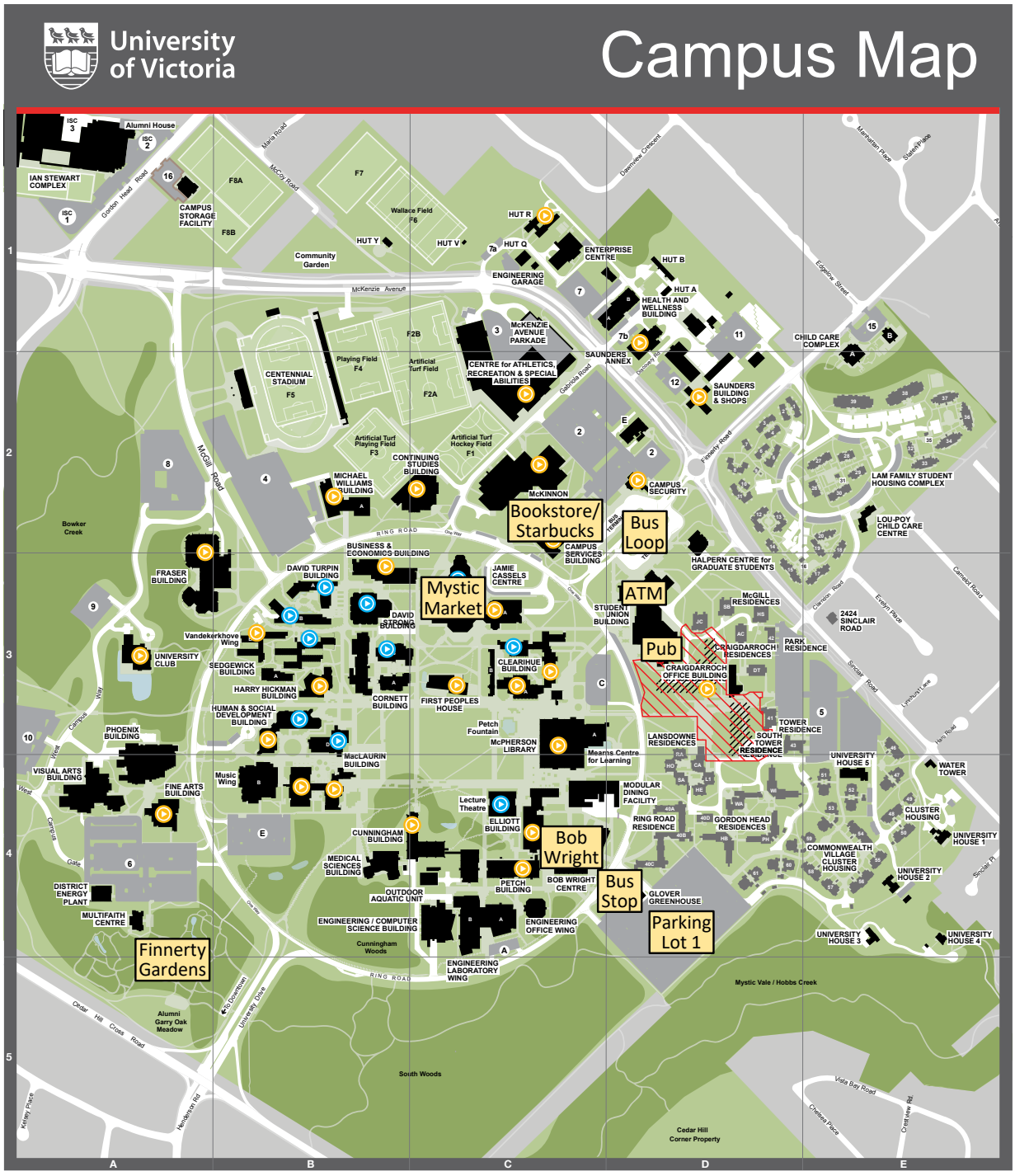
JOINT MEETING OF THE CANADIAN SOCIETY OF PLANT BIOLOGISTS WESTERN REGION AND THE UVIC FOREST BIOLOGY SYMPOSIUM

PROGRAM AND ABSTRACTS

University of Victoria

VICTORIA, BC
MAY 1 & 2, 2023


University of Victoria
Campus Map
Bookstore/ Starbucks
Bus Loop
Mystic Market
ATM
Pub
Bob Wright
Bus Stop
Parking Lot 1
Finnerty Gardens
ISC 3
Alumni House
ISC 2
IAN STEWART COMPLEX
ISC 1
CAMPUS STORAGE FACILITY
F8A
F8B
F7
Wallace Field F6
HUT R
HUT Y
HUT V
HUT Q
7a
ENTERPRISE CENTRE
HUT B
Community Garden
ENGINEERING GARAGE
McKenzie Avenue
HEALTH AND WELLNESS BUILDING
HUT A
F2B
McKENZIE AVENUE PARKADE
7b
CHILD CARE COMPLEX
SAUNDERS ANNEX
CENTRE for ATHLETICS, RECREATION & SPECIAL ABILITIES
SAUNDERS BUILDING & SHOPS
CENTENNIAL STADIUM
F5
Playing Field F4
Artificial Turf Field
F2A
Artificial Turf Playing Field F3
Artificial Turf Hockey Field F1
CONTINUING STUDIES BUILDING
MICHAEL WILLIAMS BUILDING
McKINNON
CAMPUS SECURITY
LAM FAMILY STUDENT HOUSING COMPLEX
LOU-POY CHILD CARE CENTRE
Bowker Creek
RING ROAD
BUSINESS & ECONOMICS BUILDING
CAMPUS SERVICES BUILDING
HALPERN CENTRE for GRADUATE STUDENTS
FRASER BUILDING
DAVID TURPIN BUILDING
JAMIE CASSELS CENTRE
DAVID STRONG BUILDING
STUDENT UNION BUILDING
McGILL RESIDENCES
2424 SINCLAIR ROAD
Vandekerkhove Wing
UNIVERSITY CLUB
SEDGEWICK BUILDING
CLEARIHUE BUILDING
CRAIGDARROCH RESIDENCES
PARK RESIDENCE
CRAIGDARROCH OFFICE BUILDING
HARRY HICKMAN BUILDING
CORNETT BUILDING
FIRST PEOPLES HOUSE
HUMAN & SOCIAL DEVELOPMENT BUILDING
Petch Fountain
McPHERSON LIBRARY
LANSDOWNE RESIDENCES
SOUTH TOWER RESIDENCE
TOWER RESIDENCE
PHOENIX BUILDING
MacLAURIN BUILDING
Mearns Centre for Learning
UNIVERSITY HOUSE 5
WATER TOWER
VISUAL ARTS BUILDING
FINE ARTS BUILDING
Music Wing
MODULAR DINING FACILITY
Lecture Theatre
ELLIOTT BUILDING
RING ROAD RESIDENCE
GORDON HEAD RESIDENCES
CLUSTER HOUSING
CUNNINGHAM BUILDING
UNIVERSITY HOUSE 1
COMMONWEALTH VILLAGE CLUSTER HOUSING
MEDICAL SCIENCES BUILDING
PETCH BUILDING
BOB WRIGHT CENTRE
UNIVERSITY HOUSE 2
DISTRICT ENERGY PLANT
OUTDOOR AQUATIC UNIT
GLOVER GREENHOUSE
MULTIFAITH CENTRE
ENGINEERING / COMPUTER SCIENCE BUILDING
ENGINEERING OFFICE WING
Cunningham Woods
ENGINEERING LABORATORY WING
UNIVERSITY HOUSE 3
UNIVERSITY HOUSE 4
Mystic Vale / Hobbs Creek
Alumni Garry Oak Meadow
South Woods
Cedar Hill Corner Property
A
B
C
D
E

SCIENTIFIC PROGRAM

Monday, May 1 – Bob Wright Centre (BWC) A104

9:30-9:45	**Welcome**	**Josephine Dick** – Welcome to the Territory **Peter Loock** – Dean of Science, UVic
9:45-10:10	Feature speaker **Lauren Erland** *Univ of the Fraser Valley*	T1. Resilience in nutritional quality of traditional staple crops to climate change
10:10-10:25	**Sarah Lane** *Univ of Victoria*	T2. Response of poplar, lavender, and western redcedar roots to iron deficiency stress
10:25-10:40	**Miriam Fenniri** *UBC*	T3. Postharvest quality and evolution of metabolites in wild berries of British Columbia
10:40-11:00	**Break**	
11:00-11:15	**Shakshi Dutt** *Univ of Calgary*	T4. Assessing overexpression of SOS1 from *Brassica napus* and *B. scoparia* on their ability to confer salt tolerance in *Schizosaccharomyces pombe, Arabidopsis thaliana*, and *B. napus*
11:15-11:30	**Nathan Lauer** *Univ of Victoria*	T5. Linking whole-plant responses to cell physiology in glycophytes exposed to NaCl stress.
11:30-11:45	**Udaya Subedi** *Univ of Alberta*	T6. Enhanced drought tolerance in alfalfa: Morphological, physiological, and transcriptional assessments of MsTAC1 down-regulated genotypes
11:45-12:00	**Lise Nehring** *Univ of Victoria*	T7. Assessing the contribution of Red Alder (*Alnus rubra*) to forest stand nitrogen budgets
12:00-1:10	**Lunch**	
1:10-1:35	Feature speaker **Keith Adams** *UBC*	T8. Subgenome-dominant expression and alternative splicing in response to *Sclerotinia* infection in polyploid *Brassica napus* and progenitors
1:35-1:50	**Paul de la Bastide** *Univ of Victoria*	T9. Fungal endophytes and insect herbivores affecting the health and recovery of Long's and Fernald's Braya, endangered endemic species of Newfoundland
1:50-2:05	**Melike Karaca Bulut** *UBC*	T10. Assessing the cuticular wax composition of black cottonwood
2:05-2:20	**Eerik-Mikael Piirtola** *Univ of Victoria*	T11. Poplar leaf bud resin metabolomics – seasonal patterns of leaf bud resin chemistry
2:20-2:40	**Break**	
2:40-2:55	**Tal Shalev** *UBC*	T12. Genomics of western redcedar: unlocking insights into genetic diversity and resilience in a key tree species
2:55-3:10	**Yihan Wu** *UBC*	T13. Genome-wide identification and analyses of copy number variants in 778 *Populus trichocarpa* individuals from natural populations
3:10-3:25	**Philippa Stone** *UBC*	T14. Patterns of plastid genome evolution across parasitic and mycoheterotrophic plants
3:25-3:40	**Andrew Hall** *UBC*	T15. Illuminating the diversity of cell-wall phenolics in six classes of moss
3:40-3:55	**Ravinder Goyal** *Agriculture & Agri-foods Canada*	T16. The characterization of the AP2/ERF gene family in *Pisum sativum*, and the expression profiles of some family members reveal their role in plant development
4:00-6:30	**Poster Session & Social** **BWC Lobby**	

Monday, May 1 – Poster Session - BWC Lobby

P1. Lingonberry genomics and evolution
Kaede Hirabayashi, *Univ of Victoria*

P2. Cross-species comparison of an evolutionarily conserved TF in *Arabidopsis thaliana* and tomato seed-to-seedling transition
Bailan Lu, *UBC*

P3. Is the enhanced soil carbon sequestration under N_2-fixing red alder due to increased nitrogen or diminished manganese?
Marty Kranabetter, *B.C. Ministry of Forests*

P4. Strategies for lignin manipulation without growth penalty using cell type-specific monolignol overproduction
Chak Chung Kuo, *UBC*

P5. Characterizing the interaction of protein phosphatase RLPH2 with the D group MPKs from *Arabidopsis thaliana*
Sierra Mitchell, *Univ of Calgary*

P6. Dynamics of gibberellin, glucose, and abscisic acid interactions during pea (*Pisum sativum* L.) seed development
Jocelyn Ozga, *Univ of Alberta*

P7. Characterization of AFB6 auxin receptor in pea (*Pisum sativum* L.)
Jocelyn Ozga, *Univ of Alberta*

P8. Composition of the Douglas-fir (*Pseudotsuga menziesii*) foliar mycobiome and its role in Swiss Needle Cast severity for a breeding population
Emma Hayward, *Univ of Victoria*

P9. GWAS identifies quantitative trait loci (QTLs) for limber pine resistance to white pine blister rust (WPBR)
J.-J. Liu, *Canadian Forest Service*

P10. Susceptibility of western redcedar to root and butt rot diseases as assessed by MiSeq and qPCR technologies.
J.-J. Liu, *Canadian Forest Service*

P11. Characterizing the effect of propyzamide on MOR1 protein dynamic in the *mor1-11* mutant and wild type *Arabidopsis thaliana*: Insights from fluorescence recovery after photobleaching (FRAP)
Aida Rakei, *UBC*

P12. A comparison of drought tolerance in two conifers with contrasting mycorrhizal associations
Bethany Robson, *Univ of Victoria*

P13. Enhanced drought tolerance in alfalfa: Morphological, physiological, and transcriptional assessments of *MsTAC1* down-regulated genotypes
Udaya Subedi, *Lethbridge Research and Development Centre*

P14. Landscape-level reconstruction of disturbance histories and carbon transfers from a retrospective carbon budget model as compared to sediment core records for the Sooke Lake watershed, British Columbia
J.A. (Tony) Trofymow, *Canadian Forest Service*

P15. Towards understanding the evolution of gene expression in gametophytes of mycoheterotrophic ferns and lycophytes
Marielle Wilson, *UBC*

P16. Ethanolic extract of *Ficus religiosa* prevents Cisplatin toxicity by enhancing antioxidant status in mice
Farhad Alipour, *Pune University*

P17. Physiological role of biochar and humic acid in conferring arsenic-induced oxidative stress in rice
Mirza Hasanuzzaman, *Sher-e-Bangla Agricultural University*

P18. Mulberry genes as a promising tool for enhancing crop resilience to environmental stresses
Hari Singh Meena, *Bengaluru University of Agricultural Sciences*

P19. Effect of arbuscular mycorrhizal fungi and oyster shell powder on cocoa seedlings growth and resistance against *Phytophthora megakarya* (causal agent of black pod disease) in the nursery
Paul Martial Tene Tayo, *Laboratory of Phytoprotection and Valorization of Genetic Resources*

P. 20. Assessing overexpression of SOS1 from *Brassica napus* and *Bassia scoparia* on their ability to confer salt tolerance in *Schizosaccharomyces pombe, Arabidopsis thaliana*, and *Brassica napus.*
Shakshi Dutt, *University of Calgary*

Tuesday, May 2 – Bob Wright Centre A104

9:00-9:25	Feature speaker **Susan Murch** *UBC- Okanagan*	T17. Hormonomics: A tool to understand plant growth regulators
9:25-9:40	**Milad Alizadeh** *UBC*	T18. A novel regulatory factor of plant embryonic program and its feedback regulation with seed transcription factors
9:40-9:55	**Dongeun Go** *UBC*	T19. A network of transcriptional regulators during the seed-to-seedling transition in plants
9:55-10:10	**Sean Ritter** *UBC*	T20. TOR Story: Investigating a role for CLASP in TOR-regulated growth transitions
10:10-10:25	**Cecily Costain** *UBC*	T21. Cellulose biosynthesis and COBRA – A new antibody shines a light on a previously elusive protein
10:25-10:45	**Break**	
10:45-11:30	**Sierra Mitchell** **Chris White-Gloria** **Jade Johnson** **Lana Wong** *Univ of Calgary*	T22 -T25. Insights from Quantitative Phosphoproteomics: Photosynthesis to fatty acid biosynthesis
11:30-11:45	**Tom Booker** *UBC*	T26. Local adaptation and the structure of the environment
11:45-12:00	**Adam Gilewski** *Simon Fraser Univ*	T27. Physiological and transcriptomic responses to drought in ponderosa pine
12:00-12:15	**Sachithrani Kannangara** *Simon Fraser Univ*	T28. RNAseq-based identification of a novel virus and novel virus variants in farmed blueberry plants.
12:15-1:15	**Lunch**	
1:15-1:40	Feature speaker **Soheil Mahmoud** *UBC – Okanagan*	T29. Molecular basis of flower development in *Cannabis sativa*
1:40-1:55	**Tonya Severson** *UBC*	T30. Transcriptome-wide characterization of alternative splicing in five drug-type cultivars of *Cannabis sativa*
1:55-2:10	**Reza Sajaditabar** *UBC – Okanagan*	T31. Genetic engineering of lavender glandular trichomes using trichome-specific promoters
2:10-2:25	**Dylan Perera** *UBC*	T32. Bioengineering of Montbretin A production in *Nicotiana benthamiana* – Towards scalable production of a new Type 2 diabetes treatment option
2:30-3:00	**Wrap-up & Student Prizes**	

TALKS

Resilience in nutritional quality of traditional staple crops to climate change

Lauren A.E. Erland **T1.**
Contact: lauren.erland@ufv.ca
University of the Fraser Valley, Agriculture

We are living in an era of unprecedented climate change at the same time that we need to feed a growing global population of more than 8 billion people. Almost everything you eat in a day comes from plants and globally on average nearly half the calories we consume in a day come from only three crops: corn, wheat and rice. One way to create more resilient food systems in to introduce diversity into our food systems, this can mean diversity in the species we rely on, including specialty and traditional crop species and production practices. Through the integration of climate models, microclimate and fruit quality analysis including micro and macro-nutrients and proximate analysis, our recent work has found that while yield and size of the South Pacific staple crop breadfruit (*Artocarpus altilis* var Ma'afala) is reduced, the fruit show significant nutritional resilience to changing environmental condition. We are applying the lessons learned from this study to better understand the impacts of climate change on commercial and traditional berry crops in B.C. and to use this to understand how management practices and varietal selection can be used to create more resilience berry horticultural systems.

Response of poplar, lavender, and western redcedar roots to iron deficiency stress

Sarah Lane[1], Amanda Sproule[2], David P. Overy[2], Patrick Walter[1], Jürgen Ehlting[1] **T2.**
Contact: slane@uvic.ca
[1]University of Victoria, [2]Agri-foods Canada

Iron is an essential mineral for plant metabolism yet it is poorly bioavailable, resulting in the evolution of diverse iron uptake strategies by plants and other organisms. Many plants rely on soil acidification and secondary metabolites in roots that increase iron solubility in the rhizosphere to aid in iron uptake. However, current knowledge is limited largely to a model species. Our research aims to characterize the chemical responses to iron deficiency in diverse species including poplar (*Populus trichocarpa x P. deltoides*), lavender (*Lavendula x intermedia*) and Western redcedar (*Thuja plicata*). We grew plants in soil-less cultures under normal and reduced iron conditions to stimulate production of metabolites. Roots from iron deficient plants tended to contain more phenolic compounds compared to control plants with clear species differences. We then investigated compositional differences by performing untargeted metabolomic analysis with ultra-performance liquid chromatography-high resolution mass spectrometry. Within methanol-soluble root extracts, multiple mass features were differentially abundant in roots in response to iron deficiency, but features varied across species. Metabolic responses in Western redcedar and lavender appear to be stronger compared to poplar, consistent with these species being able to tolerate alkaline soils better where iron is especially unavailable.

Postharvest quality and evolution of metabolites in wild berries of British Columbia

Miriam Z. Fenniri, Joana Pico Carbajo, Christopher Cote, Simone D. Castellarin, Abel Rosado **T3.**
Contact: Miriam.fenniri@botany.ubc.ca
University of British Columbia

Phenolics are a diverse class of secondary plant metabolites, many of which are known for health benefits, including antioxidative, chemopreventive, and neuroprotective properties. It is known that berries are a rich source of beneficial dietary phenolics, however this knowledge is mostly limited to commercial species and cultivars. The Pacific Northwest is home to over 100 edible native berry species with this number sharply increasing when naturalized, non-native berry species are also considered. Here, we explore the commercial and nutraceutical potential of a subset of wild berry species widely available in the lower mainland to identify species with desirable traits such as i) extended shelf lives, ii) minimal compositional changes over time, iii) a high accumulation of phenolics, and iv) interesting and/or novel phenolic profiles. We analyzed a variety of phenotypic traits in nine berry species from zero to four weeks post-harvest, including basic physical consumer parameters, primary metabolites, antioxidant activity, total phenolic content, and phenolic profile by HPLC/QToF. Most physical parameters and primary metabolites are stable over time in storage. Interestingly, wild berries tend to have higher total phenolic contents and antioxidant activities than their commercial counterparts, as well as unique phenolic profiles possessing previously unquantified phenolic species.

Assessing overexpression of SOS1 from *Brassica napus* and *Bassia scoparia* on their ability to confer salt tolerance in *Schizosaccharomyces pombe, Arabidopsis thaliana*, and *Brassica napus*. **T4.**

Shakshi Dutt, Muhammad Jamshed, Marcus Samuel
Contact: shakshi.dutt1@ucalgary.ca
University of Calgary

Soil salinity is a prominent abiotic stressor for agronomically important crops globally. Halophytic plants have evolved tolerance to saline environments whereas glycophytic plants remain sensitive. Canola (*Brassica napus*) is an oilseed crop of high value to Canadians as it contributes $29.9B annually to the economy. Compared to salt-sensitive glycophytic canola, the invasive broadleaf weed, Kochia (*Bassia scoparia*), is a halophytic plant. Both species contain a highly conserved salt overly sensitive (SOS) pathway responsible for helping plants combat salt stress, consisting of 3 genes: SOS1, 2, and 3. SOS1 is a transmembrane plasma membrane localized Sodium/Hydrogen (Na^+/H^+) antiporter, SOS2 is a cytosolic Serine/Threonine kinase, and SOS3 is a calcium binding protein. My study aims to overexpress the SOS1 gene from canola and kochia in salt sensitive fission yeast (*Schizosaccharomyces pombe*) lines, in wild-type and *sos1*-knockout *Arabidopsis thaliana* lines, and in wildtype Canola to determine the extent of salt tolerance conferred. We predict that the kochia SOS1 will be able to deliver an increased level of tolerance to salt compared to overexpression of canola SOS1 as shared protein sequence identity is 74%. The use of model organisms facilitates quick-yielding, proof-of-concept analyses, which will be completed concurrently with the transformation of canola.

Linking whole-plant responses to cell physiology in glycophytes exposed to NaCl stress **T5.**

Nathan Lauer
Contact: nlauer@uvic.ca
University of Victoria

The responses of glycophytic plants to NaCl stress have been well documented and include rapid decreases in root water flux, transpiration, photosynthesis, and growth. Once acclimated, plants exhibit a more conservative growth form characterized by decreased chlorophyll concentration but increased compatible solute concentrations, senescence of older leaves, and lateral root formation. This response is now known as 'systemic acquired acclimation' (SAA). Emerging evidence suggests the SAA response is regulated by systemic electrical signals sent through the phloem followed by cell signaling cascades leading to changes in cell physiology. The secondary cell signaling responses include elevated cytosolic Ca^{+2}, the enzymatic production of reactive oxygen species (ROS) and nitric oxide (NO), the induction of autophagy, the proliferation of peroxisomes and changes to organelle activity. The cell signaling processes in root cortex and guard cells are well studied whereas signaling processes governing mesophyll cells and photophysiology are mostly unexplored. This work will discuss the emerging evidence linking the SAA response to long-distance electrical signals followed by cell signaling cascades at different cell types. Also, a conceptual framework for studying the cell signaling events that potentially govern photophysiology will be discussed.

Enhanced drought tolerance in alfalfa: Morphological, physiological, and transcriptional assessments of MsTAC1 down-regulated genotypes **T6**.

Udaya Subedi[1,2], Kimberley Burton Hughes[1], Gaganpreet Kaur Dhariwal[1], Guanqun Chen[2], Surya Acharya[1], Stacy D. Singer[1]
Contact: udaya@ualberta.ca
[1]Agriculture and Agri-Foods Canada, Lethbridge Research and Development Centre; [2]University of Alberta, Department of Agricultural, Food and Nutritional Science

Drought poses a severe threat to alfalfa (*Medicago sativa* L.) production. Previously, the zinc finger transcription factor Telomerase Activator 1 (TAC1) was found to negatively regulate responses to drought and salinity in Arabidopsis. In this study, we identified a *TAC1* homolog in alfalfa and generated RNAi genotypes to investigate its role in drought stress response. Under drought stress, TAC1-RNAi genotypes exhibited less wilting and experienced smaller reductions in plant height, internode length, and shoot and root weight compared to EV controls, suggesting an enhancement in drought tolerance. Furthermore, TAC1-RNAi genotypes also demonstrated lower leaf water-loss rates and higher leaf relative water contents under drought compared to EV controls, which corresponded with significantly lower stomatal densities. Transcriptional profiling of plants under drought conditions led to the identification of numerous differentially expressed

genes between TAC1-RNAi and wild-type genotypes, with an abundance being involved in cell wall production, secondary metabolism, abiotic stress response, hormone metabolism, and redox-related processes, as well as those encoding transcription factors. This study provides valuable insight into the physiological and molecular mechanisms regulating drought resilience in alfalfa, and provides a basis for the development of transgene-free alfalfa germplasm using CRISPR/Cas technology with superior performance under drought condition.

Assessing the contribution of red alder (*Alnus rubra*) to forest stand nitrogen budgets **T7.**

Lise Nehring[1], Barbara Hawkins[1], Marty Kranabetter[2]
Contact: lisenehring@uvic.ca
[1]University of Victoria, Centre for Forest Biology; [2]B.C. Ministry of Forests

Red Alder (*Alnus rubra*) is a common coastal hardwood in British Columbia and has evolved a symbiotic relationship with the nitrogen-fixing actinomycete, *Frankia*. This research uses $\delta^{15}N$ signatures in soils, wood and litter to assess the contribution of nitrogen-fixing Red Alder to the components of stand nitrogen budgets. The stands used are part of the B.C. Ministry of Forests' long-term Experimental Project 1121.01. Planted in 1994 as part of a replacement series trial, the Holt Creek site contains stands of Douglas-fir and Red Alder in five proportions (RA: Df proportions: 100/0, 50/50, 25/75, 11/89, 0/100). Increment cores from 5 trees/species/ plot were taken along with soil and litter samples and analyzed for essential mineral elements and $\delta^{15}N$. The litter of both species did not differ in $\delta^{15}N$. Results confirmed that forest floor soil under Red Alder was enriched in total nitrogen, and $\delta^{15}N$ was elevated due to the contribution of fixed atmospheric nitrogen. The enrichment effect was visible in the tree rings of Douglas-fir in the 50/50 stand. Red Alder tree ring $\delta^{15}N$ exhibited a non-linear relationship with time. This could be due to reduced nitrogen fixation associated with declining tree vigour or negative feedback from low soil pH.

Subgenome-dominant expression and alternative splicing in response to Sclerotinia infection in polyploid Brassica napus and progenitors **T8.**

Grant de Jong, Keith Adams
Contact: keith.adams@ubc.ca
University of British Columbia, Department of Botany

Polyploidy has played an extensive role in the evolution of flowering plants. Allopolyploids, with subgenomes containing duplicated gene pairs called homeologs, can show rapid transcriptome changes including novel alternative splicing (AS) patterns. We subjected both resynthesized and natural lines of polyploid *Brassica napus*, along with the progenitors *Brassica rapa* and *Brassica oleracea*, to infection with the fungal pathogen *Sclerotinia sclerotiorum*. RNA-sequencing analyses revealed widespread divergence between polyploid subgenomes in both gene expression and AS patterns. Resynthesized *B. napus* displayed significantly more A and C subgenome biased homeologs under pathogen infection than during uninfected growth. Differential AS (DAS) in response to infection was highest in natural *B. napus* (12 709 DAS events) and lower in resynthesized *B. napus* (8863 DAS events). Natural *B. napus* had more upregulated events and fewer downregulated events. There was a global expression bias towards the *B. oleracea*-derived (C) subgenome in both resynthesized and natural *B. napus*, enhanced by widespread non-parental downregulation of the *B. rapa*-derived (A) homeolog. In the resynthesized *B. napus*, this resulted in a disproportionate C subgenome contribution to the pathogen defense response, characterized by biases in both transcript expression levels and the proportion of induced genes. Our results elucidate the complex ways in which *Sclerotinia* infection affects expression and AS of homeologous genes in resynthesized and natural *B. napus*.

Fungal endophytes and insect herbivores affecting the health and recovery of Long's and Fernald's Braya, endangered endemic species of Newfoundland **T9.**

Paul de la Bastide[1], Terrie Finston[1], Luise Hermanutz[2] and [1]Will Hintz[1]
Contact: pdelabas@uvic.ca
[1]University of Victoria, Centre for Forest Biology; [2]Memorial University of Newfoundland, Department of Biology

Long's (*Braya longii*) and Fernald's (*B. fernaldii*) Braya are endemic to the Great Northern Peninsula of Newfoundland. These herbaceous perennials are endangered due to habitat loss, chronic pathogen infections and insect herbivory. While recovery plans are being implemented, their fungal microbiome remains understudied. This study examines the fungal community and the role of insect herbivory in plant health. Plant tissues from three populations were sampled during active growth over five years, yielding 326 fungal isolates identified primarily by nucleotide sequence analysis. Isolates included 36 taxa, 16 of which were detected once; 12 taxa were detected across multiple sites, sampling intervals and years, including known pathogens of Brassicaceae. Plants frequently showed symptoms of both fungal infection and insect herbivory. Insects on Braya were sampled over three years on the same field sites to assess their fungal microbiome. Fungal isolates were very similar to those colonizing plants, with a few exceptions. Vertical transmission of fungi in seeds is under study for two sites, one pristine, one disturbed, while a metagenomics study was initiated to capture the broader fungal community in plants and compare among sites and hosts. These findings will improve our knowledge of Braya endophyte communities and inform recovery efforts.

Assessing the cuticular wax composition of black cottonwood

Melike Karaca-Bulut, Shawn Mansfield **T10.**
Contact: karacaa.melike@gmail.com
University of British Columbia

The study investigates the effects of drought stress on the productivity of *Populus trichocarpa* (black cottonwood) trees, a species with high transpiration rates, by examining changes in the composition of leaf cuticular waxes. Cuticular waxes are crucial for regulating non-stomatal water loss and include long-chain fatty acid metabolites, flavonoids, tocopherols, triterpenoids, and phytosterols. By comparing the cuticular wax composition of natural populations grown under control and drought conditions, the study identified candidate genes associated with cuticular wax biosynthesis and regulation using GWAS. The study found that the overall wax content of black cottonwood is less sensitive to drought than individual wax constituents, with alkenes, alcohols, and esters contributing to drought response and tolerance. The study uncovered two known genes, *CER1* and *FATB*, linked to fatty acid biosynthesis and novel components involved in coordinating drought responses in poplar trees, highlighting the plasticity of cuticular waxes in responding to drought environments. This research has important implications for understanding the potential impacts of climate change on poplar trees and identifying strategies for improving their drought tolerance.

Poplar leaf bud resin metabolomics – seasonal patterns of leaf bud resin chemistry

Eerik-Mikael Piirtola, C. Peter Constabel **T11.**
Contact: eemipi@uvic.ca
University of Victoria, Centre for Forest Biology

One adaptation of trees in northern latitudes is the production of resin in leaf buds. This hydrophobic resin protects the buds and developing leaves from insect herbivory and frost. Poplar resins are particularly rich in bioactive phenolics and are widely used in traditional medicine. This study aims to identify seasonal patterns in the chemical composition of *Populus trichocarpa* leaf bud resin. Here we focus on dihydrochalcones, a specialized group of phenylpropanoids found in the bud resin of balsam poplars. We analyzed the secreted resin extracted from the surface of lateral leaf buds as well as whole leaf bud extracts. The samples were collected monthly over one year. We used ultra-high performance chromatography (UPLC) coupled with mass spectrometry (MS) for targeted quantification of dihydrochalcones, and high-resolution mass spectrometry (HRMS) for nontargeted metabolomics to identify changes in total metabolites in the leaf bud extracts. We demonstrated an accumulation of dihydrochalcones in the bud extracts in the fall. Overwintering dormant buds showed high levels of dihydrochalcones compared to developing buds in the summer. An increase in dihydrochalcones was identified in surface resin in the fall when buds transition from growth to dormancy, as well as during bud break in the spring.

Genomics of western redcedar: unlocking insights into genetic diversity and resilience in a key tree species **T12.**

Tal J. Shalev[1], Omnia Gamal El-Dien[1,2], Lise van der Merwe[1], Matias Kirst[4], Carol Ritland[1], Alvin D. Yanchuk[3], John H. Russell[3], Joerg Bohlmann[1]
Contact: tal.shalev@msl.ubc.ca
[1]University of British Columbia, Michael Smith Laboratories; [2]Canadian Forest Service, Pacific Forestry Centre; [3]B.C. Ministry of Forests; *[4]University of Florida, School of Forest, Fisheries and Geomatic Sciences*

Western redcedar (WRC; *Thuja plicata*) is an ecologically, culturally, and economically important tree species in North America. By creating genomic resources for important trees such as WRC, we aim to develop a better understanding of their biology and improve breeding for growth and resilience in operational forestry. We present novel transcriptome, genome, and single nucleotide polymorphism (SNP) resources for WRC. We found that the genetic diversity of WRC is exceptionally low for a continuous tree species of its range size, likely due to range expansion from a single glacial refugium and its unique self-compatibility. Analysis of unique selfing lines revealed that WRC's adaptability and responsiveness to selection may be due to balancing selection as a result of its demography. Further, not only does WRC show limited inbreeding depression for growth, terpene chemistry, or dendrochronological traits, but appropriate selection intensity can mitigate the effects of inbreeding for growth traits. Using a genomic selection approach, we identified thousands of loci putatively associated with growth and specialised chemistry traits in WRC, with substantial variation in effect sizes of loci between different traits. We are now applying this knowledge to developing custom SNP sets for improved application of genomic selection in operational breeding.

Genome-wide identification and analyses of copy number variants in 778 *Populus trichocarpa* individuals from natural populations **T13.**

Yihan Wu, Keith Adams
Contact: yihan.wu@botany.ubc.ca
University of British Columbia, Department of Botany

Copy number variations (CNVs), including duplications and deletions of the genome ranging up to 1Mb, are an important contributor to genomic variation, and may influence phenotypic variation. They are relatively understudied compared to single nucleotide polymorphisms despite affecting a higher proportion of the genome. Using whole genome sequencing data and RNA-sequencing data, we studied the natural diversity of CNVs across the range of *Populus trichocarpa* and the effects of CNVs on gene expression. We analyzed whole genome sequencing data of 778 *P. trichocarpa* individuals to identify CNVs in the genomes and examined gene expression with RNA-sequencing data of leaf and xylem for 390 individuals. We found 24,546 deletions and 13,595 duplications covering a major percentage of the genome. Genes overlapping with CNVs were enriched in important biological processes such as reproduction, cellulose production, and defense. We also detected CNV introgression from the related species *P. balsamifera*. Analysis of CNV genotypes with expression data showed a minority of genes overlapping CNVs having a strong correlation of expression with copy number. Our identified CNVs provide insights into the extent, characteristics, and diversity of CNVs in wild populations of *P. trichocarpa* and the effects of CNVs on gene expression.

Patterns of plastid genome evolution across parasitic and mycoheterotrophic plants

Philippa Stone, Vivienne Lam, Hayley Darby, Sean Graham **T14.**
Contact: philippa.stone@botany.ubc.ca
University of British Columbia, Department of Botany

Most plants fix their carbon through photosynthesis. However, mycoheterotrophs obtain some or all of their fixed carbon from soil fungi, and holoparasitic plants from other plants. Loss of photosynthetic function has led to parallel gene loss in the plastid genome for most heterotrophic lineages, but this has not been fully characterized across angiosperms. Here we examine plastid genome structure and gene content in taxonomically diverse heterotrophs and autotrophs in order to characterize commonalities and differences in patterns of plastid genome evolution. Most heterotrophs have experienced changes in plastid genome structure. A third of species that maintain an inverted repeat (IR) have experienced loss of colinearity compared to their autotrophic relatives, and another third have completely lost their IR. We developed a novel pipeline using BLAST and tRNAscan-SE to confirm GenBank annotations for gene presence vs. absence, which are

sometimes not accurate. Non-photosynthetic species that have lost photosynthetic machinery retain a core set of non-bioenergetic genes, and several have retained full copies of *rbcL* and *atp* genes. Of the five non-bioenergetic genes expected to linger (*accD*, *clpP*, *trnE*, *ycf1* and *ycf2*), genes that are involved in lipid biosynthesis (*accD*), protein degradation (*clpP*), and heme biosynthesis (*trnE-UUC*), have the fewest independent losses.

Illuminating the diversity of cell-wall phenolics in six classes of moss

Andrew G. Hall, Sean W. Graham, A. Lacey Samuels **T15.**
Contact: andrew.hall@botany.ubc.ca
University of British Columbia, Department of Botany

The emergence of lignin was one of the most consequential evolutionary events shaping terrestrial ecosystems. Lignin is a phenolic polymer produced by the coupling of subunits derived from the phenylpropanoid pathway and is typically thought to be restricted to the vascular plants. However, the existence of polymers composed of flavonoid- and phenylpropanoid-type subunits in the cell walls of some mosses challenges a long-held assumption that moss cell walls are devoid of phenolics. The biosynthesis, distribution, and physiological roles of these structures in mosses remain largely unknown. Here we present a bioinformatic survey of phenylpropanoid pathway enzymes, coupled with a fluorescence-imaging survey of cell walls in taxa from six classes of mosses. Using a BLAST-based approach considering phenylpropanoid pathway enzymes from *Arabidopsis***,** we identified the presence of these enzymes and characterized potential gene-family expansions in mosses, based on data from the 1000 Plant Transcriptomes Initiative. Phenolic compounds produce autofluorescence when excited with ultraviolet light. We exploited this characteristic to examine the distribution of phenolic materials within cell walls and across moss taxa. We found heterogeneous distributions of autofluorescence which varied both spectrally and spatially, suggesting the presence of cell-wall phenolics in mosses with diverse composition and organization across the major lineages.

The characterization of the AP2/ERF gene family in *Pisum sativum*, and the expression profiles of some family members reveal their role in plant development **T16.**

Ravinder K. Goyal, Arun Kommadath, Jeff Ranches, Albert Hannig
Contact: Ravinder.goyal@agr.gc.ca
Agriculture and Agri-Foods Canada, Lacombe Research and Development Center

The pea (*Pisum sativum* L.) is a well-known pulse crop that is used as food and animal feed all over the world. Due to its capacity to organically fix nitrogen and the fact that it is a rich source of protein, it assumes more significance in sustainable agriculture and promotes the movement towards plant-based proteins in place of animal-based proteins. Peas' huge (4.45 Gbp) genome and lack of genetic element characterization contributed to their comparatively slow progress in several biological areas compared to other commercial crops. APETALA2 (AP2)/ Ethylene-Responsive Element Binding Protein, or Ethylene Response Factors (ERF) are plant-specific transcription factors (TFs) that bind to the cis-elements conserved in the target genes. The significance of the AP2/ERF superfamily in plant development, stress response, and hormone response has drawn attention. Using hmmsearch, a genome-wide search turned up 195 AP2-domain-containing gene sequences dispersed over 177 chromosomal locations. The gene characterization for conserved domains placed the majority of the genes into the ERF sub-class, followed by AP2 and RAV. Further classification of the genes revealed some similarities as well as distinctness from the Arabidopsis gene family. The differential expression of some family members suggests that they play a role in plant development.

Hormonomics: A tool to understand plant growth regulators

Susan J. Murch[1], Ryland T. Giebelhaus[2], Lauren A.E. Erland[3]
Contact: susan.murch@ubc.ca
[1] University of British Columbia Okanagan, Chemistry ;[2]University of Alberta, Chemistry; [3] University of the Fraser Valley, Agriculture

T17.

Plant growth regulators (PGRs) are a small signaling molecules, which function in coordination to direct all aspects of development, function and reproduction in living systems. The classic Skoog and Miller hypothesis proposed that the routes of plant growth and development are determined by the relative ratios of auxins and cytokinins. In the last 75 years, the hypothesis has been stretched and modified as we understand the roles of indoleamine, brassinosteroids, stringolactones, ethylene, gibberellins, abscisic acid, jasmonates, salicylates, karrikins and others. Endogenous PGRs are inherently present at low levels in tissues, stored in many forms and mobilized rapidly in response to a stimulus making them difficult to measure, identify and quantify. We have developed and optimized a new tool for identification, detection and quantification of PGRs. HormonomicsDB is an online searchable database that can be used to query an untargeted mass spectrometry (MS) dataset against a database of more than 260 known and predicted plant hormones, their precursors, conjugates and metabolites. The protocol encompasses sample preparation, analysis, data processing and hormone annotation and is designed to minimize degradation of labile hormones. The application of this tool to experimental systems such as Wollemi Pine, Cannabis, African Violets and Hazelnuts has discovered the complexity of PGR systems in the control of plant growth and development.

A novel regulatory factor of plant embryonic program and its feedback regulation with seed transcription factors

T18.

Milad Alizadeh, Liang Song
Contact: milad.alizadeh@botany.ubc.ca
University of British Columbia, Department of Botany

The regulation of gene networks is essential for plant development. ABA INSENSITIVE 3 (ABI3) is a master transcription factor that coordinates many aspects of seed development. A loss of function of ABI3 impairs food reserve accumulation, seed dormancy, and desiccation tolerance. During the embryonic-to-vegetative transition, many genes actively expressed in the seeds are transcriptionally switched off. Here, we report a newly characterized transcriptional corepressor of the embryonic program, SEED DORMANCY 4-LIKE (AtSDR4L). *Atsdr4l* mutants show increased seed dormancy, stunted seedlings development, elevated expression of *ABI3*, and over-accumulation of the seed storage lipids. We showed that a feedback regulation occurs between ABI3 and AtSDR4L. The genetic study of double mutants demonstrated that ABI3 is epistatic to Atsdr4l for embryonic traits. In addition, we found that penetrance and expressivity of the Atsdr4l phenotype are condition- and developmental stage-dependent. In conclusion, a self-regulating mechanism achieved by feedback regulation between ABI3 and AtSDR4L is essential for a successful seed-to-seedling transition.

A network of transcriptional regulators during the seed-to-seedling transition in plants

T19.

Dongeun Go, Alexander Wong, Liang Song
Contact: dongeun.go@botany.ubc.ca
University of British Columbia, Department of Botany

The development of seed and the following seed-to-seedling transition are intricate processes tightly regulated by a network of transcriptional regulators. In *Arabidopsis thaliana*, LEC1, ABI3, FUS3, and LEC2, collectively known as LAFL, serve as master transcription factors that regulate gene expression during embryo morphogenesis and seed maturation. During the subsequent transition from seed maturation to seed germination to seedling growth, this LAFL network is suppressed by the repressors, including a newly characterized co-repressor called *Arabidopsis thaliana* SEED DORMANCY 4-LIKE (*At*SDR4L). However, the feedback regulation among the AtSDR4L and its targets, including *LEC1,* is not well understood. Creating large segmental deletions spanning *cis*-regulatory elements of *At*SDR4L targets can facilitate further studies on the function of AtSDR4L. Here, we thus present a successful removal of the AtSDR4L targeting regions near *LEC1*, *RGL2*, and *ATPP2CA* by CRISPR-Cas9-based genome engineering. Furthermore, a CRISPR/Cas9 construct for targeting the *AtSDR4L* orthologs in a close relative of Arabidopsis, *Camelina sativa*, marked by its high oil content, was successfully

transformed, thereby suggesting the potential for further studies on *AtSDR4L* homologs in relation to the LAFL network in crops.

TOR Story: Investigating a role for CLASP in TOR-regulated growth transitions

Sean Ritter, Geoffrey Wasteneys **T20**.
Contact: sean.ritter@botany.ubc.ca
University of British Columbia, Department of Botany

As photosynthetic organisms, plants need to adapt to changing light conditions. TARGET OF RAPAMYCIN (TOR) is a protein kinase activated by growth factors and inactivated by energy deprivation, thereby acting as a master regulator of metabolic pathways in all eukaryotes. An early study in yeast by Choi et al. (2000) indicated that TOR signalling regulates microtubule stability, and physically interacts with BIK1, the yeast homolog of Cytoplasmic Linker Protein (CLIP170). Although plants lack CLIP170 proteins, they do have homologues of the CLIP-associating protein (CLASP), which is a microtubule-associated protein. A recent study has demonstrated that CLASP undergoes changes in abundance in response to light and nutrient levels. In addition, CLASP plays key roles in both BR signalling and auxin transport, two processes specifically associated with TOR signalling in plants. This study therefore explored the potential function of CLASP in the coordination of TOR activity in hormonal signalling and microtubule organization using the model system Arabidopsis thaliana. These findings and ongoing experiments provide new insight into how the nutrient-sensing capabilities of TOR are translated into altered root development, thereby furthering our understanding of how plants perceive their changing environment.

Cellulose biosynthesis and COBRA – A new antibody shines a light on a previously elusive protein

Cecily Costain, Kamryn Diehl, Geoffrey Wasteneys **T21.**
Contact: cecily.costain@botany.ubc.ca
University of British Columbia, Department of Botany

Plants produce cellulose, the most abundant biopolymer on Earth. Cellulose production is regulated by several proteins working in concert. Among these is COBRA (COB), a glycosylphosphatidylinositol (GPI) - anchored protein located at the outer leaflet of the plasma membrane of plant cells. COB contains several structural domains, including a cellulose-binding domain, a GPI-anchor attachment site, and a cysteine-rich domain (of which little is known). COB is believed to be involved in cellulose biosynthesis by modulating anisotropic cell expansion and microfibril deposition at the cell wall, but the precise molecular mechanisms by which COB functions is unclear. In this study, we use a combination of molecular and biochemical techniques such as affinity purification, mass spectrometry, and western blotting to further elucidate COB's role in cellulose biosynthesis. Our results indicate that COB function is controlled by a possible cleavage or phosphorylation event. One potential mechanism by which COB functions is through a conformational change upon its binding to cellulose after secretion. Modelling this through bioinformatic tools such as AlphaFoldTM, however, is currently not possible. We therefore intend to focus future investigations on COB regulation in vivo in a system in which COB can freely bind to cellulose.

Insights from quantitative phosphoproteomics: Photosynthesis to fatty acid biosynthesis
The Moorhead Lab
University of Calgary, Department of Biological Sciences

Characterizing the interaction of protein phosphatase RLPH2 with the D group MPKs from *A. thaliana*
Sierra Mitchell, Greg Moorhead **T22.**
Contact: sierra.mitchell@ucalgary.ca

Protein phosphorylation is a prevalent post-translational modification involved in all aspects of the cell. This is achieved through the opposing activities of protein kinases and protein phosphatases, which add or remove a phosphoryl group on proteins, respectively. In Arabidopsis thaliana four novel bacteria-like phosphatases have been identified, one of which being Rhizobiales-like phosphatase 2 (RLPH2). Using quantitative phosphoproteomics to compare the protein phosphorylation profile of WT and rlph2 KO lines, the D group mitogen activated protein kinases (MPK) were identified to be potential substrates of RLPH2, specifically regulating the TxY motif of their activation loop. From invitro peptide work, this dephosphorylation activity seemed to be dependent on the aspartic acid residue being present in the TxY motif of D group MPKs (TDY), as opposed to the glutamic acid residue found in the A, B, and C group MPKs (TEY). Invitro dephosphorylation assays with the full length proteins will be pursued to confirm the importance of the aspartic acid in RLPH2's specificity towards D group MPKs. This research is important in confirming the possible regulatory function of RLPH2 on D group MPKs and how that might affect downstream substrates of these MPKs.

SLP1: a novel regulator of photosynthesis
Chris White-Gloria, Greg Moorhead **T23.**
Contact: christopher.whiteglo@ucalgary.ca

Photosynthesis is one of the most important biological phenomena on the planet. One regulatory mechanism for this process is the post-translational modification of proteins involved in catalyzing the light (in)dependent reactions occurring at the chloroplast thylakoid membranes and stroma. Like in all other eukaryotes, protein phosphorylation is the most prevalent post-translational modification in plants and is controlled by protein phosphatases and protein kinases. In the chloroplast only a few protein phosphatases are well characterized, with their substrates mostly being thylakoid membrane proteins. Following our group's bioinformatic discovery of chloroplast stroma localized protein phosphatase *Shewanella*-like phosphatase 1 (SLP1), our phosphoproteomics study suggests that SLP1 regulates the phosphorylation status of 126 proteins in the chloroplast. This gives SLP1 a supposedly widespread role and places it at the center of many chloroplastic processes, including photosynthesis. With 21 putative SLP1 substrates involved in photosynthesis, SLP1 represents a novel regulator of photosynthetic reactions spreading across the different localities of the chloroplast.

Characterization of the chloroplast protein phosphatase *Shewanella*-like protein phosphatase 1
Jayde Johnson, Greg Moorhead **T24.**
Contact: jayde.johnson@ucalgary.ca

Plants capture energy from the sun and using carbon dioxide and water, transform it into the oxygen and biomass which sustains nearly all life on earth. These photosynthetic reactions occur in the chloroplast and due to their importance, the reactions that occur here are tightly regulated. Many of the mechanisms for regulation of chloroplast processes are known and include post-translational modifications, such as reversible protein phosphorylation, redox regulation, and pH regulation. *Shewanella*-like protein phosphatase 1 (SLP1) is a novel phosphoprotein phosphatase (PPP) that resides in the stroma of *Arabidopsis thaliana* chloroplasts. Although SLP1 was discovered by the Moorhead group close to a decade ago, the mechanism that regulate it are still largely unknown. A mass spectrometry based quantitative phosphoproteomics study was conducted to uncover SLP1 substrates by comparing phosphorylation abundance between wild-type *Arabidopsis*, SLP1 over-expressor, and *slp1* knock-out lines. The study uncovered 126 putative SLP1 substrates all predicted to be localized to the chloroplast of *Arabidopsis.* Here we use phosphorylated peptides derived from putative SLP1 substrates in an *in vitro* malachite green assay to characterize chloroplast diurnal effects on SLP1. Our results indicate that SLP1 activity is affected by both pH and the redox environment of the chloroplast.

Regulation of fatty acid biosynthesis by protein phosphorylation of the α-CT subunit of ACCase in *Arabidopsis thaliana* **T25.**

Lana Wong, Greg Moorhead
Contact: lana.wong1@ucalgary.ca

Reversible protein phosphorylation is essential in mediating most cellular functions in living organisms. *Shewanella*-like phosphatase 1 (SLP1) is a novel *Arabidopsis thaliana* protein phosphatase localized to the chloroplast and is predicted to play an antagonistic role to the constitutively active chloroplast localized kinase, casein kinase 2 (CK2). Through a quantitative phosphoproteomics study carried out by previous members of the Moorhead Lab, many putative substrates of SLP1 were identified, one of them being acetyl-coenzyme A carboxylase carboxyltransferase subunit alpha (α-CT). α-CT is a subunit of acetyl-CoA carboxylase (ACCase), an enzyme that catalyzes the first committed step of *de novo* fatty acid biosynthesis, and like SLP1, is chloroplast localized. Carboxyltransferase interactors (CTIs), a group of small plastidial proteins of the chloroplast envelope have been identified to associate with the α-CT subunit of ACCase in a light-dependent manner. As there are phosphorylation sites on the C-terminus of α-CT, there is great interest in determining whether protein phosphorylation plays a role in mediating this interaction. By studying the effects of this post-translational modification, we will gain a better understanding of the role of protein phosphorylation in regulating fatty acid biosynthesis, which will ultimately uncover new ways to increase bio-oil production in crops.

Local adaptation and the structure of the environment

Tom Booker **T26.**
Contact: booker@zoology.ubc.ca
University of British Columbia, Department of Zoology

Spatial structure is an almost ubiquitous feature of life on earth. Environmental variation across the space a species inhabits can lead to spatially varying selection that, along with restricted dispersal, can lead to local adaptation. The spatial pattern of environmental variation, and thus the selection gradients, has a strong influence on local adaptation. In this work, I analyze a combination of simulated and empirical data to describe how the spatial pattern of environmental variation affects the degree of local adaptation and the genetic underpinnings of this important process. I examine the distribution of locally adaptive effects and the statistical power to identify locally adaptive alleles under various patterns of environmental variation. This study has implications for our expectations about local adaptation in natural populations and the outlook of characterizing the genetics basis of it.

Physiological and transcriptomic responses to drought in Ponderosa pine

Adam Gilewski[1], Jim Mattsson[1], Marie Vance[2] **T27.**
Contact: agilewsk@sfu.ca
[1]Simon Fraser University, [2]BC Ministry of Forests, Lands, Natural Resource Operations and Rural Development; Forest Improvement and Research Management Branch

Ponderosa pine (*Pinus ponderosa*) is a drought-tolerant tree species of key importance for the BC interior's increasingly hot and dry forests. A provincial seed orchard contains selections based on lumber yield, but their performance under drought conditions is unknown. A comparison of half-sib family responses to well-watered and drought conditions revealed that: (1) families with high growth generally did not experience greater reduction in growth in response to drought than slow-growing families, (2) drought-stressed seedlings that grew well had higher water potentials and lower water use efficiencies, (3) fast growing individuals within the drought treatment had intermediate transcriptomic responses in needles relative to trees that grew poorly under drought stress. Finally, hydroponic experiments showed that mild osmotic stress stimulated rather than inhibited root growth. In summary, we found that some families previously selected for growth have high drought tolerance and can be used for deployment and further selection for drought resistance. Moreover, high growth and water potential together with smaller transcriptomic changes and low water use efficiency under drought stress indicate both access to and transpiration of water. We hypothesize that this is accomplished by a drought avoidance strategy such as root growth accessing deeper water.

RNAseq-based identification of a novel virus and novel virus variants in farmed blueberry plants

Sachithrani Kannangara[1], Juan Rodriguez[1], Adam Gilewski[1], Gerda de Villiers[2], Peter Ellis[2], Eric Gerbrandt[3], Jim Mattsson[1*]
Contact: skk25@sfu.ca
[1] Simon Fraser University, Department of Biological Sciences; [2] Phyto Diagnostics Company Ltd.; [3]BC Blueberry Council

T28.

Blueberry scorch and shock virus cause increasingly large production losses of highbush Blueberries in British Columbia. Moreover, correct diagnosis is important as scorch virus-infected plants will die and should be removed, whereas shock virus-infected plants recover and can be kept. In recent years, however, about 20% of diseased plants tested negative for both viruses by ELISA and PCR. To find out why we applied high-throughput sequencing of RNA in 77 diseased plants from across the BC lower mainland. We identified novel sequence variants of both scorch and shock viruses. When new PCR primers matching conserved regions among sequence variants were tested, PCR-based diagnosis improved. Moreover, we identified a novel Luteovirus. This 5078 base pairs long virus genome contains open reading frames for an RNA-dependent RNA polymerase, a coat protein, and RNA polymerase. This virus is present in nearly all tested plants, suggesting it does not cause disease alone. However, a population of diseased plants test negative for scorch, shock, and other viruses by deep sequencing but do harbor the Luteovirus, suggesting that this virus or variants of it may cause virus-like disease symptoms. We are currently testing this and other alternative hypotheses.

Molecular basis of flower development in *Cannabis sativa*

Soheil S. Mahmoud, Reza Sajaditabar, Ayelign M. Adal
Contact: soheil.mahmoud@ubc.ca
University of British Columbia Okanagan

T29.

The molecular aspects of flower initiation and development in *Cannabis sativa* have not been thoroughly investigated. In order to identify genes that control these processes, we employed RNA-Seq to obtain sequence information for transcripts that control flowering in this plant. A homology-based search in a *C. sativa* transcriptome database led to the identification of several transcripts homologous to those that control flower initiation and organ identity. Expression analysis revealed that most of these transcripts are differentially expressed during flower development. In this study, we cloned and constitutively expressed two transcription factor genes (*csSep1* and *csSep3*, which were predicted to control floral organ identity) in *Arabidopsis thaliana* plants, and evaluated the effects on flower initiation and morphology. Our results demonstrated that *csSep1* and *csSep3* do not affect floral morphology. However, they significantly impact growth and development, and flower timing in transformed *A. thaliana* plants.

Transcriptome-wide characterization of alternative splicing in five drug-type cultivars of *Cannabis sativa*

Tonya F. Severson, Keith L. Adams
Contact: tonya.severson@botany.ubc.ca
University of British Columbia, Department of Botany

T30.

Cannabis sativa is widely used for fiber, medicinal, and other purposes. Many cultivars exist, yielding varying proportions of THC, CBD, other cannabinoids, and terpenes. Some of these differences could arise from differential transcription of genes and differential splicing of transcripts, which are known to affect metabolism in other organisms. In this study, we identified alternatively splicing (AS) events from mature trichomes of five drug-type cultivars with divergent chemotypes. The AS events identified reveal that intron retention is the most common event type, followed by alternative donor, alternative acceptor, skipped exons, and mutually exclusive exons, consistent with event type distributions observed in other plants. These events included 547 unique to a single cultivar, 2661 shared by 2-4 cultivars, and 7569 common to all 5 cultivars. Genes with AS events were analyzed for enrichment, showing, for example, that genes with AS unique to a single cultivar are enriched for molecular functions related to interactions with ATP and processes involving transport within cells and across membranes. Alternative splicing of two terpene synthases (limonene and myrcene synthases) varied among cultivars. These results provide insights into the conservation and variation of AS events in drug-type cultivars of cannabis.

Genetic engineering of lavender glandular trichomes using trichome-specific promoters **T31.**

Reza Sajaditabar, Soheil S. Mahmoud
Contact: rsajadit@mail.ubc.ca
University of British Columbia Okanagan

Lavender, an aromatic shrub member of the Lamiaceae family, is widely cultivated for its essential oil (EO) which is composed of a mixture of monoterpenes. Lavender EO has a variety of applications in perfumery, hygiene, medicinal, and biofuel industries, among others. Among the 35 species of lavender, *Lavandula angustifolia*, *Lavandula latifolia* and *Lavandula intermedia* are the most economically important for their high EO content. In these plants, EO is produced in glandular trichomes (GT) which are specialized structures located on the surface of the leaves, stems and flowers. EO monoterpene composition is a key factor of its quality, and certain monoterpenes are more desirable than the others. For example, linalool and linalyl acetate are desired in perfumery while borneol and camphor are not. The aim of our study is to improve EO profile by manipulating the expression of terpene synthase genes (TPS). Previous studies have used the CaMV35S promoter to induce TPS expression and EO production. However, this approach can lead to the production of toxic levels of monoterpenes in non-GT plant cells. We propose using GT-specific promoters that have been isolated in our lab to enhance TPS expression only in GTs, thereby increasing EO production without harming the plant.

Bioengineering of Montbretin A production in *Nicotiana benthamiana* – Towards scalable production of a new Type 2 diabetes treatment option **T32.**

Dylan Perera[1], Lars H. Kruse[1], Frederick G. Sunstrum[1], Daniela Garcia[1], Guillermo Lopez-Perez[1], Sharon Jancsik[1], Macaire M.S. Yuen[1], Doug Cossar[2], Michael McLean[2], Sandra Irmisch[3], Jörg Bohlmann[1]
Contact: dsperera@student.ubc.ca
[1]Michael Smith Laboratories, University of British Columbia; [2]PlantForm Corporation, Toronto; [3]Institute of Biology Leiden, Leiden University, The Netherlands

Montbretin A (MbA) is a complex acylated flavonol glycoside isolated from the montbretia plant (*Crocosmia x crocosmiiflora*). MbA is a strong and specific inhibitor of human pancreatic α-amylase and could therefore serve as a treatment for type 2 diabetes. It is not feasible to mass-produce MbA by chemoenzymatic synthesis or by extraction from montbretia plants. However, we previously elucidated all steps of the MbA pathway in montbretia, allowing us to engineer MbA production in *Nicotiana benthamiana* (Nb) by transient agroinfiltration of 10 montbretia genes. It is now necessary to further improve MbA yields. One improvement strategy identified metabolic bottlenecks in MbA-bioengineered Nb, *e.g.,* at the first pathway intermediate myricetin-3-*O*-rhamnoside (MR). Increasing expression of the following pathway enzyme CcUT2 decreased MR accumulation and improved MbA yields. Another yield improvement strategy targeted undesired side-products, *e.g.,* side-products built around myricetin-3-*O*-glucoside (MG) vs canonical MR. Phylogenetic analysis, *in vitro* assays, and *in planta* assays identified three Nb UDP-glycosyltransferases that could mediate MG formation. Next, we will apply RNAi silencing and CRISPR/Cas9 knockouts to these enzymes with the goal of reducing side-product formation and redirecting intermediates towards MbA. This study highlights the potential of pathway engineering in Nb to overcome limitations in developing novel pharmaceuticals.

POSTERS

Lingonberry genomics and evolution

Kaede Hirabayashi, Gregory L. Owens **P1.**
Contact: khirabayashi@uvic.ca
University of Victoria, Department of Biology

Lingonberry (*Vaccinium vitis-idaea*) is a dwarf shrub that grows widely in the circumpolar region. The species has two recognized subspecies (ssp.) defined by their origin: European ssp. vitis-idaea and North American ssp. *minus*. The two subspecies are morphologically different, with the former growing relatively taller with longer/wider leaf and bigger fruits than the latter. The berries have medicinal uses including potential anti-cancer, antioxidant, and anti-inflammatory properties. The exploration of cultivars with agroeconomic benefits to initiate larger-scale lingonberry commercial production has therefore been a growing area of research. Despite extensive chemical analysis, very little genomic information has been generated for lingonberry. Moreover, genetic differentiation between the two subspecies is undefined, which means genetic identification of subspecies is currently challenging. The goal of my project is to create the genomic resource for lingonberry, and further elucidate the species history and enzymatic profiles using the genomic data. To achieve this, I first sequenced and assembled the genomes of both European and North American lingonberries and further annotated the genomes using RNAseq. Using genome alignment and population modelling, I explored the evolutionary history and population dynamics of the species.

Cross-species comparison of an evolutionarily conserved TF in *Arabidopsis thaliana* and tomato seed-to-seedling transition **P2.**

Bailan Lu, Jiayi Shan, Liang Song
Contact: bailan.lu@botany.ubc.ca
University of British Columbia, Department of Botany

Plant developmental phase transitions are under tight spatiotemporal controls. Transcription factors and co-factors (TFs) regulate the transcriptional reprogramming in these processes by forming feedback loops and resetting the epigenetic environments. The transition from seeds to seedlings is a prerequisite for plants to establish and thrive, and this phase switch requires the inactivation of embryonic programs during seedling establishment. In *Arabidopsis thaliana*, SEED DORMANCY 4-LIKE (AtSDR4L) is recently reported as a transcriptional co-repressor that suppresses seed maturation traits, storage reserve accumulation and primary dormancy, during post-embryonic growth. This gene is widely conserved in flowering plants, though the rice ortholog is suggested to affect seed dormancy oppositely to AtSDR4L. To study how well the regulatory effect of this novel TF on seed maturation programs can be generalized, tomato is included for a cross-species comparison with *Arabidopsis*. SDR4 homologous gene is knocked out in tomato cultivar M82D through CRISPR/Cas9 and tissue culture approaches. Together with AtSDR4L, their effects at the phenotypic and genomic levels will be compared. This is our first step to explore the functional conservation of SDR4 in two representative species from asterid and rosid clades of eudicots, with the aim to better understand its inter-species regulatory potential and diversity.

Is the enhanced soil carbon sequestration under N_2-fixing red alder due to increased nitrogen or diminished manganese? **P3.**

Marty Kranabetter, George Harper, Tim Philpott, Charlotte Norris
Contact: marty.kranabetter@gov.bc.ca
[1]B.C. Ministry of Forests, [2]Natural Resources Canada

As a N_2-fixing tree, *Alnus rubra* can enhance soil C sequestration. The mechanism responsible is unclear but includes two possibilities: 1) high N% leaf litter from red alder is slow to decompose and favours bacteria rather than white-rot fungi; or 2) reductions in soil pH under red alder causes a decrease in exchangeable Mn that hampers fungal production of peroxidase enzymes. We compared soil C under red alder vs. conifers and examined peroxidase activity in leaf litter, forest floor and mineral soil substrates. The upper soil profile C content under red alder increased by approx. 15 Ton C ha-1, equivalent to a 34% increase over conifers. A disparity in peroxidase activity was most notable in forest floors, with a 3-fold and 10-fold increase in Mn-peroxidase and residual peroxidases under conifers, respectively. With forest floors we found a stronger linear relationship between peroxidase activity and exch. Mn than with N%. The link between N and Mn processes likely both contribute to slower rates of C turnover. Nitrogen is the catalyst because N fixation causes sharp reductions in

forest floor pH and Mn, which, in our analysis, was more likely the cause for diminished peroxidase enzyme activity and enhanced C sequestration.

Strategies for lignin manipulation without growth penalty using cell type-specific monolignol overproduction **P4.**

Chak Chung Kuo[1], Fabrizio Chow[1], Brianna Archibald[1], Xinyi Huang[1,2], Shawn Mansfield[1,2], Lacey Samuels[1]
Contact: c.kuo@alumni.ubc.ca
University of British Columbia; [1]Department of Botany, [2]Department of Wood Science

Lignin is a rigid, hydrophobic biopolymer found in the cell wall of specialized cells such as fibres and vessels, allowing vascular plants to stand tall and transport water against gravity. Monolignols, monomers of lignin, are produced in the cytosol and then cross-linked into lignin in the cell wall. The quantity of monolignols is tightly controlled, as constitutive monolignol production throughout the Arabidopsis plant results in dwarfism, also known as lignin modification-induced dwarfism (LMID). The causes of LMID remain unknown, hindering the development of high-lignin plants for lignin-centred biorefineries. We hypothesize that LMID is influenced by the quantity of cytotoxic monolignols which induce stress and stunt growth. Using Arabidopsis, we overexpressed MYB63, which encodes a transcriptional activator of monolignol biosynthesis, with cell type-specific promoters targeting xylem vessels, xylem parenchyma, interfascicular fibres, epidermis, starch sheath, and phloem companion cells. Quantitative real-time PCR (qRT-PCR) and ultra-performance liquid chromatography (UPLC) confirmed MYB63 overexpression and increased monolignol production above wild-type levels. MYB63 expression driven by the phloem-specific SUC2 promoter was the highest among all lines and led to delayed bolting. These data suggest that the quantity and location of monolignols determine the extent of LMID, offering insight into creating high-lignin plants without compromising plant health.

Characterizing the interaction of protein phosphatase RLPH2 with the D group MPKs from *Arabidopsis thaliana* **P5.**

Sierra Mitchell, Greg Moorhead
Contact: sierra.mitchell@ucalgary.ca
University of Calgary

Protein phosphorylation is a prevalent post-translational modification involved in all aspects of the cell. This is achieved through the opposing activities of protein kinases and protein phosphatases, which add or remove a phosphoryl group on proteins, respectively. In *Arabidopsis thaliana* four novel bacteria-like phosphatases have been identified, one of which being Rhizobiales-like phosphatase 2 (RLPH2). Using quantitative phosphoproteomics to compare the protein phosphorylation profile of WT and *rlph2* KO lines, the D group mitogen activated protein kinases (MPK) were identified to be potential substrates of RLPH2, specifically regulating the TxY motif of their activation loop. From invitro peptide work, this dephosphorylation activity seemed to be dependent on the aspartic acid residue being present in the TxY motif of D group MPKs (TDY), as opposed to the glutamic acid residue found in the A, B, and C group MPKs (TEY). Invitro dephosphorylation assays with the full length proteins will be pursued to confirm the importance of the aspartic acid in RLPH2's specificity towards D group MPKs. This research is important in confirming the possible regulatory function of RLPH2 on D group MPKs and how that might affect downstream substrates of these MPKs.

Dynamics of gibberellin, glucose, and abscisic acid interactions during pea (*Pisum sativum* L.) seed development **P6.**

Harleen Kaur, Kosala Wadhuthanthri, Dennis Reinecke, Jocelyn Ozga
Contact: harleen1@ualberta.ca *or* jocelyn.ozga@ualberta.ca
University of Alberta, Plant BioSystems Group, Department of Agricultural, Food, and Nutritional Science

Gibberellins (GAs) play a key role in regulating seed growth and development in pea. The overexpression of *PsGA3ox1 ((LE)* gene encoding GA 3β-hydroxylase in the semi-dwarf (le) cultivar 'Carneval' (TG1 line) increased seed bioactive GA1 levels during early seed development and produced 10 to 23% larger seed size during the seed-filing period (8 to 20 days after anthesis, DAA) and at maturity, compared to the control C1 plants. Higher glucose levels occurred in the seed coats of TG1 seeds along with higher abscisic acid (ABA) levels in both TG1 seed coat and embryo tissues. In order to understand the possible interactions between higher bioactive GA, glucose, and ABA levels in the TG1 seeds, the expression of the ABA

biosynthetic gene, 9-cis-epoxycarotenoid dioxygenase (NCED; key rate-limiting enzyme in pathway), the ABA transporter gene *PsABCG* (ATP-binding cassette transporter subfamily G) and genes involved in sugar transport (sucrose transporter 1, *PsSUT1*; vacuolar glucose transporters, *PsVGT1* and *PsVGT2*, and tonoplast monosaccharide transporters, *PsTMT1* and *PsTMT2*) were studied in C1 and TG1 seed coat and cotyledon tissues during the seed-filling development period. Overall, these data shed further light on the dynamics of GA, glucose, and ABA interactions during pea seed development.

Characterization of AFB6 auxin receptor in pea (*Pisum sativum* L.) **P7.**

Harleen Kaur, Dennis Reinecke, Jocelyn Ozga
Contact: harleen1@ualberta.ca *or* jocelyn.ozga@ualberta.ca
University of Alberta, Plant BioSystems Group, Department of Agricultural, Food, and Nutritional Science

Pea contains members of all four auxin receptor clades TRANSPORT INHIBITOR RESPONSE 1 (TIR1), AUXIN SIGNALING F-BOX 2 (AFB2), AFB4, and AFB6. In a previous study, auxin-dependent interactions of pea auxin receptors with pea Aux/IAAs in Yeast 2-hybrid assays provided evidence that members of all four TIR1/AFB clades of pea are functional auxin receptors (Ozga et al., 2022, J Exp Bot 73:4094). Arabidopsis lacks the AFB6 clade; therefore, much less information is available on this receptor clade member. For further understanding the role of PsAFB6 in mediating auxin-induced growth and development, we generated and characterized pea plants that under- and over-express *PsAFB6*. The *PsAFB6* under-expression line had reduced main plant stem height, number of nodes per plant, and pedicels length at the first five flowering nodes compared to its null control. In contrast, the PsAFB6 over-expression lines exhibited greater main plant stem height, number of nodes per plant, and peduncle and pedicel lengths at specific flowering nodes relative to their nulls. These changes in the growth parameters of the PsAFB6 transgenic lines did not impact plant productivity. Altogether, these data further confirm that PsAFB6 is a functional auxin receptor that modulates specific aspects of auxin-regulated growth processes in pea.

Composition of the Douglas-fir (*Pseudotsuga menziesii*) foliar mycobiome and its role in Swiss Needle Cast severity for a breeding population **P8.**

Emma Hayward[1], Jürgen Ehlting[1], Jon Degner[2], Paul de la Bastide[1], Joey Tanney[3]
[1]University of Victoria, Centre for Forest Biology; [2]B.C. Ministry of Forests, Forest Improvement and Research Management Branch; [3]Canadian Forest Service, Pacific Forestry Centre

Fungal pathogens of trees are an essential component of forest ecosystems as an ecological driver of diversity and natural selection; however, they can also have devastating effects. My research aims to better understand *Nothophaeocryptopus gaeumannii*, the causal agent of Swiss Needle Cast (SNC), a disease infecting Douglas-fir (*Pseudotsuga menziesii*). This pathogen infects the needles of its host and is associated with defoliation and is endemic throughout the range of Douglas-fir. In the Pacific Northwest of the US and Canada, a rise in incidence and severity of this disease has been observed in the past few decades, which is thought to be linked to climatic changes and forestry practices. While there is a genetic component to SNC tolerance, fungal load is not correlated with needle loss. Our research investigates whether there are other fungal endophytes that may affect this interaction. We used both fungal culturing and metagenomics to characterize the foliar mycobiome of a population of SNC infected Douglas-fir located in Jordan River, BC. Preliminary analyses suggest a great diversity of fungal species across samples (covering 20 taxonomic orders of Ascomycetes and seven Basidiomycetes). However, microbiome community composition does not appear to explain SNC severity or impact growth in this population.

GWAS identifies quantitative trait loci (QTLs) for limber pine resistance to white pine blister rust (WPBR) **P9.**

J.-J. Liu[1], R. A. Sniezko[2], J. Krakowski[3], R. Sissons[4], G. Alger[4], A. Kegley[2], A. Zamany[1], H. Williams[1], B. Rancourt[1]
Contact: Jun-jun.liu@nrcan-rncan.gc.ca
[1]Natural Resources Canada, Canadian Forest Service, Pacific Forestry Centre, [2]USDA Forest Service, Dorena Genetic Resource Center, [3]Alberta Agriculture and Forestry, [4]Parks Canada, Waterton Lakes National Park

A genome-wide association study (GWAS) was performed to dissect complex genetic architectures in limber pine (*Pinus flexilis)*. Disease development and severity were assessed for three years post inoculation, and quantitative resistance (QR) were phenotypically characterized. A set of candidate genes with putative functions in resistance and defense responses

were selected for targeted sequencing. Using SNP genotypes of candidate genes, a GWAS was performed using both GLM and MLM models. The results showed that 19 SNPs distributed on Pinus consensus linkage groups (LG) 1, 2, 4, 5, and 12 were significantly associated with quantitative traits for limber pine QR to WPBR ($p < e\text{-}6$). These SNP-based QTLs were not linked to the Cr4-controlled major gene resistance (MGR) that was genetically mapped on LG8, suggesting that QR can be pyramided with MGR as a strategy for breeding of durable resistance. QR-associated SNPs identified by GWAS were annotated within nine functional genes, and six of them encoded NBS-LRR proteins while the other three each encoded one RLK, one protein of the LRR superfamily, and a glutamate receptor. The identified SNPs and candidate genes provide initial insights into the genomic architecture underlying WPBR-resistance mechanisms and will be useful in marker-assisted selection of WPBR-resistant genotypes.

Susceptibility of western redcedar to root and butt rot diseases as assessed by MiSeq and qPCR technologies. **P10.**

J.-J. Liu[1], S. Houston[1], M. Cruickshank[2], A. Zamany[1], I. Leal[1], C. Filipescu[2]
Contact: Jun-jun.liu@nrcan-rncan.gc.ca
[1]Natural Resources Canada, Canadian Forest Service, Pacific Forestry Centre; [2]Canadian Wood Fibre Centre

The current study developed disease assessment methods using genomics based MiSeq and qPCR technologies, and they were evaluated for the repeatability and efficiency in monitoring disease development using WRC seedlings. The seedlings were inoculated at three years old with several pathogenic fungi including *Armillaria ostoyae, Coniferiporia weirii, Heterobasidion occidentale*, and *Perenniporia subacida* and assessed two years post inoculation. Disease symptoms of discolored wood decay were observed in the root collars in 20% ~ 60% of the inoculated seedlings which varied by pathogen. Both MiSeq and qPCR detected the targeted fungi in a large proportion of inoculated but asymptomatic seedlings. The visual levels of decay and the detection of the inoculated fungi by MiSeq and qPCR were highly correlated, indicating their reliability. The genomics tools developed here can detect disease infection earlier than visual observation of wood decay by measuring disease progression of WRC trees in a quantitative way. Application of these tools allows selection of WRC resistance to the root and butt rot pathogens at an early infection stage, which may shorten the time in future breeding programs.

Characterizing the effect of propyzamide on MOR1 protein dynamic in the *mor1-11* mutant and wild type *Arabidopsis thaliana*: Insights from fluorescence recovery after photobleaching (FRAP) **P11.**

Aida Rakei, Geoffrey Wasteneys
Contact: aida.rakei@botany.ubc.ca
University of British Columbia, Department of Botany

Microtubule Organization 1 (MOR1) is an essential 217 kDa protein that controls microtubule polymerization through its ability to associate with microtubule polymers and bind free tubulin. Previous studies have focused on mutations in the N-terminal TOG1 domain of MOR1 that impair microtubule dynamics upon moderate temperature elevation. After screening mutations in the C-terminal domain of MOR1, we identified a single amino acid substitution allele, *mor1-11*, that causes roots to skew in a rightward direction when exposed to the herbicide propyzamide, in contrast to the left skewing response of wild-type roots. This novel mutant provides an opportunity to better understand both how MOR1 controls dynamics, and to understand the mechanism by which propyzamide, a widely used benzamide herbicide, impairs microtubule dynamics. To test the hypothesis that propyzamide alters the affinity of MOR1 to microtubule polymers, we used fluorescence recovery after photobleaching (FRAP) to compare the residency time on microtubules of fluorescently tagged wild-type MOR1 (MOR1-3xYpet) and mor1-11 (mor1-11-Ypet) +/- propyzamide. The results indicate that there were differences in fluorescence recovery rates for the MOR1-3xYpet and mor1-11-Ypet fluorescent reporters in the presence of propyzamide. We determined that propyzamide decreased MOR1's affinity for microtubules, while increasing that of the mutant mor1-11. These findings are consistent with the C-terminal domain of MOR1 having a prominent role in polymer affinity.

A comparison of drought tolerance in two conifers with contrasting mycorrhizal associations **P12.**

Bethany Robson, Barbara Hawkins
Contact: brobson@uvic.ca
University of Victoria, Department of Biology

Drought events are increasing in frequency, severity, and distribution as a result of climate change. Plants have a variety of adaptations to water stress, including symbioses with mycorrhizal fungi. Little is known about how the type of mycorrhizae (arbuscular or ecto-) may affect drought tolerance, especially in conifers that cannot associate with more than one type. The objective of this study was to determine how the type of mycorrhizae may affect drought tolerance in *Pinus contorta* and *Thuja plicata*, species that make contrasting mycorrhizal associations. Three experiments were performed using aeroponics and traditional soil culture to explore the effects of mycorrhizal association in mitigating water stress. *P. contorta* consistently outperformed both an interior and coastal population of *T. plicata* in all experiments. Quantum yield declined linearly with increasing drought stress in both treatments with mycorrhizal colonization, and non-linearly in the treatment with no colonization. These trends were consistently shown across all seedling populations, which may indicate that mycorrhizal symbioses are important in the drought tolerance of both species, regardless of type. Further investigation is needed to elucidate how mycorrhizae may influence recovery after drought in these species, as well as the mechanisms mycorrhizae may use to improve drought tolerance in hosts.

Enhanced drought tolerance in alfalfa: Morphological, physiological, and transcriptional assessments of *MsTAC1* down-regulated genotypes **P13.**

Udaya Subedi[1,2], Kimberley Burton Hughes[1], Gaganpreet Kaur Dhariwal[1], Guanqun Chen[2], Surya Acharya[1], Stacy D. Singer[1]
Contact: udaya@ualberta.ca
[1]Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre; [2]University of Alberta, Department of Agricultural, Food and Nutritional Science

Drought poses a severe threat to alfalfa (*Medicago sativa* L.) production. Previously, the zinc finger transcription factor Telomerase Activator 1 (TAC1) was found to negatively regulate responses to drought and salinity in Arabidopsis. In this study, we identified a *TAC1* homolog in alfalfa and generated RNAi genotypes to investigate its role in drought stress response. Under drought stress, TAC1-RNAi genotypes exhibited less wilting and experienced smaller reductions in plant height, internode length, and shoot and root weight compared to EV controls, suggesting an enhancement in drought tolerance. Furthermore, TAC1-RNAi genotypes also demonstrated lower leaf water-loss rates and higher leaf relative water contents under drought compared to EV controls, which corresponded with significantly lower stomatal densities. Transcriptional profiling of plants under drought conditions led to the identification of numerous differentially expressed genes between TAC1-RNAi and wild-type genotypes, with an abundance being involved in cell wall production, secondary metabolism, abiotic stress response, hormone metabolism, and redox-related processes, as well as those encoding transcription factors. This study provides valuable insight into the physiological and molecular mechanisms regulating drought resilience in alfalfa, and provides a basis for the development of transgene-free alfalfa germplasm using CRISPR/Cas technology with superior performance under drought conditions.

Landscape-level reconstruction of disturbance histories and carbon transfers from a retrospective carbon budget model as compared to sediment core records for the Sooke Lake watershed, British Columbia, Canada **P14.**

J.A. (Tony) Trofymow[1,2], K. Brown[1], B. Smiley[1], N. Hebda[3], R. Dixon[1], D. Dunn[1]
Contact: tony.trofymow@nrcan-rncan.gc.ca
[1]Canadian Forest Service; [2]University of Victoria, Department of Biology; [3]University of British Columbia, EEG Science

A retrospective C budget for the 8500ha Sooke Lake Reservoir (SLR) watershed from 1911-2012 was developed using historic inventories, disturbance data and CBM-CFS3. Stream flow and dissolved C [DOC] data from 1996-2012 for three catchments were used to parameterize decay loss fraction to CO_2 and DOC. The model estimated terrestrial C exports from the watershed to SLR. A 33cm sediment core was collected from SLR at 72m depth and sampled every 0.5cm. An age model using Pb-210 and 14C revealed the core spanned a 300yr period, the top 11.5cm from 1911-2014CE. Charcoal and magnetic susceptibility records were used to estimate fire frequency and erosion. Terrestrial C inputs to sediment were estimated by pyGCMS of C compounds. Nine charcoal peaks occurred over 300yrs. Four from 1911-2012 occurred ~10 years after nearby fires, three associated with magnetic peaks ~10 years after reservoir expansion, suggesting foreshore charcoal washed into the SLR. Charcoal peaks from fires 2500-4000m from the core were not detected. Over 127 C compounds were identified, 8 terrestrial and 3 algal markers, terrestrial C fraction increasing from 0-14cm depth. Total terrestrial C in sediments was (5145 MgC/100yr) ~17% of modeled DOC exports (30640 MgC/100yr), suggesting most DOC entering SLR was respired as CO_2 or exported.

Towards understanding the evolution of gene expression in gametophytes of mycoheterotrophic ferns and lycophytes **P15.**

Marielle Wilson, Sean Graham
Contact: Marielle.wilson@botany.ubc.ca
University of British Columbia, Cornell University

Several plant lineages have wholly or partly lost their photosynthetic ability and instead rely, to varying degrees, on carbon acquired from fungal associations. One manifestation of this mycoheterotrophic lifestyle is in the "dark" gametophytes of several fern and lycophyte groups. In contrast to their photosynthetic sporophyte generation, these gametophytes rely solely on fungal carbon for nutrition throughout their life phase. Thus, their independently living haploid and diploid generations effectively switch trophically so only the haploid stage is fully mycoheterotrophic. Initial mycoheterotrophy has arisen independently multiple times across ferns and lycophytes. Critical genetic changes accompanying this shift have yet to be explored. We are generating transcriptomes from photosynthetic sporophytes and mycoheterotrophic gametophytes of ferns (Psilotaceae, Ophioglossaceae, Gleicheniaceae, Schizaceae) and lycophytes (Lycopodiaceae). We will then contrast gene expression between generations of the same species and between mycoheterotrophic gametophytes and those of completely photosynthetic taxa. Through this, we can better understand (1) the genetic changes accompanying trophic switching within species, and (2) the evolution of mycoheterotrophy in fern and lycophyte lineages. Our study will provide insights into the evolution of mycoheterotrophy, the genetic basis of trophic switching, and nuclear genome evolution in relation to plant-fungi interactions.

Ethanolic extract of *Ficus religiosa* prevents Cisplatin toxicity by enhancing antioxidant status in mice **P16.**

Farhad Alipour
Contact: Farhad.alipour82@gmail.com
Pune University, India.

The clinical use of Cisplatin, has been limited due to the major side effects such as nephrotoxicity and hepatotoxicity. Recent reports have shown that the impairment of antioxidant defense systems is the main offender for side effects of cisplatin. The present study was undertaken to assess the protective effect of aqueous extract of *Ficus religiosa*, leaf against Cisplatin-induced oxidative dysfunction in mice. Three different doses of *Ficus religiosa*, leaf (250, 500 and 1000 mg/kg) were administered daily for fifteen days and Cisplatin was administered intra-peritoneally in 3 days interval. The animals were sacrificed 24 h after the last treatment. The liver and kidney were prepared for the biochemical investigations.

Cisplatin significantly induced oxidative stress, ultimately leading to increased serum levels of liver enzymes such as alanine aminotransferase, aspartate aminotransferase, alkaline phosphatase, total bilirubin and Lactate dehydrogenase. Renal toxicity also characterized by a significant increase in concentrations of serum creatinine and blood urea nitrogen. Supplementation of *Ficus religiosa* ameliorated the side effects of Cisplatin referenced to improved antioxidant status of liver and kidney. The results of this study concluded that the extract of *Ficus religiosa* leaf could be proposed to protect the liver and kidney damage induced by Cisplatin. This protective effect might be correlated with the antioxidant properties of leaves extract of *Ficus religiosa*.

Physiological role of biochar and humic acid in conferring arsenic-induced oxidative stress in rice (*Oryza sativa* L.) **P17.**

Mirza Hasanuzzaman, Farzana Nowroz, Md. Rakib Hossain Raihan
Contact: mhzsauag@yahoo.com
Sher-e-Bangla Agricultural University, Department of Agronomy, Bangladesh

Arsenic (As) is a naturally-occurred metalloid which is non-essential but toxic if accumulated in plants to higher levels. Biochar (BC) and humic acid (HA) are soil amendments and biostimulants for plant growth and stress tolerance. We aimed at investigating the role of BC and HA in detoxification of As toxicity in rice. Rice (Oryza sativa L. cv. BRRI dhan75) was used as test plants. Twenty-five-day old seedlings were transplanted and grown in pot with or without irrigation by 0.25 mM sodium arsenate solution for 20 days. A set of plants were treated with BC (0.2 and 0.4 g kg-1 soil) and HA (0.2 and 0.4 g kg-1 soil) at the time of transplantation. Arsenic exhibited an increased oxidative stress indicator (lipid peroxidation, hydrogen peroxide, electrolyte leakage) and proline content. Moreover, the antioxidant defense system of rice consisting of non-enzyme antioxidant contents and enzyme activities were decreased as a result of As toxicity. The damaging effect was prominent in plant height, biomass acquisition, tiller number and relative water content as well. Furthermore, chlorophyll and leaf area were also exhibited a decreasing trend due to toxicity. Arsenic exposure also disrupted the glyoxalase system. However, application of BC and HA recovered the reactive oxygen species-induced damages in plants, upregulated the effectiveness of ascorbate-glutathione pool, accelerated the activities of antioxidant enzymes and improved glyoxalase system. These positive impacts of BC and HA ultimately resulted in improved plant characteristics with better plant-water status and regulated proline content that conferred As stress tolerance of rice. So, it can be concluded that BC and HA effectively mitigated As-induced physiology and oxidative damage in rice plants. Therefore, BC and HA could be potential biostimulants and soil amendments in As-contaminated rice fields.

Mulberry genes as a promising tool for enhancing crop resilience to environmental stresses

Hari Singh Meena, M.P.S Bangari, K.H. Dhanyalakshmi, T. Thomas, S.S. Patil, K.N. Nataraja **P18.**
Contact: harisingh3212@gmail.com
Bengaluru University of Agricultural Sciences, Department of Crop Physiology, GKVK Campus, India

Plants are constantly exposed to various environmental stresses that can adversely impact their survival and performance. To overcome these challenges, plants have evolved defense responses that involve the reprogramming of gene expression and the production of certain metabolites. One of the major aspects of crop improvement is the identification of putative abiotic stress tolerance genes. Mulberry, a hardy perennial crop, exhibits remarkable characteristics such as fast growth and stress adaptability, making it an interesting model system to study abiotic stress tolerance mechanisms. In this study, a drought-specific transcriptome that was previously generated was analyzed to determine whether genes involved in drought tolerance can impart oxidative stress tolerance. Five genes were selected for *in-silico* expression analysis using the Arabidopsis *e-northern* BAR database to reveal their putative role. Further, *in-vivo* expression analysis was conducted by exposing Mulberry plants to methyl viologen (10µM) to induce oxidative stress. The results of qRT-PCR-based expression analysis showed that the expression of *MaDUF1068-like, MaCatalase, MaNCED, MaIsocitrate-dehydrogenase,* and *MaP5C* genes was significantly higher in stressed plants than in control plants after 12 and 24 hours of treatment. These results indicate that these genes may play a crucial role in developing crop resilience for multiple abiotic stress tolerances.

Effect of arbuscular mycorrhizal fungi and oyster shell powder on cocoa seedlings growth and resistance against *Phytophthora megakarya* (causal agent of black pod disease) in the nursery **P19.**

Paul Martial Tene Tayo[1], Aristide Dzelamonyuy[2], Thaddee Boudjeko[1]
Contact: martialtene@gmail.com
[1]Biotechnology Centre-Nkolbisson, Laboratory of Phytoprotection and Valorization of Genetic Resources, Cameroon; [2]Indiana University School of Medicine, Biochemistry and Molecular Biology

Application of organic amendments such as arbuscular mycorrhizal fungi (AMF) as well as chitinous sources have been proposed as a strategy for the management of diseases caused by soil borne pathogens. The aim of this study was to evaluate the combined effect of AMF and oyster shell powder soil amendment to enhance cocoa seedling growth and induce resistance against *Phytophthora megakarya* under nursery conditions. The results showed that AMF combined with oyster shells powder soil amendment significantly increased plant height, leaf number, leaf area, dry shoot and root weight more than chemical fungicide treatment after five months of growth. This treatment raised soil pH significantly and decrease *Phytophthora megakarya* load of the soil suspension by 82 %. Leaf inoculation showed the weakest disease severity index (highest level of resistance) recorded in plants treated either with AMF and oyster shell powder combined. Moreover, this resistance was correlated with the increased expression level TcPer-1, TcGlu1, TcChiB and TcMYBPA genes before and after infection. These findings demonstrated that AMF and oyster shell powder combined could be used as biofertilizer and biofungicide to improve the quality of cocoa seedling production and their resistance against *Phytophthora megakarya*.

Assessing overexpression of SOS1 from *Brassica napus* and *Bassia scoparia* on their ability to confer salt tolerance in *Schizosaccharomyces pombe, Arabidopsis thaliana*, and *Brassica napus*. **P20.**

Shakshi Dutt, Muhammad Jamshed, Marcus Samuel
Contact: shakshi.dutt1@ucalgary.ca
University of Calgary

See T4. abstract.

THANKS TO OUR SPONSORS!

CENTRE for FOREST BIOLOGY
University of Victoria

ARGUS CONTROLS

CONVIRON

BioChambers
PROVIDING GROWTH TO RESEARCH.

MOSAIC
FOREST MANAGEMENT

SelectSeed

FGC
Forest Genetics Council of British Columbia