2021 FOREST GENETICS
CFGA/WFGA STUDENT AND POSTDOC SYMPOSIUM

Symposium Proceedings

May 19-20, 2021

Co-hosted by the
Western Forest Genetics Association *and the*
Canadian Forest Genetics Association -
l'Association canadienne de génétique forestière

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2021 Forest Genetics Student & PostDoc Symposium
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2021 Forest Genetics Student & PostDoc Symposium
Program at a Glance

Los Angeles PDT	New York EDT	GMT	London BST	Paris CEST	Tokyo JST	Sydney AEST	DAY 1 — Wednesday, May 19 — Live Session Plenary	DAY 2 — Thursday, May 20 — Live Session Plenary
6:30	9:30	13:30	14:30	15:30	22:30	23:30		Session #6 (3 x 10min oral presentations)
7:00	10:00	14:00	15:00	16:00	23:00	0:00		Session #6 - 15min LIVE Q&A
7:30	10:30	14:30	15:30	16:30	23:30	0:30		Session #7 (3 x 10min oral presentations); Session #7 - 15min LIVE Q&A
8:00	11:00	15:00	16:00	17:00	0:00	1:00	*Welcome Day 1*	*Welcome Day 2*
8:30	11:30	15:30	16:30	17:30	0:30	1:30	**Keynote: Nathalie Isabel** (20mins + 10min Q&A)	**Career Panel (50mins)** 10min break
9:00	12:00	16:00	17:00	18:00	1:00	2:00	**Session #1** (4 x 10min oral presentations)	
9:30	12:30	16:30	17:30	18:30	1:30	2:30	Session #1 - 20min LIVE Q&A	**Poster Session #2**
10:00	13:00	17:00	18:00	19:00	2:00	3:00	**Session #2** (4 x 10min oral presentations)	*BREAK*
10:30	13:30	17:30	18:30	19:30	2:30	3:30	Session #2 - 20min LIVE Q&A	**Session #8** (4 x 10min oral presentations)
11:00	14:00	18:00	19:00	20:00	3:00	4:00	**Poster Session #1**	Session #8 - 20min LIVE Q&A
11:30	14:30	18:30	19:30	20:30	3:30	4:30		**Session #9** (3 x 10min oral presentations)
12:00	15:00	19:00	20:00	21:00	4:00	5:00	**Parallel Breakout Live Discussion Sessions**	Session #9 - 15min LIVE Q&A; *BREAK*
12:30	15:30	19:30	20:30	21:30	4:30	5:30	**Session #3** (3 x 10min oral presentations)	**Parallel Breakout Live Discussion Sessions**
13:00	16:00	20:00	21:00	22:00	5:00	6:00	Session #3 - 15min LIVE Q&A; *BREAK*	*BREAK*
13:30	16:30	20:30	21:30	22:30	5:30	6:30		
14:00	17:00	21:00	22:00	23:00	6:00	7:00	**Session #4** (4 x 10min oral presentations)	**Session #10** (5 x 10min oral presentations)
14:30	17:30	21:30	22:30	23:30	6:30	7:30	Session #4 - 20min LIVE Q&A	
15:00	18:00	22:00	23:00	0:00	7:00	8:00	**Session #5** (4 x 10min oral presentations)	Session #10 - 25min LIVE Q&A; **Keynote: Patrick von Aderkas** (20mins + 10min Q&A)
15:30	18:30	22:30	23:30	0:30	7:30	8:30	Session #5 - 20min LIVE Q&A; *Closing Day 1*	*Awards & Closing Remarks*
16:00	19:00	23:00	0:00	1:00	8:00	9:00		
16:30	19:30	23:30	0:30	1:30	8:30	9:30		

On-demand (both days): Welcome Exhibit Hall. Live sessions become available on-demand for 90 days.

Poster Hall (both days): Poster Session ALL (on demand).

Welcome 2021 Forest Genetics Symposium Participants,

Following the 2019 Canadian Forest Genetics Association/l'Association canadienne de génétique forestière (CFGA) and the Western Forest Genetics Association (WFGA) meetings, we expected to organize a business-as-usual joint in-person conference in the Okanagan Valley, British Columbia, for Summer 2021. A host committee was formed and hotel venue booked in early 2020. The Covid-19 pandemic, however, was just getting started. Lockdowns and travel restrictions soon made it apparent international conferences would not be permitted by federal and provincial health authorities. What was Plan B?

2021 Forest Genetics Symposium emerged to showcase the research of students and postdocs who represent the *Next Generation* of our rapidly evolving discipline. To assist us in boldly going where we have not gone before, we enlisted Podium Conference Services. Lauren Moline, Conference Manager, helped us organize a first-class virtual event, which has attracted over 150 registrants from around the world.

Many thanks to the students and postdocs who responded to our call for abstracts. Over 80 submissions were received from across North America and overseas! The scientific panel was challenged in screening and allocating the submissions to oral and poster sessions. To accommodate so many presenters (and keep us on time across several time zones), applicants were requested to submit pre-recorded videos: <10 minutes for oral presentations and <2 minutes for posters. Prizes will be awarded at the end of Day 2. Judge them for yourself by viewing at your leisure the day prior, during, and up to 90-days following the Symposium. The awards, Q&As and other sessions will be "live", so don't miss out on your chance to participate in real-time.

This event would not be possible without our Sponsors who provided generous donations during these difficult times. Please visit their virtual booths during the Symposium and thank them for their support. If you are a student, enquire about potential career opportunities.

Also, thanks to the dozens of volunteers, including keynote speakers, the scientific and career panels, Q&A moderators, breakout session leads, and judges. These volunteers include several past CFGA and WFGA oral and poster presentation prize winners! Seek them and the career panel out for tips on how to pursue your passion.

Finally, thank YOU for signing-up for this Symposium. In ancient Greece, a "Symposium" was a banquet that included drink, food and conversation accompanied by music, dancing, and recitals. Although we can't host such an event at this time, we hope this virtual one will offer the next-best experience. Looking forward to "seeing" you May 19-20, 2021!

Brian and Nick

Brian T. Barber, RPF
President, CFGA/ACGF

Nicholas Ukrainetz, Ph.D, RPF
President, WFGA

2021 Forest Genetics Scientific Program Committee

Brian Barber, President, CFGA/ACGF
Nicholas Ukrainetz, President WFGA
Andreas Hamann, University of Alberta
Barb Thomas, University of Alberta
Jill Hamilton, North Dakota State University
Patrick Lenz, Canadian Forest Service
Richard Sniezko, US Department of Agriculture
Marie Vance, BC Forest Improvement and Research Management Branch

2021 Forest Genetics Awards Committee

Dave Kolotelo, Lead, Awards Judging Panel

Dr. Sally Aitken, University of British Columbia
Dr. Jean Beaulieu, University of Laval
Dr. Andy Benowicz, Alberta Government
Dr. Andy Bower, USDA Forest Service
Dr. Andreas Hamann, University of Alberta
Dr. Jill Hamilton, North Dakota State University
Dr. Barb Hawkins, University of Victoria
Dr. Glenn Howe, Oregon State University
Dr. Keith Jayawickrama, Oregon State University
Dr. Sally John, Isabella Point Forestry Ltd.
Dr. Patrick Lenz, Natural Resources Canada
Dr. Judy Loo, Retired, Biodiversity International
Dr. Pengxin Lu, Ontario Government
Dr. Simon Nadeau, Natural Resources Canada
Dr. Tongli Wang, University of British Columbia
Dr. Greg O'Neill, British Columbia Government
Dr. Blaise Radcliffe, University of British Columbia
Dr. Deogratias Rweyongeza, Alberta Ministry of Agriculture and Forestry
Clara Schortemeyer, J.D Irving Ltd.
Dr. Rahul Singh, GenomeBC
Dr. Michael Stoehr, Retired, British Columbia Government
Dr. Marie Vance, British Columbia Government
Martin Williams, Natural Resources Canada

Conference Organizers
Lauren Moline, Podium Conference Services

2021 Forest Genetics Award Winners

The success of the conference afforded us the opportunity to award a good number prizes for the best oral and poster presentations. Thank you to Dave Kolotelo and the 23 judges who respectively lead and participated in the evaluation process.

Congratulations to the following award recipients:

Award	Prize		Winner	University / Affiliation
WFGA Critchfield Award – Best Student Poster	$ 300	US	Kaylee Rosenberger	Northern Illinois University/Morton Arboretum
WFGA Critchfield Award - Runner-up Student Poster	$ 150	US	Aaron Onufrak	University of Tennessee
WFGA Critchfield Award - Best Student Oral Presentation	$ 700	US	Francois Du Toit	University of British Columbia
WFGA Critchfield Award - Runner-up Student Oral Presentation	$ 350	US	Eddie Lauer	North Carolina State University
CFGA Gene Namkoong Award- Best Student Poster	$ 500	CDN	Lorinda Bullington	University of Montana/ MPG Ranch
CFGA Gene Namkoong Award- Runner-up Student Poster	$ 250	CDN	Bronwyn Moore	University of BC/Natural Resources Canada
CFGA Carl Heimburger Award - Best Student Oral Presentation	$ 1,000	CDN	Susan Mcevoy	University of Connecticut
CFGA Carl Heimburger Award - Runner-up Student Oral Presentation	$ 500	CDN	Heather Dun	University of Oxford
2021 Forest Genetics Postdoc Award - Best Poster	$ 500	CDN	Sam Belton	National Botanic Gardens, Dublin, Ireland
2021 Forest Genetics Postdoc Award - Best Oral Presentation	$ 1,000	CDN	Antonio Castilla	Michigan State University
2021 Forest Genetics Postdoc Award - Runner-up Oral Presentation	$ 500	CDN	Claire Depardieu	Laval University
2021 Forest Genetics Genome BC Award - Best Student Genomics Poster	$ 300	CDN	Cynthia Webster	University of Connecticut

2021 Forest Genetics Student & PostDoc Symposium Keynote Speakers

Nathalie Isabel has been a Research Scientist at Natural Resources Canada since 1996. She is Adjunct Professor with the Canada Research Chair in Forest Genomics at Laval University and is part of the Spruce-Up project. Her research interests are centred on the development of knowledge and tools to better understand the adaptability of boreal and temperate forest tree species. She studies key functional traits such as drought tolerance by combining genomic and precision phenotyping approaches. Her research also focuses on studying the genetic diversity of indicator forest species for the benefit of forest communities. With her team, she is also working on the development of a value chain traceability system and a Canadian center of expertise for wood identification to combat the illegal timber trade.

Patrick von Aderkas received his botany degrees from the University of Guelph and the University of Manchester (PhD). He post-doc'ed with Jack McLachlan at NRC in Halifax, then Jan Bonga at the Canadian Forestry Service, Fredericton. Currently, he is a Professor of Biology at the University of Victoria. The focus of his lab has been on gymnosperm reproduction including diverse aspects of anatomy, embryogenesis, cytogenetics, proteomics and transcriptomics. The major contribution from his laboratory, and the one that involved training the majority of his doctoral students, was on the evolution of sexual fluids in plants. Initially the focus was conifers, e.g. larch, Douglas-fir. He broadened his interests to include most ancient and also the most recently evolved gymnosperms: ginkgo, cycads, and gnetophytes. Most recently, he has begun working on cycads, in particular the fertilization fluids in which their giant sperm swim.

Career Perspectives Panel

After completing a PhD in Forest Science at the University of British Columbia in 2010, Dr. **Raju Soolanayakanahally** joined the federal government as a research scientist in tree improvement program with Agriculture and Agri-Food Canada. Based at the Saskatoon Research and Development Centre, Soolanayakanahally is also responsible for operational poplar and willow tree breeding programs. Since 2014, Soolanayakanahally has been further serving as the chair for the Poplar and Willow Council of Canada. He is currently playing a leadership role in a major cross-departmental federal genomics development and research initiative program, while also leading or supporting several genomics projects as well. In addition to having a strong background in forest genetics, Soolanayakanahally has formal training in plant ecophysiology. The depth of his research ranges from tree phenology, photosynthetic traits, tolerance to abiotic stressors and integrative responses to climate change. This background positions him well for collaborative work at the intersection with agroforestry systems: Soolanayakanahally is actively engaged in large-scale projects to study how short-rotation woody crops can support the emerging bioeconomy and sequester

carbon, and further plays a key role in multidisciplinary teams creating new phenotyping tools to support global food and forest security.

Dr. Jill Hamilton received her PhD at the University of British Columbia in Forestry studying adaptive introgression in forest trees following which she completed post-docs at the University of Alberta and University of California-Davis on the impact environmental cues have to important life history transitions and the genetic basis of adaptation for complex traits across environments in both forest and non-forest systems. Jill is currently an Assistant Professor in Biological Sciences at North Dakota State University and incoming Director of the Schatz Center in Tree Molecular Genetics at Penn State University.

Dr. Marcus Warwell is the Regional Geneticist for the USDA, Forest Service, Southern Region. He oversees the seed production, orchard and seed extractory resources that directly support reforestation. Dr. Warwell also facilitates the conservation of genetic diversity among the region's many forest tree species and acts as the subject matter expert in direct support of silviculture and other natural resource management activities. Prior to accepting the Regional Geneticist position in Fall 2020, Dr. Warwell worked as a geneticist for the USDA, Forest Service, Rocky Mountain Research Station for more than 20 years. His research focused on questions in genecology, bioclimate modeling, and evolutionary biology.

Greg Adams worked in the field of tree improvement for 40 years with J.D. Irving, Limited (JDI) and began consulting after retiring in 2019. JDI is a family owned, vertically integrated, diversified forest products company managing 2.5 million hectare of forest land in New Brunswick, the State of Maine and Nova Scotia, of which 1.5 million is private freehold land and the rest is under a Crown License. Since initiating tree improvement in 1979, the company has planted approximately 700 million improved seedlings - making a large different in current and future wood supplies and quality. Over his career, Greg has had extensive experience in managing silviculture programs and nursery production. He has also had the opportunity to integrate new technologies including somatic embryogenesis, genomic selection and enhanced pest tolerance through inoculation of seedlings with beneficial endophytic fungi. Greg received his BScF from Lakehead University and his MScF specializing in forest genetics and tree improvement from the University of New Brunswick.

2021 Forest Genetics Symposium Schedule

Please note: All times below are in PDT and need to be adjusted for your own time zone.

Wednesday, May 19

8:00 AM	**Welcome / Opening (LIVE)**
8:15 AM	**Keynote Session (LIVE): Nathalie Isabel**
8:45 AM	**Session #1: Operational Tree Improvement 1** **Tara Androschuk**, University of Alberta *What's the reason? Looking for answers to Alberta's lack of lodgepole pine seed* **Esteban Galeano**, University of Alberta *SNP-based analysis reveals unexpected features of genetic diversity, parental contributions and pollen contamination in a white spruce breeding program* **Dawei Luo**, University of Alberta *Forest growth in a future climate: tree improvement for white spruce and lodgepole pine in Alberta* **Yue Yu**, University of British Columbia *Using landscape genomics to delineate lodgepole pine seed and breeding zones*
9:25 AM	**Session #1 LIVE Q&A: Operational Tree Improvement 1** Moderator: Jonathan Degner Tara Androschuk, University of Alberta Esteban Galeano, University of Alberta Dawei Luo, University of Alberta Yue Yu, University of British Columbia
9:45 AM	**Session #2 - Operational Tree Improvement 2** **Francois du Toit,** Faculty of Forestry, University of British Columbia *Use of Remote Sensing Technology for Phenotyping in Tree Improvement Programs in British Columbia, Canada* **Omnia Gamal El-Dien**, University of British Columbia *Genomic Selection in western redcedar breeding program in BC: from proof of concept to application* **Jean-Philippe Laverdière**, Université Laval *Developing genomic selection to integrate drought response in multi-trait improvement of white spruce* **Iman Rashidijouybari,** Laval university *Multi-trait genetic selection for improved solid wood quality in white spruce*
10:25 AM	**Session #2 LIVE Q&A - Operational Tree Improvement 2** Moderator: Blaise Ratcliffe Francois Du Toit, University of British Columbia Omnia Gamal El-Dien, University of British Columbia Jean-Philippe Laverdière, Université Laval

	Iman Rashidijouybari, Laval University
10:45 AM	**Poster Session #1**
11:45 AM	**Parallel Breakout Live Discussion**
	How to write a Genome BC/Canada Proposal
11:45 AM	**Parallel Breakout Live Discussion**
	Tree Seed Working Group
11:45 AM	**Parallel Breakout Live Discussion**
	Conservation in Action
11:45 AM	**Parallel Breakout Live Discussion**
	Operational Tree Improvement Programs
12:30 PM	**Session #3: Population Genetics 1** **Sumaira Zaman**, University of Connecticut *Assessing the Megagenome of Coast Redwood* **Antonio Castilla**, Michigan State University *Genetic rescue by distant trees mitigates qualitative pollen limitation imposed by fine-scale spatial genetic structure.* **Lionel Di Santo**, North Dakota State University *Genome-wide sequencing to understand the evolutionary history of Torrey pine (Pinus torreyana) with implications for species conservation*
1:00 PM	**Session #3 LIVE Q&A: Population Genetics 1** Moderator: Ian MacLachlan Sumaira Zaman, University of Connecticut Antonio Castilla, Michigan State University Lionel Di Santo, North Dakota State University
1:15 PM	*BREAK*
1:30 PM	**Session #4: Climate Change and Adaptation 1** **Rainbow Desilva**, University of California, Berkeley *Association of genetic and climatic variability in giant sequoia reveals signatures of local adaptation along moisture-related gradients.* **Jill Sekely**, Philipps University *Interplay between genetics and environment in an Andean tree species* **Ian MacLachlan**, Texas A&M University *Effect sizes of multilocus genotypes to estimate climate-related phenotypes in lodgepole pine*
2:10 PM	**Session #4 LIVE Q&A: Climate Change and Adaptation 1** Moderator: Barbara Wong Rainbow Desilva, University of California, Berkeley Jill Sekely, Philipps University, Germany Ian MacLachlan, Texas A&M University
2:30 PM	**Session #5: Climate Change and Adaptation 2** **Rafael Candido Ribeiro**, University of British Columbia

	Case-control GWAS: detecting adaptive genetic variation associated with drought hardiness in coastal and interior Douglas-fir **Susan Mcevoy**, University of Connecticut *Genomic characterization of two maples highlights genes involved in the stress response to acidic soils across seasons* **Mengjun Shu**, University of California, Merced *Association genetics of drought tolerance in ponderosa pine (Pinus ponderosa)* **Claire Depardieu**, Laval University *Integrating dendroecology and genomics approaches to identify genes underlying drought adaptation in white spruce*
3:10 PM	**Session #5 LIVE Q&A: Climate Change and Adaptation 2** Moderator: David Montwe Rafael Candido Ribeiro, University of British Columbia Susan Mcevoy, University of Connecticut Mengjun Shu, University of California, Merced Claire Depardieu, Laval University
3:30 PM	**Closing Day 1 (LIVE)**

Thursday, May 20

6:30 AM	**Session #6 - Climate Change and Adaptation 3** **Roos Goessen**, Laval University *Understanding the adaptive capacity of forest species for climate change from the standpoint of Populus tremuloides, a keystone North American tree* **Brandon Lind**, University of British Columbia *Patterns and climatic drivers of adaptive genetic variation in Douglas-fir* **Anoob Prakash**, University of Vermont *The evolution of species' ranges in the face of changing environments*
7:00 AM	**Session #6 LIVE Q&A - Climate Change and Adaptation 3** Moderator: Ian MacLachlan Roos Goessen, Laval University Brandon Lind, University of British Columbia Anoob Prakash, University of Vermont
7:15 AM	**Session #7 - Climate Change and Adaptation 4** **Beth Roskilly**, University of British Columbia *Rangewide phenotypic and genomic patterns of climate adaptation in western larch to assess mitigation strategies with future climates* **Kate Peterson**, University of British Columbia *Predicting lodgepole pine mortality in a changing climate using provenance data* **Juliette Archambeau**, University of Bordeaux

	Combining climatic and genomic data improves range-wide tree height growth prediction in a forest tree
7:45 AM	**Session #7 LIVE Q&A - Climate Change and Adaptation 4** Moderator: Rafael Candido Ribeiro Beth Roskilly, University of British Columbia Kate Peterson, University of British Columbia Juliette Archambeau, University of Bordeaux
8:00 AM	**Welcome Day 2 (LIVE)**
8:15 AM	**Career Perspectives Panel (LIVE)** Moderator: Miriam Isaac-Renton, Natural Resources Canada Marcus Warwell, USDA, Forest Service, Southern Region Raju Soolanayakanahally, Agriculture and Agri-Food Canada Jill Hamilton, North Dakota State University Greg Adams, GWA Forestry and Applied Biosciences Consulting
9:05 AM	*BREAK*
9:15 AM	**Poster Session #2**
10:30 AM	**Session #8 – Population Genetics 2** **Lanie Galland**, University of Nevada, Reno *The role of history and environment in shaping fragmented distributions of the emblematic serotinous pines of the coastal Pacific Slope* **Emily Schumacher**, The Morton Arboretum *Butternut throughout space and time: examining range shifts in a rare tree* **Kathryn Uckele**, University of Nevada Reno *Landscape genomic and phytochemical variation across three juniper species and their hybrids* **Whitney Jackson**, Rutgers University *Population Structure within the Hard Maple Species Complex*
11:10 AM	**Session #8 LIVE Q&A - Population Genetics 2** Moderator: Marie Vance Lanie Galland, University of Nevada, Reno Emily Schumacher, The Morton Arboretum Kathryn Uckele, University of Nevada Reno Whitney Jackson, SaVAtree
11:30 AM	**Session #9 – Population Genetics 3** **Rami-Petteri Apuli**, Swedish University of Agricultural Science (Svenska lantbruksuniversitetet, SLU) *Deleterious load in Populus tremula across an active admixture zone in Sweden* **Mitra Menon**, University of California, Davis *Gene expression profiling provides insights into the architecture of adaptive evolution under novel selective pressures*

	Tal Shalev, University of British Columbia *The western redcedar genome: exceptionally low genetic diversity despite strong balancing selection in a self-compatible conifer*
12:00 PM	**Session #9 LIVE Q&A - Population Genetics 3** Moderator: Anthony Bourgoin Rami-Petteri Apuli, Swedish Agricultural University Mitra Menon, University of California, Davis Tal Shalev, University of British Columbia
12:15 PM	*BREAK*
12:30 PM	**Parallel Breakout Live Discussion** Genomic Selection in Tree Breeding
12:30 PM	**Parallel Breakout Live Discussion** Climate Change Strategies
12:30 PM	**Parallel Breakout Live Discussion** National Tree Seed Centre
1:15 PM	*BREAK*
1:30 PM	**Session #10 – Forest Health** **Barley Rose Collier Harris**, University of Oxford, Department of Plant Sciences *Is there resistance to Hylobius abietis in UK Sitka Spruce?* **Eddie Lauer**, North Carolina State University *Broad-spectrum resistance genes in the co-evolved fusiform rust-Pinus taeda pathosystem* **Mengmeng Lu**, University of Calgary *Genomic basis of response to Dothistroma needle blight in lodgepole pine* **Samson Osadolor**, University of Alberta *Lodgepole and Jack Pine Molecular Responses to Cronartium Harknessii, the Causative Agent of Western Gall Rust* **Heather Dun**, University of Oxford *Sudden larch death – variation in host response to infection*
2:20 PM	**Session #10 LIVE Q&A – Forest Health** Moderator: Barbara Wong Barley Rose Collier Harris, University of Oxford Eddie Lauer, North Carolina State University Mengmeng Lu, University of Calgary Samson Osadolor, University of Alberta Heather Dun, University of Oxford
2:45 PM	**Keynote Session (LIVE): Patrick von Aderkas**
3:15 PM	**Wrap Up & Awards (LIVE)**

2021 Forest Genetics Breakout Sessions (Selection)

Breakout – Tree Seed Working Group

The Importance of Cone and Seed Services

Dave Kolotelo (TSWG Chair, BC Tree Seed Centre): Dave.Kolotelo@gov.bc.ca
Melissa Spearing (TSWG Editor, National Tree Seed Centre): melissa.spearing@canada.ca
With contributions from Fabienne Colas (Berthier Tree Seed Centre, MFFP, Quebec):
fabienne.colas@mffp.gouv.qc.ca

This informal session reviewed the current Tree Seed Working Group (TSWG) mandate and activities in promoting tree seed science and technology:

1. Seed research from bud initiation to seed use
2. Identification of seed problems relating to tree improvement and forest management
3. Exchange of information on seed related problems
4. Advising on implementation practices

Chair Dave Kolotelo (RPF, Cone and Seed Officer, BC Tree Seed Centre) reviewed relevant material from the themed 2019 Lac Delage, Quebec workshop titled "Reaffirming the Importance of Cone and Seed Services". This workshop emphasized that the tree improvement delivery system cannot function without renewal and development of expertise and critical facilities. Huge investments are being made in genomics to decrease time to selection, but our membership's concern is that other aspects of the delivery system will become bottlenecks and little attention seems to be given to these core issues:

1. **Facility Closures**
   - Ontario Tree Seed Plant, Pineland Nursery, many nurseries in Canada and USA
2. **Rapid Succession in People and Programs**
   - Loss of practical wisdom, expertise, and field knowledge; serious labour shortages everywhere!
   - Divide between practitioners' needs and science is widening – few extension services to fill the gap
3. **Services Taken for Granted**

- Lack of understanding of the whole tree improvement delivery system
- Lack of funding in public research and extension in practical seed production / processing / pests
- We don't know it all and our product is changing (with climate change / orchard seed)

4. **A Tree Seed Centre requires large capital investment**
   - Not a great business case: highly variable crops, lack of substantial export markets
   - The public sector should be involved; seed fills biodiversity and stewardship mandates

Cone and seed services have changed from public to private responsibility in many jurisdictions since the TSWG's inception in 1983, and this sentiment is echoed worldwide as an area that needs greater awareness, public reinvestment, stewardship responsibility recognition and succession planning for stability. Recent losses of long-running provincial seed centres are an obstacle to knowledge exchange, future availability of tree seed and trusted third-party certification of origin, chain of custody and quality. TSWG News Bulletin Editor Melissa Spearing (Seed Biologist, National Tree Seed Centre) presented updated results from a TSWG membership priority-setting survey that emphasized the membership's top needs on training more cone collectors, optimizing seed orchard production and expertise, studying the effects of climate change on seed crops, and addressing gaps in post-secondary education related to tree seed across North America.

The membership has voted overwhelmingly to maintain and increase knowledge exchange opportunities, with more than 90% of the membership choosing webinars as their current preferred format.

Breakout – How to write a Genome BC/Canada Proposal

Rahul Singh, PhD, Sector Manager – *Agrifood and Natural Resources*

Genome BC was created in 2000 with the strategic goal of exploiting advances in genomics to build BC research capacity, applying genomics to sectors of importance to BC such as Health, Agri-Food, Forestry, Fisheries, and Mining, and for positioning BC as a place for genomics research and translational opportunities. Almost 20 years later, and close to the end of the fourth Strategic Plan (2015-2020), through education, advocacy, and investments, GBC has facilitated the positioning of BC as a genomics powerhouse for research and translation in these important sectors, has enabled the development and positioning of BC as a leader in genomics research, and built world-class research and infrastructure capacity. On April 1, GBC will embark on its next strategic plan spanning 2020-2023 with a goal of advancing basic research and research translation and deliberately focused on genomics innovation in all of our core sectors.

Applicants must demonstrate how their proposal holds a high potential for attaining concrete deliverables by the end of the funding period and therefore translate into significant social and/or economic benefits to Canada, usually within 3-5 years after the close of the project.

- Clearly describe, with supporting evidence, the deliverable(s) that will be realized by the end of the project.

- Describe the plan for next steps for translation of the deliverables: transfer, dissemination, use, application
- Team must include necessary expertise to realize benefits
- Rapid sharing of the outputs of the research (e.g., publications, data and resources) is required

Breakout – Genomic Selection in Tree Breeding

Jean Bousquet, Canada Research Chair in Forest Genomics, *Laval University*

Concerns and opportunities

• Access to cheap but reliable multi-locus genotyping is a major concern: there is little extra budget available in most tree breeding programs, and questions turned around how to set it up and where to find the funding. Some successful examples in Canada were provided of lobbying top management of organizations based on proof-of-concept demonstrations and economical assessments. Also opportunities were mentioned for tree breeding programs to access funding related to adaptation to climate change.

• Concerns were expressed about finding the expertise. Access by tree breeding programs to regional or nationwide genomic selection platforms was suggested, but participants were unsure about governance and leadership (who, where, and how). Research cooperatives and regional clustering of needs for same species were mentioned for sharing expertise and economies of scale.

• More demonstrations needed of types of breeding populations and traits where genomic selection would be most profitable. Some examples were mentioned of recently published studies assessing genomic selection from an economical perspective and assessing genomic selection for traits at the more mature stage including wood quality and resilience to pest and abiotic factors in advanced conifer breeding programs (as shown during the conference: Laverdière et al., Gamal El-Dien et al.).

• Need to access more information about how to best implement genomic selection in backward and forward selection schemes including individual tree selection.

• Climate change related opportunities: genomic selection enabling multi-trait selection (including correlation breakers) or high-intensity selection while preserving genetic diversity, by screening large populations of candidates based on their multi-locus genotypes only. The question of high genotyping costs was raised, however such costs should be compared to phenotyping costs for adaptive or wood quality traits at similar selection intensity, which could be higher notwithstanding the delays in implementing conventional selection for traits evaluated at a more mature stage.

• Possible cross-benefits: (1) genotyping for pedigree reconstruction and more realistic estimates of heritability/genetic gains using the marker-based G-matrix (realized genomic relationships) instead of the pedigree-based A-matrix; (2) the question was also raised if there was a need or opportunity for marker-assisted genetic resource management in conventional tree breeding programs (including seed orchard management, as shown during the conference: Galeano et al.); more cost/benefit assessments needed here.

• Demonstrations needed about the accuracy of genomic selection models in the next generation (cycle); need to start again? More assessments needed here.

Breakout – National Tree Seed Centre

Genomic Data of Today For the Challenges of Tomorrow

Donnie McPhee, MScF, Coordinator: donnie.mcphee@canada.ca
Melissa Spearing, Seed Biologist: melissa.spearing@canada.ca

This informal session reviewed the role of the Canadian Forest Service's National Tree Seed Centre to obtain, store and provide native Canadian tree and shrub seed for research purposes. This mandate has expanded to support cost-effective genetic resource conservation and other ex situ strategies beyond conventional seed banking since Canada ratified the international Convention of Biological Diversity (1992), Canada's Biodiversity Strategy (1996) and the federal Species at Risk Act (2002).

The NTSC maintains three distinct inventories of seed and germplasm: Active Research (available online/through CAFGRIS), Conservation (disjunct populations, SARA-listed or COSEWIC recommended species), and Reserve Collections managed under separate agreements for specific projects and organizations. As of May 2021, the publically accessible Active Research Seed List had 6,797 collections of 119 native species available and 343 collections of 47 exotic species, which are tested for viability every 10 years. Many collections from the 1950s-1990s have maintained high germination capacity, especially of Canada's pine and spruce species.

When funding or program mandates permit, new collections are made in collaboration with federal, provincial and territorial governments, forest industry and improvement councils, universities, corporations and a broad range of conservation groups to continue Canadian forest research and emerging restoration challenges. The 5-year in-kind value of seeds provided to Canadian Forest Service research programs alone is estimated at $1.1 million given the single-tree data associated with each collection to isolate genetic or climatic variables. The NTSC has also begun to routinely gather and conserve DNA samples (leaf tissue or dried branch wood) to provide additional parent-tree material to the scientific community along with viable progeny.

There is now a significant amount of data within NTSC seed testing records being harnessed for reciprocal knowledge transfer training with and for new organizations, particularly Indigenous communities and Parks Canada. A case study on the success of the 2019 bumper black ash (*Fraxinus nigra*) seed banking efforts, media attention, and continued relationship building with Indigenous Nations was presented. The effort resulted in an increase from 315 to 698 seed collections and 27 new

federal ecodistricts represented in the collection. This now ranks as the top hardwood and 9th largest single-species range-wide sampling effort since 1967.

Requests were made to a) donate small seed samples to fill gaps across the country, to back-up provincial seed centre conservation programs, and b) to participate in a national seed supply chain assessment in order to understand seed sourcing needs of domestic organizations engaged in largescale restoration projects beyond legislated reforestation. Participants discussed jurisdictional differences in seed supply infrastructure, collectors trained in NTSC-level sampling standards versus commercial seed standards, staff capacity and job opportunities.

2021 Forest Genetics Oral Presentations

Session #1: Operational Tree Improvement 1

Forest growth in a future climate: tree improvement for white spruce and lodgepole pine in Alberta

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Tree improvement, a method which has been considered effective in addressing the shrinking forest land-base in Alberta, Canada, is challenged by maladaptation associated with climate change. Using both progeny and provenance trial data of white spruce (Picea glauca (Moench) Voss) and lodgepole pine (Pinus contorta Dougl), we developed a 'Height Proportion Function (HPF)' to predict the height growth response of seedlots (unimproved (wild stand seed zone seedlot) versus improved (seed orchard breeding program seedlot)) to climate change. Merging with the top height equations in the Growth and Yield Projection System (GYPSY) and using new age-age correlation equations, we predicted the effect of climate change on the growth and yield of unimproved and improved stands in future climates.

Simulation results indicate that height growth in white spruce is strongly related to the mean coldest month temperature (MCMT), while mean annual precipitation (MAP) has the strongest effect on height growth in lodgepole pine. Regardless of climate change scenario, by 2090, climate change-related growth increases of unimproved stands and improved white spruce stands are expected to be greater in areas with low provenance origin MCMT than in areas with high provenance origin MCMT. Unimproved stands and improved lodgepole pine stands, however, are expected to show decreased height growth across Alberta due to climate change regardless of provenance origin MAP. Furthermore, irrespective of climate change scenario, stands regenerated with improved seedlots will be outgrown by unimproved stands for white spruce by 2090, while stands regenerated with improved seedlots of lodgepole pine will retain their growth advantage over unimproved stands, despite overall lower growth rates regardless of seedlot source.

These results highlight the necessity for, and offer a tool to, incorporate climate change into estimates of the benefits of tree improvement in Alberta, by predicting the growth and yield of both improved and unimproved seedlots under multiple climate change scenarios. These long-term simulation results also indicate that one strategy may not be appropriate in all regions for both white spruce and lodgepole pine and establishing a dynamic Controlled Parentage Program (CPP) region system will be necessary for future deployment from tree improvement program.

SNP-based analysis reveals unexpected features of genetic diversity, parental contributions and pollen contamination in a white spruce breeding program

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Accurate monitoring of genetic diversity levels of seedlots and mating patterns of parents from seed orchards are crucial to ensure that tree breeding programs are long-lasting and will deliver anticipated

genetic gains. We used SNP genotyping to characterize founder trees, five bulk seed orchard seedlots, and trees from progeny trials to assess pollen contamination and the impact of severe roguing on genetic diversity and parental contributions in a first-generation open-pollinated white spruce clonal seed orchard. After severe roguing (eliminating 65% of the seed orchard trees), we found a slight reduction in the Shannon Index and a slightly negative inbreeding coefficient, but a sharp decrease in effective population size (8-fold) concomitant with a sharp increase in coancestry (8-fold). Pedigree reconstruction showed unequal parental contributions across years with pollen contamination levels varying between 12-51% (average 27%) among seedlots, and 7-68% (average 30%) among individual genotypes within a seedlot. These contamination levels were not correlated with estimates obtained using pollen flight monitoring traps. Pollen contamination levels were also correlated with wind direction (Pearson's correlation = 0.92), likely from a pollen source 1 km away from the orchard under study. The achievement of 5% genetic gain in height at rotation through eliminating two-thirds of the orchard thus generated a loss in genetic diversity as determined by the reduction in effective population size. The use of genomic profiles revealed the considerable impact of roguing on genetic diversity, and pedigree reconstruction of full-sib families showed the unanticipated impact of pollen contamination from a previously unconsidered source.

What's the reason? Looking for answers to Alberta's lack of lodgepole pine seed

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Lodgepole pine seed orchards in Alberta have been failing to meet expected seed yields. Over the past decade, only 14% of pine deployment in Alberta has come from improved seed due to difficulty obtaining seed from seed orchards. Earlier work has shown that early conelet abortion, in the first year of conelet development, is a major contributor to these low yields. To investigate this further, we have selected three orchards located in central Alberta for study. Several factors are being assessed to determine causal relationships to seed yield including site location and history), seed orchard type (i.e. grafted versus seedling), environmental variables (i.e. temperature, humidity), and pollination success.

The orchards selected for study were established on old farm land which changed soil structure and introduced a hard-pan layer, factors causing poor or unsuitable conditions for root growth which could impede healthy development of planted trees. One orchard was developed from seedlings, while the other two orchards were grafted. Grafted trees are created by inserting shoots (scion) from selected parent trees into typically 1-2 year old nursery grown seedling rootstock. Grafts often remain in pots for three years before being planted at an orchard site. Grafting success depends on a variety of factors including the suitability of both scion and rootstock for a given site, how well the grafting is performed and the compatibility of the scion and rootstock.

Preliminary research indicates higher conelet abortion rates in graft origin trees as compared to seed origin trees, suggesting a potential grafting effect or latent incompatibility. To better understand this problem, we are looking at a variety of above and below ground variables. Additionally, we are looking at other factors that may contribute to early conelet abortion, which include examining canopy conditions, pollen viability, seed yields of mature cones as well as assessing conelet abortion, development and morphology. With the assistance of the Canadian Light Source, in Saskatoon, we have been able to image the internal structures and pollen tube development in 14 healthy and aborted

conelets using the Biomedical Imaging and Therapy beamline (resolution of dE/E≤10-3 mono beam). Below ground variables include soil water availability, compaction, and analyzing the root systems of trees via ground penetrating radar surveys. To determine if the observed abortion is due to unsuccessful pollination, six high and six low abortion trees in each of the grafted seed orchards will be manually cross pollinated with a pollen mix in spring 2021. Preliminary results collected by the Thomas lab indicate a spatial pattern of microsite conditions within the orchards may also be contributing to the difference in conelet abortion rates although there also appears to be a clonal effect as abortion rates are correlated across years. The goal of this study is to provide orchard managers both insight into the low seed yields in pine and offer mitigation strategies and solutions.

Using landscape genomics to delineate lodgepole pine seed and breeding zones

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Well-defined seed and breeding zones are critical for developing adaptive forest resource management strategies. These zones are traditionally delineated based on local adaptation of phenotypic traits associated with climate variables, which requires long-term field experiments. In this study, we applied a landscape genomics approach to delineate seed and breeding zones for lodgepole pine (Pinus contorta) in British Columbia and Alberta, Canada, based on genomic evidence of local adaptation of this widespread forest tree species across western North America. We used a gradient forest (GF) model to aggregate relationships between the spatial variation of 36,384 single-nucleotide polymorphism (SNPs) and 20 climate variables across 281 populations, and transformed the multidimensional climate gradients into multidimensional genomic gradients. We then used the first three principal components to represent the spatial variation of the multidimensional genomic gradients. Eight seed and breeding zones were delineated for the study area based on the change in within-zone genomic variation. We also predicted genetic offset under future climate change scenarios. Our genomic-based zones are comparable to existing breeding zones and ecosystem classifications, suggesting that this landscape genomic approach could provide an effective alternative for delineating seed and breeding zones for lodgepole pine. Our approach offers an innovative means for defining seed and breeding zones and guiding assisted gene flow in other tree species lacking phenotypic data.

Session #2: Operational Tree Improvement 2

Use of Remote Sensing Technology for Phenotyping in Tree Improvement Programs in British Columbia, Canada

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Tree improvement programs are essential for the establishment of sustainable, high yield seed sources. Currently, the selection of superior genotypes is primarily based on measures of height and diameter. These measurements are labour intensive, time consuming, and expensive. Additionally, they ignore structural and physiological processes that may provide insights into why specific trees perform better than others, and how populations will perform in future climates.

Advanced remote sensing can provide informative structural and spectral indices to measure, analyse, and maintain trials in a new way. In this presentation we describe how these technologies provide detailed and accurate measurements of crown structure, as well as functional traits. We demonstrate how high-density 3D datasets such as those derived from Light Detection and Ranging (LiDAR) and digital aerial photogrammetry, acquired from both unmanned aerial vehicles (UAVs) and aircraft can be used to develop individual-tree metrics for crown and branch characteristics. Additionally, multispectral imagery acquired at targeted wavelengths can be used to produce spectral indices which are proxies for physiological and pigment dynamics associated with photosynthesis, bud burst, drought tolerance, and cold hardiness.

Key crown spectral and structural traits of populations within common garden trials of Douglas-fir and interior spruce in British Columbia can be compared to existing information on their performance to demonstrate how remotely derived attributes can provide additional insights into future tree selection. Findings from this research can be integrated into standardized phenotyping methodologies, which are important not just for monitoring the performance of selected populations, but also for identifying trees that display resilient attributes for sustainable forest management into the future.

Multi-trait genetic selection for improved solid wood quality in white spruce

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White spruce (Picea glauca), as an important boreal conifer species for commercial wood production in Canada, especially for the lumber industry, suffers from long rotation age and adverse correlations between growth and wood quality traits. In the present study, we investigated the genetic control of solid wood quality traits and how they are correlated with other wood and growth traits at the phenotypic and genotypic levels, as well as quantified their interactions with the environment. To achieve this, we collected and analysed solid wood samples and growth records from 289 trees belonging to a polycross genetic trial established on two different sites in Quebec. Based on the results, flexural stiffness and strength, height, DBH and average wood density showed moderate to high heritability and low genotype-by-environment interactions. In addition, flexural stiffness was genetically positively correlated with flexural strength, average density, and acoustic velocity (as a proxy for modulus of elasticity, MOE), with correlations of 0.99, 0.78 and 0.78, respectively. The expected genetic gains varied between 3.6% for acoustic velocity, and 18.0% for microfibril angle (MFA). Furthermore, the efficiency of indirect selection among different wood traits revealed that selection based on wood density and acoustic velocity would result in considerable genetic gains in flexural stiffness. Several selection scenarios were tested based on combinations of multiple traits and the best scenario was identified according to priorities of the tree breeders. We conclude that indirect selection is an efficient method that can be integrated into operational white spruce breeding programs to accelerate the realization of genetic gains for growth and wood quality traits of interest.

Developing genomic selection to integrate drought response in multi-trait improvement of white spruce

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In the context of anticipated climate change, increasingly intense and frequent episodes of drought will affect water availability for boreal tree species, prompting tree breeders to consider adaptation to water stress as a priority. We used a 19-year-old comparative test of white spruce (Picea glauca [Moench] Voss) polycross progeny established on two sites affected by drought episodes to compare the genetic control and the potential for improvement of drought response, compared to more conventional growth traits. To do this, we used genomic selection (GS) based on genomic profiles and traditional selection based on pedigree information only (PS). The genetic control for drought-response traits was somewhat weaker than for growth traits, but with comparable estimated genetic gains, which makes it possible to consider the use of GS at an early age. The accuracy in predicting breeding values for drought response traits was only slightly lower than that for growth traits. We observed opposite correlations between the two sites studied between water stress resistance traits and tree radial growth, but some selection scenarios made it possible to improve all traits while sacrificing very little on height gain, which is the priority trait targeted for this species in Quebec. Our results suggest that integrating drought response into white spruce breeding programs would require only a slight sacrifice in height growth, but that the accuracy of predictions obtained by the genomic or traditional approach is negatively affected by the lower numbers of trees on single sites when the water stress episodes are temporarily and spatially different.

Genomic Selection in western redcedar breeding program in BC: from proof of concept to application

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Western redcedar (WRC, Thuja plicata), a major ecological and commercial conifer species in BC, is renowned for its natural wood durability. The species current breeding strategy is lengthy for measuring desired attributes (~25-year breeding cycles). Genomic Selection (GS), predicting phenotypes from genomic data, has created a paradigm shift through speedy evaluation and improved selection accuracy; however, in conifers GS is in its infancy due to the lack of advanced testing and validation. WRC's unique biology, including long-distance linkage disequilibrium and precocious reproduction, makes it an ideal species to evaluate the application of GS in conifers as it is expected to reduce the breeding cycle to 2 years. Here, we present one of the first GS applications at the operation level with a two-stage approach of model validation and multi-traits early selection at the seedling phase.

Using Capture-Seq genotyping technology of target genic and non-genic regions, we genotyped 113 parent trees, 1520 F1 trees (training population: 19-year- old, 26 PX families collected from 3 sites progeny test) and 3000 F1 seedlings (target population: 1-year-old, 168 FS families). These populations share 26 parents (training population female parents). After filtration, 45K high-quality SNPs were used, we divided these SNPs into three groups (genic-coding, genic-non-coding, and intergenic). The training population was phenotyped for several traits related to growth, heartwood thujaplicins and lignans (late expressed traits underlie wood durability) and foliar monoterpenes (early expressed trait underlie deer browse resistance), while the target population was phenotyped for only foliar monoterpenes.

First, we constructed the genomic relationship matrix (G matrix) to convert the 26 PX families to 447 full-sib families, and identify pedigree errors. The paternity assignment revealed significant unequal male contribution (range: 7-187 offspring/male).

Second, we compared the traditional pedigree analysis (ABLUP, using original PX pedigree) and genomic analysis (GBLUP) in the training population using all traits. The GBLUP analysis outperformed the ABLUP and resulted in increased breeding values accuracies and expected genetic gain. We also compared different SNPs groups using GBLUP.

Third, GS prediction models were fitted for 8 growth, foliar monoterpenes, and heartwood thujaplicins and lignans attributes. These models were validated first in the training population using random ten-fold cross-validation. Moreover, across-generations, -environments, -time validation, and effect of relatedness were assessed. In the second stage of models validation, we independently validated those models in the target population for foliar monoterpenes, taking advantage of assessing it at the seedling target population. The prediction accuracy (PA), the correlation between measured and predicted phenotypes, ranged between 0.08 (removing relatedness) and 0.99 (parent trees predicting training population) depending on the attribute, validation type, and the used reference to estimate PA. The average PA is around 0.7.

Finally, we used the validated models to predict growth and wood traits for the seedling target population and constructed a multi-trait selection index (growth, heartwood thujaplicins and lignans, and foliar monoterpenes) for early selection and selected the best ≈ 100 seedlings for breeding population development and possible seed orchard establishment.

Session #3: Population Genetics 1

Genetic rescue by distant trees mitigates qualitative pollen limitation imposed by fine-scale spatial genetic structure.

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Restricted seed dispersal frequently leads to fine-scale spatial genetic structure (i.e., FSGS) within plant populations. Depending on the spatial extent and pollinators' mobility, inflated kinship arising from FSGS in the immediate neighborhood can critically impoverish pollen quality. Despite the common occurrence of positive FSGS within plant populations, our knowledge regarding the role of long-distance pollination in preventing reproductive failure is still limited. Using microsatellite makers, we examined the existence of FSFG in two populations (MG and RV) of animal-pollinated tree (Pyrus bourgeana Decne). We also conducted hand-pollination experiments using pollen from individuals within and outside of the spatial patches of trees for two consecutive years. Specifically, we investigated the following hypotheses in the Iberian pear: (i) P. bourgeana exhibits significant FSGS with trees within the same patch having increased kinship; and (ii) both fruit and seed production are higher in crosses involving the mating of distant and genetically unrelated trees.

Our results revealed positive FSGS in P. bourgaeana populations, with trees separated by less than 20-70 m exhibiting significantly greater kinship than expected under the permuted null model in MG and RV populations, respectively. We also found lower fruit initiation in flowers pollinated with pollen from highly-genetically related individuals within the neighborhood. No fruits from the crossing between

trees with inflated kinship completed their development. Therefore, fruit production was limited to crosses between distant low-genetically related individuals. Furthermore, fruits coming from the crossing of distant and genetically unrelated trees exhibited heavier fruits with a greater proportion of mature seeds. Our results suggest that positive FSGS can lead to low pollen quality from nearby pollen donors, negatively impacting trees' reproductive success. Under this scenario of intrapopulation genetic rescue by distant pollen donors, highly mobile pollinators' relevance for connecting spatially and genetically distant patches of trees may be crucial to safeguarding population recruitment.

Genome-wide sequencing to understand the evolutionary history of Torrey pine (Pinus torreyana) with implications for species conservation

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Understanding how different evolutionary processes have influenced the distribution of neutral and adaptive genetic variation both across space and time can be invaluable to informing conservation decisions necessary to preserve rare species' evolutionary potential. For species that may be candidates for genetic rescue, these data can be used to evaluate potential risks associated with management decisions. In this study, we focus on Torrey pine (Pinus torreyana Parry), a critically endangered pine, endemic to California. Torrey pine is an ideal system to evaluate the contribution of demographic history, gene flow, and natural selection to population differences that span unique island-mainland distributions. This species is restricted to only two populations, one mainland population in La Jolla, CA, and one island population on Santa Rosa Island, CA, one of the Channel Islands. The combination of small population size, extremely low genetic variation, and abiotic and biotic challenges associated with climate change indicate Torrey pine may have reduced evolutionary potential to adapt to change. Thus, Torrey pine could be a potential candidate for inter-population genetic rescue. Here, we used genomic data to tease apart the respective influence of neutral and adaptive processes on population genetic structure testing demographic models of population connectivity across time and space with contemporary genome scans. Overall, we observed extremely low genetic variation and a lack of population structure within the species. Demographic simulations indicate Torrey pine has likely always suffered from low population size despite some population expansion events. In addition, there is evidence that some gene flow has persisted between island and mainland populations following divergence. Interestingly, despite small population sizes and a lack of genetic diversity, we found no evidence of inbreeding within either population. However, despite a lack of population structure genome-wide, outlier analyses identified over 2000 candidate loci putatively under strong selection. These results suggest that genomic differences between island and mainland populations likely result from selection as opposed to spatial and temporal genetic drift or inbreeding. From a conservation perspective, extremely low genetic diversity within populations indicates that opportunities for within-species evolutionary rescue may be limited. Nonetheless, these results also suggest caution is necessary for implementation of conservation strategies such as genetic rescue. Gene flow between island and mainland populations could disrupt locally adapted gene complexes important to persistence in distinct island and mainland environments.

Assessing the Megagenome of Coast Redwood

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Sequoia sempervirens, sole member of the Sequoia genus and the only hexaploid conifer, is one of the 3,654 plant species that are endangered (IUCN Red List). A long-lived tree that depends on the coastal fog for sustenance is now not only competing with rising temperatures but also habitat loss due to human interference and other light demanding conifers. Although coast redwoods are already affected by climate change, the full extent and how this differs across the range remains unclear. Answering questions regarding coast redwood's resilience under different climatic conditions as well as understanding its evolutionary history in regards to its polyploid status requires a reference genome. The recent assembly of the coast redwood genome leverages both short and long read technology. This includes 122x coverage Illumina HiSeq 4000 paired-end reads, 22x coverage Oxford Nanopore reads, and 39x coverage of short reads for Dovetail Hi-C. The combination of deeply sequenced short read data combined with long reads and capturing long-range interactions within chromosomes enabled researchers to assemble the 26 Gb coast redwood genome with an N50 of 52 Mb. The genome was queried for protein coding genes through an intensive genome annotation analysis. Proteomes of the two additional redwoods, Metasequoia glyptostroboides and Sequoiadendron giganteum, combined with other annotated land plants, were used to identify putative expansions and contractions of gene families. This comparative genomics approach allows for the discovery of unique and shared biological functions. The enrichment of specific gene families and their role in specific pathways can shed light on specific traits such as disease resistance and drought tolerance. Additionally, duplicated genes located along the genome and incongruence between gene trees can provide insight on whole genome duplication events that led to a hexaploid genome. Finally, the genomic resources developed for Sequoia sempervirens will contribute to the small fraction of gymnosperm genomes sequenced to date, and provide a basis for investigations of their adaptive potential in a rapidly changing climate.

Session #4: Climate Change and Adaptation 1

Effect sizes of multilocus genotypes to estimate climate-related phenotypes in lodgepole pine

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Forest genomic resources have expanded rapidly over the last decade as large-scale genomic data have become commonplace resources available to increasing numbers of scientists. However, accurate, repeatable, and translatable methods that integrate multilocus genotypic data with polygenic phenotypes and climate data as the basis for long-term forest management decisions, and the investments of forest stakeholders, are still to be routinely implemented.

A relatively simple genomic analysis method proposed by MacLachlan et al. (2021) used population-level frequencies of alleles with positive phenotypic effects ('positive effect alleles') to explain large proportions of phenotypic variation and identify strong genetic clines with important climatic variables. The positive effect allele (PEA) method was effective because it leverages large sample sizes within populations to count several thousand PEAs and calculate their mean frequency, but within individual seedlings counting positive effect alleles does not explain enough phenotypic variation to base forest

management decisions on. Likely reasons for this are the arbitrary nature of p-value based cut-offs commonly used to identify phenotype-associated SNPs, and the assumption that all allele effect sizes are equal, i.e. 1.0. Allele effect size estimates from genotype-phenotype associations vary greatly but are confounded by effect size inflation of low or high frequency alleles and are usually overlooked in ecological genetic studies.

Using data from lodgepole pine I demonstrate an alternative method for identifying outlier loci associated with growth, cold injury and phenology phenotypes using effect sizes and allele frequencies, rather than p-values. This leads to a simple effect size correction that removes confounding effect size variance inflation at extremes of the allele frequency range. In I turn propose simpler, more data driven summaries of multilocus genotypic variation to improve on the current positive effect allele count method. They have the potential to explain more phenotypic variation and identify stronger genetic clines among populations, and may allow improved genotypic estimates of variation in individual seedling phenotypes. Such estimates would represent a valuable genomic contribution to evolving forest management strategies that aim to select and redeploy climatically adapted genotypes.

MacLachlan I.R., Yeaman S., Rieseberg L. and Aitken S.N. (2021). Genome-wide shifts in climate-related variation underpin responses to selective breeding in a widespread conifer. PNAS (accepted, in press).

Interplay between genetics and environment in an Andean tree species

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Environmental conditions exert major selective pressures on vegetation and are a main driver of local adaptation patterns. Identifying specific effects of individual environmental factors including temperature, precipitation, and day length on the genotypes of local trees is one of the main foci of modern forest genetics. However, disentangling individual effects in situ is often complicated by landscape autocorrelation and overlapping environmental gradients. A native temperate tree species in the southernmost Andes, Nothofagus pumilio,is an ideal study organism because the mountains run almost perfectly north-to-south over the species' continuous 2000-kilometer range. The naturally narrow and linear species distribution follows clear latitude, elevation, and precipitation gradients, which allow us to examine patterns of adaptation and identify SNP loci that may be under environmental selection. We used a paired sampling site study design, in which a pair is two sites that are close enough to share a common evolutionary history but far enough apart to experience different selection pressures, generally less than 1 kilometer apart. We chose seven pairs (and one triplet) of sites along the entire species range in Argentina, and additionally sampled three single xeric sites at the edge of the distribution, for a total of 20 sites. N. pumilio is a wild non-model species that only has a transcriptome available, so we performed targeted sequencing on nDNA extracted from 496 adult trees (~25 from each site). We blasted the N. pumilio transcriptome against 1700+ genes in A. thaliana involved with interesting functions (e.g. circadian clock and stress response), then used reciprocal blast to identify putative orthologs and retained ~1600 contigs from best hits identified in each blast direction. Using this SNP set, we analysed the population genetic structure to determine general patterns of species-wide and subpopulation genetic variation and expansion following the last glacial maximum. We also performed genotype-environment associations using interpolated climactic information (CHELSAcruts dataset) to identify putative SNPs under selection. These results will inform

and fuel further downstream analyses of local adaptation within our project, including GWAS and gene flow analyses.

Association of genetic and climatic variability in giant sequoia reveals signatures of local adaptation along moisture-related gradients.

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During this century, climate warming and altered precipitation patterns will lead to habitat changes that may be detrimental to long-lived tree species. Giant sequoia, Sequoiadendron giganteum, is an iconic Sierra Nevada tree species with populations that tend to be small and highly fragmented, making them especially vulnerable to rapid environmental change. For tree species like giant sequoia, long generation times can limit migration outside of current range boundaries to track climate change. Thus, attention needs to be paid to the risks of adaptive mismatches between a population and its environment. In the face of climate change, an understanding of how environmental factors shape diversity is crucial to predicting species response and directing management. We investigate patterns of genomic variation in giant sequoia using 1364 bi-allelic single nucleotide polymorphisms (SNPs). We use an FST outlier test and two genotype- environment association methods, latent factor mixed models (LFMM) and redundancy analysis (RDA), to detect complex signatures of local adaptation. Results indicate 79 genomic regions of potential adaptive importance, with limited overlap between the detection methods. Of the 58 loci detected by LFMM, 51 showed strong correlations to a precipitation driven composite variable and seven to a temperature-related variable. RDA revealed 24 outlier loci with association to climate variables, all of which showed strongest relationship to summer precipitation. Nine candidate loci were indicated by two methods. After correcting for geographic distance, RDA models using climate predictors accounted for 49% of the explained variance and showed significant correlations between SNPs and climatic factors. Here, we present evidence of local adaptation in giant sequoia along gradients of precipitation and provide a first step towards identifying genomic regions of adaptive significance. The results of this study will provide information to guide management strategies that seek to maximize adaptive potential in the face of climate change. We caution that giant sequoia is a moisture-sensitive species with a distribution that is becoming increasingly arid.

Session #5: Climate Change and Adaptation 2

Integrating dendroecology and genomics approaches to identify genes underlying drought adaptation in white spruce

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Rapidly warming climate affects water availability for boreal conifer species, thus urging the need for assessing their adaptive capacity to better predict forest vulnerability and resilience under drier climates. In this study, we first used a dendroecological approach to determine the level of climate

sensitivity of white spruce (Picea glauca [Moench] Voss) trees grown in a provenance-family common garden. We detected a clear signal of local genetic adaptation to drought, with provenances originating from drier locations showing a higher resilience than those from wetter locations. Based on those results, we further dissected the genomic features underlying white spruce adaptation to drought, by combining gene-environment associations (GEA), genotype-phenotype associations (GPA) and transcriptomics. We identified a set of 285 genes significantly associated with climatic factors or phenotypic traits, among which 110 genes were differentially expressed under drought stress in greenhouse-controlled conditions. The interlinked phenotype-genotype-environment network revealed eight high-confidence genes involved in white spruce adaptation to drought, among which four were also drought-responsive in the expression analysis. Our findings represent a significant step towards the characterization of the genomic basis of drought resilience in conifers, and provide a new opportunity to improve drought resistance of seedlings used in reforestation.

Association genetics of drought tolerance in ponderosa pine (Pinus ponderosa)

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Background

Genotype-to-environment (G2E) association analysis coupled with genotype-to-phenotype (G2P) association analysis promises exciting advances towards discovering genes responsible for local adaptation. We combine G2E and G2P analysis with gene annotation in Pinus ponderosa (ponderosa pine), an ecologically and economically important conifer that lacks a sequenced genome, to identify genetic variants and gene functions that may be associated with local adaptation to drought.

Results

Single Nucleotide Polymorphism (SNP) markers have rapidly gained popularity due to their abundance in most genomes and their amenability to high-throughput genotyping techniques. With the genotyping-by-sequencing (GBS) technique, we identified over 4 million SNPs with 223 ponderosa pine individuals using this pipeline by aligning GBS sequence fragments to the reference genome of Pinus taeda (loblolly pine). Focusing on SNPs in or near coding regions, we found 1458 associated with 5 largely-uncorrelated climate variables, with the largest number (1151) associated with April 1st snow pack. We also planted seeds from a subset of these trees in the greenhouse, subjected half of the seedlings to a drought treatment, and measured phenotypes thought to be associated with drought tolerance, including root length and stomatal density. 817 SNPs were associated with the control-condition values of six traits, while 1154 were associated with responsiveness of these traits to drought.

Conclusions

While no individual SNPs were associated with both the environmental variables and the measured traits, several categories of genes were associated with both, particularly those involved in cell wall formation, biotic and abiotic stress responses, and ubiquitination. However, studies to determine the roles of the genes underlying these associated genetic makers are also needed, particularly as the functions of many of the associated genes have not yet been determined.

Case-control GWAS: detecting adaptive genetic variation associated with drought hardiness in coastal and interior Douglas-fir

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Drought is a growing concern in forest management and conservation of natural ecosystems, and is expected to become one of the main drivers of selection in or extirpation of natural populations of trees across the globe. In a previous study, we tested 74 natural populations of Douglas-fir (both coastal and interior varieties) for drought hardiness, and found most of the phenotypic variation for drought hardiness in seedlings is within populations and the signal of local adaptation for this trait is weak. Here, we explore the within-population variation with a case-control genome-wide association approach in order to identify putative adaptive genetic variants associated with drought hardiness within 20 of these populations. Eighty seedlings per population were submitted to a drought-to-death treatment. Chlorophyll fluorescence and visual damage were monitored over time. Slopes from linear regressions fitted for chlorophyll fluorescence vs. time for each plant were used as a proxy for drought hardiness. The ten least and ten most hardy individuals from each population were selected and pooled based on best linear unbiased predictors (BLUPs) that accounted for spatial autocorrelation within the common garden, and sequenced using exome targeted sequence capture. Cochran–Mantel–Haenszel (CMH) tests were performed in order to identify significant associations between drought hardiness and allele counts for over 1.5 million SNPs in each pooled extreme. Considering a p-value threshold of 0.05 (after correction for false discovery rate), we successfully identified 1,274 SNPs significantly associated with drought hardiness in the interior variety and 907 in the coastal variety. Next, we will annotate the genes identified in this analysis, and examine the distribution of adaptive alleles across 74 natural and 14 seed-orchard populations. Predictions of genomic vulnerability under climate change scenarios will be performed for SNPs highly associated with drought hardiness and found to be within the most relevant identified candidate genes. Results from this study, part of the CoAdapTree Project, will be used to inform breeding programs and assisted gene flow strategies for reforestation of coastal and interior Douglas-fir in the face of climate change.

Genomic characterization of two maples highlights genes involved in the stress response to acidic soils across seasons

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Acer saccharum (sugar maple) is a key ecological broadleaf tree native to Northeastern forests, and is declining in recent decades due to a variety of stressors brought on by climate change and other anthropogenic effects. Nutrient related stress exacerbated by the acidification of soils is a key factor in A. saccharum decline and creates an underlying susceptibility to a broader range of biotic and abiotic stress. Acer negundo (box elder) provides a counterpoint, with its broad native range and tolerance to a variety of abiotic stressors. Newly created reference genomes and annotations for both species allow for investigation into mechanisms of stress tolerance and the adaptive potential of these diploid, highly heterozygous trees. The sequencing design consists of deep long read coverage of Pacific Biosciences SEQUEL and Hi-C data (A. negundo, 100x; A. saccharum, 65x) resulting in moderate-sized plant genomes, estimated at 590Mbp and 440Mbp, respectively. Gene annotation combined existing and novel approaches to evaluate gene prediction methods, leveraging RNA-Seq data generated for both species.

Genomic comparisons among the three existing Acer and other land plants were used to identify putative expansions and contractions of gene families underlying the unique and shared biology of these species, including those that contribute to the iconic autumnal hues of A. saccharum. The new A. saccharum genome was used with stem tissue RNA-seq in a differential expression analysis comparing aluminum and calcium treatment plots at the Hubbard Brook Experimental Forest. This Long Term Ecological Research forest in the mountains of New Hampshire provides an ideal system to examine the impact of past, current, and future soil conditions. Integrated genomic and expression comparisons revealed insights into seasonal shifts in tolerance strategies in response to calcium deficiency, aluminum toxicity, and stress response at the systemic level.

Session #6: Climate Change and Adaptation 3

The evolution of species' ranges in the face of changing environments

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Rapid climate change and range fragmentation drastically affects long lived species like trees. As such, their ability to track shifts in climate through dispersal and gene flow becomes very restricted. Tree species thus rely on the existing plasticity and genetic variation to respond to novel climate pressures. However, the availability of adaptive plasticity and genetic responses may vary across its range due to historical processes of past range shifts and selection. We expect this variability across its range to confer a wide spectrum of resilience and vulnerability to changing climate pressures. To understand this variability, we carried out a large scale common garden study of red spruce - a climate sensitive temperate coniferous forest tree species with a fragmented distribution. In this study, 340 families were sampled from 65 populations from across its range and grown at three common garden sites located along a latitudinal gradient. In order to answer our questions, we estimated phenotypic plasticity, heritability, genetic variation for plasticity (GxE) in phenological traits across the three garden sites. The results reveal red spruce's potential for adaptive responses necessary to maintain climate adaptation, and how this variation is distributed across different regions of its range.

Patterns and climatic drivers of adaptive genetic variation in Douglas-fir

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Characterizing adaptive variation and the drivers of population differences will aid in detecting the sensitivity, resiliency, or vulnerability of natural populations, as well as improve our understanding of how species will respond to environmental change. Variation in fitness within forest tree species is often structured by climate, and novel climate forces brought on by climate change are set to further disrupt the relationship between climatic and fitness optima, exposing constituent systems to ecological and economic risk. Here, combining exome-capture pool-seq data with phenotypic and climatic data across 74 populations of interior and coastal varieties of Douglas-fir (Pseudotsuga menziesii (Mirb.), Pinaceae), we describe the patterns and environmental drivers of adaptive genetic differentiation in this species. Together with study designs targeting genomic variation underlying drought- and cold-hardiness, as well as resistance to swiss needle cast (Phaeocryptopus gaeumannii, Venturiaceae) and rhabdocline

(Rhabdocline pseudotsugae, Hemiphacidiaceae), we associate genotype to both phenotype and environment to describe spatial patterns of adaptive variation. We use this information to quantify climatic drivers of the observed structure, how this variation is partitioned across populations and varieties, and explore climatic scenarios and their impact on predicted vulnerability of populations to future climates. Together, this project will provide critical tools for increasing the resilience of Canadian forests by informing climate-based seed transfer and the breeding of trees for health and productivity under novel climates.

Understanding the adaptive capacity of forest species for climate change from the standpoint of Populus tremuloides, a keystone North American tree

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Climate change is accelerating and causing more extreme climatic event such as severe droughts. This will have negative consequences on many North American tree species. Thus, we need to understand the ability of forest tree species to persist in spite of these changes (adaptive capacity) in order to guide future forest management. Two important factors in disentangling a species' adaptive capacity are genetic makeup and phenotypic plasticity. A key species to study these aspects is the ecologically important Populus tremuloides (aspen) due to its wide distribution range that encompasses Canada, U.S. and Mexico, across varying climatic ranges including different precipitation schemes. Still, the recent decline of aspen cover observed in central Canada and west U.S. is thought to be a result of more frequent and intense drought periods due to climate change. This trend suggests that aspen stands in Eastern Canada could follow in the near future. Aspen can reproduce through seed or clonally, and it can occur as diploid or polyploid. Clonal reproduction in conjunction with polyploid occurrence are thought to be associated with dry-system environments, however such stands might be more vulnerable to climate change due to reduced fertility and genetic uniformity. This project aims to assess the adaptive capacity in Populus tremuloides. As a first step, we used genotype-by-sequencing data to analyse population structure as well as genetic diversity, occurrences of ploidy and clonality across the species' range. Four major genetic clusters were identified, and we found that triploids and clones occur mostly in clusters in drought-prone environments. Additionally, we identified regions in the genome that are under selection and might be involved in local adaptation. Further, phenotypic plasticity under different drought and temperature regimes was assessed via seed germination of Quebec and Utah populations. Genomic signatures of plasticity will be further explored with young aspen plants in a greenhouse experiment. Interestingly, germination rates under drought stress were significantly lower for Utah genotypes compared to Quebec genotypes, suggesting a seed survival strategy under drought. Future research will also focus on associating genetic variants to climate and soil variables. Altogether, these new insight in the adaptive capacity of aspen across the landscape will improve forecasting the impacts of future climate on aspen and help establish new seed zones for this important species.

Session #7: Climate Change and Adaptation 4

Rangewide phenotypic and genomic patterns of climate adaptation in western larch to assess mitigation strategies with future climates

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Shifting climates are disrupting historical patterns of local adaptation in tree populations, introducing a pressing need to understand the risks posed by climate change and mitigation strategies such as assisted gene flow. Climate niche modeling projects that areas of future suitable climate for western larch (Larix occidentalis Nutt.) will stretch far north and west of its contemporary distribution, making it a desirable candidate for assisted migration trials. It was the first conifer species approved to be operationally planted north of its native range in British Columbia, and these plantings have demonstrated its reforestation potential on many sites throughout the province. Previous common garden studies indicate weak geographic clines for growth and other adaptive traits compared to co-occurring evergreen species, suggesting western larch populations may possess high phenotypic plasticity and standing genetic variation. However, no studies have leveraged a combination of phenotype- and genotype-environment associations to test patterns of local adaptation to climate across the extent of its current natural distribution. We assessed phenotypic data on growth, phenology, cold hardiness of 52 natural populations and 28 selectively-bred families as seedlings during their second year of growth (summer 2020) in common garden experiments at the UBC campus in Vancouver, British Columbia. Moderate drought treatments were imposed in 2020 and severe drought treatments are planned for summer 2021 to assess population- and family-level plasticity (GxE) and correlations of phenotypic traits among treatments. Growth, phenology and traits related to drought tolerance will be assessed during the 2021 season. We have also generated exome-capture sequence data for pooled samples from 45 populations for genotype-environment association analyses to identify the strength of and climatic drivers of local adaptation. We will use the genomic data to test whether genetic clusters explain patterns of phenotypic differentiation for climate-related traits among populations in the common gardens. We will use this information to assess vulnerabilities related to climate change and inform strategies for matching seed sources with emerging climates.

Combining climatic and genomic data improves range-wide tree height growth prediction in a forest tree

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Predicting adaptive-trait variation across species ranges is essential to assess the potential of populations to survive under future environmental conditions. In forest trees, multi-site common gardens have long been the gold standard for separating the genetic and plastic components of trait variation and predicting population responses to new environments. However, relying on common gardens alone limits our ability to extrapolate predictions to populations or sites not included in these

logistically expensive and time-consuming experiments. We aimed to determine whether models that integrate large-scale climatic and genomic data could capture the underlying drivers of tree adaptive-trait variation, and thus improve predictions at large geographical scales. Using a clonal common garden consisting of 34 provenances of maritime pine (523 genotypes and 12,841 trees) planted in five sites under contrasted environments, we compared twelve statistical models to: (i) separate the genetic and plastic components of height growth, a key adaptive trait in forest trees, (ii) identify the relative importance of factors underlying height-growth variation across individuals and populations, and (iii) improve height-growth prediction of unknown observations and provenances. We found that the height-growth plastic component exceeded more than twice the genetic component. The plastic component was likely due to multiple environmental factors, including annual climatic variables, while the genetic component was driven by the confounded effects of past demographic history and provenance adaptation to the climate-of-origin. Distinct gene pools had different total genetic variance, with broad-sense heritability ranging from 0.104 (95\% CIs: 0.065-0.146) to 0.223 (95\% CIs: 0.093-0.363), suggesting different potential response to selection along the geographical distribution of maritime pine. Models combining population demographic history, provenance climate-of-origin, and positive-effect height-associated alleles (PEAs; identified by GEAs) predicted new observations as accurately as models relying directly on the common garden design. Strikingly, they were better at predicting new provenances, particularly in harsh environments. Our work therefore shows the potential of genome-informed modeling to improve large-scale predictions of economically and ecologically important quantitative traits.

Predicting lodgepole pine mortality in a changing climate using provenance data

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Climate change has already begun to impact British Columbian forests, and the direct and indirect impacts of climate change on forest productivity are predicted to increase in severity and magnitude. Although growth traits have been extensively studied for adaptation to climate change, the impact of climate change on tree mortality remains unclear. New tools are therefore needed to better understand the impacts of climate change on forest productivity. In this study, a climate-sensitive survival transfer function and a supporting kill selection probability model were developed using long-term, range-wide, repeatedly measured, provenance field data for lodgepole pine (Pinus contorta var. latifola Douglas) in British Columbia. A transfer function was fit to predict annual percent population survival as a function of provenance climate, climate transfer distance, and tree height, the latter variable allowing the climate transfer distance-survival relationship to vary with tree height. The transfer function can be used in conjunction with a separate probability function to predict survival probability for individual trees in a stand, which allows for implementation in a growth and yield model. The relationship between provenance mean coldest month temperature and survival was found to be population specific. Transfer to warmer climates was associated with reductions in survival for most populations, and this reduction was greatest for populations from warm climates. The reductions in survival associated with transfer to warmer climates increased with transfer distance and tree height. The results suggest that local populations at cold sites could fare better under climate warming than local populations at warm sites. This study provides a direct, implementable link between provenance-based transfer functions and growth and yield models to allow simulations of stands under possible future conditions.

Session #8: Population Genetics 2

Butternut throughout space and time: examining range shifts in a rare tree

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Understanding range movements in space and time has long been an important topic in ecology. Range shifts are key ecological and evolutionary processes because they determine community composition, coevolution, and distribution of genetic diversity. However, deciphering species movements is challenging due to the limited availability of data and their biases. Genetic methods can provide evidence of past migration or ecological processes, but these patterns can also be the result of current habitat fragmentation or climatic events. If additional, complementary data sources are used, such as species distribution modeling and fossil pollen records, we can better understand the biogeographic history of species. Juglans cinerea (butternut), a rare Eastern North American tree, has previously exhibited genetic evidence of range shifts following Last Glacial Maximum (LGM). This study re-examined butternut with additional northern range sampling as well as hindcast species distribution modeling and fossil pollen to better understand its migration history. Spatial genetic patterns in butternut are weaker than previously observed, indicating butternut has been shaped by a combination of past glaciation and modern climate. Past species distribution models and pollen records support butternut's ability to persist close to the glacial margin and track glacial retreat. These lines of evidence also support genetic structure which suggest that butternut individuals could have persisted in a cryptic refugium close to modern New Brunswick. These data add to discussion about how species shifted ranges in response to past climate and how much they are threatened by future changes to climate.

Landscape genomic and phytochemical variation across three juniper species and their hybrids

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Hybrid zones offer natural laboratories for understanding how genome variation underlies reproductive isolation and ecologically relevant phenotypes. Those involving foundational plant species may also allow insight into the extended consequences of admixture for higher trophic levels. Juniperus are foundational tree species in many arid regions of western North America, where they are prone to hybridization. Juniperus osteosperma (Utah juniper), J. occidentalis (western juniper), and J. grandis (Sierra juniper) come into secondary contact and hybridize in northwestern Nevada, where past work using cpDNA and nrDNA has suggested a gradient of introgression. We used a reduced-representation sequencing approach (ddRAD) to generate a data set of 8,882 SNPs spanning 326 individuals and 25 populations to infer spatial genetic structure and ancestry across pure and hybrid populations spanning Oregon, California, Nevada, and Utah. Hybrids exhibit ancestry from all three parental species, and are a mix of F1, backcrosses, and advanced Fn hybrids. Our results reveal complex patterns of ancestry in hybrid populations consistent with secondary contact and introgression. To elucidate patterns of phytochemical variation across the hybrid zone, we used untargeted gas chromatography-mass spectroscopy (GC-MS) to chemically profile our genotyped individuals, yielding relative concentrations of 163 unique chemical features. Principal components analysis of untargeted GC-MS data suggest

hybrids occupy a distinct position in chemospace, which is not intermediate among parental individuals. Our ongoing analyses are examining the extent to which environmental and genetic variation jointly predict phytochemical variation across the hybrid zone, and the potential roles of transgressive variation and mismatched dominance in shaping the phytochemistry of hybrids.

The role of history and environment in shaping fragmented distributions of the emblematic serotinous pines of the coastal Pacific Slope

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Pinus attenuata (knobcone pine), P. muricata (Bishop pine), and P. radiata (Monterey pine) comprise a monophyletic group of serotinous pines with fragmented distributions along the west coast of North America. In contrast to the wide distributions characterizing most pine species, these occupy restricted ranges and strongly isolated populations, making them particularly susceptible to the negative effects of warming temperatures as small, rare populations could further constrict with insufficient range expansion. To characterize the historical context of divergence and the spatial genetic structure within each species, we sampled 543 individuals across 32 populations covering the natural distributions from northern California south through Baja, Mexico. Using high throughput sequencing of reduced representation libraries (ddRADseq), we generated genotypic data for ~15,000 genome-wide single nucleotide polymorphisms (SNPs). Despite often occurring in small isolated populations, nucleotide diversity values indicate moderate levels of genetic diversity within populations. Population genetic analyses reveal pronounced spatial genetic structure across the range of each species, with populations from different regions often characterized by marked genetic differentiation. Further, remarkable patterns of genetic differentiation are apparent among discrete stands of P. muricata on Santa Cruz Island, and similarly among discrete stands of P. radiata on Cedros Island. We are currently applying genetic environment association (GEA) analyses to evaluate the influence of specific environmental variables on shaping spatial genetic variation and driving local adaptation. This work should eventually result in a basic perspective on the association of environmental variation with local adaptation in rare, range-restricted conifers, and provide an applied perspective on genetic diversity and the potential of these populations to respond to environmental change.

Population Structure within the Hard Maple Species Complex

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Sugar maple (Acer saccharum Marsh) is the most economically important member of the Hard Maple species complex, a group of related species that occupy a range between Canada and Mexico, and that are adapted to distinct ecological niches. Sugar maple has been identified as vulnerable to rapid climate change, and sustainable solutions are needed to support its role in the production of maple sugar, as well as timber and nursery production in the northeastern US. Genetic relationships between sugar maple and its allies are largely unknown. In the current study, genetic relationships of 278 individuals from six hard maple species were assessed using 20 multi-allelic microsatellite (SSR) loci. Genetic variance was partitioned into separate components for variation within and among populations, within and among species. Most of the divergence among populations (F_{PT} = 0.263) reflected inter-specific divergence (F_{ST} = 0.169), but provenances within species also differed at non-trivial scales (F_{PS} = 0.113).

Estimation and testing of paired inter-provenance divergence showed that all population pairs were statistically divergent. Principle Coordinates Analysis (PCoA) indicated that geography (and associated climatic divergence) are broadly predictive of the pattern of radiation among these taxa.

Session #9: Population Genetics 3

Gene expression profiling provides insights into the architecture of adaptive evolution in a conifer hybrid zone under different selective pressures

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Recent studies highlight that regulatory variants play a dominant role towards adaptive evolution in species with larger genomes. Gene expression patterns are modulated by regulatory variants and have been shown to be variable and strongly heritable across several studies. Coupling common garden experiments with global gene expression profiling provides us the opportunity to assess signatures of adaptive trait differentiation and of phenotypic plasticity at a more holistic scale. Further, co-expression modules obtained from transcriptome wide datasets can be thought of as multivariate traits and lend themselves to a detailed evaluation of the architecture underlying adaptive evolution under different environmental conditions. Using a common garden design with multiple population of Pinus strobiformis - Pinus flexilis hybrid zone we demonstrate strong signals of gene expression G*E effects both at the univariate and multivariate level. Irrespective of the environment the trees were grown in, among population differences in drought intensity was a major driver of adaptive trait differentiation. Further, across both the high and low elevation gardens, co-expression modules that exhibited an enrichment of univariate adaptive transcripts were themselves strongly divergent among the assayed populations but were independent of the module size and exhibited lower preservation across environments. In the low elevation garden we identified two modules strongly associated with survival & with hybrid ancestry that were not preserved across gardens but were enrichment for transcripts exhibiting adaptive evolution. Overall, preserved modules were associated with key developmental processes while adaptive modules not preserved across gardens were associated with stress response. Our work provides key insights into global patterns of gene expression rewiring in a conifer species under different selection regimes as imposed by the common gardens.

Deleterious load in Populus tremula across an active admixture zone in Sweden

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Deleterious load is a well-established phenomenon, widely known to increase under selection as well as through demographic effects, such as bottlenecks, under both domestication and range expansion. Like many other species, Populus tremula has colonized the Scandinavian peninsula after the last glacial maximum from at least two different source refugia. Trees in southern Sweden originate from a southern refugia in central Europe while the northern subpopulation originates from an eastern refugia somewhere in modern-day Russia. These two lineages meet in an active admixture zone in central Sweden. The northern population has adapted to the short growing season through a unique allele at the FT2-gene which drastically alters the timing of autumn phenology and which provides the basis for

sustainable colonization in northern environments. The FT2 allele is located in the middle of a well-established selective sweep region within the northern Swedish subpopulation but is rarely found in the southern subpopulation. The unique colonization history of Swedish P. tremula offers an exciting opportunity to study the behavior of deleterious load within an active admixture zone both across the genome and more specifically around the northern subpopulation-specific FT2 sweep.

Putatively deleterious sites were identified across the exome of P. tremula utilizing a likelihood ratio test (LRT) method based on conservation across a multiple species alignment. These deleterious mutations were subsequently scored in the entire EurAsp collection, comprising of individuals from Iceland, Scotland, Sweden, Norway, Latvia and Russia. Comparisons of deleterious allele and deleterious homozygote counts were then performed across the populations.

We found a clear signal of purging of both deleterious alleles and homozygotes in both northern and central Swedish subpopulation when compared to a Russian population used as a proxy for the eastern refugia. There were also signs of further releasing of deleterious homozygosity within the central Swedish subpopulation. Interestingly, we found that the deleterious allele count in the FT2 sweep region has the strongest negative correlation with latitude when compared to a set of randomly selected regions of similar size within the Swedish subpopulations.

At the whole genome level, the deleterious load behaved as expected with purging in the admixture zone. However, the purging extended further north than expected with both northern and central Swedish subpopulations showing signs of purging. The negative correlation of deleterious allele count and latitude within the FT2 -sweep region is in contrast to the expectations set by studies in domestication, where selection has generally been shown to increase the deleterious load. However, in P. tremula it appears that deleterious alleles have been purged rather than hitchhiked to appreciable frequencies in the region.

The western redcedar genome: exceptionally low genetic diversity despite strong balancing selection in a self-compatible conifer

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We describe the draft genome of western redcedar (WRC, Thuja plicata, Family Cupressaceae) and insights into this species' genetic diversity. A targeted genotyping approach revealed that WRC is one of the most genetically depauperate plant species currently known, with an extremely low effective population size and no significant genetic differentiation across the species' geographic range. Using a unique set of 28 genetic lines derived from up to five generations of self-fertilization (selfing), we explored the relationship between genetic diversity and WRC's mating system. Heterozygosity declined faster than expected during selfing; however, persistence of heterozygosity at a number of loci and

lower than expected reduction in heterozygosity due to inbreeding, as evidenced by observed inbreeding coefficients, suggest associative overdominance and historic purging of strongly deleterious alleles. We found 4,012 single nucleotide polymorphisms (SNPs) deviating from expectations of genetic drift during selfing, many remaining heterozygous against expectations even after four generations of selfing. Despite low genetic diversity, WRC is known to be responsive to both natural and artificial selection, making it a compelling system in which to study the impacts of selfing and reduced genetic diversity on plant adaptation to environmental change.

Session #10: Forest Health

Is there resistance to Hylobius abietis in UK Sitka Spruce?

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Sitka spruce (Picea sitchensis L.) is the most planted tree in the UK and the third largest crop by land area, so is of huge commercial interest. In the UK, the most damaging pest of Sitka spruce is Hylobius abietis (large pine weevil); a bark eating beetle which can girdle young saplings. If saplings are not treated regularly with pesticides this causes an average of 60%, and up to 100%, tree mortality.

This experiment aimed to see if there was any heritable resistance to the large pine weevil within the UK breeding population of Sitka spruce to determine if there is potential to develop a resistance breeding program. Sitka spruce is not a native species to the UK and so far no studies have looked at it's resistance to this native pest, however there was significant success in developing a resistance breeding program in Sitka Spruce to the white pine weevil in Canada.

The resistance trial looked at area of damage, on sapling stems, caused by controlled exposure to the large pine weevil. 13 improved families of Sitka Spruce and 20 full sib individuals from each family were used. The area of damage was measured every 24 hours for 3 days. This and family relationship were then used to get estimates for heritability of damage-level, used as proxy for resistance. A new method was used to determine absolute area of damage which involved tracing the area onto cellophane, photographing it, and analysing it using FIJI.

The data are currently being analysed; in two years a similar experiment is planned using saplings from various provenances across Sitka's native range.

Broad-spectrum resistance genes in the co-evolved fusiform rust-Pinus taeda pathosystem

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Fusiform rust disease, caused by the endemic fungus Cronartium quercuum f. sp. fusiforme, is the most damaging disease affecting economically important pine species in the southeast United States. In this report, we detail the genomic localization and sequence-level discovery of candidate broad-spectrum fusiform rust resistance genes in Pinus taeda L. Two full-sib families, each with 1000 progeny, were challenged with a complex inoculum consisting of over 150 pathogen isolates. High-density linkage mapping revealed two QTL on the distal end of chromosome 9, and a third QTL on chromosome 8. The

QTL on chromosome 9 were additive with respect to their effects on the probability of disease outcome. All three QTL were validated using a population of 2057 cloned pine genotypes in a six year-old multi-environmental field trial. Using long-read PacBio IsoSeq technology, a small number of candidate genes harboring SNP significantly associated with disease resistance were discovered. The results of this study constitute the first genomic evidence for broad spectrum resistance in a conifer species, showing how single qualitative resistance genes can confer effective resistance against genetically diverse mixtures of an endemic pathogen.

Sudden larch death – variation in host response to infection

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Phytophthora ramorum is responsible for disease outbreaks in a range of species, most prominently sudden oak death in the USA and sudden larch death in the UK. Our study focuses on the interactions between P. ramorum and two important forestry species in the UK, European larch (Larix decidua Mill.) and Japanese larch (Larix kaempferi (Lamb)Carr.).

Both larch species are known to be severely affected by P. ramorum often resulting total mortality of entire stands. However, there is evidence of variation in susceptibility between the two species with European larch thought to be less severely affected in the field but the results of experimental trials are inconsistent and not all are statistically significant. We have conducted inoculation experiments on potted saplings and have carried out RNAseq analysis to study the RNA transcript accumulation profiles in response to inoculation. Although not significantly different in lesion development there is an interesting difference in expression of key defence pathways between the two species. European larch has rapid induction of defence genes within 24 hours of infection followed by sustained or increasing expression to 25 days after inoculation. In comparison results in Japanese larch were more varied with fewer key defence pathways responding to infection and the observed gene expression increases were both larger and more transient compared to European larch.

This is variation in response to infection between the two species is of interest as it could help explain differences seen in the field and should be considered in the selection of trees for planting and future breeding.

Genomic basis of response to Dothistroma needle blight in lodgepole pine

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Lodgepole pine (Pinus contorta) inhabits wide ranges of the montane and interior plateau regions of Western Canada and United States, spanning various biotic and abiotic conditions, yet the basis of response to biotic stress tends to be less studied than response to abiotic stress. In recent decades, an outbreak of Dothistroma needle blight (DNB) has caused defoliation and mortality on lodgepole pine in northwestern British Columbia, raising concerns about growth and yield. We inoculated tolerant and susceptible pines with two Dothistroma septosporum isolates to investigate the gene expression response and performed genome-wide case-control association studies using 40 pine populations to

understand the genetic architecture underlying response to DNB. By analyzing the differentially expressed genes, differential exon usage, and co-expressed gene modules using RNA-seq data, we found a rapid and strong transcriptomic response in tolerant lodgepole pine samples inoculated with one D. septosporum isolate, and a late and weak response in susceptible samples inoculated with another isolate. Differentially expressed genes were enriched in PAMP- and effector-triggered immunity pathways. Genes comprising pathways and gene modules had signatures of strong selective constraint, while the highly expressed genes in tolerant samples appear to have been favored by selection to counterattack the pathogen. Using Cochran-Mantel-Haenszel method, we discovered 606 SNPs that were identified to be associated with D. septosporum pathogen response. Gene ontology terms such as peptide receptor activity, miRNA mediated inhibition of translation, are enriched in the candidate pathogen response genes. We also found that scaffolds containing candidate pathogen response genes had higher levels of linkage disequilibrium than scaffolds not containing these candidate genes, suggesting candidate pathogen response genes are under strong selection. In sum, we found a spectrum of functional genes are underlying the genetic architecture of Dothistroma pathogen response in lodgepole pine and it seems natural selection maintain these genes. We incorporated 2,485 probes corresponding disease resistance loci in our latest lodgepole pine SNP array. Our study provides insight into the resistance mechanisms of lodgepole pine to D. septosporum, and promotes the development of tools that can be used to manage DNB outbreaks in lodgepole pine.

Lodgepole and Jack Pine Molecular Responses to Cronartium Harknessii, the Causative Agent of Western Gall Rust

Samson Osadolor[1], Marion Mayerhofer[1], Chandra McAllister[1], Rhiannon Peery[1], Janice Cooke[1]
[1]*University of Alberta*

Western gall rust (WGR) is a fungal disease affecting pines across North America. Attack by the causative agent, Cronartium harknessii, leads to the production of galls on stems and branches of plants. Gall development can lead to reduction and distortion in growth of plants, including mortality of juvenile trees. C. harknessii affects particularly lodgepole (Pinus contorta) and jack pine (Pinus banksiana). Quantitative resistance has been documented in both species, with jack pine being more resistant to C. harknessii than lodgepole pine.

The goal of this study is to understand how defense responses to C. harknessii differ between lodgepole and jack pine, and also how these defense response differ between quantitatively resistant and susceptible families of lodgepole and jack pine. To address this goal, our objective is to determine whether C. harknessii-induced defense responses at the molecular level differ between more susceptible and more resistant families of lodgepole and jack pines, as well as between the more susceptible lodgepole pine and the more resistant jack pine.

Seventy-six half-sib lodgepole pine families were screened for resistance to identify the two most resistant (Pl-R1, Pl-R2) and two most susceptible (Pl-S1, Pl-S2) families. These families, together with one resistant (Pj-R1) and one susceptible (Pj-R2) family of jack pine, were either mock-inoculated or inoculated with C. harknessii, and harvested over a two week time course for hormone, transcriptomic, and quantitative RT-PCR (qRT-PCR) analyses. Quantification of the defense hormones salicylate and jasmonate in seedlings from the above experiment is underway. Since rust fungi like C. harknessii are considered to be obligate biotrophic pathogens, we predict that C. harknessii inoculation will trigger the biotroph-associated salicylate-mediated signalling network rather than the necrotroph-associated

jasmonate-mediated signalling network. Hormone profiles will be compared with expression profiles levels for genes encoding components of the salicylate and jasmonate biosynthesis and signalling pathways generated using quantitative RT-PCR (qRT-PCR).

To complement these hormone analyses, transcriptomic profiling has been carried out comparing C. harknessii- or mock-inoculated lodgepole and jack pine seedlings. Differentially expressed genes (DEGs) generated from RNA-Seq were mined to identify key WGR-responsive DEGs that will be profiled using qRT-PCR. Selection of key DEGs was based on their orthology with genes that have been functionally characterized as being involved in plant defense in annual systems, that is, genes involved in pathogen detection, signalling and secondary metabolite biosynthesis. Furthermore, genes selected for qRT-PCR showed different expression profiles in lodgepole and jack pine RNA-Seq datasets, suggesting a potential role in the differential resistance of these species. Among genes that will be profiled using qRT-PCR includes those coding for terpene synthases, chitinases, pathogenesis-related (PR) proteins and defense regulators known to be involved in plant responses to biotrophic pathogens.

We anticipate that findings from this study will provide valuable information which together with genome-wide association studies and genomic selection, can be used to identify the genetic mechanism for resistance against C. harknessii in pines.

2021 Forest Genetics Poster Presentations

Poster Session #1 – May 19th at 10:45am

1-A-4 Root Rot Resistance Locus PaLAR3 Is Delivered by Somatic Embryogenesis (SE) Pipeline in Norway Spruce (Picea abies (L.) Karst.)

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Heterobasidion root rot is the economically most severe forest pathogen across the northern hemisphere, reducing the benefit of planting elite forest material. By now, one gene leucoanthocyanidin reductase 3 (PaLAR3) is validated to play role in root rot resistance (reduces the decay spread by 27 %).

The aim of the present study was to analyze whether elite Norway spruce material carrying root rot resistantce traits could be propagated by somatic embryogenesis (SE). We analyzed the presence of the root rot resistance locus PaLAR3B among 80 Finnish progeny-tested Norway spruce plus-trees used for SE-plant production as well as in 241 SE lines (genotypes) derived from them. The SE-lines having either AA, AB, or BB genotype for PaLAR3 locus were further studied for their SE-plant propagation ability.

The results indicate that 47.5% of the studied elite trees carry the PaLAR3B allele (45% are heterozygous and 2.5% homozygous). The resistance allele was delivered to the SE-lines as expected based on Mendelian segregation and did not interfere with somatic embryo production capacity. All embryos from PaLAR3 genotypes germinated well and emblings were viable in the end of first growing season. However, in three families, PaLAR3B homo- or heterozygotes had 23.2% to 32.1% lower viability compared to their respective hetero- or PaLAR3A homozygotes. Therefore, the results indicate that there is no trade-off between root rot resistance locus PaLAR3B and somatic embryo production ability, but the allele may interfere with Norway spruce embling establishment.

1-A-5 Seed treatment by cold plasma and electromagnetic field benefit for content of biochemical compounds, antioxidant activity and photosynthesis pigments in Scots pine half-sib families

Ieva Lučinskaitė[1], Vytautas Česna[1], Valentinas Černiauskas[1], Vaida Sirgedaitė-Šėžienė[1]
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Scots pine (Pinus sylvestris L.) is the world's most widely distributed pine tree and it occupies more than 33% of all Lithuania forested areas. Scots pine has huge benefits in ecological suspect like maintenance of sustainable forest ecosystem function and in social suspect, since ability to improve human health. Unfortunately, the species is very sensitive for forest insect pathogens which can expand their nature range, especially in the process of climate change. Various biotechnology methods can be used as tools to increase Scots pine resistance for insect pests. For protection against insect pathogens, Scots pine uses its accumulated secondary metabolites (SM). One of the tools to increase the tree species total phenolic (TPC) and flavonoid (TFC) contents is using of innovative technologies such as physical stressors cold plasma (CP) and electromagnetic field (EMF), which effect highly related to tree species particular genetic family. The purpose of the research is to evaluate CP and EMF influence on TPC, TFC, antioxidant

activity and concentration of photosynthesis pigments, accumulated in different genetic families of Scots pine needles. Scots pine seeds were affected by CP 1 min., CP 2 min. and EMF 1 min. in 11 different half-sib families. Results showed that seeds treatment by CP and EMF had statistical significant increment concentration of TPC, TFC, antioxidant activity and concentration of photosynthesis pigments in 12th half-sib family of Scots pine needles. In this family after CP1 treatment TPC was increased by 0.541 mg g-1, after CP2 treatment – 0.445 mg g-1 and after EMF2 treatment – 0.1 mg g-1, compared to control. The same tendency was established in TFC and antioxidant activity (total free radical scavenging capacities were estimated by DPPH and ABTS methods). Photosynthesis pigments concentration variations in half-sib families of Scots pine needles showed that exposure of EMF increase chlorophylls a, b and carotenoids concentrations in 12th half-sib family. Chlorophyll a concentration after seeds treatment by EMF1 increases 0.237 mg g-1, compared to control. Chlorophyll b concentration after the treatment increases 0.164 mg g-1, compared to control. Carotenoids concentration after the treatment increases 0.073 mg g-1, compared to control. Our study showed that genetic selection is necessary and significant since different Scots pine half-sib families accumulate different amount of biological activity compounds, antioxidant activity and photosynthesis pigments. Furthermore, our results showed that seeds treatment by innovative technologies, such as cold plasma and electromagnetic field had a positive influence for Scots pine resistance mechanisms in a way to increase TPC and TFC, which are extremely important for the tree itself protection against insect pathogens.

Keywords: physical stressors, phenols, flavonoids, chlorophyll, carotenoid, Pinus sylvestris, genetic selection

1-B-10 Individual-based dendrochronology approach to disentangle vigor and sensitivity

Victor Fririon[1], Hendrik Davi[1], Sylvie Oddou-Muratorio[1], François Lefèvre[1]
[1]*INRAE*

Individual trees, not forest stands, respond to environmental conditions. Such an individual-scale approach has rarely been used in dendrochronology studies to analyze the radial tree growth responses to climate. The aim of this study was to apply this individual framework to assess growth diversity of trees facing variable water stress environments, and to identify sensitivity factors likely to drive growth response at stand and individual tree levels.

Using a mixed approach coupling dendrochronology methods with a process-based ecophysiological model to assess water stress level, we defined two phenotypic growth traits: the sensitivity, representing the growth response to water stress level, and the potential vigor, representing the relative capacity to grow in years with no water constrain. Here, we redefine the concept of vigor in order to dissociate it (1) from asymmetric competitive pressures within stands, and (2) from the response to stresses which also affect tree size or average growth rate. We illustrate this approach on five temperate species sampled over a wide range of ecological conditions using the French permanent plot network for the monitoring of forest ecosystems dataset (RENECOFOR, ICP forest network). We analyzed the relation between sensitivity, potential vigor and tree size at individual tree-scale, and the relation between sensitivity, average tree size, local environmental conditions (soil and climate) and species at stand-scale.

We found a positive phenotypic correlation between sensitivity and potential vigor for most of the stands (92%), revealing a growth trade-off between potential vigor and drought resistance. The

relationship between sensitivity and individual tree size was considerably variable between stands and over time within each stand, suggesting that tree social status effect is complex and modulated by local environmental conditions, stand structure and endogenous processes. The variation in sensitivity to water stress among populations was significantly correlated with environmental conditions (positively correlated with extractable soil water and summer precipitation), suggesting local adaptation and/or acclimation.

The individual-scale approach developed in this study revealed the existence of different growth strategies to perform in a context of inter-annual variation in water stress. Our results highlight that accounting for individual variation of the response of trees to climate, and considering sensitivity factors modulating this response, is necessary to understand future stand-scale performances of forests. We suggest the integration of inter-individual diversity in forest dynamics models using the dendro-phenotypic traits of sensitivity and potential vigor in order to predict more accurately how forest stands will respond to climate change and how management actions may influence their responses.

1-B-11 Genetic effects of applying Continuous Cover Forestry approach in non-native conifer UK populations.

Laura Guillardín[1], John MacKay[1], Gary Kerr[2]
[1]*University of Oxford,* [2]*UK Forest Research*

Even-aged plantations of non-native conifer species and clear-cutting silvicultural practices are widely used in UK forestry to maximize timber harvest yield. However, increasing concern for the future adaptability of forests and current policy promoting forests that support a full range of ecosystem services are leading to changes in forestry management. Continuous Cover Forestry (CCF) is an approach to forest management based on the development of diverse stand structures composed of a mixture of species, managing the ecosystem rather than the trees and encouraging natural regeneration. While the transition to this type of woodland is a well-defined silvicultural approach, there is a current paucity of studies on how the transmission of the gene pool from canopy trees to the next generation may affect the genetic diversity (GD) of future forest stands. The GD of non-native plantations may be lower compared to native woodlands. Moreover, the offspring of a population already lacking genetic diversity may be maladapted. The purpose of this project is to assess the genetic effects of applying CCF approach in non-native conifer UK populations composed by Pseudotsuga-menziesii, Thuja-plicata and Tsuga-heterophylla. Therefore, we will compare genetic diversity parameters between canopy trees and natural regeneration by testing populations from natural distributions in North America and non-native populations in the UK exhibiting different stages of CCF. The genetic diversity will be measured using a SNPs genotyping approach developed in a high-throughput microfluidic PCR system. The integration of these results will be used to develop recommendations for natural regeneration management in CCF populations.

1-B-12 DNA-based tracking of historical introductions of forest trees: the case of European beech (Fagus sylvatica L.) in Lithuania

Rūta Kembrytė[1], Darius Danusevičius[1], Jurata Buchovska[2], Virgilijus Baliuckas[12], Darius Kavaliauskas[3]
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Introduction: Is it possible to untangle the historical mosaic of human interference with the origin of forest plantations in Europe? This topic is relevant at the northern frontier of species expansion such as Fagus sylvatica in western Lithuania, where Fagus sylvatica was introduced by German foresters in the eighteenth century. Because of the climate change, especially warming winters, Fagus sylvatica started to spread northwards.The unknown origin and genetic diversity of the introduced tree species can lead to the northern region forests maladaptation.

The aim of the study was to identify the origin and assess the genetic diversity of the introduced European beech populations in Lithuania based on the DNA markers.

Materials and methods. We used 10 nuclear microsatellite loci to genotype 1260 European beech trees from the introduced populations in Lithuania and 18 natural reference populations from Germany, Sweden and Poland as the most likely sources of the introduction. We calculated common genetic diversity indexes and used several clustering approaches to investigate the genetic associations.

Results and conclusion: There was a significant differentiation among the populations at all the loci (Dest = 0.07 to 0.24). The Bayesian clustering returned high likelihood for the Lithuanian European beech stands to originate from three distinct sources: (a) the Bavarian Alps, (b) north-eastern Poland, and (c) south-eastern Poland and the Carpathian Mountains. Despite the high allelic diversity, the Lithuanian European beech populations possessed a markedly lower observed heterozygosity than the natural populations. We assume that the seeds for the Lithuanian stands were collected over a geographically wide range (resulting in high allelic diversity), but at each spot, a few adjacent and likely related trees were sampled. A DNA-based tracking system could efficiently reveal historic transfers of forest reproduce material Europe and help to improve the adaptability of future forests in climate change perspective.

1-B-13 Investigating how genotype and environment influence the growth and drought response physiology of quaking aspen trees

Kelly Kerr[1], William R. L. Anderegg[1]
[1]*The University of Utah*

Determining the extent to which phenotypic variation results from plasticity, local adaptation, or a combination of the two remains a challenge. Yet this knowledge is crucial for evaluating the capacity for tree species to survive under climate change. We are investigating within-species variation in drought response morphological and physiological traits for quaking aspen (Populus tremuloides) using both a sapling common garden and in-situ mature forest stands to answer the following questions: 1) To what extent are traits influenced by genotype and environment? 2) Is there a trait-mediated trade-off between growth under wet conditions and survival under drought conditions? Aspen propagules were grown from root segments collected from five geographic populations across Utah and Colorado and planted into a common garden on the University of Utah campus in spring 2020. Growth and drought response traits were measured in mature stands during summer 2020, and will be measured in saplings in the common garden during summer 2021.

Preliminary conclusions provide evidence that among the aspen populations investigated here, within-species variation in drought response traits may be due to both phenotypic plasticity and local adaptation. At the end of the 2020 growing season aspen saplings in the common garden showed

significant differences in growth, whereby saplings that originated from cooler, wetter climates were taller. Among the -in-situ mature forest stands, we observed substantial variation in morphological and physiological traits. Stands that occurred in cooler, wetter climates exhibited higher rates of leaf area-specific conductivity and less percent loss of conductance during summer 2020. Interestingly, stands that occurred in warmer, drier climates exhibited higher leaf area during summer 2020 which may have been due to earlier leaf out in response to warmer-than-average spring temperatures. Results from this work will help improve predictions of how tree species and populations will respond to future climate change, and inform forest management and conservation efforts.

1-B-15 Identifying biomarkers for stress in long-lived trees: the role of telomere length

Michelle Zavala-Páez[1], David Hainlen[1], Jeff Kittilson[1], Jill Hamilton[1]
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Understanding species response to stress is a major goal across diverse biological disciplines. For trees this is particularly important as they can be challenged by abiotic and biotic stresses due to their long-lived life history. Thus, identifying biomarkers that quantify response to abiotic and biotic environments are increasingly valuable as they provide information needed to accelerate decision-making in species management and conservation. One important biomarker in this context could be telomeres. Telomeres are heritable sequences of repetitive, non-coding DNA found at the tips of the chromosomes that act to enhance genomic integrity and typically shorten during the course of normal cell division. However, recently, attrition related to stress exposure indicate that trade-offs may exist in the maintenance of telomere length in response to life-history variation, disease susceptibility, and aging. Despite their potential role as biomarkers for stress few studies to date have examined telomere length dynamics in plants, and none within long-lived trees species. Populus provides an ideal biological system to assess telomere dynamics owing to its relatively small genome size, ease of clonal vegetative propagation, and economic importance as a source for lignocellulosic biomass. In this study, we will leverage clonally-replicated Poplar common garden experiments to ask what is the rate of telomere loss among the different tissue types? and what is the level of telomere attrition for Poplar clones planted across novel environments? Using genotypes of Populus trichocarpa, P. balsamifera, and their hybrids planted across North America we will quantify the role genetic variation, environmental variation and their interactions may have to telomere dynamics. We will develop a standardized protocol to measure telomere length in Poplars, combining qPCR and bioinformatic approaches. We hypothesize that telomere sequences and composition are conserved between the two species and their hybrids, but length may vary in response to environment. We predict that telomere loss may vary across tissue types and will be most notable in actively growing meristematic tissue. In addition, we predict climate transfer distance will correlate with telomere length loss, providing a metric to quantify trade-offs between the maintenance of genome integrity and exposure to novel environments. These data will provide fundamental information on the role telomere length dynamics may have to quantifying trade-offs associated with the maintenance of genomic integrity and adaptation needed for species management and conservation in forest trees.

1-B-16 Climate-based seed deployment zones for the Pacific Northwest

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Native populations of forest trees are specifically adapted to the climates they inhabit. The farther trees are moved from their local climates (i.e., as the climatic transfer distance increases), the more growth and survival tend to decrease. The transfer limit is the climatic transfer distance beyond which plantation performance is considered unacceptable. Thus, to ensure healthy and productive forests, the climatic adaptation of seedlots (i.e., seed from native stands or seed orchards) must be matched to the climate of the planting site. These concepts are important for current seed transfer and for assisted migration. Fixed zone (i.e., geographically based) seed deployment systems are frequently used to match seedlots to potential planting sites in the Pacific Northwest (PNW). However, the fixed zone method limits the deployment of seed and makes it difficult to share seed among organizations that use different zone systems. We developed analyses for a focal zone (i.e., climate-based) seed deployment system, which is available to use via the Zone Matcher web application, to enhance regeneration success, forest productivity, and adaptation to climate change.

To analyze climates in existing zone systems across the PNW, we used a climate interpolation model called ClimateNA (Wang et al. 2016). We worked with stakeholders to identify zone sets to include in our analyses, thus ensuring a relevant and usable product. We measured climatic ranges within zones to infer minimum safe transfer distances. To reduce the number of climate variables needed to calculate Euclidean climate distances among all zones, we selected climate variables that explain the largest amount of among-zone variation. To select climate variables, we partitioned climate variation within and among zones, performed Random Forest analyses, and identified highly correlated climate variables.

To enable users to explore these results and identify matches between zones, we developed the Zone Matcher web application. Users first choose a focal zone, and then Zone Matcher finds all zone matches within an acceptable climate distance. Users can also select a candidate zone to evaluate its match to the chosen focal zone. In this case, Zone Matcher shows the Euclidean climate distance and differences in 16 climate variables, photoperiod, latitude, and longitude between the focal zone and candidate zone. Zone Matcher includes climate matches for current, historic, and future climates (up to the year 2100 and for two future climate scenarios), allowing the user to adapt their seedlots on a time scale and climate scenario of their choosing.

1-B-17 Evaluating assisted gene flow as a strategy to conserve California tree species under climate change

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Anthropogenic climate change may cause many species to be maladapted to the sites where they currently occur, and is happening so rapidly that many tree species may not be able to adapt to new conditions or migrate to suitable locations due to their long lifespans. One management strategy that may allow trees to persist in parts of their range is assisted gene flow (AGF), the movement of individuals or gametes within a species range to locations where they would be pre-adapted to future climate condition. For example, individuals from warmer parts of the range could be planted in regions that will become warmer in the future. However, AGF may not be possible for all species, especially those with small ranges or climate niches. Moreover, it assumes that trees are adapted to current climate when they could be adapted to cooler climates of the past. To assess the utility of AGF for a range of species and to prioritize species, we introduce a method that takes into account which species

are 1) at the greatest risk of extinction or extirpation due to climate change, and 2) have populations that may be pre-adapted to future climates in other parts of the species' range. Using occurrence data and climate models for 46 California tree species, scores were calculated for climate risk, or the degree of change in climate a species will experience throughout its range; and AGF feasibility, or the proportion of populations in one part of the range that may be pre-adapted to future climate in other parts of the range. Because populations may be locally adapted to current climates or adapted to past climates as a result of adaptational lag, both present climate and climate at the last glacial maximum were evaluated when calculating AGF feasibility. These results identify tree species that could be good candidates for AGF.

1-B-18 Bibliometric analysis of the structure and evolution of research on assisted migration

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Assisted migration is increasingly proposed as a proactive management strategy aimed at mitigating the consequences of maladaptation predicted under climate change. However, Knowledge's structure, research gaps, future research directions need to be explored to develop framework necessary to apply assisted migration strategies. Here we use bibliometric analysis to examine the intellectual, social, and conceptual structure of assisted migration research using these data to identify gaps and opportunities for future research. Data of publications were collected from Scopus and the Web of Science databases, merged, processed, and analysed using R and VOSviewer softwares. Assisted migration research per se started in 2007 and number of publications increased steeply from 2007 to 2015 to reach 44 publications per year, thereafter, the number of publications fluctuates slightly between 2015 and 2020. Co-citation and keywords co-occurrence networks were overlaying and identified three major conceptual groups. The first conceptual group focused on theory, and risk of assisted migration of threatened and endangered species and identified plant and animal conservation ecologists; the second group assessed the impact of climate change on realized and fundamental climate and geographic niches; the third group focused on assisted population migration and was composed mostly of forest geneticists. Collaboration network identified three social core hubs: North America, Europe and Australia where the United States and Canada were both the most productive and the most collaborative countries. Topics where increased research was expected include assessment of species and population response to extreme climate events. Avenues for future research include rules of epigenetic memory, biotic interactions and atmospheric CO2 in population performance and temporal evaluations of species fitness in response to climate change. Overall, more interdisciplinary training and international collaborations will be necessary to address gaps and challenges underlying the implementation of assisted migration.

1-B-19 *Gender assessment in Populus tremuloides, a North American keystone species*

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To guide future forest management and conservation efforts, we need to understand the ability of forest tree species to persist under predicted climate change. The species Populus tremuloides (Quaking aspen) is exposed to a variety of different local environments across its natural distribution which ranges from Alaska to Central Mexico and across Canada. Therefore, Quaking aspen is our species of choice for studying genetic adaptation to local climate. Aspen is also dioecious, and dioecious species often exhibit spatial segregation of the sexes, which can make them more vulnerable to climate change. The overarching goal of the study is to test the hypothesis whether male individuals are more common in low-resource microsites and females are more common in high-resource microsites, assuming higher cost of sexual reproduction in females, which could lead to a biased sex ratio. To start, we obtained insights into the distribution of female and male aspen trees (1,156 individuals) within natural aspen stands and across the North American landscape, by using a simple PCR-approach that is based on the presence/absence patterns for the male-specific gender locus TOZ-19 (see Figure). While gender assessment was our exploratory study, ultimately, we want to determine whether certain environmental factors drive the distribution of males and females in P. tremuloides.

1-B-20 Gene expression meta-analysis identifies candidate genes involved in abiotic stress response: difference between forest species and short-life species

Cesare Garosi[1], Roberta Ferrante[1], Cristina Vettori[2], Donatella Paffetti[1]
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Plants live in constantly changing environments that are often unfavourable or stressful for growth and development. The negative effects of these abiotic stresses are exacerbated by climate change, which has been predicted to increase the frequency of extreme weather phenomena. To survive, sessile plants have to cope with the above-mentioned stress conditions, either individually or, more commonly, in combination. The direct proportion between phenotypic plasticity potential and genetic diversity is now widely recognised. Plants exhibit a great variety of genetic expression, metabolic pathways and physiology in relation to different environmental stimuli. The acquisition of new knowledge about these dynamic molecular events has always been a topic of great interest. Despite the focus that this area has received in recent years, there is still a considerable knowledge gap. Most of the studies are on short life cycle plants, and information on forest species is scarce and limited to model species. However, the increasing availability of tree species genomes associated with improvements in the field of new generation sequencing (NGS) techniques provides a powerful tool to understand the genetic architecture behind the response to abiotic stress. To fill the knowledge gap on the molecular response of plant to climate change, we conducted a meta-analysis to verify the presence of possible differences in the expression of some candidate genes between European forest species and the principal short-cycle plant species. We conducted the analysis using a database of candidate genes, developed within the LIFE project SySTEMiC. In the first phase we conducted a systematic review of gene expression studies on short-cycle plant species of selected candidate genes. Then we conducted a meta-analysis using two software tools: Comprehensive Meta-Analysis Version 2.0 and JASAP (graphical interface based on the R language). The analyses are still in progress. This first study will be useful to validate the meta-analysis protocol in order to extend the research to other genetic databases of different forest species. The results obtained will allow us to deepen our knowledge about the different mechanisms of response of plant species. This work is part of LIFE18 ENV/IT/000124 SySTEMiC (Close-to-nature forest sustainable management practices under climate changes) project with the aim of developing a

combination of advanced landscape genomics, applied genetics, modelling and silvicultural as a tool for sustainable forest management in the changing climate.

1-B-6 Linking dendroecology and molecular signatures of adaptation in Pinus halepensis

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Tree productivity is expected to decline in dry environments such as those typical of Mediterranean forests under climate change. However, the particular responses to environmental factors may substantially differ among individuals as a consequence of intra- and inter-specific genetic differentiation and the presence of local adaptation. In this study, we linked dendrochronological and genetic records obtained from a common garden experiment located in central-eastern Spain in order to characterise population differences in radial growth responses to climate factors and their genetic control for a widespread Mediterranean conifer species (Pinus halepensis Mill.). The analysis comprised 20-yr ring-width series of 130 P. halepensis trees from 23 populations representative of the natural distribution range of the species. Using factorial regression models, population by year and tree-nested-to-population by year interactions were described in relation to (i) key climate factors involved in radial growth determination and (ii) a set of single nucleotide polymorphisms (SNPs) known to be related to primary and secondary growth dynamics, leaf area and photosynthetic pigments. The main aim was to contribute to understanding the genetic basis of growth determination for the species by linking genes and phenotypes – structured in populations – with potential climate drivers of growth. Overall, we found that inter-annual growth of the whole set of trees was positively influenced by current spring precipitation and winter minimum temperature and negatively by previous autumn and spring maximum temperature. However, populations reacted differentially to maximum temperature of current May, precipitation of previous November, drought index (SPEI) at 1-month scale of previous September, and SPEI index at 6-months scale of current October which altogether explained ca. 60% of population by year interactions. On the other hand, three SNPs explained about 8% of population differences in inter-annual growth variability. Once both models were assembled, we found one SNP involved in vertical growth showing reaction to a particular climate factor (drought occurring in previous September) at the population level; the interaction between this SNP and climate, however, explained barely 2% of population by year interaction. This study represents a first attempt to integrate genetic and environmental information into statistical models explaining differential radial growth responses of populations to climate for a species of high ecological interest such as P. halepensis.

1-B-7 Predicting the global fundamental climate niche of lodgepole pine based on provenance trials

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Provenance-trial-based fundamental niches of plant species can better facilitate assisted migration for adaptation to climate change than the species-occurrence-based realized niches. This study developed a model to predict the fundamental niche for lodgepole pine based on tree-height from a wide-ranging provenance trial dataset. The model integrated genetic and environmental effects of climate into a single model and could predict the performance of any population at any planting site. The model was built through comparisons and optimizations of two candidate models, universal response function (URF) and universal transfer function (UTF), with linear and linear mixed-effect forms and varying

sample sizes. Both URF and UTF models had the same prediction accuracy, but the URF was more straightforward in identifying optimal provenance climate for a given planting site. Linear mixed-effect models did not show clear advantages over linear models in model predictions but prevented including additional predictors. Our final model predicted the fundamental niche of lodgepole pine at high accuracy on the global scale. We found that suitable habitat for lodgepole pine was widely distributed over the world for the current and future periods, which provided enormous potential for assisted migration. Our findings provided insight for model development in forest genecology and provided a basis for assisted migration at the species level and assisted gene flow at the population level to optimize adaptation and productivity for lodgepole pine under a changing climate.

1-B-8 Variation in aspen seedling performance based on family and gender under drought stress

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Trembling aspen (Populus tremuloides Michx.) is a diecious clonal tree species native to North America, which has seen a recent decline in health across much of its range, primarily due to drought. Based on the hypothesis that females may carry a higher cost to reproduction than males, we tested the performance of seedlings, subjected to abiotic stress, to determine if there are differences in size or growth rate at an early age. We hypothesize that male seedlings will outperform female seedlings, due to possible early somatic costs of reproduction in females. In addition to gender, genetics and family origin (provenance) could also potentially influence performance. We expect seedlings originating from drier regions to be more tolerant to drought conditions when compared to seedlings from less drought prone regions, based on the assertion that selection pressure favours individuals adapted to the water availability of the local environment. The objectives of this study were to: i) test if female and male aspen seedlings perform differently under drought stress, and; ii) explore the strategies of families from two different provenances under drought conditions. Catkins were collected and seed extracted from 19 different open-pollinated aspen trees, from two climactically different regions in Alberta (Peace River, higher Climate Moisture Index; CMI; and Camrose, lower CMI). Seeds were commercially grown for one year and leaf tissue was used to determine gender in 48 seedlings per family. The following year, one-year old seedlings were grown in a greenhouse for 10 weeks under well-watered (90% field capacity) and sustained drought conditions (75% field capacity based on mass weight) in a split-plot replicated block design experiment. Height, diameter, bud-burst and gas exchange were measured throughout the experiment before harvesting the seedlings for total leaf area and biomass of roots, shoots and leaves. Preliminary results will be presented.

1-B-9 Exploring Drought Stress Relevant Gene Variants of Abies alba in the Alpine Region

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[1]*Austrian Research Centre for Forests (BFW),* [2]*University of Natural Resources and Life Sciences, BOKU*

The inneralpine Vinschgau valley in South Tyrol harbours silver fir (Abies alba Mill.) populations on notably dry sites. The high vitality of these populations which are located on the margin of the species climatic distribution range, gives reason to suggest local adaptation. Signatures of drought adaptation were investigated by applying an environmental association analysis (EAA) based on both single-nucleotide polymorphisms (SNPs) and simple sequence repeats (SSRs). This is achieved by comparing populations with contrasting water balance in Tyrol and South Tyrol. Neutral genetic differentiation

between populations north and south of the main Alpine ridge is low (FST = 0.01-0.02), indicating common postglacial recolonization routes. Both neutral and adaptive genetic diversity is elevated in South Tyrol. Thirteen sets of single-base extension primers were successfully designed in the framework of this study. SNP 102.1 is highly differentiated (FST ~ 9%) between populations in Tyrol and South Tyrol and was associated with annual precipitation differences by multiple linear regression. None of the analysed SNPs was associated with the same environmental factor consistently by both partial Mantel test and linear regression. The majority of the 13 SNPs display higher genetic differentiation between the regions compared to SSR-based estimates. Overall SNP differentiation is elevated between the populations in South Tyrol, indicating adaptive differences at the small regional scale. Due to the limited number of loci and study sites, the adaptive role of the analysed SNPs to drought stress response should be validated on a broader geographical scale, ideally in combination with phenotypic measurements. We conclude that populations in South Tyrol are particularly valuable under projected climate change scenarios due to their elevated adaptive capacity and adaptation to both cold and drought periods.

1-C-21 GeneNet: mapping the genetics of Ireland's native forests in a European context.

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Of Europe's 265 native tree species, 42% are at a high risk of extinction. The severity of this risk partly depends on the abundance of its forest genetic resources (FGR). If the FGR for a given species are low, its adaptive potential against future environmental challenges will also be low. Mapping Europe's FGR is therefore critical for understanding which populations need to be prioritised in future conservation efforts. GeneNet, which is funded by the Irish Department for Agriculture, Food and the Marine, is a 2-year collaborative project between The National Botanic Gardens and Trinity College Dublin. The project sets out to map Ireland's native FGR for the purpose of updating the European FGR database, EUFGIS. This database was initiated by the European Forest Genetic Resources Programme (EUFORGEN), an EU-wide network that promotes and shares information on FGR conservation. EUFGIS maps locations known as "conservation units" which are likely to possess important FGR. Preliminarily, Ireland has 17, although none of these have been characterised genetically. The two main aims of GeneNet are to: (1) update the Irish EUFGIS section with a more detailed geographical information system (GIS) using the most up-to-date Irish Woodland surveys and forestry databases (e.g., the 2003-2008 National Survey of Native Woodlands), and (2) genetically characterise the 17 initial conservation units along with a further 25 units. Genetic characterisation will involve haplotyping 7 'high-priority' species, including black alder, ash, downy birch, silver birch, sessile oak, common oak and Scots pine. Haplotyping will mainly be achieved using established chloroplast DNA and microsatellite markers which have been used to characterise other European populations. Currently, molecular analysis is underway on over 600 individual trees sampled across 20 ancient woodland sites. The results of GeneNet will be used to resolve broad phylogeographic patterns across Europe and elucidate the contribution of Ireland's native trees to the overall FGR of Europe.

1-C-22 Seeing the forest and the trees: landscape scale genetic diversity in three Canadian conifers

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Landscape-level genetic diversity considerations in reforestation are essential for resiliency and for the continued supply of economic and social benefits that forests provide to Canadians. As breeding programs for BC's economically important forestry tree species enter into advanced generations, improved seed with increasing levels of genetic gain is being used in broad-scale reforestation. At the same time, climate change is generating stochastic risks to tree growth and survival. Although genetic diversity will buffer against future uncertainty, it must be balanced against selection for economically valuable traits in breeding programs. Tree breeders manage population size and relatedness to maintain genetic diversity in breeding populations, and seed orchard managers estimate diversity-related parameters in improved seed to meet requirements for reforestation. In light of new forest policies and new knowledge about the genomics of growth and climate adaptation, genetic diversity of planted forests at the landscape scale needs to be evaluated. In this project, we will use genomic datasets for lodgepole pine (Pinus contorta Dougl. ex. latifolia Engelm.), Douglas-fir (Pseudotsuga menziesii Mirb.), and interior spruce (Picea glauca [Monech] Voss x Picea engelmannii Parry ex Engelm.) to evaluate the adequacy of current methods for estimating genomic diversity and determine how diversity within improved seed compares to seed from natural stands. We will genotype mature planted stands of Douglas-fir and interior spruce that have experienced the cumulative effects of selective breeding, nursery practices, natural regeneration, competition and other sources of mortality to assess the implications of increasing the area of planted forest on landscape genetic diversity over time. Using this genomic data, we will use population-genetic simulation models to evaluate the long-term implications of reforestation strategies on landscape-level diversity. Once completed, results from this project will be used to assess current policies and practice, and to recommend any needed changes.

1-C-23 Conserving hemlock: Utilizing genomic resources

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Hemlock forests contribute a significant amount to the forest cover in Eastern North America. Covering over 1.3 million hectares, these 800-year-old trees are foundational to their habitat- supporting unique flora and fauna like the red-backed salamanders and red-spotted newts. In the 1950s, the hemlock woolly adelgid (HWA) was introduced to the North American continent, and would later become the cause of massive destruction. These adelgids target the cuticle of these trees, causing the leaves to fall, thereby reducing photosynthesis and stomatal conductance until the trees starve. On average, it takes five to ten years for hemlock stands to die. Given this rate, a concentrated effort is needed to save these forests. There are three main strategies towards this effort- using chemical control in the form of pesticides, or biological control by using native or related predators; or leveraging the innate genome resources of these trees against the HWA. Different species of hemlock range in their responses to the adelgid, with the Chinese hemlock (Tsuga chinensis) being the most tolerant to the pest, and the Carolina (T. caroliniana) and eastern hemlocks (T. canadensis) being the most susceptible. Interestingly, even within species of hemlocks, there are individuals of hemlocks that show different levels of tolerance to the HWA. to combat this threat and understand more about Tsuga evolution, a high-quality reference genome for the Carolina hemlock is underway as part of the Open Green Genomes Project. Apart from being the first genome of its genus, this high-quality genome will facilitate comparative genomics in and across hemlocks to fully understand differential responses to HWA.

1-C-24 Creating practical sampling guidelines for endangered IUCN Red List Oak species through simulation

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Collecting and conserving genetic diversity from plant populations for ex situ collections is a major conservation objective of seed banks and botanic gardens. However, current guidelines for collecting germplasm to preserve plant species ex situ might not adequately capture the genetic diversity of wild plant populations. In particular, sampling guidelines tailored to rare species are lacking, but can be produced by simulation. Here, we aim to recommend minimum sample sizes for several IUCN Red List oak species to aid in practical seed sampling guidelines. Oaks have high ecological importance, as they are keystone species in many environments. In addition, oaks are exceptional species, meaning they cannot be seed banked using traditional methods. Thus, it becomes increasingly important to develop sampling strategies that efficiently and effectively capture the genetic diversity of these rare species. In this project, we used genetic simulations to represent several rare oak species and 'sample' from these populations using R. Specifically, we aim to quantify performance of sampling across the range of possible sizes--from 1 individual to the total population size. From this, we determined the minimum sample size required to capture 95% of the species' genetic diversity, which is a common threshold for sufficient genetic diversity. With this data, we aim to recommend a minimum sample size to capture sufficient genetic diversity for each of these oak species, which would be directly useful to botanic gardens and arboreta. We can also answer the question, "Does one sampling strategy fit all rare oak species?"

1-C-25 Setting the baseline for genetic monitoring of Alnus glutinosa in Lithuania

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Ever-increasing climate changes affect natural ecosystems at regional, national and international scales. Riparian ecosystems are among the ones that are most heavily affected. Alnus glutinosa (black alder) is the key species that forms forest riparian ecosystems in Europe and Lithuania, therefore in the era of climate change the future of this species is uncertain.

Black alder is the only tree species that tolerates flooding over long periods, therefore it is abundant in river valleys, around the wetlands and forms unique yet confined ecosystems. Currently in Lithuania this tree species comprises 7.8 % percent of country's forested area. However, wetlands are among the most threatened habitats, affected by currently occurring climate change.

Currently, implemented genetic monitoring programs for forest tree species that evaluate genetic diversity changes over time are scarce worldwide, and only few are being implemented. A. glutinosa is not represented in any of them and this key riparian ecosystem tree species has never been genetically monitored in Europe. There are several studies that deal with its genetic characterization, however the temporal changes in black alder populations has never been studied before.

The aim of the present study is to assess genetic diversity of mature trees and natural regeneration young trees in A. glutinosa populations in Lithuania, establishing a baseline for future genetic diversity evaluation, following the protocols of Aravanopoulos (2011, 2016).

For this study ten natural A. glutinosa populations in existing GCU's for black alder in Lithuania were sampled (Figure 1). In each of the sampled population 30 mature (approx. 60 years old) trees and 30 individuals of the natural regeneration (≥ 20 years old) were sampled. To capture as much of genetic diversity as possible in a GCU the trees were evenly sampled over the corresponding GCU area at a minimum distance of 50 m. Wood samples of mature trees and leaf samples of the natural regeneration were collected for DNA analysis.

To assess genetic diversity of the mature trees and the natural regeneration we selected 20 polymorphic SSR primers, following protocols of Lepais and Balces 2011; Drašnarová et al. 2014.

Poster Session #2 – May 20th at 9:15am

2-D-26 Comparative Transcriptomic Analysis of Juvenile and Adult Leaf Morphologies in Conifers

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In land plants, heteroblasty broadly refers to a drastic change in morphology during growth through ontogeny. Juniperus flaccida (Schlechtendal) and Pinus cembroides (Zuccarini) are conifers of independent lineages known to exhibit leaf heteroblasty between the juvenile and adult life stage of development. Juvenile leaves of P. cembroides develop spirally on the main stem and appear decurrent, flattened and needle-like; whereas, adult photosynthetic leaves are triangular or semi-circular needle-like, and grow in whorls on secondary or tertiary compact dwarf shoots. By comparison, J. flaccida juvenile leaves are decurrent and needle-like, and adult leaves are compact, short and scale-like. A transcriptomic analysis was performed to evaluate differences in anatomy and gene expression patterns between both species (P. cembroides and J. flaccida). RNA from twelve samples was sequenced on HiSeq 2500 (100bp PE) and analyzed with available software. Because there are no reference genomes for these species, they were assembled de novo from the RNA-Seq reads. Following assembly, 63,741 high quality transcripts were functionally annotated in P. cembroides and 69,448 in J. flaccida. Evaluation of the orthologous groups yielded 4,140 shared gene families among the four references. Interestingly, activities related to cell division and development were more abundant in juveniles than adults in P. cembroides, but vice versa in J. flaccida. Overall, there were 509 up-regulated and 81 down-regulated genes in the juvenile condition of P. cembroides and 18 up-regulated and 20 down-regulated in J. flaccida. In comparing the expression patterns between juvenile and adult P. cembroides samples, we detected proteins responsible for the synthesis of cellulose and xyloglucans that make up the cell wall, proteins involved in cuticle biosynthesis through processing of long and very long fatty acids to produce wax and cutin, and five type II MADS-box genes. In J. flaccida samples, we detected changes in proteins related to regulation of photosystem metabolism and secondary metabolites production.

2-E-27 Secondary metabolites, antioxidant activity and photosynthesis pigments variation on Scots pine in the process of Lymantria monacha mass outbreaks

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Scots pine (Pinus sylvestris L.) is one of the prevailing tree species distributed in north temperate and boreal zones in North America, Europe and Asia continents. The species plays an unquestionable role in forest ecosystem and in human lives owing to emitting a large amount of phytoncides that help to increase people health. Biotic stressors such as forest insect mass outbreaks disturb forest ecosystem, especially by causing changes on fungal communities. Scientists revealed that insect outbreaks highly related to climate change, they have dramatically increased over the last years and new pest insects have been expanded their natural range. The same tendency has fixed with one of the hazardous insect pest in Central Europe nun moth (Lymantria monacha L.) which recurrent mass outbreaks have been detected in Finland from 21st century and also grown more abundant in there. Lymantria monacha mass outbreaks were established in 2019 and 2020 summers in temperate zone in Lithuania and they had enormous impact on Scots pines health. For protection it was used spray "Foray 76B" which had been made of Bacillus thuringiensis bacteria. Despite the fact that spraying helps to destroy Lymantria monacha grubs which gnaw Scots pine needles, it can has negative consequences for the tree growth and health in the future. Based on that, there is looking for Scots pine internal properties which could help to increase resilience against insect mass outbreaks. The purpose of the research is to evaluate coherence of the Scots pine needles accumulated secondary metabolites (total phenolic content (TPC), total flavonoid content (TFC)), antioxidant activity and concentration of chlorophylls with Lymantria monacha mass outbreaks in Lithuania. The results showed that Scots pine exploits its TPC and TFC in a way of itself protection against the pest mass outbreaks and as the outbreaks last longer, the Scots pine losses its accumulated TPC and TFC. According to the results of the research, there was bigger TPC and TFC during the 1st year mass outbreaks than the 2nd year outbreaks in all variants (Control (C) – the outbreaks and no spraying; Not sprayed (N) – no outbreaks and no spraying; Sprayed (S) – the outbreaks and spraying) – 4.45±0.19 mg/g-1 and 3.94±0.52 mg/g-1 in C; 4.43±0.27 mg/g-1 and 3.67±0.15 mg/g-1 in N; 4.46±0.38 mg/g-1 and 3.38±0.29 mg/g-1 in S. Moreover, it was established a possible correlation between flavonoids and antioxidant activity in both years outbreaks. Concentrations of chlorophylls a and b were bigger in not sprayed than in control (0.856±0.002 mg/g-1 and 0.795±0.002 mg/g-1, relatively in the 1st outbreaks; 0.826±0.003 mg/g-1 and 0.735±0.003 mg/g-1, relatively in the 2nd outbreaks). The research showed that TPC, TFC, antioxidant activity and chlorophylls a and b have a huge value for the trees internal protection against dangerous Lymantria monacha which is not known to be established in North America so far.

Keywords: phenols, flavonoids, chlorophylls, Pinus sylvestris, nun moth

2-E-28 CartograTree: Cyberinfrastructure to improve forest health and productivity in the context of a changing climate

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Climate change is threatening forest health and productivity. To date, it remains largely unknown whether tree breeding can keep pace with the rate and direction of environmental change. In addition, the frequency and impact of invasive pests and pathogens is increasing as a consequence of globalization and climate change. Hence, the identification of genes controlling traits which provide tolerance or resistance to biotic and abiotic stresses constitutes one of the most important research objectives in evolutionary ecology. However, this research is often hindered by challenges associated with the access and integration of genotypic, phenotypic and environmental data sets.

CartograTree is the first web-based application, connected to analytic workflows, that integrates genotypic, phenotypic and environmental data, from georeferenced trees. Currently 16.8M genotypes and/or 1.2M phenotypes from over 8M trees and 148 studies are available. They are integrated with 16 environmental layers that address regional and global variables. The target analytic workflows are designed to facilitate meta-analysis for association studies, allowing the use of both measured traits (GWAS) and environmental variables (GEA). The use of these two approaches together (GWAS and GEA) may uncover patterns induced by adaptive processes that cannot be detected using one approach alone. Moreover, meta-analysis of GWA and GEA datasets can increase the power to detect association signals by increasing sample size and by examining more variants throughout the genome than each dataset alone. These workflows take advantage of the strengths of CartograTree: the diversity of data types (genotypic, phenotypic and environmental), metadata collection on study designs, and robust integration of regional and global environmental layers.

Populus trichocarpa is serving as the model tree species for the development of the CartograTree workflows given its well resolved genome, economic and ecological importance, rapid growth and multitude of range-wide genomic and phenotypic resources. By developing this workflow, we also aim to demonstrate the utility of meta-analysis to identify locally adapted SNPs related to fitness-related traits in this species (phenology and height).

Future forest health and productivity will depend on the match between genotypes (and their resulting phenotypes) and new environments. Thus, tools that collect, integrate, and facilitate this assessment are critical. Here, we describe the recent updates in data sources, functionalities, and workflows offered by CartograTree.

2-E-29 Citizen Science and the Search for Disease Resistance to Rapid ʻŌhiʻa Death

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Metrosideros polymorpha, known locally as ʻōhiʻa, is ecologically and culturally Hawaii's most important species. Starting in 2010, ʻōhiʻa began being killed by two Ceratocystis fungal species (C. lukuohia and C. huliohia; often referred to as Rapid ʻŌhiʻa Death or ROD). Many Hawaiian forests have seen 90%+ ROD-related tree mortality, and ROD continues to spread across the state. Preliminary evidence suggests that some wild type ʻōhiʻa trees display genetic resistance to ROD, and based on these findings, a large-scale ROD screening effort was launched in 2018. To expand capacity for screening while also providing learning and professional development opportunities for Hawaiʻi Island students, the Teaching Change Partnership created the Community Science for Hawaiian Forests Project (CSHFP), which aims to get local students involved with cutting edge phenology and disease resistance research on ʻōhiʻa.

To achieve these outcomes, the CSHFP relies on a three pronged approach: 1) in-classroom biocultural learning about forest genetics and pathology; 2) ʻŌhiʻa grow kit packages, including locally collected ʻōhiʻa seeds, for student led propagation; and 3) disease resistance training including exposure to inoculation based screening methodologies. To date, students have received educational packets containing moʻolelo, or legends, about ʻōhiʻa lehua as well as instructional worksheets on how to collect their own phenology data through kilo, or careful observation, and how to use that data to help in the fight against ROD. Students have also received grow kits, with which students' can propagate ʻōhiʻa trees. With these kits, students will track seedling progress through early life phases. By the end of the project, students will have two healthy ʻōhiʻa trees, one of which they can outplant into their own backyard, and one which will be donated back to the USDA Forest Service's greenhouse to help in disease resistant research. There, each tree will be screened for ROD resistance, with the support of advanced students.

Central to this effort is the discovery of disease resistant wild type ʻōhiʻa. In order to achieve this goal, seed collected from a large number of individuals representing a distinct seed zone must be propagated and screened for resistance to ROD. To this end, this project will result in the following outcomes: (i) hundreds of local students will gain a high quality, hands-on experience in forest genetics, including concepts of seed zones, genetics of disease resistance, and disease resistance screening; (ii) over one hundred healthy ʻōhiʻa individuals from a Hawaiʻi Island wet forest seed zone will be propagated for eventual disease resistance screening; finally (iii) these citizen scientists will support the perpetuation of ʻōhiʻa through identification of disease resistant material for their seed zone, helping to advance understanding of a disease that presents an unprecedented threat to Hawaii's native forests.

2-E-30 Variation in Juglans nigra phytobiome driven by geographic and host genotypic variation has implications on Thousand Cankers Disease severity

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Thousand Cankers Disease of Juglans spp. and Pterocarya spp. is present in 15 U.S. states and Italy, and is hypothesized to have originated in the arid western U.S. The disease is caused by a bark beetle vector Pityophthorous juglandis and the fungus Geosmithia morbida which forms cankers that girdle and kill host trees. The most susceptible TCD host is J. nigra, an important timber and nut crop present in urban and natural forests. Thousand Cankers Disease severity is greater in the introduced range of J. nigra in the western U.S compared to the host's native range in the eastern U.S. We hypothesized that these differences are driven in part by geographical and genotypic variation in the host phytobiome or the consortium of microorganisms that aid in plant defense, resource acquisition, and stress tolerance. To begin characterizing the role of the phytobiome in mediating Thousand Cankers Disease severity, we evaluated differences in the J. nigra phytobiome in portions of the host's native (Indiana and Tennessee) and introduced ranges (Washington) across four different grafted clone accessions and open-pollinated populations present in each state. DNA was extracted from bulk soil and branch (caulosphere) tissues and ITS and 16S regions were sequenced for characterization of fungal and bacterial communities. We found that fungal and bacterial communities in the caulosphere and soil differ between the native and introduced ranges and contain different mutualistic and pathogenic microorganisms and that host genotype only significantly explained differences in the composition of caulosphere fungal communities.

Additionally, caulosphere fungal and bacterial communities in the introduced range were depauperate compared to the native range, suggesting that plant-associated microbial communities in the host's native range possess greater levels of functional redundancy and multifunctionality compared to the introduced range, and may serve to protect trees from G. morbida via competitive exclusion. We also found higher network complexity in the caulsophere of trees in the introduced range and evidence for two alternative stable community states associated with diseased and healthy trees. Our results indicate that host genotype is less significant in determining phytobiome structure compared to geography. Additionally, our results provide support for the hypothesis that geographical variation in Thousand Cankers Disease severity is partially driven by differences in the phytobiome of J. nigra in its introduced and native ranges.

2-E-31 Above and belowground fungal symbionts alter tree defenses, with potential consequences on resistance to fungal pathogens and disease

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Hundreds of asymptomatic fungal taxa live inside healthy white pine tissues. Recent studies suggest that these fungi can influence the frequency and severity of infections by fungal pathogens such as Cronartium ribicola, the causal agent of white pine blister rust. In a full-factorial experiment, we inoculated western white pine (Pinus monticola) from six seed families with foliar fungal endophytes (FFE) or ectomycorrhizal fungi (EMF, genus: Suillus), as well as a combined fungal treatment (FFE+EMF), and a control treatment (no inoculation). The six seed families consisted of half-siblings and full-sib progeny, with both high and low levels of known disease resistance. Four months post-inoculations, we infected a subset of seedlings from all four treatments with the rust to determine the individual and shared effects of FFE and EMF on resistance to white pine blister rust as well as seedling performance. We measured tree defensive chemistry (terpenes) for all treatments immediately before, and four months after infection, as disease symptoms began to appear.

Seed family influenced both initial disease severity and terpene composition in all seedlings. Terpene composition did not differ among fungal treatments immediately before pathogen infection. However, there was a strong treatment effect on terpenes after pathogen infection (p < 0.005), indicating that fungal inoculations altered seedlings' induced defense responses. EMF inoculations had the greatest influence, while EMF+FFE treated seedlings were more similar to untreated control seedlings, suggesting an interaction between above and belowground fungi. How these differences in induced defensive responses translate to disease resistance will be assessed with ongoing monitoring of disease progression.

2-F-32 A linear DNA amplification-based approach to investigate gene promoter regions in Scots pine

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As a high-quality genome sequence assembly for Scots pine is not publicly available, analysis of 5' flanking sequences (which include gene expression promoters, and other transcription regulation motifs) of Scots pine genes is currently challenging. To obtain sequences of these regulatory regions, a

linear DNA amplification-based approach is proposed. One hundred genes with the highest differential gene expression in an inoculation experiment were targeted. Using transcriptome data, primers were designed to anneal to the 5' region of expressed genes, orientated to amplify 5' flanking genomic regions. Using high molecular weight DNA as a template, 5' phosphorylated primers were used in a multiplex linear DNA amplification reaction to generate single stranded DNA (ssDNA) template. The obtained ssDNA fragments were circularised, and used as a template for rolling circle amplification. Following rolling circle amplification, massive parallel sequencing will be used to obtain 5' flanking sequences. This work is in progress (currently at the post-rolling circle amplification stage). Results of intermediary steps and obstacles are discussed.

2-F-33 Identifying and Classifying Potential Disease Resistance Genes in White Pine Species

Akriti Bhattarai[1], Jill Wegrzyn[1]
[1]*University of Connecticut*

The white pines comprise the subsection Strobus of the genus Pinus, with species native to North America, Europe, and Asia. White pines are susceptible to a devastating disease known as white pine blister rust (WPBR) caused by the fungus Cronartium ribicola. Since being introduced in the early 1900s, WPBR has spread across a large portion of the native range of North American white pines. Major resistance loci (Cr1 to Cr4) have been identified in four North American species (P. lambertiana, P. strobiformis, P. flexilis, P. monticola). Candidate genes for these loci have been categorized as NLRs, which consist of an N-terminal domain, nucleotide binding domain (NB-ARC), and leucine-rich repeat domain (LRR). In addition to major resistance, white pines may be resistant or tolerant to WPBR through other loci contributing partial resistance. These can be identified through their characteristic domains. Existing transcriptomic resources (Illumina RNA-Seq reads sourced from NCBI) for fifteen white pine species were re-assembled de novo using Trinity (v2.6.6). In order to have more complete resources for protein domain analysis, eight species with a BUSCO completeness of at least 80% were retained. Six of these species were Asian or European species (P. armandii, P. bhutanica, P. cembra, P. kwangtungensis, P. wallichiana, P. wangii), which have co-evolved with C. ribicola and show resistance to the pathogen. This allowed for comparisons with the North American species (P. lambertiana and P. strobus) that are both susceptible to WPBR. To characterize NLRs, the assembled transcripts were translated into protein sequences using Transdecoder (v5.3.0). InterProScan (v5.35-74.0) was used to scan the sequences for known NLR domains using the Pfam and SMART databases. The RGAugury pipeline was also used to identify potential resistance genes in the transcriptomes. A reference genome is available only for P. lambertiana, and potential resistance genes were identified from both the genome annotation as well as a genome scanning approach using NLR annotator. The total number of identified resistance genes varied greatly among the white pine species (ranging from 132 to 855), with the most identified in P. lambertiana, P. cembra, and P. strobus. Most identified transcripts were incomplete resistance genes, lacking one or more of the NLR domains. Motif analysis of the NB-ARC domains using MEME (v 5.2.0) identified common functional motifs previously described in conifer NLR genes. To understand the resistance genes in an evolutionary context, the relative number and type of resistance genes were compared across species and orthologous gene groups were identified using Orthofinder (v2.3.3). Exploring these relationships may provide additional insights into the evolution of important resistance genes in the white pines.

2-F-34 Investigating Genetic Signatures Associated with Reduced Mortality Against Emerald Ash Borer in Green Ash

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[1]*University of Connecticut,* [2]*University of Notre Dame*

Emerald Ash Borer (Agrilis planipennis), an invasive pest that is threatening the sustainability of the entire North American ash tree population (genus: Fraxinus), can kill a susceptible tree within five years of detection. Efforts to prevent, treat, and remove afflicted trees are culminating to billions of dollars, and the eradication of this species is impacting all landscapes. Among impacted populations, individuals that survive longer are identified as "lingering", though these account for less than 1% of the population. To complement breeding efforts, we conducted double-digest RAD-Seq across a phenotyped population of 107 green ash (Fraxinus pennsylvanica) and low-coverage whole-genome shotgun sequencing on 11 samples, representing 9 families. Variant detection conducted on the Illumina sequence provided 30,000 SNPs for analysis. Linkage map curation was performed based on SNP and pedigree information to produce 3655 markers, spanning a sex-averaged genetic distance of 158 cM. The families were phenotyped with a greenhouse egg bioassay, where EAB larvae are applied to the stem and after six weeks the percentage of larvae killed (by the host) and the mean weight of surviving larvae are measured. QTL analysis was conducted with a reference genome to examine regions associated with partial resistance to EAB. The information gathered here will be used to improve conservation efforts and generate populations of green ash that are more resistant to EAB.

2-F-35 Septoria musiva Resistance of Populus Taxa

Montariel Minor[1], Joshua Adams[1]
[1]*Louisiana Tech University*

Septoria musiva (S. musiva) is an invasive disease that have threatened the survival of Populus taxa or at least limit growth. Eastern cottonwood and other Populus species are being utilized for their vigor properties. Poplar hybrids are currently highly desirable due to their biomass and biofuel contributions involving rapid growth rate, planting stock, low sulfur content, and replacing fossil fuels. However, hybrids deployed in the southern regions have demonstrated severe vulnerability to S. musiva. This disease is a leaf and stem canker disease that can devastate hybrids within 4 years. Our research focuses on how S. musiva affects various Populus hybrid cloned taxa's. Through comparing single nucleotide polymorphism (SNPs) markers through sequencing genomic polymerase chain reaction (PCR) products we will examine how hybrids are individually influenced by S. musiva. The hybrid taxa's involved are the poplar taxa: Populus deltoides (D×D), P. deltoides × P. maximowiczii (D×M), P. deltoides × P. trichocarpa (D×T), P. trichocarpa × P. maximowiczii (T×M), and P. deltoides × nigra (D×N). The results expected would benefit to the Populus library and determine which markers may indicate a hybrid's resistance to S. musiva.

2-G-36 A population-genomic and taxonomic study of Eucalyptus argophloia and E. bosistoana

Seol-Jong Kim[1], Clemens Altaner[1], Luis Apiolaza[1], Tammy Steeves[1], Pieter B Pelser[1]
[1]*University of Canterbury*

The New Zealand Dryland Forests Initiative (NZDFI) aims to create plantations of high-value Eucalyptus timber species in dry environments on the east coast of New Zealand. This would enable the sustainable

production of naturally-durable hardwood in New Zealand as a substitute for CCA-treated pine and unsustainably harvested tropical hardwoods. For this purpose, Australian seed collections of five promising Eucalyptus species have been used since 2009 to establish progeny trials in New Zealand. These trials are used to select and breed plant lines with growth and wood properties that are desirable for the New Zealand environment. As part of this effort, NZDFI is interested in understanding how genomic and environmental variation interacts to influence commercially important traits in the NZDFI progeny trials. My PhD research project is a component of this project. Its specific research questions are: 1) what is the taxonomic identity of a morphologically deviating population of E. bosistoana, 2) what are the patterns of genetic diversity and structure of E. argophloia and E. bosistoana, and 3) what is the mating system of E. bosistoana. To address these questions, I generated Single Nucleotide Polymorphism (SNP) data of ~1300 and ~100 individuals of E. bosistoana and E. argophloia, respectively, using a recently developed Eucalyptus 65kSNP Axiom array. Here, I present the preliminary results of analyses aimed at understanding the patterns of genetic diversity and structure of 25 populations of E. bosistoana.

2-G-37 Searching for genomic adaptation to climate in sugar maple

Alix Pugeaut[1], Yann Surget Groba[1]
[1]Institut des sciences de la forêt tempérée

Current climate disorder is a threat to global biodiversity and related ecosystem services. When climatic conditions change abruptly, as currently observed, living organisms can either adapt to their new living conditions or migrate to a more favorable habitat. This PhD project aims to study climate-related genomic adaptations in sugar maple, a species widely distributed in eastern North America. Sugar maples from localities dispersed in Québec and United States were sequenced using GBS methods. Using bioinformatics, we are currently analysing the genomic structure in these populations. We aim to identify a genomic structure that would be correlated to climatic variables. We are also preparing the collect of black maples individuals to add to the sampling. This will help us see if genetic flow is important between these two species and further discuss of the role of this genetic flow for sugar maple adaptation to climate. This project will be the first large-scale study to discuss genetic adaptations in response to changing climate conditions in sugar maple. In addition, understanding the adaptability of sugar maple to climate change may be useful for decisions related to the conservation of this economically important species. This would maximize the adaptive potential and resilience of maple forests to climate change.

2-G-38 Range-wide population structure and demographic history analysis of remnant American chestnut populations

Alexander Sandercock[1], Jared Westbrook[2], Jason Holliday[1]
[1]Virginia Polytechnic Institute and State University, [2]The American Chestnut Foundation

The American chestnut (Castanea dentata) is a deciduous tree with a widespread historical range in the eastern United States and southeastern Canada. C. dentata was ubiquitous in American forests and had served as an important economic and ecological resource for the region. Approximately 100 years ago, a fungal blight (Cryphonectria parasitica) began to decimate American chestnut populations, killing approximately four billion trees. An estimated 400 million trees remain, predominantly as stump sprouts that rarely reach reproductive maturity. Thus, it is essential to describe the population genomics of

remaining American chestnut trees to aid in current and future conservation efforts. We are using whole-genome re-sequencing to describe the genetic diversity, population structure, and demographic history of remnant American chestnut populations. To date, 96 leaf samples have been sequenced and used to develop a dataset consisting of ~47 million SNPs and INDELs, which shows evidence of a genetically diverse historical population. A DAPC analysis and ADMIXTURE software was used to estimate population structure, and preliminary results suggest a two and three population model, respectively. Finally, an SMC++ analysis was used to estimate the demographic history of C. dentata, showing a history of bottleneck events and a more recent increase in the effective population size. These preliminary findings indicate that past demographic events may have led to a population that is genetically diverse and that the current population structure can be defined by a two or three population model.

2-G-39 Disentangling the influence of spatial proximity and genetic similarity on individual growth of Picea glauca in Alaska

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The arctic region is expected to warm the most in the course of climate change. To investigate how forest trees are keeping up with such changes, we studied natural white spruce stands (Picea glauca) in Alaska. We established three study sites in nearly monospecific white spruce stands. Each study site contains two plots, one plot at the treeline ecotone and one plot at lower altitudes in a closed canopy forest. Two study sites represent the presumably temperature limited range edge of white spruce, with the first site in Central Brooks Range located at the northern treeline and the second site in the Alaska Range located at the elevational treeline. The third site, Interior Alaska, is located at a steep south exposed bluff which represents a water-limited treeline. All trees within these 1 ha plots were genotyped using 11 microsatellites and mapped with a GPS device. Additionally, adult trees were cored to obtain dendrochronological data. A data base of climate variables is available. The program STRUCTURE was used to investigate the population structure. We applied a hierarchical analysis of molecular variance as well as Mantel tests to evaluate the influence of isolation by distance vs. isolation by environment. Estimating gene flow among populations was done by a neighborhood model. To test the genetic and spatial influence on growth performance of white spruce stands, we used a two-step analytical framework. First, we employed random slope mixed-effects models to quantify the effects of climate and tree size on growth. Then we extracted the individual parameters from the models, which contain the individual growth performances including climate and size effects. Further the individual parameters were tested against genetic and spatial variables and their fine-scale spatial arrangements were estimated.

The overall genetic diversity of white spruce populations is high due to gene flow among populations favored by high seed and pollen immigration rates. Whereas gene flow is higher into edge than core populations. The high gene flow rates are also reflected in the low degree of genetic differentiation among populations which can be rather explained by geographic distance than differing environmental conditions. This leads to the assumption that genetic drift plays a bigger role in structuring white spruce populations in Alaska than local selection induced by climate. Further, in Alaskan white spruce, tree size has a bigger influence in tree growth than climate conditions. Climate variables which drive tree growth differ depending on the growth limiting factor at the site, with temperature at the cold-limited treeline

and precipitation at the moisture-limited treeline. Microenvironment is likely to be more relevant for tree growth than genetic similarity.

2-H-40 Importance of differences in abiotic factors between seed origin and provenance trial sites in performance of Pacific madrone (Arbutus menziesii)

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[1]*Duke University,* [2]*University of Kentucky,* [3]*USDA Forest Service,* [4]*Washington State University*

Climate shifts and concomitant weather extremes such as extended droughts make it difficult to determine the best seed sources for reforestation. Seed source selection based on current climate conditions avoids further disrupting already stressed systems, but seed source selection could also be based on adaptation and survival in anticipated novel conditions. Knowledge of relationships between seed sources and adaptation to climatic variables helps evaluate options. This study used four common gardens of Pacific madrone (Arbutus menziesii Pursh) to model seed source performance in height growth, dieback, mortality, and phenology using abiotic variables from the seed source's geographic origins. While the degree of variation explained by even the best models was relatively low, there were some trends. Patterns of growth and mortality differed across common garden sites, but ecoregion of origin and transfer distance consistently explained the greatest amount of variation in growth, dieback, and mortality. Mean summer precipitation, an indication of potential drought stress, only explained mortality variation at the driest common garden site. Seed sources more local to a provenance study site generally had lower mortality and higher growth. However, some Willamette Valley sources not local to a provenance site had relatively greater growth and low mortality so could be good candidates for broader seed movement. The abiotic factors that best explain growth and mortality differed between less stressful and drought + cold stress years, with the models for stress years explaining more variation. Abiotic variables were better at explaining timing of spring leaf flush than the performance metrics, where seed sources from lower latitudes/elevations and drier conditions flushed sooner in the spring. Our results support the importance of abiotic factors in predicting growth, mortality, and phenology in Pacific madrone, but their predictive capacity and relative importance depends on the site, the degree of drought and cold stress, and may vary even for sites in close proximity.

2-I-41 Economic return of planting improved coastal Douglas-fir at four initial planting densities

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Significant investments in tree breeding for coastal Douglas-fir in British Columbia (BC) are projected to lead to significant volume gain at rotation age. Recent research has indicated that growth gains are accumulating as expected in realistic planting scenarios across a range of site qualities, but it is not yet clear to what degree these volume gains translate into economic gains for end-users. This research aims to quantify expected economic gains from planting improved coastal Douglas-fir under various silviculture scenarios. We use discounted cash flow analysis techniques to estimate the economic gains expected by planting trees representing three levels of genetic worth (a 0% control, +10% and +18%)

under four initial planting densities (625 sph, 1189 sph, 1890 sph and 3906 sph). These economic analyses rely on a growth and yield model calibrated with data from a 20-year realized gain trial, which was installed on five sites ranging in productivity (site index from 36 – 44). We account for log grades, increased carbon sequestration, shortened rotation ages, and a variety of economic conditions. Preliminary results suggest significant economic gains associated with planting top-crosses at all sites under baseline economic scenarios. Planting improved seed sources at the most productive sites appears to provide the highest financial return. The optimal planting densities to maximize return seem to vary at the site level, however. Traditional approaches suggest the optimal harvest age ranges from 40 to 45 years, depending on site productivity. Harvest ages may be further reduced by up to 10 years by planting improved sources. However, incorporating a low carbon price suggests higher socioeconomic returns could be achieved by harvesting later. This research provides insights to optimize return on investment when planting stands with improved trees.

2-J-42 Genetic influence on wood density variation in white-spruce (Picea glauca)

André Soro[1], Patrick Lenz[2], Jean-Romain Roussel[1], Jean Bousquet[1], Alexis Achim[1]
[1]Université Laval, [2]Natural Resources Canada

Conifer breeding programs are more and more considering wood quality among selection criteria to improve besides growth also fibre quality from future forest plantations. As wood density is one of the most commonly used indicators of wood quality, there is a growing interest to consider this trait in selection and to enhance the end-use properties of planted trees. However, wood density varies at different scales within trees, with pith-to-bark (low-frequency) trends and interannual (high-frequency) fluctuations representing two important sources of variation. From both physiological and end-use points of view, it is desirable to produce stems with limited low- and high-frequency wood density variation. In the present study, we assessed patterns of low- and high-frequency variation in 2197 wood density trends and evaluated the genetic control of traits characterizing this variation. The experimental data came from a 15-year-old white spruce genetic trial representing 93 full-sib families sampled in two contrasting environments in Quebec, Canada. A model was developed first to describe pith-to-bark patterns of variation in the mean ring density of individual disc, and thus separate low-frequency from high-frequency variation. We observed that low-frequency variation is poorly controlled by genetics unlike high-frequency signal of which only latewood is under genetic control. Our approach could help identify trees or families that tend to have limited pith-to-bark and yearly variation in wood density as part of tree genetic selection programs.

2-K-43 Effect of disruptive genetic variants on the expression of secondary cell wall deposition genes in Populus trichocarpa

Anthony Piot[1], Ilga Porth[1], Juan Carlos Villarreal Aguilar[1]
[1]Université Laval

Wood is a renewable organic material widely used for human needs thanks to its unique characteristics. The secondary cell wall (SCW) constituting most of the wood tissue is mainly composed of lignin, cellulose and hemicellulose. The proportion of these three components can be manipulated to give the wood varying properties to fit specific usages. Genetic variants with high effect on wood properties would prove very useful to efficiently modify wood properties. Disruptive variants leading to the expression of a predicted defective gene product are promising targets for molecular breeding and

biotechnologies approaches to wood improvement. Here, we review the research literature for genes known to be involved in SCW deposition (SCWD), an important part of wood formation. Using existing genomic and transcriptomic datasets, we investigated the extent and expression of disruptive variants in the identified SCWD genes. We show that disruptive variants are almost always expressed despite their predicted deleterious effect. The amount of allele-specific expression of disruptive variants, however, is variable among genes and individuals. In heterozygous individuals for a disruptive variant, the expression of the alternative allele compared to the reference one is not always similar. In addition, the presence of a disruptive variant in one or the two copies of a SCWD gene does not always change the gene expression. These results point at effects of gene expression regulation and RNA stability control mechanisms in determining the overall expression and allele-specific expression of SCWD genes. These findings are promising toward the use of disruptive variants in molecular breeding and biotechnology techniques for wood improvement. However, more information on the mechanisms at play to regulate the expression of disruptive variants and those acting to eliminate defective gene products are needed in order to better understand the effect of disruptive variants on wood properties.

2-L-44 Biochemical response in populus hybrids and clones under the impact of different environmental conditions during rooting

Valda Gudynaitė-Franckevičienė[1], Gintarė Bajerkevičienė[1], Alfas Pliūra[1]
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To meet the needs of carbon sequestration and production of raw materials from renewable natural resources for the bioenergy and timber market of the European Union, it is necessary to expand forest plantation areas. The efficiency of short-rotation forestry depends primarily on the selection of hybrids and clones, suitable for the local environmental conditions. We postulate that ecogenetic response, ecogenetic plasticity and genotypic variation of different hybrids of poplars (Populus L.) depend on the hybrids and clones, environmental conditions at rooting time and on their genetic pre-adaptations to native environmental conditions of their origin. The aim of the study was to estimate biochemical response, genotypic variation, heritability, genetic gain of photosynthesis pigments of Populus hybrids in relation to simulated environmental conditions at their rooting time. The research was performed with the cultivars and experimental clones of one intraspecific crosses of poplars (P. trichocarpa Torr. & Gray.) and four different interspecific hybrids of poplars (P. deltoides L. × P. nigra, P. deltoides × P. trichocarpa, P. maximowiczii A. Henry × P. trichocarpa, and P. balsamifera L. × P. trichocarpa). The results indicated that there are different responses of hybrids and clones to rooting-growing conditions, which later determine changes in photosynthesis pigments content. Analysis of variance showed that the effect of plant growing conditions in Phytotrone greenhouse on all the pigments content and the chlorophyll ratio in trees outplanted in field trial was highly significant (P <0.001). The impact of rooting conditions of cuttings in greenhouse was highly significant (P <0.001) on chlorophyll A, caratinoids and chlorophyll ratio of outplanted trees, but not on chlorophyll B (P = 0.0195). The most sensitive to environmental conditions according to chlorophyll A changes was P. deltoides × P. nigra hybrid. Results lets predict that changing levels of chlorophyll A due to stressors during rooting could negatively affect the process of photosynthesis, which is directly related to plant growth. Under changing environmental (rooting-growing) conditions carotenoid amount mostly varied in P. trichocarpa × P. trichocarpa – from 0.38 to 0.9 µg/g. P. deltoides × P. trichocarpa characterized by highest chlorophyll A and B ratio, while P. maximowiczii × P. trichocarpa – lowest.

2-L-45 Tweaking reference-based bioinformatic pipelines for differential expression analyses in Pinus radiata

Mikel Hurtado González[1], Álvaro Soto2, Unai López de Heredia[2], Pablo G Goikoetxea[1]
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RNAseq is becoming the preferred tool to analyze transcriptomics for both specific and general trait analysis. This NGS method generates large amounts of data that need complicated processing steps to obtain meaningful results. This makes bioinformatic analyses a heavyweight part of the process leading to discovery of new transcripts and genes from the studied species, to the mining of variants and to differential gene expression analysis. As time goes by, more and more species genomes are publicly available in databases, which simplifies the bioinformatic process and ensures better results. Bioinformatic pipelines have been standardised for model species and for new species with complete genome resources. However, when working with non-model species without a reference genome, bioinformatics becomes challenging, especially when referring to species with complex megagenomes harbouring large amounts of repeated sequences, genome duplications and paralogous sequences, such as those from many conifers, mainly within the Pinaceae. Two alternatives exist to face this problem; either using the reference of a phylogenetically close species, or performing a de novo assembly. However, de novo assemblies produce error and biases disrupting differential expression analyses. Using a related species genome as the reference has two main drawbacks, especially if the quality of the reference genome is not optimal due to fragmentation in scaffolds rather than in chromosomes. First, the information from previously unidentified sequences that do not align to the reference will be lost; and second, the uncertainty of the alignments for duplicate and paralogous sequences. Within this framework the alignment rates will depend on the distance between species and the completeness of the sequenced genome, leading to two potential related issues: (1) how low alignment rates affect the differential expression pipelines and (2) how tweaking the alignment step will affect such analyses.

To solve this problem, we have assembled a de novo Pinus radiata transcriptome, a worldwide economically important tree species lacking freely available genomic resources, from 3 adult and 3 young trees. The assembled transcriptome was then used to simulate RNAseq libraries with known differentially expressed genes (DEGs) that were analysed with state-of-the-art reference-based DE pipelines using P. taeda genome. This allowed us the benchmarking of the different pipelines in terms of true vs false positives. Our results show that the different DE pipelines rescue similar numbers of true positives, but showed differences in false positive rates. In addition, the tweaked alignment mode increased true positive rates similarly in all pipelines but it also increased the false positive rates. Overall, the most suitable alignment mode could vary depending on the objectives of each study, but HTSeq-count/DESeq2 combination will always deliver the lowest numbers of false positives.

2-L-46 TreeSnap, a Mobile and Web Platform for Tree Location and Phenotype Data Collection

Joseph West[1], Abdullah Almsaeed[1], Noah Caldwell[1], Ellen Crocker[2], C. Dana Nelson[3]
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TreeSnap (https://treesnap.org/), originally designed as a citizen science outreach project, has been expanded to support research data collection. With TreeSnap citizen scientists can use their mobile phones to tag forest trees of interest to scientists, including North American ashes, American chestnut, eastern and Carolina hemlocks, butternut, pinyon pine, and American elm. We have recently expanded

the app to support individual research programs that sample trees, suitable for projects including genetic diversity, population structure, landscape genomics, and phenotype to genotype. Anyone wishing to organize the collection of GPS coordinates, images, and basic phenotype information for a set of trees can register a new project on the TreeSnap website. All affiliated collectors (students, staff, the public) can be added to the project, and then use the app on their own phones to record each collected sample and information such as tree health, reproductive structures, surrounding habitat descriptions, and project-specific phenotypes. For projects where physical samples are being collected, users can scan barcodes on bags or tubes to associate the sample with the digital record. Once collections are complete, the project leader can curate and filter the full set of observations from all collectors, and download digital data by barcode. Work is ongoing to enable the observations and associated genotype and phenotype data to be imported into CartograTree (https://treegenesdb.org/ct), a platform that enables integration of environmental layers and sophisticated landscape genomics software pipelines for data analysis.

2-L-47 An interactive web tool to teach the scientific method and forest genomics utilizing a nation-wide network of Populus common gardens

Joseph Braasch[1], Jill Hamilton[1]
[1]*North Dakota State University*

There is increased effort to teach topics in science through deductive reasoning and inquiry-based learning. These pedagogical methods can be difficult to implement for lessons in plant biology, because indoor lessons are often divorced from the ecological context that structures the genetics of plant populations. Additionally, many students lack familiarity with outdoor settings, making inquiry-based lessons in biology especially challenging to administer and execute. Common gardens in particular could serve as useful resources for education, but schools rarely lack the expertise or resources to establish and maintain them.

Here we introduce a network of poplar common gardens established nationwide and an accompanying, publicly available educational module built with R-based web tools in the "shiny" framework. As sites of active research, these gardens will expose students to cutting edge research in tree genetics, climate adaptation, and plant ecology while providing the opportunity for exploratory learning. We will introduce the online learning module which walks students through the scientific method. First, the web app provides students with interactive maps that can be used to digitally explore the climates individual trees were collected from and compare them to the climates of their local common garden. The application will then assist students with the process of generating a hypothesis for how one of many plant traits they can measure in their common garden, such as height or phenology, changes with the climate of collection. Importantly, this part of the application will produce a graphical hypothesis that can be compared to real data that is either collected and uploaded from the garden by students themselves or provided by the application from previous surveys of the garden. With this final step, students will evaluate whether the data supports their hypothesis and discuss alternative explanations for the patterns they observed. The efficacy of this tool will also be evaluated by student and teacher response surveys to evaluate how well it works as a model which can be extended to other topics in biology. By brining together cutting edge research with these relatively novel tools for education this program should improve student retention of core concepts in evolution and climate change while being while learning about science as a career.

2-L-48 TreeGenes: Resources for Forest Tree Genetics

Emily Grau[1], Irene Cobo[1], Risharde Ramnath[1], Peter Richter[1], Jill Wegrzyn[1]
[1]*University of Connecticut*

TreeGenes is a web-based information resource designed to serve the diverse needs of the forest tree genomics research community by uniting information resources with visualization and analytic tools. A full suite of data related to forest trees is hosted, including genetic, phenotypic, environmental, and supporting literature. Community resources including a colleague directory, employment listings, and community events (meetings/courses) are also maintained. Over 2100 tree species are represented in the database including 166 with genome assemblies. The TreeGenes database, the Hardwood Genomics Project, and the Genome Database for Rosaceae have linked searching capability to allow users to easily find resources from all three databases from any of the three sites. All of these resources are hosted via the open-source platform known as Tripal which enables this cross-communication..

The data available in TreeGenes is sourced from public sources such as NCBI and Dryad as well as direct user submissions. Submissions are made via the Tripal Plant PopGen Submit module, a pipeline for accepting direct submissions from researchers. This module collects relevant metadata while reducing the burden on the researcher for submission. Ontology terms are leveraged to standardize metadata collection and allow linking across datasets. Submitted studies are associated with a permanent identifier (DOI) for future access.

In addition to search and download functionalities, users can access visualization tools and run analytic workflows using TreeGenes' computational resources. Users may visualize genetic maps and genome assemblies or visually browse orthologous gene sets using OrthoQuery. The OrthoQuery module identifies orthologous genes from TreeGenes-generated unigene sets, runs OrthoFinder analysis and visualizes relationships among families. Users may also quickly perform sequence similarity searches against hosted genomes and transcriptomes using the TSeq module.

Association mapping and landscape genetics analysis is accessible through CartograTree, a map-based application which integrates environmental, phenotypic, and genotypic data for georeferenced trees. The module works with the open source Galaxy project for executing custom-designed workflows that are tailored to the needs of the research community.

TreeGenes integrates multiple resources in addition to novel informatic tools to support and facilitate research that leverages a wide range of high throughput sequencing and phenotyping technologies. The researchers that access and submit data to TreeGenes are addressing questions related to forest health, conservation, and productivity.

2021 Forest Genetics Attendee List

Alphabetical by Last name

Sally Aitken

Maurice Amee

Tara Androschuk

Rami-Petteri Apuli

Juliette Archambeau

Kevin Astridge

Brian Baltunis

Brian Barber

David Barker

Gabe Barrett

Jean Beaulieu

Sam Belton

Lahcen Benomar

Andy Benowicz

Jean-Paul Bielech

Jean Bousquet

Andrew Bower

Joseph Braasch

Geoff Bradley

Willie Brink

Lorinda Bullington

Melike Bulut

Rafael Candido Ribeiro

Charlie Cartwright

Antonio Castilla

Vytautas Čėsna

Zeynep Cicekli

Barley Rose Collier Harris

Zach Cook

Carole Coursolle

Catherine Cullingham

Jeff Debell

Josianne Deblois

Jeff Degraan

Florian Deisenhofer

Claire Depardieu

Rainbow Desilva

Lionel Di Santo

Raiany Dias De Andrade Silva

Chen Ding

Trevor Doerksen

James Domes

Francois du Toit

Meaghan Duke

Heather Dun

Aziz Ebrahimi

Jaanika Edesi

Shakila Ekanayaka Mudiyanselage

Ken Elliott

Jonathan Feichter

Ciara Fenimore

Arnaldo Ferreira

Domen Finzgar

Kathleen Forbes

Kathy Fraser

Victor Fririon

Dreama Galbraith

Esteban Galeano

Lanie Galland

Omnia Gamal El-Dien

Cesare Garosi

Sebastien Gerardi

Julie Godbout

Felysia Green

Jeannette Griese

Valda Gudynaitė-Franckevičienė

Laura Guillardin

Jia Guo

Andreas Hamann

Jill Hamilton

Christoph Hartleitner

Barbara Hawkins

Katelyn Hengel

Andrew Hicks

Sean Hoban

Glenn Howe

Mikel Hurtado

Sahari Inoue

Miriam Isaac-Renton

Nathalie Isabel

Whitney Jackson

Keith Jayawickrama

Sally John

Stephen Joyce

Renata Kamakura

Dasvinder Kambo

Darius Kavaliauskas

Stephen Keller

Rūta Kembrytė

Kelly Kerr

Seoljong Kim

Dave Kolotelo

Mebarek Lamara

Manuel Lamothe

Eddie Lauer

Jean-Philippe Laverdière

Patrick Lenz

Jong Leong

Brandon Lind

Erica Lombardi

Judy Loo

Judy Loo

Carol Loopstra

Pengxin Lu

Mengmeng Lu

Ieva Lučinskaitė

Dawei Luo

Ian MacLachlan

Alexia-Agapi Malaspina

Laura Manerus

J A Martin

Meridith Mcclure

Kerry McLaven

Donnie McPhee

Brianna Mcteague

Eleanor Mcwilliams

Alayna Mead

Mitra Menon

Ashley Meyer

Shona Millican

Montariel Minor

David Montwe

Simon Nadeau

David Noshad

Judith Nuhu

Marissa Ochoa

Funda Ogut

Stuart Olshevski

Greg O'Neill

Aaron Onufrak

Samson Osadolor

Guillaume Otis Prud'Homme

Donna Palamarek

Aliki Papadopoulou

Thomas Parchman

Kate Peterson

Anthony Piot

Anoob Prakash

Alix Pugeaut

Juliane Raschke

Iman Rashidijouybari

Blaise Ratcliffe

Edouard Reed-Métayer

Stefan Richard

Etienne Robert

Randy Roeh

Kaylee Rosenberger

Beth Roskilly

Ngaire Roubal

Valerie Russell

Deogratias Rweyongeza

Hareram Sahoo

Alexander Sandercock

Eric Schallon

Clara Schortemeyer

Emily Schumacher

Nikki Scott

Gianluca Segalina

Jill Sekely

Tal Shalev

Bikash Shrestha

Mengjun Shu

Rahul Singh

Vilnis Šķipars

Erica Smith

Richard Sniezko

Raju Soolanayakanahally

Victoria Sork

Victoria Sork

André Soro

Mariana Souza Da Silva

Katherine Spencer

Andrew Starovoitov

Regan Steller

Fatih Temel

Barb Thomas

Lisa Tischenko

Lyne Touchette

Hayley Tumas

Kathryn Uckele

Amy Vallarino

Elizabeth (Lise) Van Der Merwe

Annette Van Niejenhuis

Marie Vance

Rita Verbylaitė

Patrick von Aderkas

Angelika Voronova

Tia Wagner

Tongli Wang

Marcus Warwell

Cynthia Webster

Jill Wegrzyn

Martin Williams

Ann Willyard

Jack Woods

Jessica Wright

Zhengyang Ye

Yue Yu

Melanie Zacharias

Michelle Zavala Paez

Yueru Zhao