis we determine IADF frequency for Norway spruce populations tested on IUFRO 1972 provenance trails. As a climatic factors triggering IADF frequency we applied standardized precipitation evapotranspiration index (SPEI) and Palmer drought severity index (PDSI) from global gridded SPEI dataset. We used nuclear microsatellite variation (SSR markers) to define genetic diversity between provenances. Based on generalized linear mixed model (GzLMM) we confirmed significance of the trees origin as well as genotype × environment interaction (G × 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 reflected to genetic distance (Fst) based principal coordinate analysis (PCoA). This may be related to the neutral nature of the SSR markers used in analysis. For climate-growth relationships studies, we created three groups of provenances (N, E, S). In 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 leads us to assumption that populations' adaptive capacity depends on "climate shift" which means differences between site climate and provenance origin climate.

*) Corresponding author's email: m.klisz@ibles.waw.pl

Genetic control of the natural resistance of *Picea glauca* against *Choristoneura fumiferana*

Claudia Méndez-Espinoza[1,2,3,†], Isabelle Giguère[1,2], Geneviève Parent[1,2,4], Patrick Lenz[5,], Éric Bauce[1], John MacKay[1,2,4]*

[1]) Centre d'étude de la forêt, Département des sciences du bois et de la forêt, Université Laval, Québec, Qc, G1V 0A6.
[2]) Institute for Integrative Systems Biology, Université Laval, Québec, Qc, G1V 0A6, Canada.
[3]) Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias, Centro Nacional de Investigación Disciplinaria en Conservación y Mejoramiento de Ecosistemas Forestales, Ciudad de México, CP 04010.
[4]) Department of Plant Sciences, University of Oxford, 0X13RB, UK.
[5]) Canadian Wood Fibre Center, Natural Resources Canada 1055 Du P.E.P.S. Street, P.O. Box 10380, Québec, Qc, G1V 4C7, Canada.

Abstract: *Choristoneura fumiferana*, the spruce budworm (SBW) is the most damaging native defoliator in North America. In the province of Quebec alone, more than 6.3 million hectares have been damaged from 2006 to 2015, during the current SBW epidemics. Recently, a constitutive resistance mechanism was identified in white spruce. 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 the 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 illuminate our understanding of the evolvability of resistance traits against defoliators and imply that considerable gains could be expected from genetic selection.

*) Presenter
[†]) Corresponding author's email: claudia.mendez-espinoza.1@ulaval.ca

Differences in pine resistance to Dothistroma needle blight in Alberta at the species, provenance and family levels

Andy Benowicz*, Deogratias Rweyongeza, Tom Hutchison

Alberta Agriculture and Forestry, Forest Management Branch, 9920-108 Street, Edmonton, AB T5K 2M4, Canada

Abstract: Dothistroma needle blight caused by *Dothistroma septosporum* is a serious pine disease in many regions around the world. Until recently the disease was unknown 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, jack pine and their hybrids while WM is a lodgepole pine progeny/provenance test. At the time of infection the 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 2142 tree were assessed. The mean percent of healthy foliage was 35% in CL and 52% in 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 in both test sites. Likewise, the open pollinated families in WM showed different levels of resistance with breeding values ranging from 34% to 92% healthy foliage. There were seven common provenances present in CL and WM. The ranking of these provenances was stable across the two sites (r=0.93).

*) Corresponding author's email: andy.benowicz@gov.ab.ca

Adaptive variation in lodgepole and jack pine population responses to mountain pine beetle fungal associates and abiotic stresses

Kate R. St.Onge*, Catherine I. Cullingham, Rhiannon Peery, Chandra McAllister, Bianca Sacchi and Janice E.K. Cooke

University of Alberta, Department of Biological Sciences

Abstract: Mountain pine beetle (MPB) is an 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, the ancestral host, and jack pine, 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 the western North America, moving eastward we transition to jack pine, whose distribution range extends from Alberta to the Atlantic 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 hypothesize that genetic variation along this gradient in lodgepole and jack pine also correspond 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 our 18 populations. We observed wide variation between our 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/

*) Corresponding author's email: krstonge@ualberta.ca

Genetic approaches to identifying western gall rust resistance in lodgepole pine

Chandra H. McAllister*, Michael Mbenoun, Eden McPeak and Janice E.K. Cooke

University of Alberta, Department of Biological Sciences

Abstract: Western gall rust (WGR) caused by *Endocronartium harknessii* (J. P. Moore) Y. Hiratsuka, is a damaging autoecious fungal rust of hard pines, including lodgepole pine (*Pinus contorta* Dougl. ex Loud. spp. *latifolia*) and jack pine (*Pinus banksiana* Lamb.). 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, i) identify phenotypic responses of pine to *E. harknessii* infection that definitively lead to gall formation, ii) identify genes through RNA-Seq that are differentially expressed in the early phases of infection, and may contribute to pathogen resistance, and iii) 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.

*) Corresponding author's email: chandram@ualberta.ca

What do we know about the genetics of seed longevity?

Fiona Hay*

International Rice Research Institute, Laguna, Philippines.

Abstract: 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 seed lots within a species, it was originally thought that variation in longevity would correlate with the initial viability of the seeds and that all seed lots 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 seed lots within a species. This presentation will present our current understanding of the genetic basis of variation in seed longevity.

Bio: Dr. Fiona Hay is has been working in seed ecology and physiology for the past 20+ years and currently holds the position of Senior Scientist and Deputy Head of the T.T. Chang Genetic Resources Center at the International Rice Research Institute (IRRI) in the Philippines. She started her career with a PhD studying the development of seed longevity in wild plant species at the UK's Millennium Seed Bank (MSB). During her years at the MSB, her work included researching seeds of UK aquatic species, developing a comparative longevity protocol for wild seeds and enhancing our understanding of the relationship between seed moisture content and longevity, as well as supervising a number of undergraduate and doctoral students. Her MSc in Applied Statistics and Operational Research has enabled her to guide both students and colleagues around the globe in the correct use of statistics in seed research. Dr. Hay and her research team at IRRI study seed development, dormancy and germination in addition to seed longevity and optimising genebank procedures. Fiona is the coordinator for the Global Strategy for the Ex Situ Conservation of Rice. She is also Chief Editor of Seed Science and Technology.

Further information:

Website: http://irri.org/about-us/our-people/specialists/fiona-hay

*) Corresponding author's email: f.hay@irri.org

Responding to the influence of pests in forestry genetics, seed production, and deployment of improved material

Ward Strong*

Tree Improvement Branch, BC Ministry of Forests, Lands and Natural Resource Operations, Vernon, British Columbia.

Abstract: Pests (insects and diseases) influence our tree improvement activities in many ways, from tree breeding through seed deployment. This talk will explore 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, spruce leader weevils, gall rust, Comandra rust, spruce budworm, 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, the fir coneworm, spruce gall adelgids, and cone midges. We have 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 for white pine blister rust resistance; early selections have been made and will be established in seed orchards within a few years.

Bio: I am a forest entomologist with the BC government, where I have spent many years researching the biology, impact, and management of pests in BC's seed orchards. Recently I have contributed to the development of pest screening in the effort to breed trees with resistance to insects and diseases. I have a PhD in entomology from Corvallis, Oregon, and have been a P.Ag. for many years. After work I like to cross country ski, alpine ski tour, cycle, garden, backpack, and kayak, and have recently started rock climbing, much to my wife's angst!

*) Corresponding author's email: ward.strong@gov.bc.ca

Resin vesicles in conifer seeds: morphology and allelopathic effects.

Christopher I. Keeling[1],*, Andrew R. Lewis[2], David Kolotelo[3] and Allison R. Kermode[1]

[1]) Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC, Canada V5A 1S6
[2]) Department of Chemistry, Simon Fraser University, 8888 University Drive, Burnaby, BC, Canada V5A 1S6
[3]) BC Provincial Tree Seed Centre, Tree Improvement Branch, Ministry of Forests, Lands and Natural Resource Operations, 18793 32 Ave, Surrey, BC V3S 0L5

Abstract: 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-*in*sensitive (*abi3-6*) seeds were unaffected.

*) Presenting author's email: ckeeling@alumni.sfu.ca

Reference seedlot monitoring program: What have we learned in 36 years?

Lindsay Robb*

Alberta Tree Improvement & Seed Centre
Government of Alberta

Abstract: The Alberta Tree Improvement & 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 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 will be discussed.

*) Corresponding author's email: lindsay.robb@gov.ab.ca

Challenges in a high elevation pine seed orchard in Alberta

Thomas, B.R.*

University of Alberta, Department of Renewable Resources, 442 Earth Sciences Building, Edmonton, Alberta, Canada T6G 2E3

Abstract: 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 1200-1600m, 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 injections 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 will be 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:

*) Corresponding author's email: bthomas@ualberta.ca

Breeding neem tree (*Azadirachta indica*) for multiple uses

S. K. Kundu*

Director (Former), Wildlife Center, Forest Directorate, Ban Bhabon, Mohakhali,
Dhaka-1212, Bangladesh

Abstract: The neem tree (*Azadirachta indica* A. Juss) is an important multipurpose species with enormous potential especially for protection of environment and developing sustainable agriculture and forestry. Individual neem tree exhibits great variation in morphological and chemical makeup. Rural people can easily get 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 more amount of bio-active compound (limonoids) as well as desired agronomic characters. Higher fruit yield usually related with the production of high amount of biochemical compounds. These compounds have high values in producing medicines, pesticides, fungicides, nematicides, cosmetics, animal feed and organic manure. Agronomic traits such as quality timber, fuel wood, agro-forestry species, shelterbelts, avenue trees, drought and disease resistance are of good choice for selection breeding. In this paper yield parameters such as provenance variation, cline, physiological and isozymes variation are 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 plantation. 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 plan are also suggested.

Further Information:

Kundu, S.K. & Tigerstedt, P.M.A. 1999. Variation in net photosynthesis, stomatal characteristics, leaf area and whole-plant phytomass production among ten populations of neem (*Azadirachta indica*). Tree Physiology 19: 47-52. (https://doi.org/10.1093/treephys/19.1.47)

Kundu, S.K. 1999. Comparative analysis of seed morphometric and allozyme data among four populations of neem (*Azadirachta indica*). Genetic Resources and Crop Evolution. 46(6): 569-577. (https://doi.org/10.1023/A:1008761503500)

*) Corresponding author's email: sunilkundu98@gmail.com

LIFEGENMON: LIFE for European Forest Genetic Monitoring System.

Hojka Kraigher[1,]*, Barbara Fussi[2], Filippos Aravanopoulos[3], Monika Konnert[2], Fotis Kiourtsis[4], Živan Veselič[5], Veronika Vodlan[6], Marjana Westergren[1]

[1]) Sloveian Forestry Institute, Ljubljana, Slovenia
[2]) Bavarian Office for Forest Seeding and Planting
[3]) Aristotle University of Thessaloniki
[4]) General Directorate of Forestry and Agric. Affairs, Decent. Adm. of Macedonia, Thrace
[5]) Slovenia Forest Service
[6]) Centre for information service, co-op. and development of NGOs

Abstract: 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 project LIFEGENMON (LIFE ENV/SI/000148) 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 and Silver fir were established in Germany, Slovenia and Greece, FGM guidelines for these two and five additional species of different biology are to 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 will be 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; formation of future action plans to establish a discussion line with policy makers on development and implementation of the FGM system shall be addressed.

Further information:
Fussi, B., Westergren, M., Aravanopoulos, F. et al. 2016. Forest genetic monitoring: an overview of concepts and definitions. Environ Monit Assess 188: 493. doi:10.1007/s10661-016-5489-7
Project website: http://www.lifegenmon.si

*) Presenting & corresponding author's email: hojka.kraigher@gozdis.si

Forest genetic monitoring (FGM) applied: first results from two FGM sites in Greece

F.A. (Phil) Aravanopoulos[1], E. Avramidou[1], E. Malliarou[1], N. Tourvas[1], V. Kotina, I. Korompoki, I. Ganopoulos[1], P. Alizoti[1], E. Barbas[1], P. Bekiaroglou[2], P. Hasilidis[2], G. Roussakis[2], F. Kiourtsis[2], N. Fragiskakis[2]

[1]) Department of Forestry and Natural Environment, Laboratory of Forest Genetics and Tree Breeding, Aristotle University of Thessaloniki, University Campus, Thessaloniki, 54I II4, Greece
[2]) General Directorate of Forests and Agricultural Affairs, Decentralized Administration of Macedonia, Thrace

Abstract: 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: (a) demographic assessments (age, height, DBH, % filled seeds, % germination, regeneration abundance), and (b) 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 are presented and discussed in light of the 2nd 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.

Adaptive capacity and climate refugia for interior *Pinus albicaulis*

Mary F. Mahalovich* and Mark J. Kimsey

USDA Forest Service, Northern, Rocky Mountain, Southwestern and Intermountain Regions
Intermountain Forestry Cooperative, University of Idaho

Abstract: 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 indicate 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.
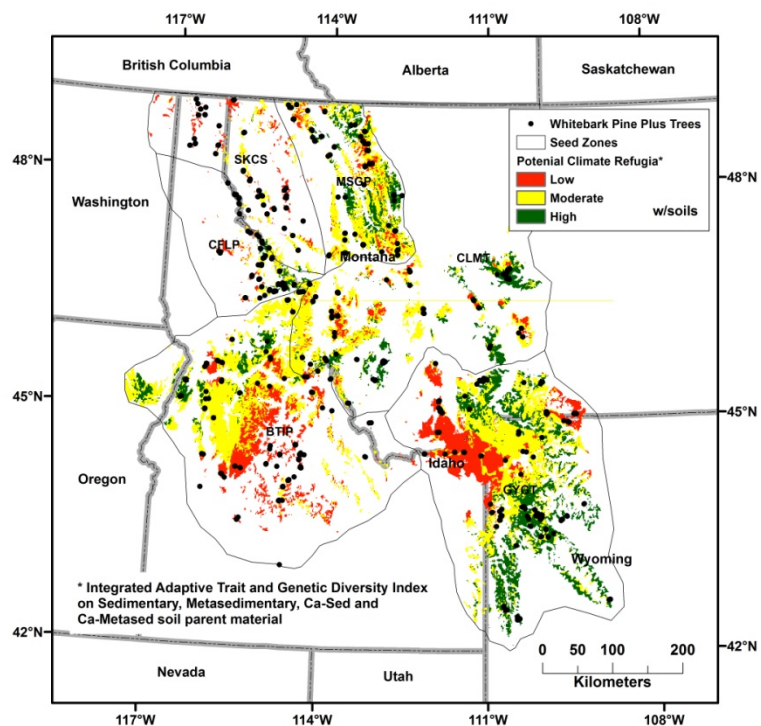
*) Corresponding author's email: mmahalovich@fs.fed.us

Assessing range-wide genetic diversity and structure in subalpine larch (*Larix lyallii*)

Marie Vance*, Patrick von Aderkas

Centre for Forest Biology, University of Victoria

Abstract: 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, I sampled 62 populations distributed across the species' natural range. 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.

*) Corresponding author's email: marie@uvic.ca

Tree breeding in the southern US: genetic gain equals productivity and profitability for landowners

Steve McKeand*, J.B. Jett, Trevor Walker, Austin Heine, Daniel Genung
Tori Brooks, April Meeks, Ross Whetten, and Fikret Isik

North Carolina State University, Department of Forestry and Environmental Resources, Raleigh, North Carolina, United States

Abstract: 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* L.) 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. We will summarize 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 derive 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 will be presented.

Bio: Steve McKeand has been a Professor of Forestry and Environmental Resources for over 30 years and is Director of the Cooperative Tree Improvement Program at NC State University. In addition to directing the program, Steve conducts research in support of the Tree Improvement Cooperative, teaches graduate and undergraduate courses in forest genetics, directs graduate students, and conducts outreach and extension programs for the 34 company and government agency members of the Cooperative as well as for foresters and forest landowners throughout the southern US. Steve received his BS in Forestry from Purdue University in 1976 and his MS in Forest Genetics in 1978, also from Purdue. In 1983, he completed his PhD in Forest Genetics at NC State University.

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

*) Corresponding author's email: Steve_McKeand@ncsu.edu

The genomic basis of adaptive and plastic responses to climate in conifers

Sam Yeaman*, Hodgins KA, Lotterhos KE, Suren H, Nadeau S, Degner JC, Nurkowski KA, Smets P, Wang T, Gray LK, Liepe K, Hamann A, Holliday JA, Whitlock MC, Rieseberg LH, Aitken SN

University of Calgary, Department of Biological Sciences

Abstract: 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 use 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 compare RNAseq expression profiles under 7 different environmental treatments and characterize genes that respond similarly vs. differently in their expression. We also explore the genetic basis of adaptive differences among populations using exome capture and phenotype- and environment-association analyses. We find 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, western larch, and jack pine, as well as to study the basis of resistance to dothistroma in lodgepole pine, and Swiss needle cast in Douglas-fir.

Bio: Dr. Sam Yeaman works at the University of Calgary in the Department of Biological Sciences as an Assistant Professor and AIHS chair in computational biology and bioinformatics. He did a B.Sc. at Trent University and his Ph.D. at University of British Columbia under the supervision of Mike Whitlock. Further research took him to Neuchâtel for a postdoc with Laurent Lehmann, before returning to UBC to work with Sally Aitken and Loren Rieseberg on climate adaptation in conifers. His research focuses on how evolution gives rise to adaptation, using a combination of theoretical and empirical studies in a range of organisms including conifers, fruit flies, sunflower, and stickleback.

Further information:

Yeaman S, Hodgins KA, Lotterhos KE, Suren H, Nadeau S, Degner JC, Nurkowski KA, Smets P, Wang T, Gray LK, Liepe K, Hamann A, Holliday JA, Whitlock MC, Rieseberg LH, Aitken SN. Convergent local adaptation to climate in distantly related conifers. *Science*. **353**:1431-1433.

Yeaman S, Hodgins KA, Nurkowski K, Holliday JA, Rieseberg LH, Aitken SN. 2014. Conservation and divergence of gene expression plasticity over ~140 million years of evolution in lodgepole pine (*Pinus contorta*) and interior spruce (*Picea glauca* x *Picea engelmanii* and their hybrids). *New Phytologist*. **203**:578-591.

Lab website: http://yeamanlab.weebly.com
*) Corresponding author's email: samuel.yeaman@ucalgary.ca

Do long-term provenance trials and rapid genomic approaches paint the same picture of climate adaptation?

Sally Aitken[1,], Ian MacLachlan[1], Jon Degner[1], Jeremy Yoder[1], Tongli Wang[1], Pia Smets[1], Sam Yeaman[2], Katharina Liepe[3], Andreas Hamann[3]*

[1]) University of British Columbia
[2]) University of Calgary
[3]) University of Alberta

Abstract: 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 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 BC. Custom ~50K SNP arrays were developed and 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 indicate that genomic approaches can rapidly characterize climate adaptation patterns in widespread tree species.

Further information:

Liepe KJ, A Hamann, P Smets, CR Fitzpatrick, SN Aitken. 2016. Adaptation of lodgepole pine and interior spruce to climate: Implications for reforestation in a warming world. Evolutionary Applications 9: 409-419.

Suren, H., Hodgins KA, Yeaman S, Nurkowski KA, P. Smets, Rieseberg LH, Aitken SN, Holliday JA. 2016. Exome capture from spruce and pine giga-genomes. Molecular Ecology Resources 16: 1136-1146.

Project website: http://adaptree.forestry.ubc.ca/

*) Corresponding author's email: sally.aitken@ubc.ca

Lack of thermal acclimation of needle respiration and photosynthesis of two white spruce seed sources tested along a regional climatic gradient

Lahcen. Benomar[1,], Mohammed S. Lamhamedi[2], Jean Beaulieu[1], André Rainville[2], Jean Bousquet[1], Steeve Pépin[1], Hank A. Margolis[1]*

[1]) Faculté de foresterie, de géographie et de géomatique, Pavillon Abitibi Price, Université Laval, Québec, QC G1V 0A6, Canada

[2]) Direction de la recherche forestière, ministère des Forêts, de la Faune et des Parcs, 2700 rue Einstein, Québec, QC G1P 3W8, Canada

Abstract: Knowledge about the thermal acclimation potential of physiological processes of boreal tree species is important to (i) determine the ability to adapt to predicted global warming (ii) assist reforestation decisions under a changing climate and (iii) reduce the uncertainty regarding forest ecosystem-climate change feedback on 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 seed sources (from south and north of the commerial 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 the 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. The 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.

*) Corresponding author's email: lahcen.benomar.1@ulaval.ca

Identifying adaptive variation in lodgepole and jack pine: outlier detection across methods and landscapes.

Catherine Cullingham*, Janice Cooke, David Coltman

Department of Biological Sciences, University of Alberta

Abstract: Lodgepole and jack pine are two economically and ecologically important tree species that hybridize in western Canada, an area of recent mountain pine beetle 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.

Further information:

Cullingham, C.I., Cooke, J.E.K. and Coltman, D.W. 2014. Cross-species outlier detection reveals different evolutionary pressures between sister species. New Phyt. 204:215-229.

*) Corresponding author's email: cathy.cullingham@ualberta.ca

Exome genotyping and association genetics of quantitative traits in a clonally tested loblolly pine population (*Pinus taeda* L.)

Mengmeng Lu*[1, 2, 3], Konstantin V. Krutovsky[1, 2, 4, 5, 6], C. Dana Nelson[7, 8], Jason B. West[1, 2], Tomasz E. Koralewski[1], Thomas D. Byram[1, 9], Nathalie A. Reilly[10], Carol A. Loopstra[1, 2]

[1]Department of Ecosystem Science and Management, Texas A&M University, 2138 TAMU, College Station, TX 77843-2138, USA; [2]Molecular and Environmental Plant Sciences Program, Texas A&M University, 2474 TAMU, College Station, TX 77843-2474, USA; [3]Department of Biological Science, University of Calgary, 507 Campus Drive NW, Calgary, AB T2N4S8, Canada, [4]Department of Forest Genetics and Forest Tree Breeding, Georg-August-University of Göttingen, Büsgenweg 2, Göttingen 37077, Germany, [5]N. I. Vavilov Institute of General Genetics, Russian Academy of Sciences, 3 Gubkina Str., Moscow 119333, Russia; [6]Genome Research and Education Center, Siberian Federal University, 50a/2 Akademgorodok, Krasnoyarsk 660036, Russia; [7]USDA Forest Service, Southern Research Station, Southern Institute of Forest Genetics, 23332 Success Road, Saucier, MS 39574, USA; [8]University of Kentucky, Forest Health Research and Education Center, 730 Rose Street, Lexington, KY 40546, USA; [9]Texas A&M Forest Service, 2585 TAMU, College Station, TX; [10]Department of Biology and Marine Biology, University of North Carolina Wilmington, 601 S. College Road, Dobo Hall 102, Wilmington, NC 28403-5915, USA

Abstract: Loblolly pine (*Pinus taeda* L.) 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 the 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.

Further information:

Lu M, Krutovsky KV, Nelson CD, Koralewski TE, Byram TD, Loopstra CA (2016) Exome genotyping, linkage disequilibrium and population structure in loblolly pine (Pinus taeda L.). BMC Genomics. doi:10.1186/s12864-016-3081-8

Lu M, Krutovsky KV, Nelson CD, West JB, Reilly NA, Loopstra CA (2017) Association genetics of growth and adaptive traits in loblolly pine (Pinus taeda L.) using whole-exome-discovered polymorphisms. Tree Genet Genomes 13:57

[*]) Presenting and corresponding author's email: mengmeng.lu3510@gmail.com

Realized gain trials in coastal Douglas-fir: 20-year results

Michael Stoehr*

Tree Improvement Branch, BC Ministry of Forests, Lands and Natural Resource Operations
Saanich Seed Orchard, Saanichton, BC, V8M 1W4

Abstract: 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, one of the most important timber species in BC, we have 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 controls (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.

*) Corresponding author's email: michael.stoehr@gov.bc.ca

A tale of two series: latitudinal effects on aspen growth in Alberta

J.S. Brouard*

Western Boreal Aspen Corp.

Abstract: Two aspen (Populus tremuloides Michx.) clone trial series were established on the same three sites in north-western 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 propagated vegetatively 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 were tested in the G814 series and 39 clones in the G813 series, but not all clones were represented on all sites. This paper examines 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 are clear provenance differences in aspen growth response in relation to latitudinal transfer, there is 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 average 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.

*) Corresponding author's email: johnbro@saltspring.com

Is hybrid vigour possible in native balsam poplar breeding?

Yue (Bobby) Hu*, Barb R. Thomas

[1]Deartpemetn of Renewable Resouces, 442 Earth Sciences Building, University of Alberta, Edmonton, Alberta. T6G 2E3.

Abstract: Poplars (*Populus* L.) 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 (ie: hybrid vigour/heterosis).

In this project, we are testing the hypothesis that within species breeding of widely spaced populations of balsam poplar will lead to the expression of hybrid vigour. We are exploring 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 on 6-year height and diameter from the Alberta field sites only, indicate 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 a 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 was 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.

*) Corresponding author's email: yhu6@ualberta.ca

Tree improvement in Canada – past, present and future

Stefan G. Schreiber[1,2,]*, Barb R. Thomas[2], Michael Stoehr[3], Andy Benowicz[4], William R. Schroeder[5], Newton Philis[6], Margot Downey[7], Pierre Perinet[8], Dale Simpson[9], Michele Fullarton[10], Mary Myers[11], David Steeves[12], Basil English[13]

[2]) University of Alberta, Dept. of Renewable Resources, Edmonton, AB
[3]) Government of British Columbia, Ministry of Forests, Lands and Resource Operations, Tree Improvement Branch, Victoria, BC
[4]) Government of Alberta, Alberta Tree Improvement and Seed Centre, Edmonton, AB
[5]) Agroforestry Solutions, Indian Head, SK
[6]) Government of Manitoba, Sustainable Development, Forestry and Peatlands Management Branch, Winnipeg, MB
[7]) Government of Ontario, Ministry of Natural Resources and Forestry, Crown Forests and Lands Policy Branch, Sault Ste. Marie, ON
[8]) Direction de la recherche forestière, Ministère des Forêts, de la Faune et des Parcs du Québec, Québec, QC
[9]) Government of Canada, Natural Resources Canada, Atlantic Forestry Centre, Fredericton NB
[10]) Government of New Brunswick, Dept. of Energy and Resource Development, Forest Management Branch, Island View, NB
[11]) Government of Prince Edward Island, Department of Communities, Land and Environment, Forests, Fish and Wildlife Division, Charlottetown, PE
[12]) Government of Nova Scotia, Dept. of Natural Resources, Forestry Division, Truro, NS
[13]) Government of Newfoundland and Labrador, Department of Fisheries, Forestry and Agrifoods, Forest Ecosystem Management Division, Corner Brook, NL

Abstract: 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 summarizes the past, present and anticipated future state of tree improvement by province and highlights objectives, management and productivity associated with these programs. We are also attempting 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.

*) Corresponding author's email: stefan.schreiber@ualberta.ca

Seed Trek: the Next Generation

Greg O'Neill*

Tree Improvement Branch
BC Ministry of Forest, Lands and Natural Resource Operations

Abstract: 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 propose 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.

Further information:

O'Neill, G., T. Wang, N. Ukrainetz, L. Charleson, L. McAuley, A. Yanchuk, and S. Zedel. 2017. A proposed climate-based seed transfer system for British Columbia. Prov. B.C., Victoria, B.C. Tech. Rep. 099. www.for.gov.bc.ca/hfd/pubs/Docs/Tr/Tr099.htm

*) Corresponding author's email: Greg.ONeill@gov.bc.ca

Can climate niche model predict among-population variation in forest trees?

Tongli Wang[1],*, Greg O'Neill[2], Elizabeth Campbell[3], Sally Aitken[1]

[1]) Department of Forest and Conservation Sciences, University of British Columbia
[2]) BC Ministry of Forest, Land and Natural Resource Operations
[3]) Natural Resources Canada

Abstract: 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-trail-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 trails for many tree species. Can climate niche models help? To explore such a possibility, we used lodgepole pine, 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 is encouraging, but it is critical to select the right model and to optimize the modeling process.

*) Corresponding author's email: tongli.wang@ubc.ca

Protecting Locally Adapted Genetic Diversity of Alberta's Native Tree Species

Jill Sekely*, Andreas Hamann

Department of Renewable Resources, University of Alberta, Edmonton AB Canada

Abstract: 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. Here, we conduct a conservation gap analysis for the Canadian province of Alberta, in which we use ecological sub-regions as proxy for genetic population differentiation of native tree species to assess the effectiveness of the current reserve system. The analysis is 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/

*) Corresponding author's email: sekely@ualberta.ca

Water use efficiency mediated the photosynthesis ability of two pine species and their hybrids in response to water availability

de la Mata, R.[1, 2,]*, Erbilgin, N*[1]*., Thomas, B. R*[1].

[1]) Department of Renewable Resources, University of Alberta, 442 Earth Sciences Building, Edmonton, Alberta, Canada
[2]) Fruticulture, Institute for Agrifood Research and Technology, Caldes de Montbui, Catalonia, Spain

Abstract: 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 pines (*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, tradeo-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 ✕ 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 was monitored over 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. Hybrid pines showed similar net photosynthesis as compared with pure lodgepole pines under drought, but were intermediate between pure pine species when water was available. Hybrid families shows a promising results for selecting families with high growth potential while maintaining the ability to cope with drought.

*) Corresponding author's email: delamatapombo@yahoo.es

Adaptation of white spruce to climate: cold hardiness and long-term field performance

Jaime Sebastian Azcona*, Uwe Hacke, Andreas Hamann

Department of Renewable Resources, University of Alberta

Abstract: Under the 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 the adaptation to climate of different species 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 years old provenance trial in central Alberta with 10 provenances from a wide range of the white spruce 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 in 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 suggest a potential of southern provenances having an increased productivity with a better use of an extended growing season under climate change, but a good synchrony with frost events seems to be key for a good survival in the field.

*) Corresponding author's email: jaime4@ualberta.ca

Differences in stable carbon isotope content of white spruce (*Picea glauca*) populations in Alberta.

Deogratias M Rweyongeza[1], and Robert D Guy[2]*

[1]) Forest Management Branch, Alberta Agriculture and Forestry, Edmonton, AB, Canada
[2]) Department of Forest and Conservation Sciences, University of British Columbia, Vancouver, BC, Canada

Abstract: In Alberta, Canada, white spruce (*Picea galuca* [Moench] Voss) 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 has 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 broad geography ($52^o33'$ – $59^o53'$N and $110^o13'$ – $119^o40'$W), elevation ($180 – 1341$m) and climate (degree days $< 0^o$C $= 1310 – 3004$; degree days $>5^o$C $= 952 – 1382$). Wood core extracted from selected trees of these populations on two test sites provided samples for ^{13}C analysis during the driest year identified by the size of the growth rings and for the whole 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 $> 5^o$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 clanging climate.

*) Corresponding author's email: Deogratias.Rweyongeza@gov.ab.ca

Genetic parameters of maritime pine radial growth during a specific drought event

Laurent Bouffier[1,2,], Raphaël Segura[1,2], François Ehrenmann[1,2], Jean-Marc Gion[3]*

[1]) INRA, BIOGECO, UMR 1202, 33610 Cestas, France
[2]) University Bordeaux, BIOGECO, UMR 1202, 33400 Talence, France
[3]) CIRAD, UMR AGAP, 69 Route Arcachon, Cestas, France

Abstract: Main selection criteria of French maritime pine (*Pinus pinaster*) breeding program are growth at 12 years old and stem straightness. Scenarios of climate changes 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 thus to be able to evaluate growth in the future climatic conditions characterized by low precipitations during the growth period.

A maritime pine genetic trial was established 19 years ago on two contrasting sites (humid and dry sites) with half-sib families. 150 high resolution dendrometers have been installed on 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 considered (2015 and 2016) were characterized by contrasting climate (dry spring in 2015 and wet spring in 2016). Soil humidity 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 low or for high precipitation level. This methodology allows to estimate the genetic variability for growth in dry versus wet conditions and to identify the genotypes best adapted to the future climate.

*) Corresponding author's email: laurent.bouffier@inra.fr

Transcriptome of yellow-cedar (*Callitropsis nootkatensis*) during seed stratification and germination.

Christopher I. Keeling*, Allison R. Kermode

Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC, Canada V5A 1S6

Abstract: Yellow-cedar is a culturally, economically and environmentally significant species in the North Pacific coastal rainforest between California and Alaska. The deep dormancy and the poor germination rates of seeds in this species favors 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 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 (<u>AB</u>SCISIC ACID <u>I</u>NSENSITIVE<u>3</u>), a component of the abscisic acid (ABA) signal transduction pathway, which plays a major role during seed development and dormancy.

*) Corresponding author's email: ckeeling@alumni.sfu.ca

In the right place: habitat suitability models for endangered whitebark pine and limber pine to support recovery and management.

Jodie Krakowski[1,], Robin Kite[2], Ann Blyth[2]*

[1]) Alberta Agriculture and Forestry, Forest Management Branch, Edmonton, AB
[2]) Caslys Consulting Ltd., Saanichton, BC

Abstract: 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 and limber pine, species-specific habitat mapping and modelling 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.

*) Corresponding author's email: jodie.krakowski@gov.ab.ca

Productivity and adaptation of selected poplar (*Populus* spp.) cultivars under climatic conditions of Poland

Marzena Niemczyk[1],*, Krzysztof Mudryk[2], Marcin Jewiarz[2], Marek Wróbel[2]

[1]) Forest Research Institute, Department of Silviculture and Tree Genetics, Braci Leśnej St. no 3, Sękocin Stary, 05-090 Raszyn, Poland
[2]) Laboratory of Technology for Production and Quality Assessment of Biofuels, Faculty of Production and Power Engineering, University of Agriculture in Krakow, Balicka St. 120, 30-149 Kraków, Poland

Abstract: Ten poplar cultivars used in Europe commercially in short-rotation forestry systems were tested to compare their productivity and adaptation to the climatic conditions of Poland. Additional aim 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 share 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 for cultivars 'NE-42' and 'Fritzi Pauley'). Data for the 'AF-6' and 'MON' cultivars were not analysed because of their cold-tenderness and their high mortality. Of the eight cultivars analysed, 'AF-8' had the poorest growth parameters, and produced approximately 3 t dry mass ha^{-1} yr^{-1}. The share 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 indicate the importance of testing cultivars under local climatic conditions before planting on a commercial scale.

*) Corresponding author's email: m.niemczyk@ibles.waw.pl

White spruce wood quality in Alberta breeding regions D1, H and I

Robert T. Matheson*, Barb R. Thomas

University of Alberta, Department of Renewable Resources, 442 Earth Sciences Building,
Edmonton, Alberta, Canada T6G 2E3

Abstract: The majority of tree improvement (TI) programs focus upon 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 the characteristics of the wood 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 tree improvement programs have been 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.

*) Corresponding author's email: rtmathes@ualberta.ca

Drought tolerance and growth of populations in a wide-ranging tree species indicate climate change risks for the boreal north

David Montwé[1,2,], Miriam Isaac-Renton[1], Andreas Hamann[1], Heinrich Spiecker[2]*

[1]) University of Alberta, Dept. Renewable Resources, Edmonton, AB, Canada, T6G 2H1
[2]) Albert-Ludwigs-Universität Freiburg, Institute of Forest Science, Chair of Forest Growth, Freiburg, Germany, 79106

Abstract: Choosing drought-tolerant planting stock in reforestation programs may help adapt forests to climate change. To inform such reforestation strategies, we test lodgepole pine (Pinus contorta Doug. ex Loud. var latifolia Englm.) population response to drought, and infer potential benefits of a northward transfer of seeds from drier, southern environments. The objective is 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. The 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. and 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.

*) Corresponding author's email: david.montwe@ualberta.ca

Using the legacy of pan-Canadian provenance tests: tree ring analyses and association genetics for studying sensitivity to climate

Simon Nadeau[1,2,*], Johann M. Housset[2,3], Isabelle Duchesne[1], Patrick Lenz[1,4], Claire Depardieu[2,4], Nathalie Isabel[2,4], Martin P. Girardin[2,3]

[1]) Natural Resources Canada, Canadian Wood Fibre Centre, 1055 du P.E.P.S, P.O. Box 10380, Stn. Sainte-Foy, Québec, QC, G1V 4C7, Canada
[2]) Natural Resources Canada, Canadian Forest Service, Laurentian Forestry Centre, 1055 du P.E.P.S., P.O. Box 10380, Stn. Sainte-Foy, Québec, QC, G1V 4C7, Canada
[3]) Centre for Forest Research, Université du Québec à Montréal, C.P. 8888, succ. Centre-ville, Montréal, QC, H3C 3P8, Canada
[4]) Canada Research Chair in Forest Genomics, Université Laval, Sainte-Foy, QC, G1V 0A6, Canada

Abstract: 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 (EWP), white spruce (WS), and black spruce (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, evidencing 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 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.

*) Corresponding author's email: patrick.lenz@canada.ca

Assessing the intraspecific interactions among six different provenances of aspen based on a stress gradient hypothesis

Waqas Noor*, Andreas Hamann

University of Alberta, Department of Renewable Resources

Abstract: 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 in understanding the facilitation and competition interspecifically. Plant-plant interactions are recognized as importance 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 (Latitude: 54^o53, Longitude: 113^o18`W) using six different aspen provenance seedlot: ABf (Alberta Foothill), BC (British Columbia), cAB (Central Alberta), MN (Minnesota), nAB (Northern Alberta) and SK (Saskatchewan). The data was collected for plant height, diameter at breast height (DBH) and root collar diameter (RCD) from 2002 to 2005 and 2008 and was correlated with annual mean temperature and rainfall. Repeated measures one-way ANOVA revealed that provenance MN yielded highest overall plant height and DBH. However, under stress conditions, northern resources perform 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.

*) Corresponding author's email: wnoor@ualberta.ca

Improving seed quality and genetic diversity in native boreal reclamation species

Lindsay Robb*

Alberta Tree Improvement & Seed Centre
Government of Alberta

Abstract: 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 & 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.

ATISC began research on non-tree seeds four years ago starting with hazels 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 take years for completion.

*) Corresponding author's email: lindsay.robb@gov.ab.ca

In situ quantification of blue stain fungi in jack, lodgepole and hybrid pine.

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

University of Alberta, Dept. of Biological Sciences

Abstract: *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. My main objective is to develop a quantitative PCR (qPCR) assay to quantify the amount of fungal DNA within the xylem of *G. clavigera*-inoculated jack, lodgepole 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 (*Pinus contorta* var. *latifolia*) or jack pine (*P. banksiana*) 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*.

*) Corresponding author's email: bianca@ualberta.ca

Dead or Alive: Molecular assays for pathogen detection

Barbara Wong[1], Isabel Leal[2], Nicolas Feau[1], Richard Hamelin[1]*

[1]) University of British Columbia, Department of Forest Science and Conservation, 2424 Main Mall, Vancouver, BC, Canada, V6T 1Z4
[2]) Natural Resources Canada, Pacific Forestry Centre, 506 Burnside Rd W, Victoria, BC, Canada, V8Z 4N9

Abstract: 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.

*) Corresponding author's email: barb.wong@ubc.ca