Eastern Regional Meeting 2017

Canadian Society of Plant Biologists

November 24-25, 2017

Conférence régionale de l'est 2017

Société canadienne de biologie végétale

24-25 novembre 2017

McGill

MACDONALD

110TH Anniversary

Eastern Regional Meeting 2017

Canadian Society of Plant Biologists

November 24-25, 2017

Conférence régionale de l'est 2017

Société canadienne de biologie végétale

24-25 novembre 2017

McGill

MACDONALD

110TH Anniversary

Dear Colleagues,

Welcome to the Canadian Society of Plant Biologists' 2017 Eastern Regional Meeting. We are delighted to welcome you to McGill University on the 110th anniversary of the Macdonald Campus for a day of plant biology research and communication.

We have the pleasure of presenting three plenary talks, thirty selected talks in concurrent sessions, and more than 20 poster presentations running the gamut of topics, tools, and scales of contemporary plant biology.

We would like to thank our many volunteers, session chairs and judges for the Poster and Oral Presentations. We would especially like to acknowledge Michael Stasiak for his excellent web support, Daphne Goring for organizing judges for the student competitions, Peter Summers for providing valuable guidance from his experience with last years' ERM, and Diane Chan-Hum for administrative support. We would also like to thank the Faculty of Agricultural and Environmental Science and Department of Plant Science for generously providing with access to their facilities and for their support of the event planning process.

We would like to thank our sponsors for their generous support of this meeting. Please take some time to visit their exhibitions during the coffee and lunch breaks.

Finally, we would like to thank the CSPB-SCBV Executive, the plenary speakers, all presenters and meeting participants.

We wish you all a great day of plant science!

Jean-Benoit Charron and Olivia Wilkins

Co-Chairs of the CSPB/SCBV ERM 2017 Organizing Committee

Photo : Raymond Building 1920s

Chers collègues,

Bienvenue à la conférence régionale de l'Est 2017 de la Société canadienne de biologie végétale. Nous sommes ravis de vous accueillir à l'Université McGill à l'occasion du 110e anniversaire du Campus Macdonald pour une journée de recherche et d'échange de savoir en biologie végétale.

Nous avons le plaisir de présenter trois conférenciers pléniers, 35 présentations orales sélectionnées lors de séances simultanées et plus de 20 affiches couvrant toute la gamme de sujets, d'outils et d'échelles de la biologie végétale contemporaine.

Nous tenons à remercier nos nombreux bénévoles, modérateurs et juges ainsi que Michael Stasiak pour son excellent soutien informatique, Daphne Goring pour l'organisation des différents concours étudiants, Peter Summers pour ses précieux conseils et Diane Chan-Hum pour son soutien administratif. Nous aimerions également remercier la Faculté des sciences de l'agriculture et de l'environnement et le Département de sciences végétales de l'Université McGill d'avoir généreusement donné accès à leurs installations et d'avoir aidé à la planification de l'événement.

Nous aimerions également remercier nos commanditaires pour leur généreux soutien financier. Veuillez prendre le temps de visiter leurs kiosques pendant les pauses-café et l'heure du diner.

Enfin, nous aimerions remercier les membres du comité exécutif de la Société canadienne de biologie végétale, les conférenciers pléniers, tous les présentateurs et les participants à la conférence.

Nous vous souhaitons une bonne journée de science végétale!

Jean-Benoit Charron et Olivia Wilkins

Coprésidents du Comité d'organisation CSPB / SCBV ERM 2017

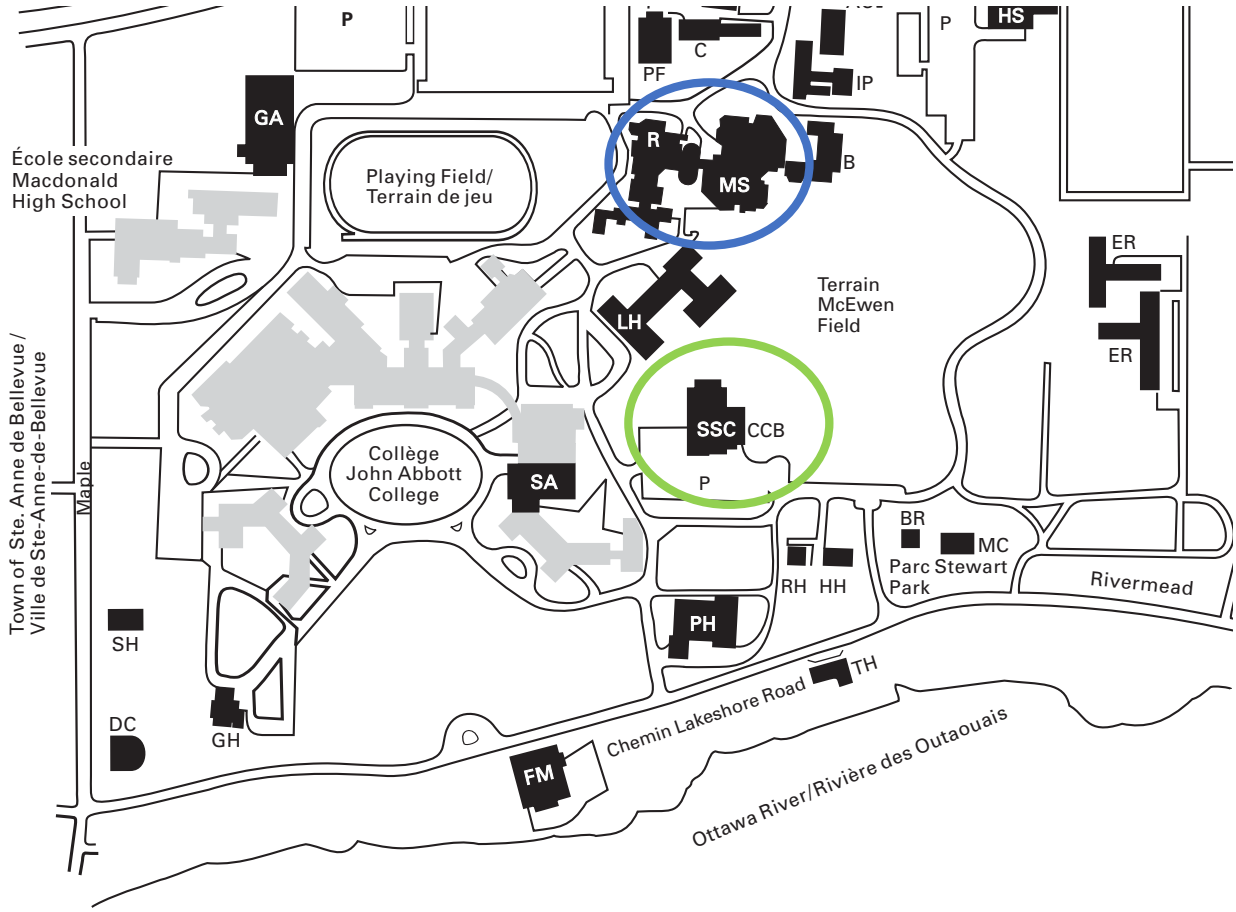
Photo: Macdonald College c. 1930s

Message from Macdonald Campus:

McGill University is pleased to welcome members of the Canadian Society of Plant Biologists for the 2017 ERM to celebrate the 110th anniversary of the Macdonald Campus. McGill University has two campuses each providing a different learning and research environment. Tucked along the waterfront a little more than a half-hour from the bustling downtown of Montreal in Sainte-Anne-de-Bellevue, the Macdonald Campus is a beautiful campus of 650-hectares (1600 acres) that includes classrooms, laboratories, research facilities, green space, herbarium, farmlands, fields and forests, all used for teaching and research. Established in 1907 as Macdonald College, the "Mac" Campus is now home to the Faculty of Agricultural and Environmental Sciences (FAES), the School of Human Nutrition, the Institute of Parasitology, and the McGill School of Environment. With over 100 academic staff and 2100 students at all academic levels, the "Mac" Campus is a mix of anglophone, francophone and international staff and students who significantly contribute to the vibrancy of both the academic and non-academic aspects of life on campus. The Faculty is at the forefront of some of the greatest challenges facing humanity - food security, quality and safety, climate change, water and natural resource scarcity and the relationship between nutrition, health and disease. Our researchers are world-class academics who push the limits of knowledge in fields as diverse as crop science, animal welfare, parasitology, food safety and nutrition, biofuel production, and precision farming. For more information about Macdonald Campus please watch https://www.youtube.com/watch?v=TnuzMazBa1g or feel free to contact Professor Anja Geitmann, Dean of the Faculty of Agricultural and Environmental Sciences and McGill University, Associate Vice-Principal (Macdonald Campus) anja.geitmann@mcgill.ca.

Photo: Macdonald campus today

Campus Map



Friday night's events will be hosted in the Centennial Centre (SSC Building, green circle).

Saturday's events will be hosted in the Raymond and Macdonald-Stewart Buildings (R and MS Buildings, blue circle)

Parking

There is ample parking on campus. Please park in any available non-reserved spot.

WIFI

McGill Username: guest.303089@mcgill.ca
McGill Password: z445bb2c
Used by: CSPB-ERM 2017
Wireless Network SSID:wpa.mcgill.ca or mcgill.ca

Thank you to our Gold Level Sponsors

Gold Level Sponsors, continued

McGill

FACULTY OF
Agricultural and
Environmental Sciences

FACULTÉ DES
Sciences de l'agriculture
et de l'environnement

THE CANADIAN SOCIETY OF PLANT BIOLOGISTS • LA SOCIÉTÉ CANADIENNE DE BIOLOGIE VÉGÉTALE •

Thank you to our Bronze Level Sponsors

Bronze Level Sponsors, continued

WOODSMEN
DEMONSTRATION
McGill MACDONALD

We are pleased to invite you to a spectacular demonstration of a few select lumberjacking events performed live by the McGill Woodsmen/women at **13h10,** just outside of the cafeteria.

Founded in 1954 at the Macdonald College, the McGill Woodsmen/women are McGill's pride. In the last 40 years Macdonald's men and women teams have had their names etched on trophies over 100 times, with the greatest winning record of all McGill teams. Since 1997, the team as joined the Canadian Intercollegiate Lumberjack Association was established. There are six schools currently registered as C.I.L.A. members:

- Algonquin College
- Dalhousie Agricultural Campus
- Maritime College of Forest Technology
- McGill University
- Sir Sandford Fleming College
- University of New Brunswick

Program Schedule – Overview

Friday, November 24

18:30-20:00	**Registration,** The Ceilidh, Centennial Centre
18:30-21:00	**Opening Mixer,** The Ceilidh, Centennial Centre, Registrants are invited to an informal social gathering where a variety of refreshments will be available

Saturday, November 25

7:30-9:50	**Registration, light breakfast, poster setup,** Macdonald-Stewart Building
8:50-9:00	**Welcoming remarks,** Raymond Building (R2-045), CSPB President Anja Geitmann
9:00-9:50	**Plenary Lecture I: How plants use physics to survive and thrive?** Raymond Building (R2-045), Anne-Lise Routier-Kierzkowska
9:50-10:40	**Plenary Lecture II: GxE and the genomic basis of environmental response in plants,** Raymond Building (R2-045), David Des Marais
10:40-11:00	**Coffee Break,** Macdonald-Stewart Building
11:00-12:30	Concurrent session I (R2-045): Plant Development Concurrent Session II (R2-046): Regulation and Metabolism Concurrent Session III (R3-045): Abiotic Stress
12:30-13:30	**Lunch,** Macdonald-Stewart Building
13:15-13:30	**Macdonald Campus Woodsmen Exhibition,** Outdoors
13:30-14:30	**Poster session and Sponsor Exhibitions,** Macdonald-Stewart Building
14:30-16:00	Concurrent Session IV (R2-045): Biotic Interactions Concurrent Session V (R2-046): Growth and Regulation Concurrent Session VI (R3-045): Bioinformatics and Molecular Tools
16:00-16:20	**Coffee Break,** Macdonald-Stewart Building
16:20-17:10	**Plenary Lecture III: How parasitic weeds wake up: Cracking the germination code,** Raymond Building (R2-045), Shelley Lumba
17:10-17:30	**Closing remarks and awards,** Raymond Building (R2-045)

Program Schedule - Detailed

Friday, November 24

	18:30-20:00	**Registration,** The Ceilidh, Centennial Centre
	18:30-21:00	**Opening Mixer,** The Ceilidh, Centennial Centre, Registrants are invited to an informal social gathering where a variety of refreshments will be available

Saturday, November 25

	7:30-9:50	**Registration, light breakfast, poster setup,** Macdonald-Stewart Building
	8:50-9:00	**Welcoming remarks,** Raymond Building (R2-045), CSPB President Anja Geitmann
	9:00-9:50	**Plenary Lecture I: How plants use physics to survive and thrive?** Raymond Building (R2-045), Anne-Lise Routier-Kierzkowska, Institut de recherche en biologie végétale - Université de Montréal
	9:50-10:40	**Plenary Lecture II: GxE and the genomic basis of environmental response in plants,** Raymond Building (R2-045), David Des Marais, Massachusetts Institute of Technology
	10:40-11:00	**Coffee Break,** Macdonald-Stewart Building

Concurrent session I: Plant Development (R2-045)
Chair: D. Kierzkowski

PD1	11:00-11:15	**An integrated model of simple and compound leaf organogenesis.** D. Kierzkowski*, A. Runions, F. Vuolo, S. Strauss, H. Jenke, R. Lympouridou, A-L. Routier-Kierzkowska, R.S. Smith, M. Tsiantis
PD2	11:15-11:30	**Effect of cell shape and growth orientation on mechanics of the epidermis.** A.J. Bidhendi*, B. Altartouri, M.S. Zamil, A. Geitmann
PD3	11:30-11:45	**Compatible pollen signalling in Arabidopsis thaliana: the proposed role of stigma-expressed RLCKs.** J. Doucet*, N.Udugama, D.R. Goring
PD4	11:45-12:00	**Lunapark proteins suppress the membrane fusion activity of RHD3 for the formation of tubular ER network.** J. Sun*, H. Zheng
PD5	12:00-12:15	**The concomitant evolution of angiosperms produced leaves with coordinated mesophyll surface area, cell diameter, vein, and stomatal traits to maximize exchange surface under a low CO_2 world**. G Théroux-Rancourt*, J.M. Earles, M.E. Gilbert, M.A. Zwieniecki, C.K. Boyce, A. McElrone, C. Brodersen
PD6	12:15-12:30	**The expansion pattern of *Arabidopsis* pavement cells is determined by the mechanical properties of the cell wall.** B. Altartouri*, T. Tani, G. Scarcelli and A. Geitmann

Concurrent Session II: Regulation and Metabolism (R2-046)
Chair: F. Marsolais

RM1	11:00-11:15	**The activity of key fermentative enzyme Alcohol Dehydrogenase 1 from Arabidopsis thaliana is differentially altered by several redox post-translational modifications.** S. Dumont*, N.V. Bykova, A. Khaou, Y. Besserour, J. Rivoal

RM2	11:15-11:30	**The Role of SNF1-Related Protein Kinase 1 (SnRK1) in Regulating Intermediary Metabolism in Arabidopsis thaliana.** Y. Wang*, B.J. Micallef, I.J. Tetlow, R. Mullen, R. Feil, J.E. Lunn, M.J. Emes
RM3	11:30-11:45	**Regulation of Arabidopsis Starch Branching Enzyme 2.2.** G.J. MacNeill*, I.J. Tetlow, M.J. Emes
RM4	11:45-12:00	**GmMYB176 interactome and regulation of isoflavonoid biosynthesis in soybean.** A.K.A. Vadivel*, S. Dhaubhadel
RM5	12:00-12:15	**Identification and characterization of a pectin acetylesterase from the seed coat of common bean (Phaseolus vulgaris).** J. Palmer, A. Pajak, F. Marsolais*
RM6	12:15-12:30	***Norbelladine synthase* – A novel gene involved in Amaryllidaceae alkaloid metabolism in *Narcissus pseudonarcissus* 'King Alfred'.** A Singh*, I. Desgagné-Penix

Concurrent Session III: Abiotic Stress (R3-045)

Chair: P. Ryser

SA1	11:00-11:15	**Thriving or just surviving: examining heat-stress induced mortality of Tamarack under extreme climate conditions.** B.K. Murphy*, D.A. Way
SA2	11:15-11:30	**Winter is coming: Root lifespan and overwintering strategies for two wetland species, Sagittaria latifolia Willd. (Alismataceae) and Carex crinita Lam. (Cyperaceae), in contrasting climate zones.** A. P. Rayon1*, M.C. Eppes, P. Ryser
SA3	11:30-11:45	**Exploring the cold acclimation mechanisms under freeze-thaw cycles in *Brachypodium distachyon*.** B.F. Mayer*, J.-B. Charron
SA4	11:45-12:00	**A domesticated transposable element is essential for salinity defense in Arabidopsis thaliana.** Y. Shao*, T. Bureau
SA5	12:00-12:15	**Exploring the role of XERICO in Arabidopsis thaliana development and stress response.** E. Vonapartis*, D. Mohamed, C. Carianopol, S. Gazzarrini
SA6	12:15-12:30	**CYP86A1, a Key Enzyme in Suberin Biosynthesis, is Important in the Response of Arabidopsis to Salt Stress.** S.-M. Wang*, P. Wang, L. Gao, N. de Silva, O. Rowland
	12:30-13:30	**Lunch,** Macdonald-Stewart Building
	13:15-13:30	**Macdonald Campus Woodsmen Exhibition,** Outdoors
	13:30-14:30	**Poster session and Sponsor Exhibitions,** Macdonald-Stewart Building

Concurrent Session IV: Biotic Interactions (R2-045)

Chair: D. Desveaux

BI1	14:30-14:45	**Nuclear localized fungal effector suppresses the transcriptional responses to pathogens and mislead the host.** B. Ahmed*, H. Germain
BI2	14:45-15:00	**Investigating the role of BLADE-ON-PETIOLE genes in plant defense.** C. Bergin*, B.O. Oyetoran, Y. Wang, S. Chatfield, L. Bauer, R. Datla, R. Subramaniam, M.L. Smith, S.R. Hepworth
BI3	15:00-15:15	**Maturation and intercellular movement of Turnip mosaic virus (TuMV) replication vesicles require ROOT HAIR DEFECTIVE 3.** N. Movahed*, J. Sun, H. Vali, J.F Laliberté, H. Zheng

BI4	15:15-15:30	**A candidate fungal effector protein Mlp124357 targets the vacuolar structures to promote virulence.** M.H. Madina*, H. Zheng, H. Germain
BI5	15:30-15:45	**Elucidating the substrate specificities of acyl-lipid thioesterase enzymes from diverse plant taxa.** R.S. Kalinger*, I.P. Pulsifer, and O. Rowland
BI6	15:45-16:00	**Metabolomics of resistant and susceptible potato genotypes reveals several resistance related metabolites involved in late blight resistance.** S. Joshi*, A. Gagnon, A.C. Kushalappa

Concurrent Session V: Growth and Regulation (R2-046)

Chair:

GR1	14:30-14:45	**Deciphering species-specific pollen tube guidance in *Solanum*.** V. Joly*, C. Viallet, Y. Liu, A. Zaro, F. Ceriotti, D. P. Matton
GR2	14:45-15:00	**Investigating the role of autophagy in *Arabidopsis* self-incompatibility.** H. Nelles*, D.R. Goring
GR3	15:00-15:15	**Diversification of the histone acetyltransferase GCN5 through alternative splicing in *Brachypodium distachyon.*** A. Martel*, H. Brar, B.F. Mayer, J.-B. Charron
GR4	15:15-15:30	**The possible role of SPL/miR156 module in controlling growth phase transition in barley.** R.K. Tripathi*, J. Singh
GR5	15:30-15:45	**Functional Characterization of Germination Associated Thaumatin-like Proteins in Barley.** I. Iqbal*, R.K. Tripathi, O. Wilkins, J. Singh

Concurrent Session VI: Bioinformatics and Molecular Tools (R3-045)

Chair: M. Strömvik

BT1	14:30-14:45	**Rapid gene function analysis using a new Barley Stripe Mosaic Virus system.** A. Cheuk* and M. Houde.
BT2	14:45-15:00	**On the path towards a pan-genome model for potato.** M. Kyriakidou*, J.H. Gálvez, C.Y. Tang, H.H. Tai, N.A. Barkley, D. Ellis, M.V. Strömvik
BT3	15:00-15:15	**Evaluating the genetic basis of gene co-regulation in wheat.** R. Goessen*, L. Lukens, E. Raherison
BT4	15:15-15:30	**Optimization of the INTACT system to profile guard cell gene expression in *Arabidopsis* leaves.** A. van Weringh*, N.J. Provart
BT5	15:30-15:45	**Using Chlorophyll Fluorescence for High Precision Phenotyping of Drought Stressed Breeding Populations of White Spruce.** A.E. Besik*, P. D'Odorico, N. Isabel, I Ensminger

	16:00-16:20	**Coffee Break,** Macdonald-Stewart Building
	16:20-17:10	**Plenary Lecture III: How parasitic weeds wake up: Cracking the germination code,** Raymond Building (R2-045), Shelley Lumba, University of Toronto
	17:10-17:30	**Closing remarks and awards,** Raymond Building (R2-045)

Abstracts: Plenary Session

PL1. How do Plants Use Physics to Survive and Thrive? A.-L. Routier-Kierzkowska**,** *Institut de recherche en biologie végétale, Université de Montréal, Montreal, QC.*

Plants are smart mechanical engineers. Despite their lack of muscles, plants can use physics principles to move at surprising speeds, for example to catch insect preys or spread their seeds as far as possible. The architecture of young plant organs is optimized to produce a stiff structure and use as little "building material" as possible. This makes it possible for roots and shoots to grow quickly in search of light or nutriments, while their capacity to synthetize new cell walls is limited. Plants can even sense mechanical forces, e.g. due to wind or a pathogen attack, and adapt their physiology in consequence.

From a mechanical viewpoint, plant cells are relatively simple objects. In the last years, we have developed a collection of methods to investigate plant cell mechanics and understand their growth and mechano-sensitivity. However, we only start to uncover the complexity of plant biomechanics at the tissue or organ level. In this presentation, I will expose my research plans to explore the mechanical tricks used by plants to optimize their chance of survival and reproduction.

PL2. GxE and the genomic basis of environmental response in plants. D. Des Marais. *Department of Civil and Environmental Engineering, MIT Associate of the Arnold Arboretum of Harvard University*

Plants live in a constantly changing, often unpredictable world and have evolved diverse strategies to cope with this environmental uncertainty. Some of these strategies represent a "best guess" by the plant about what conditions it may encounter over its lifetime. Other strategies leave some flexibility regarding the physiological and developmental traits expressed, contingent upon environmental signals. Natural populations harbor abundant genetic variation for environmentally-responsive traits. I will describe work determining the molecular basis of these traits and understanding how genetic diversity in molecular processes drives evolutionary change. I focus on the genetic basis of plant-water and temperature interactions, and show that natural variation in signaling pathways drives the evolution of local populations to climate. These studies point to a critical role for understanding the genetic architecture of abiotic stress response as we develop strategies to maintain natural diversity in the face of climate change and as we adapt our agricultural systems to meet growing human need.

PL3. How parasitic weeds wake up: Cracking the germination code of *Striga*. M. Bunsick[1], K. Nemrish[1], P. Sung[1], C. Adityani[1], A Collaku[1], H. McKay[1], S. Toh[2], Y. Tsuchiya[2], S. Lumba[1]*. *[1]Dept. of Cell and Systems Biology, University of Toronto and [2]Division of Biological Science, Nagoya University*

In Africa, the parasitic weed, *Striga hermonthica*, infects major food crops which results in devastating yield losses for over 100 million subsistence farmers. Because *Striga* is an obligate parasite, it is essential for *Striga* seed to germinate in the vicinity of a plant host. Roots of hosts exude the hormone, strigolactones (SLs), which are perceived by *Striga* seed to indicate that a host is nearby and thereby germinate. In higher plants, various signals like hormones, light and nutrients are transduced by signaling pathways into combinations of gene expression which compose a "germination code". *Striga*, however, has modified its response to signals that would typically promote germination of seeds from non-parasitic plants. Instead, *Striga* has evolved high sensitivity to SLs which override other germination cues. Because *Striga* is not amenable to genetics studies, it has been challenging to elucidate the molecular mechanisms underpinning *Striga* germination. To study a non-model system like *Striga*, we have developed three strategies: (1) chemical probes to dissect SL receptor function in *Striga*; (2) heterologous expression of *Striga* genes in *Arabidopsis* to analyze function; and (3) biochemical approaches including large-scale yeast two-hybrid methods to identify interactions among *Striga* proteins. To determine how *Striga* has 'rewired' the germination code of autotrophic plants, we are constructing StrigaNet, the first *Striga* interactome based on our protein interaction studies. By comparing protein interaction networks from *Striga* with those from *Arabidopsis*, we will determine the extent of evolutionary conservation of germination pathways in parasitic and non-parasitic plants.

Concurrent Session I: Plant Development

PD1. An integrated model of simple and compound leaf organogenesis. D. Kierzkowski[1]*, A. Runions[2], F. Vuolo[2], S. Strauss[2], H. Jenke[2], R. Lympouridou[2], A-L. Routier-Kierzkowska[1], R.S. Smith[2], M. Tsiantis[2]. *[1]Dept. of Plant Science, University of Montreal, Canada and [2]MPI for Plant Breeding Research, Cologne, Germany.*

A current challenge in biology is to understand the diversity of organismal form. Although the genetic basis of morphogenesis is relatively well characterized, it is still unclear how gene action translate into divergent morphologies. We investigate this problem by comparing leaf development in two closely related species, *Arabidopsis thaliana*, which has simple leaves with serrations, and *Cardamine hirsuta* with compound leaves subdivided into individual leaflets. By using time lapse imaging and genetics, we decompose the development of complex leaf shapes, into their constituent elements underlying growth, patterning and differentiation. We show that, despite their very different final forms, overall developmental patterns are conserved between these species. The differences in shape originate mainly from quantitative modification of local growth inhibition, and the timing of cell differentiation. This work shows how the interplay of spatial and temporal genetic cues operating within a mechanically connected tissue produces organ shape diversity.

PD2. Effect of cell shape and growth orientation on mechanics of the epidermis. A.J. Bidhendi[1]*, B. Altartouri[1], M.S. Zamil[2] and A. Geitmann[1,2]. [1]*Institut de recherche en biologie végétale, Département de sciences biologiques, Université de Montréal, Montréal, QC H1X 2B2, Canada and 2Department of Plant Science, McGill University, Sainte Anne de Bellevue, QC H9X 3V9, Canada.*

The epidermis is the first layer of defense against environmental antagonists, and it is mechanically designed to resist pathogen invasion and tear. We used onion epidermis to investigate how the orientation of the cell growth axis affects tensile and failure properties of the epidermis. The results indicate that, in hydrated state, the tissue failure does not occur by cell delamination (detachment). However, tearing tests demonstrate a marked anisotropy in tear-resistance of the epidermis. The tears induced along the long axis follow a relatively straight path mostly by interfacial delamination in cells. This observation is in contrast to previous studies on damage evolution in plant tissues with primary walls. However, the tear trajectory perpendicular to the cells' long axis tilts, assumes a nearly 45-60° angle, and eventually aligns with the cell axis. The latter seems to occur when the angle of the tear path becomes too sharp with regard to cell-cell interfaces. Fluorescent micrographs suggest that the initial shift of tear path from 90° to 45-60° angle may result from cellulose orientation. This is however in contrast to previous reports suggesting a longitudinal direction for cellulose microfibrils in onion epidermis. Tensile tests also indicate that, while the tissue is initially stiffer longitudinally, it exhibits a marked strain-stiffening in the transverse direction when stretched. Moreover, the ultimate tensile strength of the tissue was found to be higher in this direction supporting our initial observation of a semi-transverse orientation for cellulose bundles. Together, the results indicate a potential for cell orientation to fine-tune the stiffness and damage resistance of the tissue advertently.

PD3. Compatible pollen signalling in Arabidopsis thaliana: the proposed role of stigma-expressed RLCKs. J. Doucet[1]*, N. Udugama[1], and D.R. Goring[1]. [1]*University of Toronto Department of Cell and Systems Biology, Toronto, ON.*

The characteristic dry stigmas in the Brassicaceae means that compatible pollen must first be recognized by stigma papillae for successful germination, but relatively little is known about cellular responses to compatible pollen. In our working model, upon compatible pollen recognition, vesicle trafficking is initiated in the stigmatic papilla towards the plasma membrane under the pollen contact site. This regulated secretion allows for water release and cell wall modifications to mediated pollen hydration, germination, and subsequent pollen tube growth. Although the physiological process of compatible

pollinations have been well-described, the signalling events that precede them remain elusive. Transcriptome datasets have provided a wealth of potential candidates involved in this process, including receptor-like kinases and other genes which undergo transcriptional changes in response to pollination. We have identified two stigma-expressed receptor-like cytoplasmic pseudokinases which may function as part of the conserved signalling pathway in the Brassicaceae family of plants. Although this work represents one small piece of the puzzle of early pollen recognition in the stigma, it validates utilizing a reverse-genetics approach to identifying other potential key players in the compatible pollen acceptance pathway. These may include other stigma-expressed receptor-like kinases or membrane proteins. This project represents an exciting first step towards understanding the basal compatible pollen response pathway in the stigmatic papillae.

PD4. Lunapark proteins suppress the membrane fusion activity of RHD3 for the formation of tubular ER network. J. Sun[1*], H. Zheng[1]. *[1]Biology Department, McGill University, Montreal, QC, Canada.*

The endoplasmic reticulum (ER) is a network of tubules and sheets playing important roles in eukaryotic cells. The formation of the ER requires homotypic membrane fusion, which is mediated by a Dynamin-like large GTPase protein family. In Arabidopsis, ROOT HAIR DEFECTIVE3 (RHD3) is an ER membrane fusogen, but little is known about how the activity of RHD3 is regulated in mediating the ER fusion. Here we show that Lunapark (LNP) proteins, a conserved ER membrane protein family, physically interact with RHD3 at 3-way junctions of the ER, and stabilize the nascent 3-way junctions. Arabidopsis *lunapark* knockout mutants exhibit short root hairs with sheeted ER in many cells. We show that LNPs and RHD3 act antagonizingly in the fusion of ER membranes at the molecular and genetic levels. We thus suggest a model in which LNPs suppress RHD3 to regulate the formation of the ER network and cell growth. RHD3 mediates ER tubular membrane fusion to create 3-way junctions, after which LNPs are recruited to the 3-way junctions. LNPs recruited by RHD3 promote the degradation of RHD3, so to stop further fusion thereby a 3-way junction can be stabilized. A loss of LNP activity would lead to an elevated expression level of RHD3, which cause an excessive ER fusion resulting a sheeted ER in cells.

PD5. The concomitant evolution of angiosperms produced leaves with coordinated mesophyll surface area, cell diameter, vein, and stomatal traits to maximize exchange surface under a low CO_2 world. G. Théroux-Rancourt[1]*, J.M. Earles[2], M.E. Gilbert[1], M.A. Zwieniecki[1], C.K. Boyce[3], A. McElrone[4,5], C. Brodersen[2]. *[1]Department of Plant Sciences, University of California Davis, Davis, CA, 95616, USA [2]School of Forestry & Environmental Studies, Yale University, New Haven, CT 06511, USA [3]Department of Geological Sciences, Stanford University, Stanford, CA 94305, USA [4]USDA-Agricultural Research Service, Davis, CA 95616, USA* [5]Deparment of Viticulture and Enology, University of California, Davis, CA 95616, USA

The evolution of plant leaves, through the marked increased in certain anatomical features has allowed the angiosperms to dominate and to have a transformative effect on the globe. This is in part due to the higher assimilation rates associated with improved control over water loss through higher vein and stomatal densities. However, little is known about the diversity of leaf mesophyll surface area, which strongly affects CO_2 diffusion and assimilation. Using data from the literature and from our high-resolution X-ray computed tomography (microCT) dataset, we studied if there was an evolutionary trend in mesophyll surface area. By considering the exposed surface of the mesophyll to the intercellular air space on a mesophyll volume (A_{mes}/V_{mes}) rather than leaf area basis (S_m), we demonstrate that angiosperms and ferns have constructed leaves with more A_{mes}/V_{mes} than gymnosperms, but that angiosperms present the broadest range of values. Within all plants clades, higher A_{mes}/V_{mes} is associated with smaller mesophyll cell diameter. By concomitantly improving vein and stomatal density with A_{mes}/V_{mes}. angiosperms were able to explore a broad trait space of vein, stomatal, and mesophyll cell properties, and outperform ferns and

gymnosperms who were confined to specific habitats due to anatomical limitations. Hence, the mesophyll surface area and cell diameter could be viewed as a link between the improvement of vein density and stomatal traits, which allowed angiosperms to conquer new habitats as atmospheric CO_2 declined since the end of the Cretaceous.

PD6. The expansion pattern of *Arabidopsis* pavement cells is determined by the mechanical properties of the cell wall. B. Altartouri[1*], T. Tani[2], G. Scarcelli[3] and A. Geitmann[1,4]. [1]*Department of Biological Sciences, University of Montreal, Montreal, QC H1X2B2, Canada* [2]*Cellular Dynamics Program, Marine Biological Laboratory, Woods Hole, MA 02542, USA* [3]*The Fischell Department of Engineering, University of Maryland, College Park, MD 20742, USA* [4] *Faculty of Agricultural and Environmental Sciences, McGill University, Sainte-Anne-de-Bellevue, QC H9X3V9, Canada*

Plant cell development and growth are determined by the expansion pattern of the primary cell wall. Among the principal structural components in the primary wall are the cellulose microfibrils. They are thought to dominate the mechanical strength of the wall and thus determine the cellular expansion pattern. The objective of this study is to investigate the role of cellulose during the morphogenesis of epidermal pavement cells of *Arabidopsis* cotyledon. We employed polarized fluorescent microscopy to study cellulose arrangements and noncontact light Brillouin spectroscopy to investigate the mechanical rigidity of the cell wall during early stages of pavement cells. We investigated the *Arabidopsis* wildtype and the mutant *any1* which is characterized by a significant reduction in the cellulose crystallinity. The results of this study revealed a characteristic spatial distribution of the cell wall strength in the periclinal wall of individual pavement cells in the early developmental stages. The spatial occurrence of the mechanical strength is in agreement with the spatial distribution of cellulose microfibrils. The rigidity of the wall on the neck side of a bend is significantly higher than that on the lobe side of the bend. Moreover, the rigidity of the periclinal wall in the mutant cells was decreased significantly compare to the wildtype. Interestingly, we detected a slight difference between the strength of the neck and lobe regions in the mutant cells. These results suggest that lobe formation in pavement cells involves the spatially control of cell wall rigidity at subcellular level despite the presence of crystalline cellulose.

Concurrent Session II: Regulation and Metabolism

RM1. The activity of key fermentative enzyme Alcohol Dehydrogenase 1 from *Arabidopsis thaliana* is differentially altered by several redox post-translational modifications. S. Dumont[1]*, N.V. Bykova[2], A. Khaou1, Y. Besserour[1], J. Rivoal[1]. [1]*Département de sciences biologiques, Université de Montréal and* [2]*Morden Research and Development Centre, Agriculture and Agri-Food Canada.*

Several environmental factors can lead to oxygen limitation in plants, causing hypoxia or anoxia. Paradoxically, hypoxia is also known to cause an increase in production of reactive oxygen species (ROS) and reactive nitrogen species (RNS). An accumulation of these molecules can lead to oxidation of thiol groups on protein Cys residues. During hypoxia, plant cells rely on fermentative pathways to cope with the energy deficiency caused by respiration failure. Here, we focus on the terminal enzyme of ethanol fermentation, Alcohol Dehydrogenase (ADH) from *Arabidopsis thaliana*. We have demonstrated that an oxidative treatment of *A. thaliana* suspension cell cultures with H_2O_2 leads to a significant decrease in ADH specific activity. We purified recombinant *A. thaliana* ADH1 and demonstrated that treatments with H_2O_2 and nitric oxide (NO) led to significant decreases in catalytic activity. ADH1 inhibition by NO, but not H_2O_2, was reversed by DTT. We found that the binding of ADH1 to NAD^+ or NADH prevents the enzyme from inhibition by ROS or RNS, suggesting that the coenzymes limit the availability of sensitive Cys residue(s). We have also shown that the treatment of recombinant ADH1 with oxidized or reduced glutathione in the presence of the glutathionylation promoting agent diamide led to protein *S*-glutathionylation without affecting the

enzyme activity. Mass spectrometry analysis showed that two Cys residues in ADH sequence can be modified by glutathione, whereas six other Cys participate in intrachain disulfide bond formation. These results suggest that ADH is subject to several redox post-translational modifications that affect its enzymatic activity.

RM2. The Role of SNF1-Related Protein Kinase 1 (SnRK1) in Regulating Intermediary Metabolism in *Arabidopsis thaliana*. Y. Wang[1]*, B.J. Micallef[2], I.J. Tetlow[1], R. Mullen[1], R. Feil[3], J.E. Lunn[3], Michael J. Emes[1]. [1]*Department of Molecular and Cellular Biology, University of Guelph, Guelph, Canada N1G 2W1* [2]*Department of Plant Agriculture, University of Guelph, Guelph, Canada N1G 2W1* [3]*Max Planck Institute of Molecular Plant Physiology, 14476 Potsdam-Golm, Germany.*

The Sucrose Non-fermenting-1-Related Protein Kinase 1 (SnRK1) is a highly conserved heterotrimeric protein kinase in plants. It possesses a catalytic subunit (α) and two regulatory subunits (β and γ). The effects of altered expression of AKINβ1 on carbohydrate metabolism and gene expression in leaves were investigated in an Arabidopsis T-DNA insertion mutant. The contents of key intermediates in the tricarboxylic acid (TCA) cycle of the mutant leaves were markedly reduced throughout the diurnal cycle, coupled with a decrease in measurable respiration rate. Compared to wild type, 2485 genes and 188 genes were expressed differentially in leaves of the akinβ1 mutant in response to light and darkness respectively. Among these, several genes exhibited very substantial decreases in expression. Notably, expression of particular isoforms of multigene families involved in malate and lipid metabolism, and nitrate uptake showed decreases of 50-240 fold during the light period, but not during darkness. The subcellular localization of AKINβ1 and the regulatory function of N-myristoylation on the subcellular localization of AKINβ1 were investigated, showing that AKINβ1 localizes to Golgi. A model is hypothesized to explain the effects of AKINβ1 on metabolism and gene expression in Arabidopsis.

RM3. Regulation of Arabidopsis Starch Branching Enzyme 2.2. G.J. MacNeill*, I.J. Tetlow, M.J. Emes. *Department of Molecular and Cellular Biology, College Biological Sciences, University of Guelph, Ontario, Canada.*

Starch is a water insoluble carbon store found in higher plants and is a major component of the human diet. Transient starch is produced and degraded in chloroplasts over the diurnal cycle. Biosynthesis occurs through the coordinated activity of multiple classes of enzymes. Starch synthases polymerize ADP-glucose into α-glucan chains, while starch branching enzymes (SBE) introduce branch points to the growing glucan, and debranching enzymes modify glucan architecture. SBEs form phosphorylation dependent complexes with other starch biosynthetic enzymes. Two functional isoforms of SBE exist in Arabidopsis, of which SBE2.2 accounts for most of the measurable activity. Recombinant SBE2.2 was phosphorylated by soluble plastid extracts on residues Ser^{290} and Ser^{301}. A putative protein-protein interaction domain, conserved across all class II SBEs, has also been identified. Site-directed mutagenesis is being used to alter this conserved domain, Ser^{290} and Ser^{301}, and a C-terminal Cys residue to investigate their importance in catalysis and the formation of heteromeric complexes *in* vitro. The *in vivo* relevance of these post-translational modifications is being investigated by functional complementation of a *sbe* Arabidopsis null lines with wt and mutated SBE2.2. Effects on starch biosynthesis and structure will be determined. This research is significant for its potential applications to crop production and targeted manipulation of starch structure.

RM4. GmMYB176 interactome and regulation of isoflavonoid biosynthesis in soybean. A.K.A. Vadivel[1,2*], S. Dhaubhadel[1,2]. [1]*London Research and Development Centre, Agriculture and Agri-Food Canada, London, ON,* [2]*Department of Biology, Western University, London, ON.*

MYB transcription factors are one of the largest transcription factor families characterized in plants. GmMYB176 is an R1MYB transcription factor that regulates *Chalcone synthase 8* (*CHS8*)

gene expression and isoflavonoid biosynthesis in soybean. Silencing of *GmMYB176* suppresses the expression of the *GmCHS8* and reduces the accumulation of isoflavonoids in soybean hairy roots. However, overexpression of *GmMYB176* does not alter either *GmCHS8* gene expression or isoflavonoid levels suggesting that GmMYB176 alone is not sufficient for *GmCHS8* gene regulation. It is hypothesized that GmMYB176 acts cooperatively with another factor(s) for the regulation of *GmCHS8* gene expression and it may also regulate other isoflavonoid biosynthetic genes in soybean. The objective of this research was to identify the GmMYB176 interactome for *GmCHS8* gene regulation and elucidate the role of GmMYB176 in isoflavonoid biosynthesis in soybean. GmMYB176 interacting proteins were identified using two translational fusion baits (GmMYB176-YFP and YFP-GmMYB176) by co-immunoprecipitation, followed by liquid chromatography-tandem mass spectrometry. The interaction of selected candidates with GmMYB176 was validated *in planta* and their DNA binding activities determined. Our results reveal that GmMYB176 forms a transcriptional complex with Gm04bZIP and/or Gm05bZIP and this complex may regulate *GmCHS8* expression. RNA-seq and metabolomics analyses of soybean hairy roots in which *GmMYB176* was either silenced or over-expressed revealed that GmMYB176 regulates multiple genes in the isoflavonoid biosynthesis pathway, affecting the production of metabolites such as phenylalanine, liquiritigenin, daidzin, genistin, glycitein, and glyceollin.

RM5. Identification and characterization of a pectin acetylesterase from the seed coat of common bean (*Phaseolus vulgaris*) J. Palmer, A. Pajak, F. Marsolais*. *London Research and Development Centre, Agriculture and Agri-Food Canada.*

Common bean is rich in dietary fibre, a major component of which is pectin present in the seed coat. Pectin is produced as an esterified polymer in the Golgi apparatus, which can be de-esterified after it is secreted. The enzyme pectin acetylesterase participates in this process. De-esterification can change the structural properties of the cell wall. Esterification decreases calcium binding and gelation of pectin. A gene designated *PAE1* was characterized which encodes a major pectin acetylesterase in the seed coat. This gene is differentially expressed at all stages of seed development between germplasm lines SARC1 and SMARC1N-PN1, with transcript levels higher in SMARC1N-PN1 by 5- to 16-fold according to microarray data. The transcript was found to accumulate specifically in the seed coat, and the difference in expression between genotypes was confirmed by quantitative RT-PCR. Protein accumulation was observed in seed coat extracts of SARC1 and SMARC1N-PN1 by Western blot, with levels higher in SMARC1N-PN1 by approximately 2-fold. Initial velocity of pectin acetylesterase in seed coat extracts was higher by approximately 3-fold in SMARC1N-PN1. The acetate content of purified pectin from mature seed coats was 2.8 fold higher in SARC1 than SMARC1N-PN1. The difference in pectin acetylesterase expression is associated with an insertion of 150 base pair insertion in the promoter of SARC1. SMARC1N-PN1 was found to have a decreased seed water absorption and germination as compared with SARC1, specifically in older seeds.

RM6. *Norbelladine synthase* – A novel gene involved in Amaryllidaceae alkaloid metabolism in *Narcissus pseudonarcissus* 'King Alfred'. A Singh[1]*, I. Desgagné-Penix[1,2]. *[1]Department of chemistry, biochemistry and physics, Université du Québec à Trois-Rivières, Trois Rivières, Québec, CANADA. [2]Centre SÈVE, Université de Sherbrooke, Sherbrooke, Québec, CANADA*

Plants of Amaryllidaceae family produce more than 600 Amaryllidaceae alkaloids (AAs) with large range of biological activities. Some examples of AAs include galanthmine - acetylcholine esterase inhibitor, lycorine - antimitotic activity and narciclasine – anticancerous agent. However, their biosynthesis in plants is poorly studied. Therefore, efforts are required for AAs biosynthesis genes elucidation to allow AAs pathway metabolic engineering for drug development. Through an integrated analysis of transciptomic and metabolomic database of *Narcissus pseudonarcissus* 'King Alfred', we identified *Norbelladine synthase*

gene responsible for condensation of tyramine and 3,4 -DHBA to yield Norbelladine, a crucial intermediate of AAs biosynthesis pathway that provides a core structure to all AAs. Transcriptome of *Narcissus pseudonarcissus* 'King Alfred' was used to BLAST search *norcoclaurine synthase* (NCS) homolog. The resulting candidate gene was selected for cloning and characterization. *NBS* expressed well in E.coli Rosetta^{TM} (DE3) pLysS host strain at 37°C and 0.9mM IPTG concentration, followed by purification using nickel affinity column. Protein sequence lacked N-terminal signal peptide and shared similarity with PR-10/ Bet v1 at phylogenetic level. RT-PCR results shows NBS transcript expressed highest in bulb tissues. Enzyme assays analyzed on LC-ESI-MS/MS confirmed protein to be *norbelladine synthase* that catalyzes Pictet-Spengler reaction to form norbelladine.

Concurrent Session III: Abiotic Stress

SA1. Thriving or just surviving: examining heat-stress induced mortality of tamarack under extreme climate conditions. B.K. Murphy[1*] and D.A. Way[1,2]. *[1]Department of Biology, University of Western Ontario, London, ON, N6A 3K7, [2]Nicholas School of the Environment, Duke University, Durham, NC, USA 27708.*

As temperatures and greenhouse gas emissions increase, so will the frequency of climate-induced tree mortality events. This will affect the future functioning of northern forests and could impact global carbon cycling. While interactive effects of drought and heat stress have been studied, there is little known about the impact of heat stress alone on tree mortality. In a previous experiment by the Way lab, tamarack (*Larix laricina* [Du Roi] K. Koch) seedlings were grown under ambient (400 ppm) and elevated (750 ppm) CO_2 concentrations combined with ambient (average London, ON temperatures), ambient +4 ˚C, and ambient +8 ˚C growth temperatures. Despite being well watered, there was mortality of tamarack in **only** the ambient CO_2 and +8 ˚C chamber. I mimicked these growth conditions to examine carbon fluxes of tamarack as they develop and die to investigate whether carbon limitations are causing mortality. First, I compared carbon balance parameters of healthy seedlings across all six chambers. There was no acclimation of photosynthesis, but there was a significant decrease in respiration ($P<0.05$) and a significant increase in V_{cmax} ($P<0.01$) across increasing temperatures. Next, I examined the carbon balance parameters between healthy and dying seedlings in the ambient CO_2 and +8 ˚C chamber. Possibly due to variation between individual trees, there was no significant difference, but rather a trend of decreasing A_{net}/R_{dark} in dying seedlings compared to healthy seedlings ($P=0.0931$). Further analyses, including root respiration and carbohydrate pools, should give insight into whether carbon limitations are the cause of observed mortality.

SA2. Winter is coming: Root lifespan and overwintering strategies for two wetland species, *Sagittaria latifolia* Willd. (Alismataceae) and *Carex crinita* Lam. (Cyperaceae), in contrasting climate zones. A.P. Rayon[1]*, M.C. Eppes[2] and P. Ryser[1]. *1Department of Biology, Laurentian University and 2Department of Geography and Earth Sciences, University of North Carolina.*

In Northern Ontario, roots of some perennial wetland plant species senesce in autumn, while others maintain their roots over winter. Such contrasting strategies of root economics reflect different responses to an unfavourable season. The question arises, do such strategies change along a gradient of growing season length. This study investigates the effect of growing season length on root phenology of two species with contrasting root seasonal behaviour in two contrasting climate zones within their natural distribution: *Sagittaria latifolia* with autumn-senescing roots and *Carex crinita* with overwintering roots. Plants of local origin were grown in mesocosms in Sudbury, Ontario (growing season 150 days) and Charlotte, North Carolina (growing season 208 days). Four harvests were conducted throughout a year in each location to assess the timing of spring root production and autumn root senescence. In both species, the timing of leaf emergence and leaf senescence corresponded with the local climate. *C. crinita* roots remained alive (>80%) throughout the winter in both sites. In Sudbury, *S.*

latifolia roots senesced completely in the autumn and to about 90% in Charlotte. This indicates that the species-specific root winter strategy remains the same regardless of the growing season length. However, the absence of complete senescence in roots of *S. latifolia* in Charlotte where 5-10% of roots survived until spring suggests that complete root senescence by late fall, as observed in Sudbury, is a specific adaptation to a long winter. This is supported by a longer delay in leaf senescence of Charlotte plants when grown in Sudbury.

SA3. Exploring the cold acclimation mechanisms under freeze-thaw cycles in *Brachypodium distachyon*. B.F. Mayer*, J.-B. Charron. *Dept. of Plant Science, McGill University*

Temperate cereals have the capacity to increase their tolerance to freezing by undergoing cold acclimation, a process that naturally occurs during the fall and increases winter survival. The grass model *Brachypodium distachyon* has been shown to cold acclimate and to modestly increase its freezing tolerance when exposed to constant low temperature. In this study, we have exposed *Brachypodium distachyon* plants to freeze-thaw cycles similar to those observed in their natural environment. Following this repetitive treatment whole plant freezing tests were conducted and survival to freezing was compared to that of plants exposed to constant low non-freezing temperature (4°C). Higher freezing tolerance was observed in plants subjected to freeze-thaw cycles. These plants also accumulated higher levels of cold-regulated gene transcripts than those exposed to 4°C. Furthermore, cold-regulated genes displayed distinctive expression profiles over several freeze-thaw cycles suggesting the presence of adaptive transcriptional responses that could include transient transcriptional memories. We also show that these transcriptional responses differ between winter and facultative Brachypodium accessions which suggests the presence of a range of adaptation strategies to low temperature in *Brachypodium distachyon*.

SA4. A domesticated transposable element is essential for salinity defense in *Arabidopsis thaliana*. Y. Shao[1]*, T. Bureau[1]. [1]*Department of Biology, McGill University, Montreal, Quebec Canada H3A 1B1.*

Transposable elements (TEs) were once thought to be junk DNA, with no benefits towards the host. They are classified into DNA transposons and retrotransposons. In recent decades, some DNA transposon-derived genes were found to be functional in plants. These types of genes are defined as domesticated transposable elements (DTEs). The reported DTEs in plants including the MUSTANG and FAR1/FHY3 gene families, both of which evolved from the MULE TE superfamily, and the DAYSLEEPER gene, derived from the hAT TE superfamily, are transcriptional regulators and play important roles during plant development. Here we found *MUG4*, a member of the MUSTANG gene family, is essential for abiotic stress adaptation. Two T-DNA insertion lines were both shown to be hyper-sensitive to KCl and NaCl, but not sensitive to osmotic stresses induced by mannitol or PEG. Molecular complementation experiments confirmed the *mug4* salt sensitive phenotype. These results suggest MUG4 may be specifically involved in ion toxicity defense but not directly involved in osmotic stress response. MUG4 was found to be in the nucleus, however, unlike FAR1 nor FHY3, MUG4 did not show transcriptional activation. All the results above indicate MUG4 has novel functions compared to previously reported DTEs, and opens a new door for valuable roles of DTEs in plant adaptation to stress.

SA5. Exploring the role of XERICO in *Arabidopsis thaliana* development and stress response. E. Vonapartis[1]*, D. Mohamed[1], C. Carianopol[1], S. Gazzarrini[1,2]. [1]*Dept. of Cell and Systems Biology, University of Toronto* [2] *Dept. of Biological Sciences, University of Toronto.*

Plants continually face a multitude of abiotic stresses due to their sessile nature, which can severely compromise their ability to survive through the growing season. To mitigate the effects of a harsh environment, plants have evolved various developmental and physiological strategies through which they can effectively balance growth and defense against stressors.

Arabidopsis XERICO (XER) is a putative RING E3 ubiquitin ligase that increases intracellular abscisic acid (ABA) levels and promotes drought tolerance. To further characterize the role of XER in development and stress response, we began by analyzing its expression pattern using fluorescent transcriptional fusions in *Arabidopsis*. In addition, using transgenic lines expressing a fluorescent RING-inactive XER variant, we show that XER is targeted to the endoplasmic reticulum. To broaden our understanding of *XER* transcriptional regulation by stress, we conducted a yeast one-hybrid screen and isolated six potential upstream regulators, most of which are stress-responsive. Furthermore, a high-throughput yeast two-hybrid screen of an ABA-regulated protein library was carried out to identify XER interactors and shed light on the molecular mechanism through which XER may regulate stress response. From this screen, 40 potential downstream targets have been isolated. Data on select XER upstream regulators and downstream targets will be discussed. We propose that upon XER induction by a stress stimulus, it functions to regulate stomatal development, ultimately encouraging plant growth and survival during unfavourable growth conditions such as drought.

SA6. CYP86A1, a Key Enzyme in Suberin Biosynthesis, is Important in the Response of Arabidopsis to Salt Stress. S.-M. Wang[1,2]*, P. Wang[2], L. Gao[2], N. de Silva[1], O. Rowland[1]. [1]*Department of Biology and Institute of Biochemistry, Carleton University, Ottawa, ON, Canada,* [2]*State Key Laboratory of Grassland Agro-ecosystems, College of Pastoral Agriculture Science and Technology, Lanzhou University, Lanzhou, P. R. China*

Salinity is one of the major environmental stresses that restricts agricultural production. Vascular plants have several protective strategies to adapt to salt stress, including having apoplastic and transcellular barriers to limit the radial transport of ions (*e.g.* Na^+) in roots. Suberin is a hydrophobic heteropolymer containing aliphatic and phenolic compounds that is deposited in the cell walls of various tissues, such as root endodermis and periderm. Suberin is thought to help control the movement of ions and water in roots, however, it is still unknown how suberin functions in response to salt stress. In this study, the functional mechanisms of suberin in plant adaptation to salt stress were investigated by using a *cyp86a1* (*horst*) knock-out mutant of *Arabidopsis thaliana*, which has significant reductions in aliphatic suberin. Results showed that NaCl induced *CYP86A1* transcript levels and increased suberin content in roots of wild-type, while suberin did not change significantly in *cyp86a1*. Additionally, the *cyp86a1* knock-out mutant displayed a salt-hypersensitive phenotype. The mutation of *CYP86A1* resulted in more Na^+ accumulation in shoots via the trans-cellular transport pathway, and led to a change in root hydraulic conductivity and photosynthetic capacity. Taken together, our results indicate that suberin affects Na^+ accumulation, root water permeability and leaf photosynthetic capacity under salt stress including via increases in suberin content. Finally, we propose a model for the function of suberin in response to salt stress of Arabidopsis.

Concurrent Session IV: Biotic Interactions

BI1. Nuclear localized fungal effector suppresses the transcriptional responses to pathogens and mislead the host. B. Ahmed*[1,2], H. Germain[1], [1]Department of Chemistry, Biochemistry and Physics, University of Quebec, Trois-Rivières, QC, Canada, [2] Department of Plant Science, McGill University, Sainte-Anne-de-Bellevue, QC, Canada.

The basidiomycete *Melampsora larici-populina* causes poplar leaf rust, invading leaf tissue and secreting effector proteins through specialized feeding structures known as haustoria. The mechanisms by which rust effectors promote pathogen virulence are poorly understood. The present study characterized Mlp124478, a candidate effector of *M. larici-populina*. We used the model plants *Arabidopsis thaliana* and *Nicotiana benthamiana* and established that Mlp124478 accumulates in the nucleus and nucleolus, however only its nuclear accumulation is required to promote growth of the oomycete pathogen *Hyaloperonospora arabidopsidis*. The localization of Mlp124478 in nucleoli indicates that GFP is not masking the Mlp124478 localization sequence, thus localization is driven

by the effector sequence. When Mlp124478 was excluded from the nucleolus and present only in the nucleus, the increased susceptibility to *H. arabidopsidis* remained, indicating that the nucleolar localization is facultative for its virulence function. Stable constitutive expression of *Mlp124478* in *A. thaliana* altered leaf morphology, observed through increased waviness of rosette leaves and repressed expression of genes involved in immune responses. Our results indicate that Mlp124478, which contains a DNA-binding domain, interacts with the TGA1a-binding sequence. Taken together, our results suggest that Mlp124478 exerts its virulence activity in the nucleus of host cells and would binds the TGA1a promoter to suppress genes induced in response to pathogen infection.

BI2. Investigating the role of *BLADE-ON-PETIOLE* genes in plant defense. C. Bergin[1]*, B.O. Oyetoran[1], Y. Wang[1], S. Chatfield[1], L. Bauer[2], R. Datla[3], Subramaniam[1,2], M.L. Smith[1], S.R. Hepworth[1]. *[1]Department of Biology, Carleton University, Ottawa, Ontario, Canada, [2]Agriculture and Agri-Food Canada, Ottawa Research and Development Center, Ottawa, Ontario, Canada, [3]National Research Council Canada, Saskatoon, Saskatchewan, Canada*

Plants have evolved multiple layers of defense to detect and fight invading pathogens. The most ancient and basal form of immunity is PAMPs-triggered innate immunity (PTI) which relies on the recognition of pathogen associated molecular patterns (PAMPs) by pattern recognition receptors in the plasma membrane. *BLADE-ON-PETIOLE (BOP)* genes encode an evolutionarily conserved subclade of BTB-ankyrin proteins that control development within the NON-EXPRESSOR OF PATHOGENESIS-RELATED GENES1 (NPR1) family of plant defense regulators. NPR1 and its closest homologs are master regulators of a broad-based immune response called systemic acquired resistance (SAR) whereas *BOP* genes lack a known role in plant defense. Here, we provide evidence that Arabidopsis BOP1/2 are required in PTI. We used a microarray approach to investigate the transcriptome of *BOP1* overexpressing plants. Gene Ontology (GO) analysis of these data revealed that 35% of upregulated genes are associated with plant defense, in particular innate or PTI. Among these genes were Clade I TGA factors that interact with BOPs to control development and have a previously characterized role in PTI. Using direct pathogen testing, plants overexpressing BOP1 show increased innate resistance to *Pseudomonas syringae* accompanied by a stronger oxidative burst and increased callose deposition. BOP1 overexpressing plants also have a heightened growth-inhibition response to a PTI elicitor (flg22). Conversely, PTI-associated responses are diminished in *bop1 bop2* mutants. Preliminary results suggest that BOP1/2 and Clade I TGA factors co-regulate a subset of genes involved in PTI. Collectively, these data reveal that Arabidopsis BOP1/2 have dual functions in development and defense.

BI3. Maturation and intercellular movement of Turnip mosaic virus (TuMV) replication vesicles require ROOT HAIR DEFECTIVE 3. N. Movahed[1]*, J. Sun[1], H. Vali [2,3], J.F Laliberté[4], H. Zheng[1]. *[1]Dept. of Biology, McGill University; [2]Facility for Electron Microscopy Research, McGill University; [3]Dept. of Anatomy & Cell Biology, McGill University;[4] INRS-Institut Armand-Frappier, Laval.*

Turnip mosaic virus (TuMV) is a member of the potyviridae family that infects a broad spectrum of *Brassica* plants. TuMV induces the formation of small viral replication vesicles at the ER exit sites through the action of a transmembrane viral protein called 6K2. The viral replication vesicles then mature and move from the ER to plasmodesmata (PDs) and to adjacent cells. The contribution of the host proteins in these processes is poorly defined. Here, we observed a considerable delay in the development of the TuMV disease in an Arabidopsis mutant called *root hair defective3 (rhd3)*. RHD3 is involved in mediating the fusion of different ER membrane tubules. Western Blot confirmed that RHD3 is involved in the replication as well as the intercellular movement of TuMV. We found by fluorescent microscopy and transmission electron microscopy that, RHD3 is required for maturation and intercellular movement of the viral replication vesicles to adjacent cells. 6K2

physically interacts with RHD3 in our yeast two-hybrid and Bimolecular Fluorescence Complementation analyses. Furthermore, 6K2 can redirect RHD3 from the ER to viral replication vesicles, but 6K2(GV), a non-productive 6K2 that is localized to Golgi, failed to direct RHD3 from the ER to viral replication vesicles. More importantly, Golgi-localized 6K2 also failed to co-localized with RHD3. Based on these results, we concluded that Maturation and intercellular movement of Turnip mosaic virus (TuMV) replication vesicles require RHD3.

BI4. A candidate fungal effector protein Mlp124357 targets the vacuolar structures to promote virulence. M.H. Madina[1*], H. Zheng[2] and H. Germain[1]. *[1]Dept. of Chemistry, Biochemistry and Physics, Université du Québec à Trois-Rivières, 3351 boul. des Forges, Trois-Rivières, Québec, Canada G9A 5H7. [2]Department of Biology, McGill University, 1205 Dr. Penfield Avenue, Montréal, Québec, Canada H3A 1B1*

The obligate biotrophic fungus *Melampsora larici-populina* (*Mlp*) is one of the most devastating pathogen responsible for leaf rust disease on poplar tree. Research on the genome of *Mlp* revealed that it secretes many effector proteins, some of which have been considered candidate effectors to modulate plant function. Determining the function of effectors inside of cells is the key to understand pathogenicity mechanisms and improve our ability to protect crops from disease. In this study, to investigate the function of a candidate fungal effector in pathogenesis, we developed a stable transgenic *Arabidopsis* line expressing Mlp124357 fused with the green fluorescent protein (GFP). The confocal microscopy analysis revealed that Mlp124357-GFP fusion protein labeled the tonoplast, transvacuolar strands and other smaller spherical bright structure which were previously described as bulbs. A predicted GXXXG motif (X being any amino acid) present in the protein sequence of Mlp124357 is required for proper subcellular localization since replacement of the glycine residues with alanine (Mlp124357^{GA}) led to the delocalization of Mlp124357 into the nucleus and cytoplasm. We used immunoprecipitation and mass spectrometry to identify Mlp124357 interaction partners. We selected five proteins that localized to tonoplast from the IP interactor list. We screened their knock-out line, crossed them with Mlp124357 line, and assessed if their absence led to a relocalization of the effector in *Arabidopsis*. We also found that Mlp124357 enhances plant susceptibility to the bacteria *Pseudomonas syringae* and the oomycete *Hyaloperonospora arabidopsidis*.

BI5. Elucidating the substrate specificities of acyl-lipid thioesterase enzymes from diverse plant taxa. R.S. Kalinger*, I.P. Pulsifer, O. Rowland. *Institute of Biochemistry and Department of Biology, Carleton University.*

Plants produce a wide variety of lipid metabolites. These include volatile medium-chain (6-16 carbon) fatty acids and methylketones, which serve to attract insect pollinators and deter predatory insects. The Rowland lab discovered a family of four acyl-lipid thioesterase genes (*At*ALT1-4) in *Arabidopsis thaliana*, which encode plastid-localized enzymes that generate medium-chain fatty acids or β–keto fatty acids by cleaving the thioester bond between growing fatty acyl chains and their carrier proteins. ALT homologs exist in all plant taxa, indicating that their products are biologically important; however, they are nearly all uncharacterized. Despite high sequence similarity, *At*ALT1-4 generate vastly different fatty acid products, suggesting that ALT homologs in other plants also have highly varied activities. In this study, the diversity of ALT-like enzymes was investigated by screening the substrate specificities of 15 ALT homologs from monocots, eudicots, a lycophyte, a green microalga, and the ancient gymnosperm *Gingko biloba*. Enzymes were expressed in *Escherichia coli*, and their lipid products were profiled via gas chromatography and mass spectrometry. Overall, these enzymes displayed highly varied substrate specificities compared to one another and *At*ALT1-4, and could be classified into four functional groups consisting of members from diverse species and taxa. Medium-chain fatty acids are used to manufacture insecticides, pharmaceuticals, and biofuels, and ALT-like proteins are ideal candidates for metabolic

engineering to produce specific fatty acids in significant quantities. Also, continuing to probe the substrate specificities of ALT-like enzymes from diverse plant species will lead to a greater understanding of their evolutionary origins and biological roles.

BI6. Metabolomics of resistant and susceptible potato genotypes reveals several resistance related metabolites involved in late blight resistance. S. Joshi[1*], A. Gagnon[2], A.C. Kushalappa[1] *[1]Department of Plant Science, McGill University, Ste.-Anne-de-Bellevue, Quebec, Canada [2]Progest2001 Inc. Marie-Victorin Sainte-Croix, Quebec, Canada*

Late blight of potato is a destructive disease caused by an oomycete, *Phytophthora infestans*. It has a worldwide occurrence, leading to yield loss of up to 40%. Managing the pathogen is still a difficult task. Resistance to late blight is either qualitative or quantitative. The quantitative resistance is durable, but the governing mechanisms are not completely deciphered, which limits its breeding applications. The objective of this study was to identify the resistance genes and their mechanisms, in a resistant genotype (Libertas) and a commercial susceptible genotype (AG704.10). These genotypes were grown in greenhouse, both leaves and stems were *P. infestans* or mock inoculated. Disease severity and pathogen biomass was monitored to quantify resistance. The late blight severity was assessed by measuring the lesion diameter overtime. The area under disease progress curve (AUDPC) was calculated using the lesion diameter and found to be significantly ($P < 0.01$) higher in AG704.10 (AUDPC = 177.97), as compared to Libertas (AUDPC = 96.69). The resistance related (RR) metabolites, with high fold change in resistant genotype compared to the susceptible, were identified. Several constitutively accumulated metabolites belonging to the flavonoid and alkaloid groups were found in Libertas. Also, key phenylpropanoids and flavonoids were found to be accumulated in Libertas leaves and stem post pathogen inoculation. These metabolites might be involved in late blight resistance. Moreover, the constitutive resistance appears to be the major mechanism imparting resistance in Libertas.

Concurrent Session V: Growth and Regulation

GR1. Deciphering species-specific pollen tube guidance in *Solanum*. V. Joly[1]*, C. Viallet[1], Y. Liu[1], A. Zaro[2], F. Ceriotti[3], D. P. Matton[1] *[1]Institut de Recherche en Biologie Végétale, Dép. de Sciences biologiques, Université de Montréal, Québec, Canada [2]Facultat de Biologia, Universitat de Barcelona, Catalonia, Spain [3]Laboratorio de Genómica Evolutiva, Grupo de Evolución Molecular de Plantas, Instituto de Biología Agrícola de Mendoza, CONICET-UNCuyo, Mendoza, Argentina.*

Small, secreted cysteine-rich proteins (CRPs) combine a highly stable cysteine spacing, ensuring conservation of their 3D structure and function, and hypervariable inter-cysteine blocks, allowing quick evolution of specific recognition domains. Interestingly, several CRPs were shown to control key pollen-pistil interactions in a species-specific way. The most emblematic example is perhaps the LURE defensin-like family, controlling directional guidance of pollen tubes (PTs) in *Torenia* and *Arabidopsis*.

We chose wild potatoes (*Solanum* sect. *Petota*) as a case study to investigate the impact of rapid CRP divergence in plant speciation. Gathering ~200 close species with overlapping distribution areas, this taxon indeed exhibits strong reproductive isolation. Lab-on-a-chip microfluidic experiments carried out on 4 species show that species-preferential PT attraction is a key factor in this isolation. We suspect polymorphic CRPs to control this attraction.

High-throughput sequencing technologies were applied to profile the ovule secretome as well as the reproductive transcriptomes of our 4 species of interest. To screen out candidate genes, we developped KAPPA, a sequence search algorithm specifically dedicated to CRPs, and obtained a set of 32 defensin-like groups expressed in ovules.

Five promising chemoattractant candidates exhibiting (i) ovule-specific expression, (ii) down-regulation in guidance-defective ovules, and (iii) interspecific divergence were selected for further characterization. They are currently being investigated with on-gel assays and specific microfluidic devices tailored for *Solanum* PTs. This study will lead to a better understanding of CRP-mediated PT chemoattraction as one of the

major species-specificity checkpoints that must be "unlocked" by pollen tubes in the pistil.

GR2. Investigating the role of autophagy in *Arabidopsis* self-incompatibility. H. Nelles[1]*, D.R. Goring[1,2]. [1]*Department of Cell and Systems Biology, University of Toronto and* [2]*Centre for the Analysis of Genome Evolution and Function, University of Toronto*

In the flowering plants, fertilization is controlled by a series of interactions between pollen and pistil. Members of the Brassicaceae have dry stigmas, allowing a plant to strictly regulate pollen acceptance through the selective hydration of compatible pollen grains. Most species within this family have acquired an outcrossing mechanism, known as self-incompatibility (SI), where self-pollen is rapidly rejected at the stigma surface. SI is achieved by disrupting the vesicular trafficking of stigmatic compatibility factors to the pollen contact site, thus preventing the germination of incompatible pollen. While the upstream SI signaling components, S cysteine-rich (SCR) and S-locus receptor kinase (SRK), have been characterized in *Arabidopsis lyrata*, the downstream signaling events require further investigation. In this study, we have transformed the inbreeding species *A. thaliana* with three genes from *A. lyrata* to establish a stable SI line. Stigmas from the SI line showed a specific rejection of self-pollen, resulting in a substantial reduction in seed set. We plan to further investigate the genetic requirements of SI and the putative role of autophagy in this mechanism. A GFP:ATG8 marker was introduced into SI lines and preliminary confocal work has revealed autophagosome formation in self-pollinated stigmatic papillae. The requirement for autophagy in SI will be further explored using autophagy T-DNA KO lines (*atg 5-1*, *atg7-2*) and by generating additional KO lines using CRISPR/Cas9 deletion.

GR3. Diversification of the histone acetyltransferase GCN5 through alternative splicing in *Brachypodium distachyon.* A. Martel[1*], H. Brar[1], B.F. Mayer[1], J.-B. Charron[1]. [1]*Department of Plant Science, McGill University, Macdonald Campus, Sainte-Anne-de-Bellevue, QC, Canada.*

The epigenetic modulatory SAGA complex is involved in various developmental and stress responsive pathways in plants. Alternative transcripts of the SAGA complex's enzymatic subunit GCN5 have been identified in *Brachypodium distachyon*. These splice variants differ based on the presence and integrity of their conserved domain sequences: the histone acetyltransferase domain, responsible for catalytic activity, and the bromodomain, involved in acetyl-lysine binding and genomic loci targeting. *GCN5* is the wild-type transcript, while alternative splice sites result in the transcriptional variants termed *L-GCN5* and *S-GCN5*. Absolute mRNA quantification revealed that, across eight *B. distachyon* accessions, *GCN5* was the dominant transcript isoform, followed by *L-GCN5* and *S-GCN5*. A cycloheximide treatment further revealed that the *S-GCN5* splice variant was degraded through the non-sense mediated decay pathway. All alternative *BdGCN5* transcripts displayed similar transcript profiles, being induced by heat and accumulating to higher levels in the crown, compared to aerial tissues. All predicted protein isoforms localize to the nucleus, corroborating their purported epigenetic functions. S-GCN5 was incapable of forming an *in vivo* protein interaction with ADA2, the transcriptional adaptor that links the histone acetyltransferase subunit to the SAGA complex, while both GCN5 and L-GCN5 interacted with ADA2. Therefore, a complete histone acetyltransferase domain is required for BdGCN5-BdADA2 interaction *in vivo*. Thus, there has been a diversification in *BdGCN5* through alternative splicing that result in differences in conserved domain composition, transcript fate and *in vivo* protein interaction partners. Furthermore, our results suggest that *B. distachyon* may harbor compositionally distinct SAGA-like complexes.

GR4. The possible role of SPL/miR156 module in controlling growth phase transition in barley. R.K. Tripathi*, J. Singh. *Dept. of Plant Science, McGill University, McGill University, Sainte Anne de Bellevue, QC, Canada.*

Barley, a major cereal grown worldwide, is self pollinating and diploid plant species. Plant

architecture of barley is a complex agricultural trait which undergoes vegetative to reproductive phase transition after embryogenesis and determines final grain yield. The growth phase transition in barley is under complex regulatory circuit which needs thorough investigation. In *Arabidopsis*, the growth phase transition is regulated by antagonistic actions in between certain *SQUAMOSA* promoter binding like transcription factors (SPLs) and miR156. The miR156 negatively regulates *SPL* genes which positively regulates *miR172*. However, knowledge about this regulatory hub in barley is limited. To study the control of growth phase transition and spike architecture, we examined the SPL/miR156 module and its interaction with miR172 in barley.We identified 13 barley *SPL* genes, within seven distinct groups, that are orthologs to *SPL* genes described in *Arabidopsis*, wheat and rice. Further, 9 of 13 *SPLs* produced splice variants with transcripts and proteins of different lengths and showed differential expression pattern at vegetative to reproductive phase development. Interestingly, 4 of 13 *SPLs* were found as a target of miR156. Tissue specific differential expression patterns were observed for miR156-targeted *SPLs* as compared to non-targeted. An antagonistic expression pattern of miR156 when compared to *SPLs* & miR172 during the vegetative and the reproductive phases was observed and signifies their roles in barley growth phase transition.

GR5. Functional Characterization of Germination Associated Thaumatin-like Proteins in Barley. I. Iqbal*, R.K. Tripathi, O. Wilkins, J. Singh. *Department of Plant Science, McGill University, Sainte Anne de Bellevue, QC, Canada.*

The superfamily of Thaumatin-like Proteins (TLPs) belongs to a large, highly intricate and conserved PR-5 gene family of pathogenesis-related (PR) proteins. They play a substantial role in abiotic stress tolerance, binding to hormones, apoptosis, antifreeze activity, enzyme inhibition, fruit ripening, and seed germination. However, structural and functional information about TLPs in barley is limited. A prominent proportion of barley grains is processed into malt, whose quality is predominantly dependent upon endosperm β-glucan metabolism. Higher level of β-glucan grounds poor malt filtration, high wort viscosity, and haze formation. Recently, a barley TLP has been recognized as a potential interactor partner with (1,3,1,4)-β-glucan. Using rice TLP genes as a query, 28 TLP homologs were identified in barley. Our data indicates that there are 16 true TLPs in barley genome that possesses thaumatin family signature. Amino acid analysis suggests that some newly identified TLPs are rich in cysteines and varies between 10 to 24 residues. Our data shows that TLPs from rice, *Brachypodium*, barley and *Arabidopsis* clustered in 11 groups in the phylogenetic analysis. 62% of the newly identified TLPs produce splice variants and only 5 TLPs contain carbohydrate binding motif (CQTGDCGG). Gene structure analysis revealed that exon number ranged from 1 to 3 and two TLPs were found to be intronless. Spatio-temporal expression of barley TLPs shows that have differential expression in different tissues of barley. To investigate the role of *HvTLP8* for the regulation of (1,3,1,4)-β-glucan activity, *HvTLP8* RNAi and over-expresser barley mutant lines are being developed through genetic transformation.

Concurrent Session VI: Bioinformatics and Molecular Tools

BT1. Rapid gene function analysis using a new Barley Stripe Mosaic Virus system. A. Cheuk* and M. Houde. *Département des Sciences Biologiques, Université du Québec à Montréal.*

Understanding genetic and molecular bases of gene function is of increasing importance to harness their potential to produce plants with novel traits. One important objective is the improvement of plant productivity to meet future demands in food crop production. Gene function is mostly characterized through overexpression or silencing in transgenic plants. This approach is a lengthy procedure, especially in cereals. Plant viral expression systems can be used for rapid expression of proteins. However, current systems have a small cargo capacity and have mostly been used for gene silencing. Here, a four-component Barley Stripe Mosaic Virus-based (BSMV) system with high cargo capacity was constructed for rapid and stable expression of recombinant proteins in different plant species allowing

function analyses at different stages of development. Fluorescent marker proteins are expressed at high levels within a week and a proof of efficient function analysis is shown using the aluminum malate transporter-1 gene. In addition to the ability of gene cotransformation, this work demonstrates that the four-component BSMV system allows overexpression of cDNAs of up to 2100 nucleotides (encoding a protein of ca 78 kDa) thereby providing an invaluable tool to accelerate functional genomics and proteomic research in monocot and dicot species.

BT2. On the path towards a pan-genome model for potato. M. Kyriakidou[1*], J.H. Gálvez[1], C.Y. Tang[1], H.H. Tai[2], N.A. Barkley[3], D. Ellis[3], M.V. Strömvik[1]
[1]*Department of Plant Science, McGill University, Montreal, Canada* [2]*Fredericton Research and Development Centre, Agriculture and Agri-Food Canada, Fredericton, Canada* [3]*International Potato Center, Lima, Peru*

A reference sequence based on one individual representing a species' genome, is unable to capture the genetic variability among the organisms of that species. A great number of genes affected by Copy Number Variations (CNVs) contribute to diversity of many agronomic traits. Potato (*Solanum tuberosum* L.) is an important staple crop with a highly heterozygous and complex genome. Major efforts for potato improvement have been attempted but the expansion of the available genomic and transcriptomic resources is necessary to explore novel traits. Genomic re-sequencing data from six diploid potato landraces was used to identify structural variation compared to the current reference genome. The genomes were assembled by combining *de novo* and reference based methods. The results of a CNV analysis showed that in the majority of the genomes, the number of the genes affected by deletion events was greater than those affected by duplications. Here, we focus on the genomic analysis of chromosome 12 in these six potato germplasm as all of them appeared to have a high number CNVs per Mb. In particular, genes involved in metabolic process of polysaccharides, in environmental stress tolerance, and in disease response had increased copy number in these genomes.

BT3. Evaluating the genetic basis of gene co-regulation in wheat. R. Goessen*, L. Lukens, E. Raherison, *Department of Plant Agriculture, University of Guelph*

Quantitative trait differences are caused by the differential expression of many genes. However, gene expression differences caused by many unlinked loci would be difficult or impossible to retain in segregating populations. Thus, we hypothesized that in plant improvement, selection would favor 1) the fixation of linked genes with similar regulatory control and 2) single master regulatory loci that control the expression of many downstream genes. We tested these hypotheses in wheat. Using RNA-sequencing data from a segregating population derived from a recent x heritage cultivar cross, we constructed a co-expression network. We identified several groups of co-expressed genes controlled by single trans e-QTL. These groups suggest selection for defense response traits and flowering time traits, among other processes, that have driven wheat improvement. We also find evidence of similar regulatory patterns and functional similarity amongst linked genes at an unusually high frequency. We conclude that both trans regulation and genetic linkage have ensured gene co-regulation during wheat improvement. We propose that the molecular changes selected in wheat improvement may be shared by other crops.

BT4. Optimization of the INTACT system to profile guard cell gene expression in *Arabidopsis* leaves. A. van Weringh*, N.J. Provart, *Department of Cell & Systems Biology, University of Toronto.*

Guard cells allow plants to adapt to environmental changes by altering the aperture of stomatal pores. Narrowing or widening stomatal pores allow plants to dynamically balance their photosynthetic rate against the availability of necessary resources such as sunlight, water and carbon dioxide. When water becomes limited guard cells are a first point of adaptation, a target cell of the earliest production of the stress hormone Abscisic Acid. To better understand how this cell type adapts to water availability we

chose to use the INTACT system, a method to isolate cell type specific RNA or chromatin. We have optimized the INTACT system to extract guard cell RNA from adult *Arabidopsis* leaves. INTACT has the benefit of using few plants per sample, and tissue may be frozen early in the protocol. Therefore, this approach is well suited to sample dynamic gene expression changes under physiologically relevant conditions. We will use this method to profile gene expression changes in guard cells during the onset of drought in adult *Arabidopsis*.

BT5. Using Chlorophyll Fluorescence for High Precision Phenotyping of Drought Stressed Breeding Populations of White Spruce. A.E. Besik[1,3*], P. D'Odorico[1], N. Isabel[2], I Ensminger[1,3] [1]*Department of Biology, University of Toronto Mississauga, Mississauga, ON, Canada* [2]*Laurentian Forestry Centre, Canadian Forest Service Natural Resources Canada Québec (Sainte-Foy), Canada* [3]*Graduate Program in Cell and Systems Biology, University of Toronto, Toronto, ON, Canada*

Climate change is expected to cause mismatch between locally adapted white spruce populations and the environment where they naturally occurred, leading to maladaptation. The field of tree genomics has greatly advanced over the past decade providing genomic tools for improved tree breeding and selection, which will help to identify and select genotypes that are better adapted to future warmer and drier climates. However, technological development in phenotyping has lagged behind advances in genomics, causing phenotyping to be the limiting step for high-throughput identification and connection of specific traits with these genomic resources. The long-term objective of this experiment is to develop a precise method for phenotyping white spruce grown in the field for use as ground validation data for high-throughput phenotyping using drone imaging. Another aim is to analyze and compare the contribution of genetics, environment and their interaction to phenotypic performance. One pedigree population (2000 genotypes of white spruce genotyped previously for 9000 single nucleotide polymorphisms) has been clonally replicated and established across four different field sites in Quebec and Ontario. For this study, a subset of genotypes have been selected for data collection. The phenotypic response of these genotypes to naturally occurring drought stress has been quantified and compared using leaf level measurements of chlorophyll fluorescence, pigment composition, and water potential. Data obtained from the leaf level measurements will eventually be up-scaled to validate proxies of photosynthesis obtained from multispectral imagery acquired with a drone. Preliminary findings show variation among genotypes in response to minor drought stress.

Poster Session

PS1. *Ac/Ds* Transposons Tagging System as a Tool for Functional Genomics in Oat (*Avena Sativa*). M. Mahmoud*[1], R. Kaur[2], N. Tinker[3], J. Singh[1]. [1]*Dept. of Plant Science,* [2]*Dept. of Bioresource Engineering, McGill University,* [3]*Agriculture and Agri-Food Canada, Ottawa, ON, Canada.*

Oat (*Avena sativa*) is one of the most important cereals worldwide, due to its multifunctional uses for animal feed and human food. This crop has one of the largest and most complex hexaploid genomes among cereals. However, in respect to genetic and genomic studies, oat has lagged behind. This limitation impedes its further improvement. Thus, development of new genomic approaches in oat is imperative, not only to characterize its genome, but also to increase its diversity by creating novel random mutations. Heterologous maize *Activator* (*Ac)/ Dissociation (Ds)* transposon-based gene tagging system has been successfully applied in many crop species including barley. Here, we report the progress of our *Ac/Ds*-mediated genomic approach, developed first time in oat. Highly regenerative calli derived from mature oat seeds, cultivar (Park), were genetically bombarded or co-bombarded with various *Ac/Ds* constructs, using biolistic gun.

Our molecular and biochemical analyses confirmed a total of 20 unique successful transformation events, where *Ac* and *Ds* elements were successfully introduced into the oat genome. Individual *Ac* and *Ds* lines are being crossed, to develop genetic populations for their

use in exploring the *Ds* mutants, and thereby, identification of novel oat genes. A new form of transposon-based activation tagging approach used in this project has great potential to overcome gene and genome redundancy in this complex genome. This resource will be used as a base for the identification of novel genes associated with the desirable traits in oat.

PS2. Identification of gene regulatory network to differential water deficits and diel rhythms in two hybrid poplars. R. Chen*, O. Wilkins, *Dept. of Plant Science, McGill University, Ste. Anne de Bellevue, QC*

Drought accounts for about 32% decrease in the growth of aspens, more than any other stressor. Thus, to understand functional interplay between drought and other environmental signals and reveal the gene regulatory network underlying is imperative. We cultivated two hybrid poplar clones, Okanese and Walker, in three different water sufficient conditions. We then analysed physiology, transcriptome and chromatin accessibility on a variety of tissues from these conditions respectively. Eventually, we would like to identify how gene regulatory network within poplar responds to drought throughout a diel period and to lay the root for clarification of global gene regulatory networks in xylophyta.

PS3. Investigating a role for homeodomain transcription factors in differentiating abscission zones in Arabidopsis. L. Corrigan[1]*, V. Pautot[2], S. R. Hepworth[1]. *[1]Dept. of Biology, Carleton University [2]Instit. Jean-Pierre Bourgin, France.*

The shedding, or abscission, of plant organs such as leaves, fruits and flowers occurs at predetermined positions in the plant called abscission zones (AZs). Premature abscission is undesirable in crops because it reduces yield. AZs typically form at organ boundaries. Studies in Arabidopsis have identified boundary genes *BLADE-ON-PETIOLE1/2* (*BOP1/2*) as essential for the differentiation of AZs in flowers. Downstream effectors of BOP1/2 in this process are unknown. In other contexts, BOP1/2 require the downstream activity of three-amino-acid-loop-extension (TALE) homeodomain proteins: a BELL-like factor ARABIDOPSIS THALIANA HOMEOBOX GENE1 (ATH1) and its KNOX binding partner KNOTTED-like from ARABIDOPSIS THALIANA6 (KNAT6). Here, we use a genetic approach to examine the requirements for these TALE factors in abscission. Our data show that mild abscission defects in *ath1* mutants are progressively enhanced by *knat2, knat6, and knat2 knat6* mutations. Increasing loss of TALE activity leads to structural defects at the base of flowers including an expanded and disorganized AZ. In *ath1 knat2 knat6* triple mutants, there is a lengthy delay in AZ formation and the separation of organs is incomplete. These data provide insight into the role of boundary genes in plant organ abscission.

PS4. **EPR1 a transcription factor at the interface of high temperature response and the circadian clock.** J. Gelinas-Belanger, O. Wilkins *Dept. of Plant Science, McGill University, Ste. Anne de Bellevue, QC*

Asian rice (*Oryza sativa)* is a very important staple crop, being the primary source of calories for more than 30 % of the world's population, and is currently used as a model to understand crop gene regulation under various agro-environmental conditions. Rice is a crop that is very susceptible to high temperature, and global yields are predicted to be reduced by 10-15 % due to extreme heat events caused by climate change while they should be increased by 1 %/year to meet the needs of the rising world demand. Identifying and characterizing key elements of the heat response regulatory network in rice is a promising avenue to cope with these rising stresses. Recent studies have shown that the gene expression of Early Phytochrome Responsive 1 (OsEPR1, LOC_Os06g51260, 2 splice variants), a MYB Transcription Factor acting as a core element of the rice's circadian clock and binding to the Evening Element, increases dramatically under heat stress. However, current studies show that many of its target genes do not seem to be affected by heat stress which suggests that one or multiple genetic factor impede its action. My project objectives are to functionally validate the regulatory functions of OsEPR1 isoforms in relation to heat stress using a multi-genomic

approach (RNA-seq, ATAC-seq, etc.) and quantify their expression using RT-qPCR. The findings of this research will lead to a greater understanding of the regulatory mechanisms that control genetic responses toward abiotic stresses in commercial grain crops and generate insights to improve breeding practices.

PS5. Signal vs. Noise in Low-Affinity Na^+ Fluxes. A.M. Hamam[1*], T.M. Alozzi[1], D.T. Britto[1], H.J. Kronzucker[2]. *[1]Department of Biological Sciences and the Canadian Centre for World Hunger Research (CCWHR), University of Toronto [2]School of BioSciences, University of Melbourne.*

Although salinity is a major threat to agriculture globally, little is known about mechanisms underlying low-affinity NaCl transport across the plasma membranes of root cells. It has long been known, however, that nutrient deficiency can increase Na^+ absorption rates, but this characteristic has not been explored in the modern context of rapid, channel- and SOS1-mediated Na^+ cycling in roots. Here, we measured influx of the $^{24}Na^+$ radiotracer into roots of barley (*Hordeum vulgare* L.) seedlings grown hydroponically under four regimes: nutrient-replete ("GF"); $CaSO_4$ only ("G0"); K^+-deficient ("GF -K^+"); and K^+ with $CaSO_4$ only ("G0 +K^+"). Variable starvation periods, radioactivity-loading times, and NaCl concentrations were used to determine Na^+ influx maxima and inhibitory profiles. GF and G0 +K^+ conditions elicited the lowest fluxes, on which the ATPase inhibitor DES (diethylstilbestrol), and the K^+-channel blockers Cs^+ (cesium) and TEA^+ (tetraethylammonium) had no inhibitory effect. The highest fluxes were found after 24 h of G0 or GF -K^+ treatment, and, while these could be partially inhibited, effects were seen only when plants were loaded in radioactive solutions for much longer periods (20 min) than are typically recommended in recent literature (2 min). Our results suggest that the current model of rapid, transmembrane sodium cycling (RTSC) under saline conditions may be in error.

PS6. Metabolic characterization of potato cell cultures subjected to nutritional phosphate deficiency indicates the persistence of futile substrate cycling during stress. J.Z. He, S. Dorion, M. Lacroix, J. Rivoal.* *Institut de Recherche en Biologie Végétale, Université de Montréal.*

Heterotrophic potato (*Solanum tuberosum*) cell cultures were grown in MS media under conditions of phosphate (Pi) sufficiency (+Pi = 2.5 mM) or Pi deficiency (-Pi = 125 µM). Using this material, we investigated the metabolic changes occurring in central carbon metabolism during the response to Pi starvation for up to 12 days of stress. The specific activities of 28 glycolytic and respiratory enzymes were measured in +Pi and -Pi conditions. We found an increase in the level of several enzymes potentially catalyzing futile substrate cycles. A targeted metabolomic approach was used to quantify cell and medium Pi as well as key glycolytic intermediates, adenylates, and pyridine nucleotides. Results show that -Pi cells were able to maintain a relatively low but stable pool of cellular Pi throughout the Pi deficiency period. Despite significant decreases in total cellular adenylates and in several glycolytic phospho-esters, the energy charge of -Pi cells was not different from that of +Pi cells. In addition, no major difference was observed in total O_2 uptake between the two treatments. These data indicate that the level of cellular Pi is tightly controlled in -Pi conditions in order to maintain a critical level necessary to preserve respiration. Using [U-^{14}C] glucose as a metabolic tracer, we provide evidence that -Pi cells maintain a futile cycling between hexoses and hexose phosphates. This indicates that the apparently wasteful consumption of ATP maintained in potato cells under Pi deficiency could be part of a mechanism used to preserve a critical level of cellular Pi.

PS7. The expansion and diversification of HSFs gene regulatory networks in Asian rice. V. Vaidya*, B. Ahmed, O. Wikins. *Dept. of Plant Science, McGill University, Ste. Anne de Bellevue, QC*

Abiotic and biotic stresses induce developmental and physiological changes in plants which alter expression level of different genes to coordinate these changes and also impose harm thus decreasing productivity. *Oryza sativa* (Rice) is an

important crop as staple food to large populations in majority of the world. It is easy to genetically modify and is a model crop for cereal genetic modification studies. It is highly sensitive to abiotic stresses of heat and drought, independently and as a combination of both. A number of genes encoding Heat shock proteins are induced in plants to confer tolerance against extreme conditions. It is now known that Heat shock factors (Hsfs) respond to multiple stresses besides heat stress. Rice consists of 25 Hsfs and Wilkins *et al.,* found that 9 Hsfs respond to both heat and water deficit while 6 Hsfs respond to just drought. Hsfs are conserved through evolution and have diverse roles due to gene and genome duplications. They interact with conserved Heat shock elements (HSE) present in the promoter of Heat shock protein (Hsp) genes. Identification of Hsfs that respond to multiple stresses will allow identification of the bound DNA regions i.e. *cis* regulatory elements (CREs) through techniques like DAP seq. Heat stress responding Hsfs bind to conserved HSE but CRE to which drought responsive Hsfs binds is unknown. Variation in sequence of CREs can impact gene expression. Sequence variation in CREs will allow them to be used for crop breeding programs to develop plants adaptable to climate change.

PS8. The effect of a delayed spring on late growing season root and shoot senescence in *Rhynchospora alba* (L.) Vahl (Cyperaceae). K. Byne[1]*, P. Ryser[1]. [1]*Dept. of Biology, Laurentian University.*

The warming climate advances plant growth in spring, changing species' phenological patterns. The effects of an early spring on autumn senescence are not clear, especially for herbaceous plants in natural environments. The present study addresses how the timing of the start of the growing season affects autumn phenology in the wetland graminoid *R. alba*. Overwintering bulbils of *R. alba* were stored in a refrigerator, and were either planted on May 6 in pots in an experimental garden in a cold-frame, or kept in the refrigerator for further three weeks before planting. Flowering time of the plants was monitored, and beginning in mid-August, three plants from each of the treatments were harvested every two weeks to be analysed for number of leaves, and the dry mass of green and senesced shoots, roots, and components of sexual and vegetative reproduction. Root vitality was tested using TTC. The three weeks delay in the start of the growing season resulted in delayed flowering and delayed senescence of both leaves and roots. Plants with a delayed start also had a lower dry mass of their overwintering bulbils, but a larger number of leaves, compared to plants with an early start. We conclude that for the northern temperate *R. alba* an early spring does not result in a longer growing season, but allows it to invest more into vegetative reproduction. The species shifts its phenology to match the changes in spring, but is unlikely to respond to an extended autumn after finishing its life cycle.

PS9. Pectate lyases promote pollen germination and lubricate the path of the pollen tube in *Arabidopsis thaliana*. Y. Chebli* and A. Geitmann. *Dept. of Plant Science, McGill University.*

The pollen tube is a cellular cylindrical protuberance formed by the pollen grain upon its contact with the stigma. Its main purpose is to ensure sexual plant reproduction by delivering the sperm cells to the female gametophyte. To be able to accomplish this task, the elongating pollen tube has to emerge from the pollen grain by breaking through its thick wall and it has to penetrate the pistillar tissue without precociously bursting. Both situations require the loosening of cell wall material - during germination the pollen intine proper has to yield and during pollen tube elongation the apoplast of the transmitting tract needs to be softened to allow for pollen tube passage. Here we investigate the putative role of the pectin digesting enzymes pectate lyases (PLs) in these processes. Using mutant analysis, microscopical observations of fluorescently tagged PLs combined with fluorescence recovery after photo-bleaching (FRAP) experiments and immuno-detection, we show that PLs are required for intine loosening during the first steps of pollen tube germination. During pollen tube elongation, PLs are secreted by the pollen tube into transmitting tract, likely contributing to the digestion and loosening of the pollen tube path. Our data provide direct evidence for the long-standing assumption that pollen tubes extrude

enzymes to the extracellular space with the likely purpose to interact with the transmitting tissue.

PS10. Post-translational Regulation of Starch Synthase IIa, a Key Enzyme of Starch Biosynthesis in Maize Endosperm. S. Mehrpouyan[1*], I.J. Tetlow[1] and M.J. Emes[1]. [1]*Department of Molecular and Cellular Biology, University of Guelph, Ontario, Canada, N1G 2W1.*

Starch is the most abundant storage carbohydrate in plants, providing 70% of human caloric intake and has many industrial applications. Starch biosynthesis involves the coordination of starch synthases (SSs), starch branching enzymes (SBEs) and debranching enzymes.
In cereals, some starch biosynthetic enzymes function via formation of multi-enzyme complexes, and protein phosphorylation plays a crucial role in their assembly. In maize, the isozyme SSIIa, forms the core of a heteromeric protein complex with SBEIIb and SSI, and is responsible for the localization of this complex in the starch granule. The catalytic activity of this particular protein complex is crucial for normal starch biosynthesis in maize. When maize amyloplast extracts were analysed by western blots, following non-denaturing PAGE, multiple bands of SSIIa were identified. The relative mobility and distribution of SSIIa bands was markedly different between samples treated with ATP or alkaline phosphatase, suggestive of major conformational changes and/or association with other proteins caused by protein phosphorylation. Results will be presented showing effect of phosphorylation on the catalytic activity of enodgenous and recombinant forms of SSIIa as well as on formation of enzyme complexes with other enzymes of starch biosynthesis. The sites of SSIIa phosphorylation have been investigated by site-directed mutagenesis and data on the amino acid residues involved will be discussed. The present study provides new insights into our understanding of the signal transduction system regulating amylopectin biosynthesis in plants. This work is of strategic importance and has the potential to identify novel genes for crop improvement.

PS11. Evolution and mechanism of the mitochondrial *cox1* intron horizontal transfer in Angiosperms. L.F. Ceriotti[1]*, L.E. García[1,2] and M.V. Sánchez-Puerta[1,2,3]. [1]Facultad de Ciencias Exactas y Naturales, UNCuyo, [2]Instituto de Biología Agrícola de Mendoza, CONICET-UNCuyo and [3]Facultad de Ciencias Agrarias, UNCuyo.

The most frequent case of horizontal gene transfer in angiosperms involves the group I intron in the *cox1* mitochondrial gene, originally acquired from a fungal donor and followed by more than 100 subsequent inferred plant-to-plant transfer events. This promiscuous behaviour is thought to be due to its encoded DNA *homing* endonuclease, whose cleavage site is in *cox1* intron-less alleles. The study of homologous introns in yeast suggests that intron insertion occurs through the double-strand break repair (DSBR) pathway without crossover, process called *intron homing*. So, this mechanism has been proposed to participate in angiosperms *cox1* intron propagation. However, other repair mechanisms supposed to occur in plant mitochondria could participate. These mechanisms can be distinguished because they are supposed to generate crossovers (CO) and/or non-crossovers (NCO) in different proportions. In order to detect possible alternative repair mechanisms involved in *cox1* intron propagation, we analyzed 139 angiosperm species with the intron. The analysis consisted in the identification of CO and NCO events comparing exon1, exon2 and intron phylogenetic relationships. When sequences were available the analyses was extended to intergenic regions flanking the exons. In contrast with original DSBR model, where COs and NCOs are expected to occur in similar proportions, only NCO events where detected in our analyses. We propose an alternative repair pathway called synthesis-dependent strand annealing (SDSA), which can only produce NCO results, as the most probable mechanism involved in the *cox1* intron propagation in angiosperms.

PS12. Identification of candidate *Fusarium graminearum* effectors during infection of *Arabidopsis thaliana* using biotin identification (BioID). M. G. Miltenburg[1]*, C. Rampitsch[2], M. Khan[3], D. Desveaux[3], R. Subramaniam[1]. [1]*Dept.*

Of Biology, Carleton University and Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, [2]Morden Research and Development Centre, Agriculture and Agri-Food Canada, [3]Dept. of Cell and Systems Biology, University of Toronto.

Fusarium graminearum is a fungal pathogen that causes Fusarium head blight (FHB) in wheat, barley, and other cereal crops. Infection results in the buildup of the mycotoxin deoxynivalenol (DON), making the grain unfit for livestock feed and human consumption. To develop new ways of combatting FHB, it is necessary to improve our understanding of plant-pathogen interactions. This includes identifying potential effector proteins that are associated with infection.

The aim of this project is to use a technique known as proximity-dependant biotin identification (BioID) to identify potential *Fusarium* effector proteins that are present in *Arabidopsis* seedlings during infection. BioID is a technique that can be used to identify proximal proteins and potential interactions. It uses a promiscuous biotin ligase (BirA) localized to the cytoplasm or membrane, which biotinylates proximal proteins that can then be isolated by affinity purification and mass spectrometry.

Preliminary results confirm that BirA promiscuously biotinylates proteins in *Arabidopsis* seedlings grown in liquid media supplemented with exogenous biotin. The next steps for this project are to optimize the setup to capture *Fusarium* proteins. As well, we hope to generate *Arabidopsis* expressing BirA in the chloroplast or nucleus, to identify effectors that may target these organelles. Once potential effectors have been identified, further research will be conducted to confirm their function and role in infection.

PS13. Getting to the root of the matter: Relationships between chemical characteristics of softwood biochar, torrefied biosolids and early corn (*Zea mays*) root development and N uptake. R. Backer[1]*, M. Ghidotti[2], T. Schwinghamer[3], D. Fabbri, P. Dutilleul[1], P. Seguin[1], D.L. Smith[1]. [1]Dept. of Plant Science, McGill University and [2]Department of Chemistry "Giacomo Ciamician", CIRI-EA and CIRSA, University of Bologna

Biochar, produced by pyrolysis of biomass at temperatures above 350 ˚C, offers the potential to 1) return carbon to the soil due to its high content of stable C and 2) improve soil fertility by altering soil pH and nutrient-holding capacity. In contrast, materials produced by torrefaction of biomass at temperatures lower than 350 ˚C have lower C contents but retain higher concentrations of plant available nutrients. In this experiment, we characterized the chemical properties, including the volatilomes, of a biochar produced from softwood chips at 500 ˚C (PYR) and torrefied biosolids (produced at 270 ˚C, ALT, and at 320 ˚C, AHT). The volatilome data showed that organic compounds were released in air and water preferentially by ALT and AHT. We attempted to relate these characteristics to plant growth effects in corn (*Zea mays* L.). Multivariate statistics of germination data revealed that low H/C of PYR was positively correlated with longer root systems while the higher H/C, volatile matter and available N and K concentrations of AHT and ALT were negatively correlated with root growth. Under greenhouse conditions, compared to the control, corn plants grown on soil amended with 26 Mg $ha^{-1,}$ ALT and AHT had reduced root lengths while plants grown on soil amended with 26 Mg $ha^{-1,}$ PYR had increased root length. AHT improved biomass accumulation and N uptake. These effects could not be attributed to individual volatile or water-soluble compounds, however appeared to be related to the high concentration of N-containing organic compounds in ALT and AHT.

PS14. Exploring the evolution of the cytokinin receptor. S. Gerayli[1*], D. P. Maxwell[1] *[1]Department of Biology, Western University, London, Ontario, Canada*

LHK1 (*Lotus histidine kinase 1*) is a cytokinin receptor which has been shown to be required and sufficient for nodule organogenesis in *Lotus japonicus*. To gain insights about how and when the cytokinin signaling system was established, a comprehensive phylogenetic analysis was undertaken that involved searching for LHK1

homologs among nine different groups of algae (Rhodophyta, Cryptophyta, Dinophyta, Heterokontophyta, Haptophyta, Chlorarachniophyta, Euglenophyta, Chlorophyta), Liverworts, Mosses, Hornworts, Clubmosses, Ferns, Gymnosperms and Angiosperms. The LHK1 protein has three functional domains; CHASE, KINASE and RECEIVER, we looked for similarity of these three domain in the mentioned group. Domain profiles of characteristic proteins involved in the cytokinin network were obtained from the public HMMER database (http://www.ebi.ac.uk/Tools/hmmer/) which provides access to the protein homology search algorithms found in the HMMER software suite. The domains of proteins involved in cytokinin signaling were investigated to identify potential components in cytokinin signaling. The phylogenetic relation of these protein domains was analyzed to conclude on the evolution of the respective protein domains and the proteins they are part of. The most surprising finding from this analysis was the inability to detect the CHASE domain in some groups of land plants and most likely this domain was acquired by certain eukaryotic lineages through horizontal gene transfer from bacteria. Also, one possible vector could have been a virus. In this context it is interesting to note that the genome of the virus *Ectocarpus siliculosus virus-1*, which integrates into the genome of its brown algae host, *Ectocarpus siliculosus*, encodes a CHASE domain containing His kinase.

PS15. *Lactobacillus plantarum* (ATCC 9019) cell-free supernatant promotes growth of tomato in sandy media. J.R. Lamont[1]*, D.L. Smith[1], O. Wilkins[1]. [1]*Dept. of Plant Science, McGill University.*

Lactobacillus is a ubiquitous member of plant microbiomes, however, it has not been thoroughly evaluated at a plant growth promoting microorganism. The objective of this work was to determine if *Lactobacillus plantarum* (ATCC 9019) (*Lb.*9019) cell-free supernatant (CFS) could improve growth and development of tomato grown under stressful conditions imposed by a sandy medium. Tomato (*Solanum lycopersicum* cv Moneymaker) seeds were sown in 2" pots containing sand and turface mixed in equal proportions and watered in with either DI water, or 100x diluted *Lb.*9019 CFS supernatant from a 24h culture. Pots under the *Lb.*9019 treatment were watered with redissolved *Lb.*9019 CFS at the same rate twice per week throughout the experiment. Shoot height, shoot dry weight, root dry weight, total root length, total root volume, average root diameter, total root surface area and number of root tips for each plant were measured 40 days after seeds were sown. Lb.9019 CFS was analyzed for nutrient and phytohormone content Plants treated with *Lb.*9019 CFS were larger and more developed than control plants after 40 days growth. Dry shoot and root weights, shoot length, root length, root surface area, root volume, average root diameter, and number of root tips were all significantly greater for plants treated with *Lb.*9019 CFS than for control plants. Analysis of *Lb.*9019 CFS revealed it contained negligible nutrients but appreciable quantities of indole-3-acetic acid and abscisic acid. The stimulatory effects on tomato, and analysis of *Lb.*9019 CFS suggest *Lb.*9019 secretes plant-growth-promoting compounds including phytohormones, and perhaps others.

PS16. Identification of potential *Arabidopsis thaliana* receptors involved in perception of *Fusarium graminearum* infection via GFP labelling. N.K. Manes[1]*, E.K. Brauer[2], R. Subramaniam[1]. [1]*Dept. of Biology, Carleton University and Ottawa Research and Development Centre, Agriculture and Agrifood Canada and* [2]*Ottawa Research and Development Centre, Agriculture and Agrifood Canada.*

Arabidopsis thaliana perceives the presence of microbes via its transmembrane localised pattern recognition receptors (PRRs). PRRs recognize evolutionary conserved regions of a protein present on the microbes, referred to as microbe associated molecular patterns or MAMPs. Perception of microbes leads to activation of defense responses (called basal immunity) that involves at cellular levels such as the activation of ROS (reactive oxygen species), activation of MAPK (mitogen-activated protein kinase) cascades, and induction of defense related genes

such as FRK1, WRKY53 and PHI-1. Widely characterised PRRs have been studied in context to bacterial pathogens but very little is known about fungal associated PRRs. Here in this study, a high throughput screen using GFP-labelled *Fusarium graminearum* has revealed potential PRRs which are involved in reducing infection caused by the harmful cereal crop pathogen responsible for diseases such as Fusarium Head Blight (FHB).

PS17. MKP1 controls stomatal cell fate differentiation during stomatal development in *Arabidopsis.* F. Tamnanloo*, H. Damen, J.S. Lee. *Department of Biology, Concordia University, Montreal, QC, Canada*

MAP Kinase phosphatases (MKPs) are important regulators of the activation levels and kinetics of MAP kinases. This is crucial for a large number of physiological processes during interactions with the environment as well as growth and development. Stomata are pores in the plant epidermis that open and close in response to water stress and thereby control water loss from the plant and at the same time regulate CO_2 uptake. Although much is known about the potential upstream MAPKKs and biological role of MPK3 and MPK6 during stomatal development, the process by which they are inactivated remains unclear. Here we report the identification of MKP1 as a key regulator promoting stomatal cell fate differentiation. A loss-of-function *mkp1* mutation occasionally developed clusters of small cells failed to differentiate into stomata. A genetic analysis showed that MPK3 and MPK6 are epistatic to MKP1, consistent with the predicted function of MKP1 as a MAPK phosphatase. Our biochemical analysis using stomatal signal provide evidence that MPK3 and MPK6 are indeed physiological substrates of MKP1 during stomatal development. These findings help determine the role of phosphatase in controlling MAPK signaling specificity in stomatal development and create a deeper understanding of MAPK signaling cascades in plants.

PS18. The Biogenesis of Photosynthetic Membranous Vesicles. S. Bakhtiari*, Y. Sun, M. Valente-Paterno, W. Zerges. *Dept. of Biology, Concordia University.*

Chloroplasts are essential organelles found in plants and algae. Inside the chloroplast, thylakoid membranes form a network of vesicles and contain the complexes of the photosynthetic electron transport system. Despite our detailed knowledge of the composition and function of thylakoid membranes, the cytological organization of their biogenesis is poorly understood. We show that de novo photosystem II (PSII) biogenesis occurs in discrete regions in differentiating chloroplasts and mature chloroplasts which are growing and dividing. Results of biochemical fractionation experiments revealed "chloroplast translation membranes" (CTM) which are enriched in marker proteins for PSII biogenesis (and the T-zone) and, therefore, are proposed to serve as a platform for PSII biogenesis. Proteomic analyses of CTM support their role in thylakoid biogenesis and potentially reveal new proteins in this process. Our results provide insights into spatiotemporal organization of the biogenesis of organellar membranes which is separate from the membrane biogenesis in the endomembrane/secretory system.

PS19. Transcription promotes plastid genome instability in Arabidopsis. J. Pérez Di Giorgio, E. Lepage, S. Truche, S. Tremblay-Belzile, A. Loubert-Hudon, and N. Brisson *Department of Biochemistry and Molecular Medicine, Université de Montréal, Montréal, Québec, Canada*

Conflicts between transcription and replication are a potent source of genome instability. For instance, the transcription machinery may generate R-loops as the nascent transcript reanneals with the template DNA strand, forming a DNA:RNA hybrid and leaving the non-templated DNA single-stranded. Unregulated R-loops can be susceptible to lesions and stall replication fork progression, generating double-stranded breaks (DSBs) and inducing hyper-recombination.
Here we evaluate impact of transcription on plastid (pt) genome stability in *Arabidopsis thaliana.* We show that reduced pt transcription limits the accumulation DNA

rearrangements on a genome-wide scale by favoring conservative repair. Using light and heat stresses known to impact plastid transcription, we showed that modulation of plastid transcription leads to a similar modulation of plastid genome instability.

We further demonstrate that transcription leads to error-prone ptDNA repair especially under defective fork progression conditions caused by the absence of the pt genome maintenance actors such as Whirly proteins, RecA1 and PolIB. Similar results were observed under high levels of DSBs induced by ciprofloxacin, at whole-genome scale, or by an exogenous endonuclease cleaving at a single site in the pt genome, establishing a link between plastid transcription and DSB repair.

Additionally, we show that transcription rates correlate with the appearance of R-loops in the plastid, that R-loops increase in the absence of Whirly proteins, and that removing R-loops reduces genome instability. Taken together, our results suggest that plastid transcription can threaten plastid genome stability by inducing R-loops and preventing conservative DNA repair and thus, needs to be tightly controlled.

PS20. Quantitative assessments of wax-only water barriers on *Pinus strobus* and *P. resinosa* needles using a modified experimental set-up. C. Buschhaus*. Crandall University

With extreme weather events predicted to increase, the contribution and plasticity of cuticular wax (as compared to other epidermal components) as a primary barrier to environmental stressors must be quantified. Most studies demonstrating that plant wax restricts excessive water loss have analyzed leaves or fruit using a chamber apparatus that maintains a saturated state at the physiologically inner surface of the cuticle. This set-up permits measuring the same leaf area before and after a treatment. Conversely, studies of narrow cylindrical plant parts such as needles or thin stems have relied on primitive dehydration techniques that do not allow further treatments on the same plant material. Here we modify the chamber apparatus to examine the minimum water conductance of needles and narrow stems in order to allow paired comparisons, such as before and after wax removal. Results using needles from *Pinus strobus* and *P. resinosa* indicate resistances to water movement comparable to published values for other leaves followed by a substantial decrease after solvent extraction of cuticular wax. Application of this method to and preliminary results for Arabidopsis stems will be also shown. Further use of this method should allow quantitative assessments of the wax (only) contribution to the water barrier in Arabidopsis wax mutants as well as the plasticity of cuticular wax water barriers necessary for extreme environmental conditions likely to be experienced by conifer needles.

Meeting delegates

Delegate	Institution	Participation
Ahmed, Bulbul	McGill University	BI1, PS7
Altartouri, Bara	Université de Montréal	PD2, PD6
Backer, Rachel	McGill University	PS13
Bakhtiari, Shiva	McGill University	PS18
Bannister, James	University of Waterloo	
Barraj, Abdel-Rahman	Zeiss	Sponsor
Bede, Jacquie	McGill University	
Begg, Caroline	McGill University	
Bergin, Christopher	Carleton University	BI2
Besik, Ariana	University of Toronto	BT5
Bidhendi, Amir	Université de Montréal	PD2
Bouard, William	Université du Québec à Montréal	
Brisson, Normand	Université de Montréal	PS19
Buschhaus, Christopher	Crandall University	PS20
Byne, Kyelle	Laurentian University	PS8
Ceriotti, Federico	Instituto de Biología Agrícola de Mendoza - Université de Montréal IRBV	GR1, PS11
Charron, Jean-Benoit	McGill University	SA3, GR3
Chebli, Youssef	McGill University	PS9
Chen, Ruite	McGill University	PS2
Chen, Wei-Yuan	McGill University	
Cheuk, Arnaud	Université du Québec à Montréal	BT1
Clayton, Emily	Western University	
Corrigan, Laura	Carleton University	PS3
Cumming, Matthew	University of Toronto	
de Zwaan, Todd	LemnaTec	Sponsor
Des Marais, David	Massachusetts Institute of Technology	PL2
Desveaux, Darrell	University of Toronto	PS12
Doucet, Jennifer	University of Toronto	PD3
Dumont, Sébastien	Institut de recherche en biologie végétale - Université de Montréal	RM1,
Emes, Michael	University of Guelph	RM2, RM3, PS10
Ensminger, Ingo	University of Toronto	BT5
Francoeur, Francois	Integrated DNA technologies	Sponsor
Geitmann, Anja	McGill University	PD2, PD6, PS9
Gélinas, Jérôme	McGill University	PS4
Gerayli, Sina	Western University	PS14
Goessen, Roos	University of Guelph -Wageningen University	BT3
Goring, Daphne	University of Toronto	PD3, GR2

Haldar, Aparna	Agriculture and Agri-Food Canada - Ottawa Research and Development Centre -University of Ottawa	
Hamam, Ahmed	University of Toronto	PS5
Hepworth, Shelley	Carleton University	BI2, PS3
Houde, Mario	Université du Québec à Montréal	
Hunt, Steve	Qubit Systems	Sponsor
Iqbal, Irfan	McGill University	GR5
Joly, Valentin	Institut de recherche en biologie végétale - Université de Montréal	GR1
Joshi, Sripad	McGill University	BI6
Kalinger, Rebecca	Carleton University	BI5
Kapoor, Karuna	McGill University	
Kierzkowski, Daniel	Institut de recherche en biologie végétale - Université de Montréal	
Klein, Dan	Carleton University	
Kyriakidou, Maria	McGill University	BT2
Lai Dang, Qing	Lakehead University	
Lamont, Jack	McGill University	PS15
Le Dreff-Kerwin, Eric	University of Waterloo	
Liu, Ruoxi	McGill University	
Lumba, Shelley	University of Toronto	PL3
Macfie, Sheila	Western University	
MacNeill, Greg	University of Guelph	RM3
Madina, Hur	Université du Québec à Trois-Rivières	BI4
Mahmoud, Mohannad	McGill University	PS1
Manes, Nimrat	Carleton University and Ottawa Research and Development Centre	PS16
Marsolais, Frédéric	Agriculture and Agri-food Canada - London Research and Development Centre	RM5
Martel, Alexandre	University of Toronto	GR3
Martinez, Julian	McGill University	
Mayer, Boris	McGill University	SA3, GR3
Mehrpooyan, Sahar	University of Guelph	PS10
Micallef, Barry	University of Guelph	
Michell, Eric	Phyto Sciences Distribution	Sponsor
Miltenburg, Mary Gwen	Carleton University	PS12
Moffett, Peter	Université de Sherbrooke	
Movahed, Nooshin	McGill University	BI3
Murphy, Bridget	Western University	SA1
Nadeau, Katia	Bio-Rad Laboratories	Sponsor
Nelles, Hayley	University of Toronto	GR2
Ouellet, Francois	Université du Québec à Montréal	

Overbeek, Wiliam	McGill University	
Pérez Di Giorgio, Juliana	Université de Montréal	PS19
Priebe, Mark	Systems for Research Corp.	Sponsor
Rayon, Andrea	Laurentian University	SA2
Rivoal, Jean	Institut de recherche en biologie végétale - Université de Montréal	RM1, PS6
Rosenbaum, Phillip	McGill University	
Routier-Kierzkowska, Anne-Lise	Institut de recherche en biologie végétale - Université de Montréal	PL1, PD1
Rowland, Owen	Carleton University	SA6, BI5
Ryser, Peter	Laurentian University	SA2, PS8
Shao, Yang	McGill University	SA4
Singh, Aparna	Université du Québec à trois-Rivière	RM6
Stromvik, Martina	McGill University	BT2
Subramaniam, Rajagopal	Carleton University and Ottawa Research and Development Centre	PS12, PS16
Sun, Jiaqi	McGill University	PD4, BI3
Tamnanloo, Farzaneh	Concordia University	PS17
Theroux Rancourt, Guillaume	University of California Davis	PD5
Tremblay-Belzile, Samuel	Université de Montréal	
Tremblay, Frédérique	McGill University	
Tripathi, Rajiv	McGill University	GR4, GR5
Tyree, Melvin T		
Vadivel, Arun Kumaran Anguraj	Western University	RM4
Vaidya, Vanya	McGill University	PS7
Van Brenk, Jordan	Western University	
van Weringh, Anna	University of Toronto	BT4
Vonapartis, Eliana	University of Toronto	SA5
Wang, Suo-Min	Lanzhou University	SA6
Wang, You	University of Guelph	RM2
Wees, David	McGill University	
Wilkins, Olivia	McGill University	GR5, PS2, PS4, PS7, PS15
Zamil, Shafayet	McGill University	PD2
Zaro Sanchez, Anna	Universitat de Barcelona - Université de Montréal IRBV	GR1
Zhang, Yiyi	McGill University	
Zheng, Hugo	McGill University	PD4, BI3, BI4
Zheng, Yaping	McGill University	