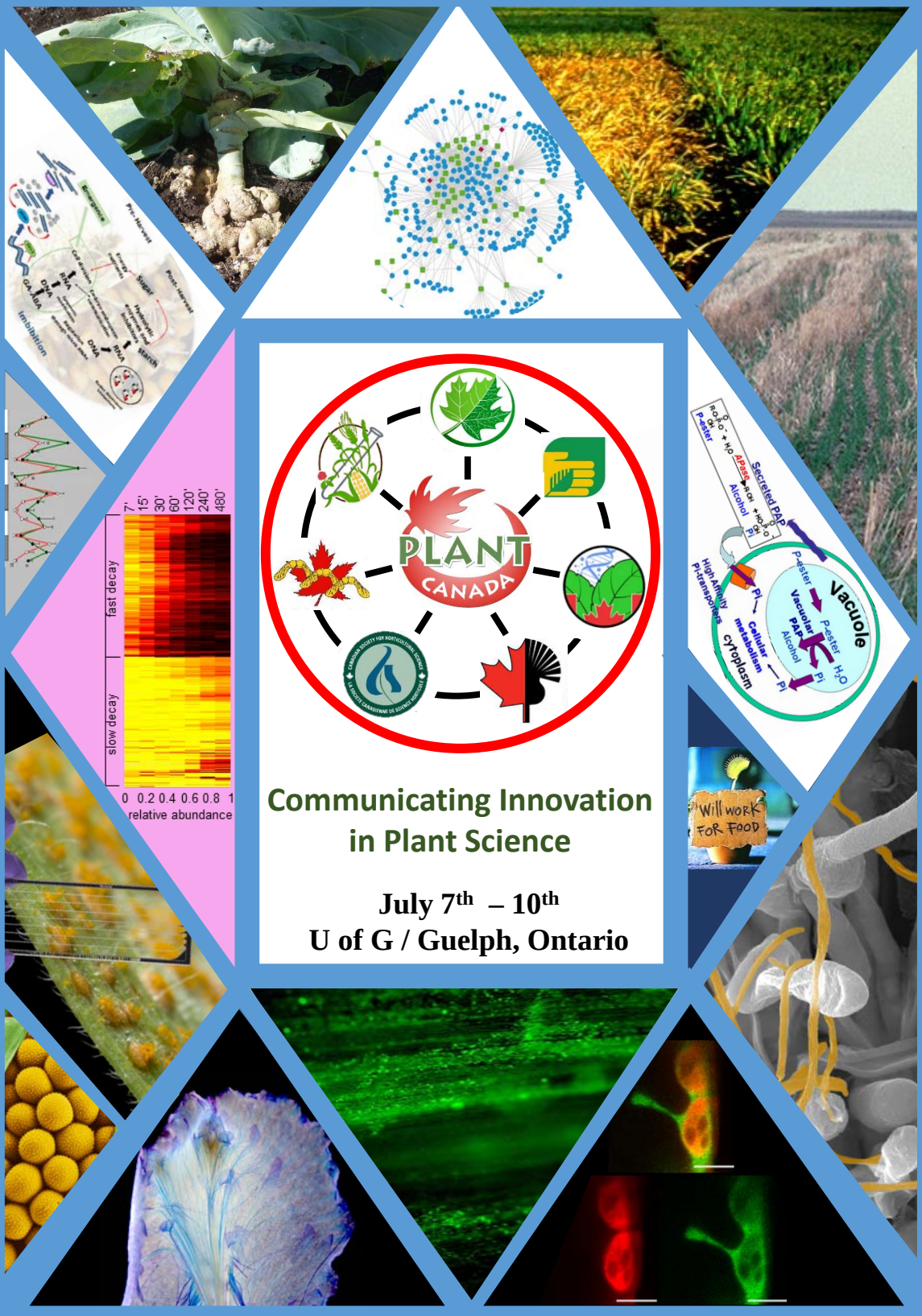
PLANT CANADA 2019



Communicating Innovation in Plant Science

July 7th – 10th

U of G / Guelph, Ontario

PROCEEDINGS

On the front cover:

1. An example of a gene regulatory network (figure courtesy of Siobhan Brady and Allison Gaudinier, University of California-Davis, USA).

2. A comparison between control and genome-edited rice in the field shows that genome editing of pathogen-responsive elements in rice SWEET (sugar transporter) genes leads to broad-spectrum resistance to bacterial blight (image courtesy of Bing Yang, University of Missouri, USA).

3. No-till winter wheat seeded into standing stubble for snow trapping, spring, north-central Saskatchewan (image courtesy of Brian Fowler, University of Saskatchewan, Canada).

4. Model showing that vacuolar and secreted purple acid phosphatases (PAPs) are upregulated by Pi-deprived plants to scavenge Pi from intra- & extracellular Pi-esters (figure courtesy of William Plaxton, Queen's University, Kingston, Ontario, Canada).

5. Hyphal network of *Pseudozyma flocculosa* developing around powdery mildew colonies (image courtesy of Richard Bélanger, Université Laval, Québec, Canada).

6. A stromule emerging from a chloroplast labeled with GFP fused to carbonic anhydrase (image courtesy of Maureen Hanson, Cornell University, New York, USA).

7. Far red light increases $^1O_2$ levels in corn; singlet oxygen was detected using SOSG reagent and fluorescence microscopy (image courtesy of Clarence Swanton, University of Guelph, Ontario, Canada).

8. Rhizoids on the underside of a cleared specimen of the liverwort, *Marchantia polymorpha* (image courtesy of Victor Jones, University of Oxford, UK).

9. (a) Yellow rust spores on a wheat leaf and a sequencing slide used to introduce a sample to a high-throughput genetic sequencer (image courtesy of Andy Davis, John Innes Centre, UK). (b) Yellow rust spores from inside a wheat leaf (SEM image courtesy of Kim Findlay, John Innes Centre, UK).

10. An RNA decay rate heat map (data courtesy of Leslie Sieburth, University of Utah, USA).

11. A model for the regulation of pre- and post-harvest grain germination in cereals (figure courtesy of Jaswinder Singh, McGill University, Montreal, Québec, Canada).

12. Clubroot on cabbage caused by *Plasmodiophora brassicae* Wor. (image courtesy of Mary Ruth McDonald, University of Guelph, Ontario, Canada).

*****The nitrate uptake rate over a 3-day period in tomato shows a circasemidian pattern in a 12 or 24 h photoperiod (data courtesy of Barry Micallef, University of Guelph, Ontario, Canada).

Welcome to the Meeting / Bienvenue au la Congrès 2019

Federation of Canadian Plant Science Societies

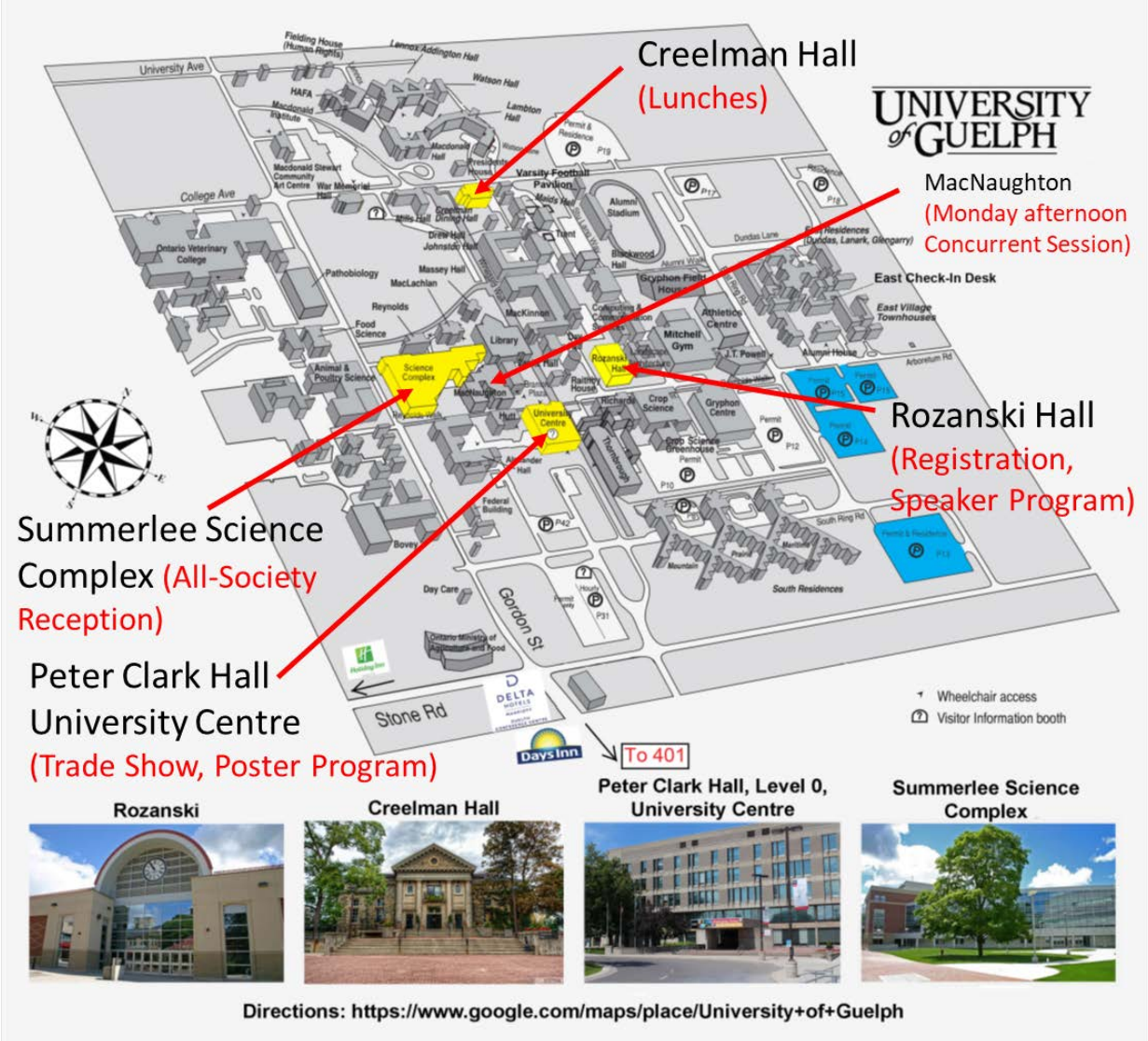
Fédération des Sociétés Canadiennes des Sciences Végétales

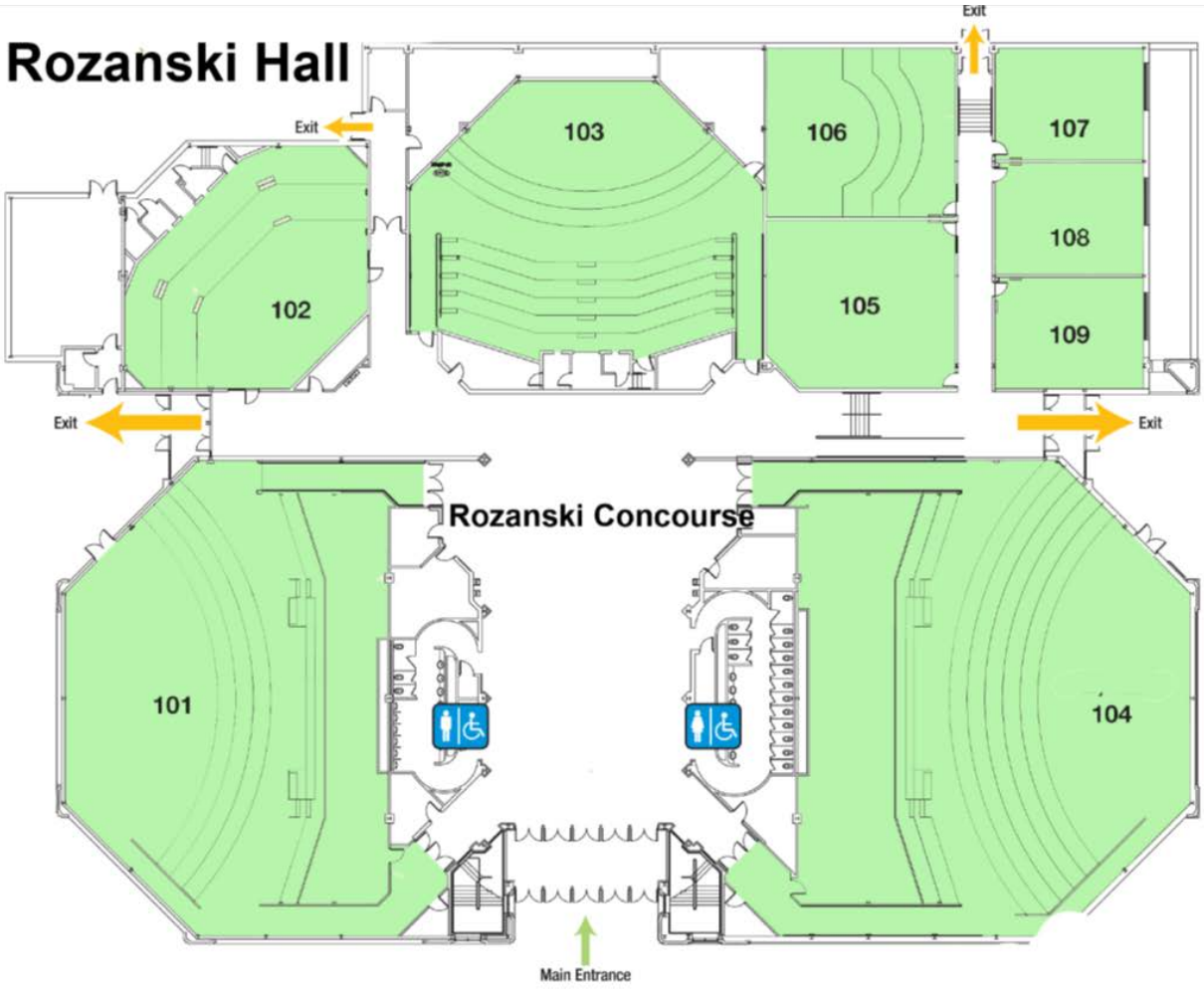
The University of Guelph
Guelph, Ontario, Canada

July 7th – July 10th, 2019

Table of Contents

Map of the University of Guelph

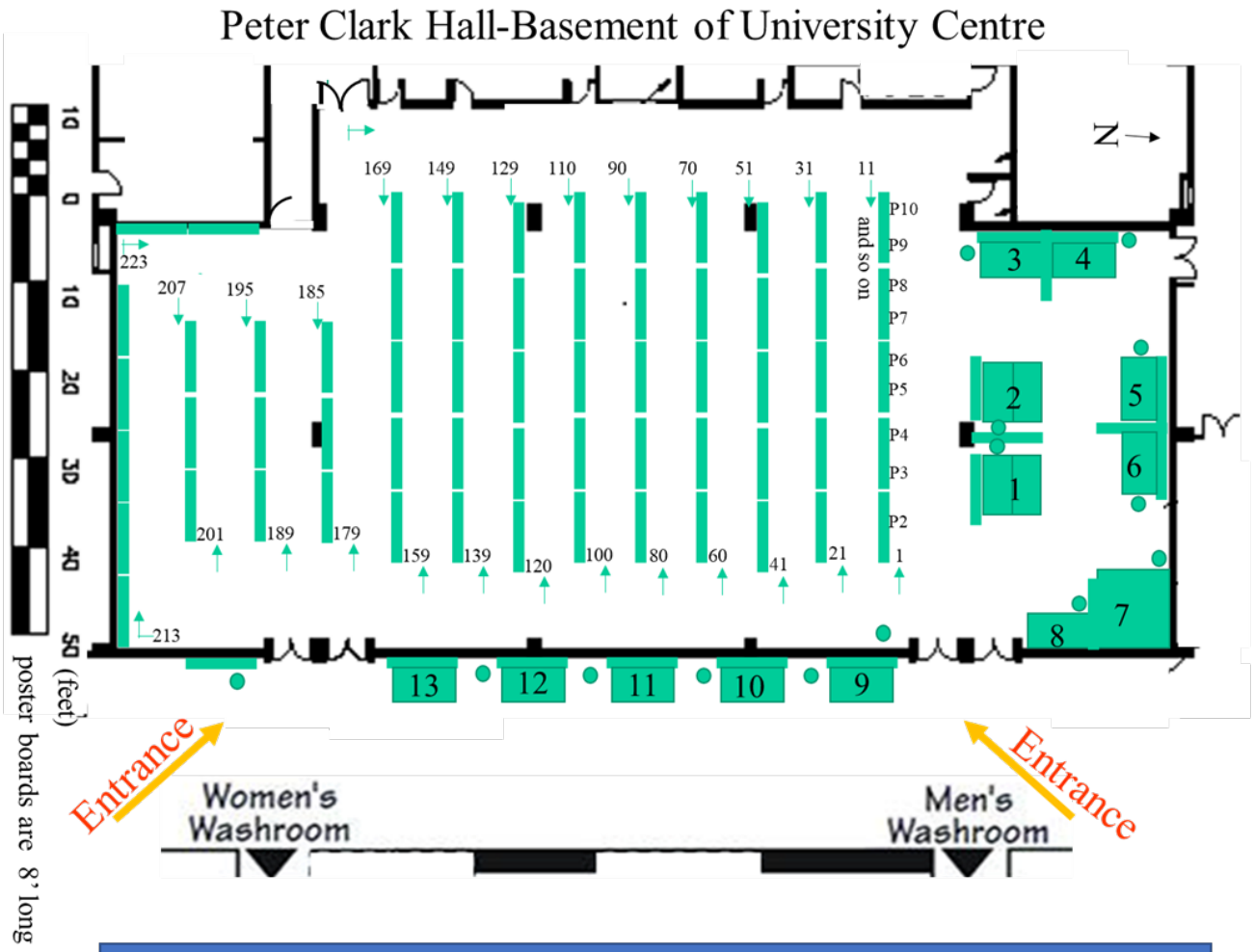




West side of building

Room Number	Capacity
Rozanski 101	400
Rozanski 102	120
Rozanski 103	200
Rozanski 104	600
Rozanski 105	60
Rozanski 106	40
Rozanski 107	30
Rozanski 108	30
Rozanski 109	30

Poster and Exhibitor Area for Plant Canada 2019



Exhibitors at Plant Canada 2019

- BASF-2
- Biochambers Inc.-3
- Canadian Science Publishing-4
- Cedarlane-8
- Conviron-7
- Hoskin Scientific-5
- Innotech Alberta-1
- LI-COR Biosciences-6
- New England Biolabs-12
- Norgen Biotek Corp.-10
- Platform Genetics-13
- Taylor and Francis Group-9
- We Vitro Inc.-11

THANK YOU to the **UNIVERSITY of GUELPH** for hosting & sponsoring Plant Canada 2019

Silver Sponsor ($5,000)

The University of Guelph, Office of Research, oversees a $146 million research enterprise across seven colleges, our regional campus at Ridgetown, 15 research stations and the University of Guelph/Ontario Ministry of Agriculture, Food and Rural Affairs partnership. We are committed to supporting the research programs of University of Guelph faculty across all disciplines.

From the three founding Colleges: the Ontario Veterinary College (1862), the Ontario Agricultural College (1874) and the MacDonald Institute (1903), the University of Guelph, established in 1964, has grown to be one of Canada's top comprehensive universities. Dedicated faculty and staff are at work making communities, environment, food and health better.

https://www.uoguelph.ca/research/

Bronze Sponsors ($2,500 each)

The Ontario Agricultural College (OAC) of the University of Guelph is internationally renowned for its research, teaching and knowledge extension. Our community has a strong sense of shared purpose: To Improve Life by inspiring leaders, generating knowledge and creating innovative solutions for food, agriculture, communities and the environment.
https://www.uoguelph.ca/oac

****

Canada's largest and most diverse applied plant biology department. We are a research-intensive department within the Ontario Agricultural College dedicated to teaching, research and service related to horticultural crops, turfgrass, landscape species and field crops. We provide hands-on learning opportunities from nationally and internationally recognized experts to students at the diploma, undergraduate and graduate levels.
https://www.plant.uoguelph.ca/

****

https://www.uoguelph.ca/cbs/

https://www.uoguelph.ca/mcb/

The College of Biological Science is a globally-recognized academic faculty with a mission to expand the understanding of life, from DNA to cells to complex ecosystems. It produces intrepid and interdisciplinary research in a student-centred learning environment that encourages and promotes comprehensive understanding of the systems that govern life.

THANK YOU to our **INDUSTRY SPONSORS** for making Plant Canada 2019 possible

GOLD Supporter ($6000)

InnoTech Alberta

SILVER Supporter ($3000-$5999)

- BASF
- BioChambers
- Canadian Science Publishing
- Conviron
- Hoskin Scientific
- Li-Cor Inc
- Regent Instruments
- Western Grains Research Foundation

Bronze Supporter ($1000-$2999)

- Ag West Bio
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- Corteva Agrisciences
- CropLife
- Fisher Scientific
- Grain Farmers of Ontario
- Koch Agronomic Services
- Medicago
- Performance Plants
- Syngenta
- Vineland Research and Innovation Center

InnoTech Alberta https://innotechalberta.ca/

InnoTech Alberta offers you access to research talent, technical expertise, and unique facilities that can help accelerate technology development that serves both the private and public sector.

Sponsor of Monday Afternoon Session 2:

Cannabis Production and Disease Management

Presented in MacNaughton r. 113

Please Visit Innotech at Booth #1

BASF https://www.basf.com/ca/fr.html

Sponsor of the Wednesday morning Coffee Break

Please Visit BASF at Booth # 2

****

BioChambers Inc https://www.biochambers.com/

Sponsor of the Tuesday afternoon Coffee Break

Please Visit Biochambers at Booth # 3

Canadian Science Publishing https://www.nrcresearchpress.com/

Canadian Science Publishing

Sponsor of the Monday morning Coffee Break

Please Visit CSP at Booth # 4

****

Conviron http://www.conviron.com/ Please Visit Conviron at Booth # 7

Sponsor of the Monday afternoon Coffee Break

Hoskin Scientific https://www.hoskin.ca/

Sponsor of

Poster Session #2

Please Visit Hoskin Scientific at Booth # 5

****

LI-COR Biosciences https://www.licor.com/

Sponsor of Poster Session #1

Please Visit LI-COR at Booth # 6

Western Grains Research Foundation https://westerngrains.com/

Sponsor of the Tuesday morning Coffee Break

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Regent Instruments http://regent.qc.ca/

Sponsor of the Wednesday afternoon Coffee Break

Ag West Bio https://www.agwest.sk.ca/

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Cargill https://www.cargill.ca/en/home

****

Cedarlane https://www.cedarlanelabs.com/

Please Visit Cedarlane at Booth # 8

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Corteva Agriscience

https://www.corteva.ca

CropLife
https://croplife.ca/fr/

https://croplife.ca

****

Fisher Scientific https://www.fishersci.ca/ca/fr/home.html

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Grain Farmers of Ontario https://gfo.ca/

****

Koch Agronomic Services https://kochagronomicservices.com/

Medicago https://www.medicago.com/fr/

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Performance Plants http://www.performanceplants.com/

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Syngenta https://www.syngenta.ca/

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Vineland Research and Innovation Centre https://www.vinelandresearch.com/

Federation of Canadian Plant Science Societies
Fédération des sociétés canadiennes des sciences végétales

Plant Canada President's Message

Greetings from Plant Canada

On behalf of the Board of Directors of Plant Canada, I am pleased to invite you to attend the **Plant Canada 2019 meeting with the theme communicating innovation in plant science**, to be held from July 7-10, 2019 in Guelph, Ontario, Canada. The conference will include a keynote speech, plenary lectures, symposia, workshops, many concurrent oral sessions and poster presentation sessions. We are expecting about 600 delegates, so it will be a great meeting for networking and developing collaborations among the members of seven plant science societies of Plant Canada.

About Plant Canada

Plant Canada - Federation of Canadian Plant Science Societies, a not-for-profit corporation, is an umbrella organization that seeks to bring together researchers, educators, extension personal, postdoctoral fellows and students in plant science and related disciplines in Canada. The purposes of Plant Canada are: a. to organize and sponsor regular, effective scientific meetings and workshops under a national umbrella for plant science and related disciplines in Canada, b. to operate and maintain a strong communication network among Member Societies and their individual members, and c. to be a strong and effective force for public education and advocacy in plant and related sciences in Canada and globally. Plant Canada organizes Plant Canada conferences every four years.

Plant Canada Incorporation

Although founded in 2000, Plant Canada - Federation of Canadian Plant Science Societies (referred to as Plant Canada through the document) was incorporated as a Not-for-profit corporation on July 31, 2015 under the new Canada Not-for-profit Corporations Act.

Plant Canada Member Societies

As of July 2019, Plant Canada membership includes seven Canadian plant societies: Canadian Association for Plant Biotechnology (CAPB), Canadian Botanical Association (CBA), Canadian Phytopathological Society (CPS), Canadian Society of Agronomy (CSA), Canadian Society for

Horticultural Science (CSHS), Canadian Society of Plant Biologists (CSPB) and Canadian Weed Science Society (CWSS).

2015-19 Plant Canada Highlights

- Plant Canada was incorporated as a federal corporation on July 31, 2015.
- Initiated first steps after incorporation and developed PC by-laws.
- Completely redesigned Plant Canada website
- Fostered collaboration among Canadian Plant Science societies
- Contributed to the Canadian Plant Health Network consultations
- Each year sponsored a Plant Canada student presentation award
- Organized the Plant Canada 2019 meeting with a theme of Communicating Innovation in Plant Science from July 7- 10, Guelph, ON.

Plant Canada Officers and Board of Directors 2018-19

Dr. Deena Errampalli

PC President

Dr. John Markham

PC Vice President

Dr. Diane Edwards

PC Secretary

Dr. Gayle Jesperson

PC Treasurer

Dr. Shahrokh Khanizadeh

PC Past President

The Plant Canada Board of Directors (2018-19) is made up of two representatives from each of the seven-member societies (normally the president, Vice president, past president or president elect):

Dr. Rima Menassa

Canadian Association for Plant Biotechnology

Dr. Abdelali Hannoufa

Canadian Association for Plant Biotechnology

Dr. Art Davis

Canadian Botanical Association

Dr. John Markham

Canadian Botanical Association

Dr. Lone Buchwaldt

Canadian Phytopathological Society

Dr. Barry Saville

Canadian Phytopathological Society

Dr. Helen Booker Canadian Society of Agronomy

Dr. Jaswinder Singh

Canadian Society of Agronomy

Dr. Karen Tanino

Canadian Society for Horticultural Science

Dr. Valérie Gravel

Canadian Society for Horticultural Science

Dr. Geoffrey Wasteneys Canadian Society of Plant Biologists

Dr. Daphne Goring

Canadian Society of Plant Biologists

Dr. Rory Degenhardt

Canadian Weed Science Society

Dr. David Clements

Canadian Weed Science Society

Since the Botany 2015 meeting in Edmonton, Alberta, your Plant Canada board has met four times a year for the first three years. During the 2018-19, the Board met monthly to organize the Plant Canada 2019 meeting. In between, individual board and committee members have been heavily involved in meetings, as required. Although the Plant Canada member societies meet once every four years at the Plant Canada meeting, the individual societies held their society meetings annually either alone or jointly with other Plant Canada member societies or other plant science societies.

Plant Canada's global involvement

Plant Canada is a member of the Global Plant Council, which supports plant science internationally. Plant Canada was a founding member of the Global Plant Council. In 2015, 2016, 2017 and 2019 the Plant Canada President attended the GPC annual meetings and represented Plant Canada. Deena Errampalli, President of Plant Canada was elected as the Treasurer of GPC in 2017.

Thank you to PC Board members

On behalf of the Plant Canada, I wish to express my thanks to the 2018-19 and the past Board of Directors and committees for their time and energy on the Board. Their hard work has enabled us to move the objectives of the Plant Canada from 2015-2019. The contributions made by Diane Edwards (PC Secretary; 2014-2019) Shahrokh Khanizadeh (Immediate Past President; 2015-19), John Markham (PC Vice president; 2015-19), and Deena Errampalli (PC President; 2015-2019) who will be completing their term are gratefully acknowledged and your dedication to Plant Canada is much appreciated.

Plant Canada meetings:

By joining forces of its seven-member societies, the Plant Canada offers one large meeting every four years, with numerous invited speakers and other events like teaching workshops, presentations from NSERC, etc. It further creates a loud voice and maintains a strong communication network and collaboration amongst Member Societies and their individual members nationally. Six societies participated in the last five PC meetings organized and lead by one or more of its member societies (with input from all member societies). In 2015, CAPB became a member of Plant Canada.

*List of Plant Canada meetings***:**

Plant Canada 2000 meeting led by CBA and CSPB in London, Ontario

Plant Canada 2003 meeting lead by CBA in Antigonish, Nova Scotia,

Plant Canada 2005 meeting lead by CSPP in Edmonton, Alberta,

Plant Canada 2007 meeting lead by CPS in Saskatoon, Saskatchewan,

Plant Canada 2011 meeting lead by CSA and CSHS in Halifax, Nova Scotia

Plant Canada 2015 Meeting led by CBA and was held jointly with Botanical Soc. of America in Edmonton, Alberta

Current meeting:

Plant Canada 2019 Meeting lead by CSPB in Guelph, Ontario

The current meeting would not have been possible without the hard work and dedication of **Plant Canada 2015 Meeting Scientific Organizing Committee:** Geoffrey Wasteneys, chair

(Canadian Society of Plant Biologists), Abdelali Hannoufa (Canadian Association for Plant Biotechnology), Art Davis (Canadian Botanical Association), Lone Buchwaldt (Canadian Phytopathological Society), Jaswinder Singh (Canadian Society of Agronomy), Valérie Gravel (Canadian Society for Horticultural Science), Rory Degenhardt (Canadian Weed Science Society); **Local Arrangements Committee:** Barry Micallef (Chair) and **Fundraising Committee**: Robert Mullen and Barry Micallef (Co-chairs), Plant Canada 2019 meeting website webmaster: Michael Stasiak (CSPB), and the **Plant Canada Board of Directors.** Plant Canada acknowledges **the generous contributions from our sponsors** for Plant Canada 2019 meeting in Guelph, Ontario.

Join Plant Canada

Any society or organization can become a member of Plant Canada, which is free, as long as the organization's interests are related to plant science disciplines in Canada. The applications can be submitted to the Plant Canada Board for consideration. We believe that collectively we can advance plant science in Canada.

In closing, it has been a busy, challenging and rewarding four-year term for me. I thank my former employer, Agriculture and Agri-Food Canada for allowing me to contribute to Plant Canada as its President from 2015 to until my retirement in April 2018. Special thanks to my husband, Dr. Andrew Piggott, for his patience and encouragement during my four-year term as the President of Plant Canada. I offer a heartfelt thank you to the seven Plant Canada member societies for giving me the opportunity to serve the organization and to represent you nationally and internationally. I hope you feel that I have served the Plant Canada well.

Respectfully submitted,

Dr. Deena Errampalli

President, Plant Canada (2015-19)

For more information on Plant Canada visit our

website at http://www.plantcanada.ca/
Facebook: https://www.facebook.com/PlantCanada/
Twitter: https://twitter.com/plantcanada

Welcome Address from the Scientific Program Organizing Committee

On behalf of the Scientific Program Organizing Committee, I welcome you to Plant Canada 2019. All seven Plant Canada member Societies and Associations participated in a planning process that began over two years ago. One goal was to put together a program reflecting our diverse interests, while highlighting excellence that will be of broad interest to all attendees. I believe that we have achieved that goal.

The theme Plant Canada 2019, *Communicating Innovation in Plant Science* reflects the scientific achievements that will be communicated by our twelve invited plenary speakers, and will be the focus of a keynote lecture by media personality Dan Riskin, who will provide insights into effective communication of the work we do to the broader community. How we communicate the work we do as plant scientists is of critical importance, particularly these days, as we face serious environmental challenges. It is clear that our research activities have enormous potential for addressing these challenges. Convincing governments and funding agencies to prioritize what we do, while heading off misconceptions surrounding and opposition to the biotechnologies we rely on, requires a concerted effort across the fields of plant biology.

In addition to the twelve plenary lectures, the Plant Canada 2019 program includes 212 oral presentations in the concurrent sessions, and more than 215 poster presentations. Several workshops, information sessions pre-conference tours and field trips will complement the scientific program. Be sure to attend the trade displays of our sponsors in the exhibit hall, as well as the sponsor information session on Sunday afternoon.

A huge team effort had gone into organizing the scientific program and coordinating the events of this meeting. Along the way, we have been guided by the Plant Canada President, Deena Errampalli, and assisted by the Plant Canada Secretary Diane Edwards. The event would be impossible without huge efforts from the Local Arrangements Committee led by Barry Micallef, and the financial support of our many corporate and academic sponsors, the efforts of the fundraising committee, which was chaired by Robert Mullen and Barry Micallef, and finally the University of Guelph. As President of this year's host society for the 4-yearly Plant Canada meeting, I would also like to extend my gratitude to members of the CSPB executive and communications committee for the extra workload they endured in the run up to this meeting.

Thank you for attending, and I hope you will be inspired at Plant Canada 2019.

Geoffrey Wasteneys

Chair, Scientific Program Organizing Committee for Plant Canada 2019

Plant Canada 2019 Organizational Committees

Scientific Program Organizing Committee

CSPB & Committee Chair: Geoff Wasteneys, UBC geoffrey.wasteneys@ubc.ca
CSHS: Valérie Gravel, McGill U valerie.gravel@mcgill.ca
CSA: Andrew Burt, AAFC Brandon andrew.burt@canada.ca
CWSS: Rory Degenhardt, Corteva Agroscience Edmonton RDegenhardt@dow.com
CPS: Lone Buchwaldt, AAFC Saskatoon lone.buchwaldt@canada.ca
CAPB: Abdelali Hannoufa, AAFC London Abdelali.Hannoufa@AGR.GC.CA
PC & *Ex officio*: John Markham, U Manitoba John.Markham@umanitoba.ca
PC & *Ex officio*: Deena Errampalli, Plant Canada, deenaerrampalli@bell.net

Fund Raising Committee

CSPB & Co-Chair: Robert Mullen, U Guelph rtmullen@uoguelph.ca
CSPB & Co-Chair: Barry Micallef, U Guelph bmicalle@uoguelph.ca
CBA: Art Davis, U Saskatchewan art.davis@usask.ca
CPS: Lone Buchwaldt, AAFC Saskatoon lone.buchwaldt@canada.ca
CSHS: Karen Tanino, U Saskatchewan karen.tanino@usask.ca,
Youbin Zheng, U Guelph yzheng@uoguelph.ca
CAPB: Rima Menassa, AAFC London rima.menassa@canada.ca
CSA: Rigas Karamanos, Koch Fertilizer Canada, Calgary Rigas.Karamanos@kochind.com
CWSS: Matthew Underwood, Syngenta Canada, Plattsville Matthew.Underwood@syngenta.com
PC: Gayle Jesperson, Plant Canada Treasurer, gdjesperson@gmail.com

Local Arrangement Committee

CSPB & Committee Chair: Barry Micallef, U Guelph bmicalle@uoguelph.ca
CPS: Lone Buchwaldt, pre-conference tour organizer, AAFC Saskatoon lone.buchwaldt@canada.ca
CBA: Mihai Costea, pre-conference tour organizer, WLU mcostea@wlu.ca
CSPB: Bernie Grodzinski, controlled-environment facility tour organizer, U Guelph bgrodzin@uoguelph.ca
CAPB: Max Jones, audiovisual, U Guelph amjones@uoguelph.ca
CSPB: Mina Kaviani, postdoc rep, U Guelph mkaviani@uoguelph.ca
CSA: Istvan Rajcan, pre-conference tour organizer, U Guelph irajcan@uoguelph.ca
CSHS: Sara Stricker, grad student rep, U Guelph strickes@uoguelph.ca
CSPB: Ian Tetlow, poster logistics, U Guelph itetlow@uoguelph.ca
CSHS: Laura Van Eerd, pre-conference tours organizer, U Guelph-Ridgetown Campus lvaneerd@uoguelph.ca

Individual reports

from the member societies of Plant Canada

Plant Canada 2019 is a joint meeting of the following seven scientific societies from Canada:

Canadian Association for Plant Biotechnology

Canadian Botanical Association

Canadian Phytopathological Society

Canadian Society of Agronomy

Canadian Society for Horticultural Science

Canadian Society of Plant Biologists

Canadian Weed Science Society

Canadian Association for Plant Biotechnology

The Canadian Association for Plant Biotechnology was founded in 1970-1971 as the International Association for Plant Biotechnology Canada (IAPB Canada). The association went through multiple name changes (in 1998 and 2006), and in 2015, renamed as **Canadian Association for Plant Biotechnology (CAPB)**. Our goals are to promote interaction among Plant Biotechnology researchers in Canada, liaise with the International Association of Plant Biotechnology, advocate for Plant Biotechnology research, bridge the gap between academia/basic research and industry and serve as a contact point for Plant Biotechnology-related information in Canada. CAPB provides a forum of communication for its members to further the development of Plant Biotechnology in Canada. It also provides an excellent opportunity for new collaborations among industry leaders and researchers, helping to connect people who conduct plant biotechnology research. The association holds biennial meeting in Canada. More information can be found at https://www.canadianplantbiotech.ca/

CAPB Executives (2019-2020)

President, National Correspondent and Government Liaison	Dr. Rima Menassa
Vice-President, Deputy National Correspondent and Secretary	Dr. Abdelali Hannoufa
Director of Communication	Dr. Dominique Michaud
Academic and Industry Liaison	Dr. Sangeeta Dhaubhadel
Membership	Dr. Susanne Kohalmi
Treasurer	Dr. Pankaj Kumar Bhowmik
PostDoc and Student Affairs	Mr. Dinesh Adhikary
Webmaster	Dr. Gary Tian
Immediate past president as Observer	Dr. Yafan Huang

More information on Executive Committee can be found at
https://www.canadianplantbiotech.ca/iapb-canada-executive-committe/

CAPB at Plant Canada 2019 Meeting

Guelph, ON

Co-sponsored Symposia

- Genome editing enables disease resistance in plants - **Dr. Bing Yang**
- Improving photosynthesis in C3 plants- **Dr. Maureen Hanson**

CAPB-led concurrent sessions and workshops

- CAPB1: Bioproducts production in plants
- CAPB2: Genome editing and molecular plant improvement
- CAPB3: Genome editing workshop

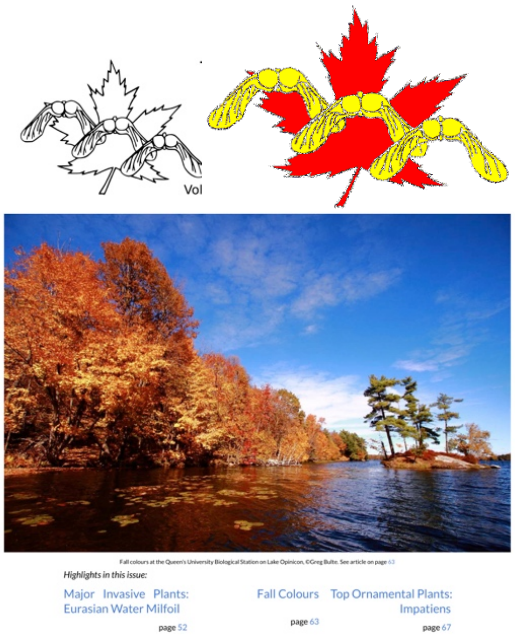
CAPB and Plant Canada Business and Social Meetings

- Executive meeting on July 7 at 4:00-5:30 pm
- **Pioneering & Distinguished Canadian Plant Biotechnologist Award winner, Dr. Margie Gruber**, will be receiving the award on July 7 at 6:45-7:30 pm
- Annual General Meeting on July 8 at 11:15 am-1:00 pm
- CAPB co-sponsored Student Social for student members on July 8 at 8:30-10:30 pm
- Two oral and two poster presentation awards for students will be presented on July 10 at 12:30-1:30 pm
- Travel awards for students will be presented on July 10 at 12:30-1:30 pm

Canadian Botanical Association
L'Association Botanique du Canada

The CBA-ABC

- provides a national organization for botanists in Canada and encourages the participation of professional botanists working in universities, colleges, schools, government and industry, as well as interested students, technicians and amateurs
- represents Canadian botany and botanists in the national and international arenas and responds rapidly and professionally on matters that are of concern to Canadian botanists
- provides a national annual meeting for botanists at which there are opportunities to give papers, attend symposia, participate in field trips, and to meet in smaller, special interest sections that reflect the main areas of botanical activity in Canada
- provides means for studying issues that particularly concern botanists, and provides national support to certain activities
- regularly publishes a bulletin that provides news of botany and botanists in Canada



Join us in 2020 for our Annual Meeting!!

At Université du Québec en Abitibi-Témiscaminque (UQAT)
in Rouyn-Noranda, Québec

Theme: ***Heading North - Botany in Canada's Boreal Biomes***
May 31 – June 4, 2020

Plenary Symposium: "Botany Heading North" plus Section Symposia, Spring Flowers,
and a Field Trip to the Research Forest and Station

Contributed Papers including Student Talks and Posters,
plus up to 5 post-conference field trips

ANNUAL AWARDS PROVIDED BY CBA - ABC

Each year, the Canadian Botanical Association/L'Association Botanique du Canada provides awards to botanists studying in Canada and/or to Canadian botanists studying abroad. CBA-ABC offers a number of awards to support students investigating botanical topics.

STUDENT AWARDS:

- for papers published within the past year ($500-1000)
Porsild-Consaul Award for the best paper in systematics and phytogeography.
Stan Rowe Award for the best paper in plant ecology.
Taylor A. Steeves Award for the best paper in plant development or structure.
Luella Weresub Award for the best paper in mycology or lichenology.

- for best presentations at the Annual Meeting ($500)
Lionel Cinq-Mars Award for the best oral presentation.
Iain and Sylvia Taylor Award for the best poster presentation.

- for travel to participate at the Annual Meeting ($150-500)
John Macoun Travel Bursary for graduate students.
Keith Winterhalder Travel Award for undergraduate students.

- for research ($1300)
Laurie Consaul Northern Research Scholarship for research in Canada's north.

MAJOR AWARDS:

George Lawson Medal for excellence in contributions to Canadian botany.

Mary Elliott Service Award for meritorious service to CBA-ABC.

Magister Award for excellence in teaching plant science within Canada.

For further information about CBA-ABC activities and awards,
please visit **www.cba-abc.ca**

CBA-ABC Board of Directors for 2018-2019

President - Dr. Julian Starr (University of Ottawa)
President-Elect - Dr. Nicole Fenton (Université du Québec en Abitibi-Témiscamingue)
Past-President – Dr. Art Davis (University of Saskatchewan)
Vice-President / Liaison for Plant Canada – Dr. John Markham (University of Manitoba)
Secretary – Ms. Deborah Metsger (Royal Ontario Museum)
Treasurer – Dr. Shelley Hepworth (Carleton University)
Editor, *CBA-ABC Bulletin* – Dr. Tyler Smith (Agriculture & Agri-Food Canada, Ottawa)
Webmaster – Dr. Zoe Panchen (University of British Columbia)
Directors – Dr. Richard Caners (Royal Alberta Museum) (west)
Ms. Nadia Cavallin (Royal Botanical Gardens) (east)
Dr. Bruce Ford (University of Manitoba) (west)
Dr. Julissa Roncal (Memorial University of Newfoundland) (east)
Dr. Patrick von Aderkas (University of Victoria) (west)
Student Representative – Mr. Dylan Johnston (University of Saskatchewan) (west)
Student Representative – Ms. Kirsten Reid (Wilfrid Laurier University) (east)

Executive Assistant – Ms. Vanda Wutzke (Aberdeen, Saskatchewan)

CBA-ABC Section Chairs for 2018-19

DEVELOPMENT SECTION
Co-Chairs: Dr. Simon Chuong (University of Waterloo)
Dr. Moira Galway (Saint Francis Xavier University)

ECOLOGY SECTION
Co-Chairs: Dr. André Arsenault (Atlantic Forestry Centre)
Dr. Nicole Fenton (Université du Québec en Abitibi-Témiscamingue)

MYCOLOGY SECTION
Co-Chairs: Dr. Shannon Berch (British Columbia Ministry of the Environment)
Dr. Hugues Massicotte (University of Northern British Columbia)

SYSTEMATICS AND PHYTOGEOGRAPHY SECTION
Co-Chairs: Dr. Geraldine Allen (University of Victoria)
Ms. Deborah Metsger (Royal Ontario Museum)

TEACHING SECTION
Co-Chairs: Dr. Adam Brown (University of Ottawa)
Dr. Martha Mullally (Carleton University)

Canadian Phytopathological Society / La Société Canadienne de Phytopathologie

The Canadian Phytopathological Society (CPS) is a scientific society for plant pathologists which was formed in 1929. The objective was to encourage research, education, and the dissemination of knowledge on the nature, cause, and control of plant diseases. The society has more than 350 members in Canada and abroad. Its members have expertise in all facets of plant pathology from applied field research to investigations of host-pathogen interactions at the molecular level. The membership includes graduate students, postdoctoral fellows, research associates, technical assistants, extension plant pathologists, research scientists and university professors. In addition, several grower organizations and private companies are sustaining members.

A Board of Directors and several committees guide the society's work. For 2018-2019 the CPS Board consists of

President	Dilantha Fernando
President Elect	Barry Saville
Vice President	Lone Buchwaldt
Past President	Denis Gaudet
Secretary	Tom Fetch
Treasurer	Kenneth Conn
Membership Secretary	Vikram Bisht
CJPP Editor in Chief	Zamir Punja / Steven Strelkov
Senior Director at Large	Phillippe Tanguay
Junior Director at Large	David Joly

The CPS is responsible for publication of the *Canadian Journal of Plant Pathology* (CJPP) through Taylor and Francis. This year, the CJPP's editorial board was enhanced by adding more Section and Associate Editors to ease the flow of manuscripts through the review process. The CPS is also considering whether to publish all papers as Open Access. The society publishes a quarterly Newsletter and maintains a web site https://phytopath.ca/. This year marks the 100th Anniversary for publication of the Canadian Plant Disease Survey (CPDS). Past surveys are assessable through the CPS web site, but in the future, they will be published in the CJPP. The society presents several types of awards including 'Award for Outstanding research', 'Outstanding young scientist award' and several awards for graduate students.

To promote communication among plant pathologists, CPS members have the opportunity to meet nationally once a year. In addition, there are eight regional societies that also meet annually. Furthermore, the CPS collaborates with the American Phytopathological Society (APS) and the British Society of Plant Pathology (BSPP) primarily by amalgamation of annual meetings and funding of invited speakers. This year, the CPS will celebrate its 90th Anniversary during the Plant Canada meeting.

The following highlights CPS' participation during Plant Canada

Sunday July 7

CPS Field Tour #4 Horticultural and Agricultural plant pathology on farms from University of Guelph to Niagara, from 8 AM to 5 PM organized by Dr. Albert Tenuta, OMAFRA.

Monday July 8

CPS concurrent sessions.

CPS President's Reception by Invitation, 7:30-9:30 PM at Delta Hotels, Guelph Conference Centre.

Tuesday July 9

CPS concurrent sessions.

CPS Annual General Meeting 11:15 AM – 1:00 PM. Please pick up a provided bagged lunch and bring it to the meeting.

CPS 90th Anniversary and Awards Banquet at Delta Hotels, Guelph Conference Centre.

Wednesday July 10

CPS/CSHS Plenary Session with three invited speakers Dr. Mary Ruth McDonald, University of Guelph, Dr. Richard Bélanger, Université Laval and Dr. Diane G.O. Saunders, John Innes Centre, UK.

Canadian Society of Agronomy
La Société Canadienne d'Agronomie

agronomycanada.com | @agronomycanada

The Canadian Society of Agronomy (CSA) is dedicated to enhancing cooperation and coordination among agronomists, recognizing significant achievements in agronomy and providing the opportunity to report and evaluate information pertinent to agronomy in Canada.

Attending annual meetings, volunteering for service, and contributing to our society journal help our members to network and connect to fellow agronomists. CSA membership stands at 135 as of May 1, 2019.

The CSA offers a robust yearly awards and recognition program.

Ali Navabi Student Travel Award

The Student Travel Awards were established in 2013 to encourage student attendance at the CSA Annual Meetings and is available to any graduate student CSA member. The award is $500 and up to 4 are awarded annually. Students participate in oral and poster presentations at the AGM Conference.

Recently, CSA board named the travel awards after Dr Ali Navabi's name in his memory and contributions to the society.

Graduate Student Pest Management Award

The CSA Pest Management Award of $500 is made available annually to qualified graduate students enrolled at Canadian universities with research programs relevant to pest management. The award comes with a travel grant of up to $1,000 to allow the successful applicant to attend and present at the CSA annual conference.

Graduate Student Presentation and Poster Awards

The CSA provides a number of awards for the best oral and poster presentations given by student members. These awards are given to acknowledge the contributions that graduate students make to the society and to encourage excellence in graduate student research and presentation. The awards range from $250 - $700.

Early Career Agronomist

The Early Career Agronomist Award is given to a candidate who has made an outstanding contribution to Agronomy, is within 10 years of the start of his/her career or within 10 years of earning his/her last degree. The award includes $500 and an inscribed plaque.

CSA Fellow Award

The CSA awards a Fellowship to a member of the CSA with at least 10 years membership and a distinguished record of service in agronomy. The recipient is named “Fellow of the Canadian Society of Agronomy” and is presented with $500 and an inscribed plaque at the AGM.

Best Paper Award

The CSA offers an award each year for the best agronomy-related paper published that year in The Canadian Journal of Plant Science (CJPS). This award is based on reviews by the agronomy Editor of CJPS and a panel of CSA members. The award is an honorarium of $500 plus and invitation to give an oral presentation of the best paper at the CSA AGM.

Distinguished Agronomist

The Distinguished Agronomist Award is given to a duly nominated member of 15 years or more of regular membership who is nearing retirement (or is retired) and has a distinguished record of service to the CSA and in the field of agronomy. The award includes an inscribed plaque and $500.

2018 award winners were Dr. Yousef Papadopoulos (Distinguished Agronomist), Dr. Tarlok Singh Sahota (CSA Fellow Award), Afsaneh Sedaghatkish (Pest Management Award) and Dr. Bill Deen (Best Paper in CJPS for previous year). 2018 Travel Awards recipients included Amy Mangin (University of Manitoba), Caleb Niemeyer (University of Guelph), Cameron Ogilvie (University of Guelph) and Asfaneh Sedaghatkish (University of Guelph). The Student Oral and Poster Competition was judged by Dr. Mumtaz Cheema, Dr. Jaswinder Singh and Dr. Sheri Strydorst. Judges assessed 5 student presentations for their scientific merit, content and presentation style. In the category of 15-minute oral presentations, first prize ($750) was awarded to Cameron Ogilvie MSc. Student at the University of Guelph, second prize ($500) was awarded to Caleb Niemeyer, MSc. Student at the University of Guelph.

In the category of Poster/5-Minute Rapid Oral presentations, first prize ($500) was awarded to Amy Mangin, PhD student at the University of Manitoba and the Second prize ($250) was awarded to Amy Mangin.

The Canadian Journal of Plant Science (CJPS) is our society journal and members participate by contributing manuscripts, providing peer review, and serving on the editorial board. The CJPS is supported by three societies: the CSA, the Canadian Weed Science Society (CWSS), and the Canadian Society of Horticultural Sciences (CSHS). The board was restructured in 2018 and now has three technical editors (TE), Dr. Bourlaye Fofana (CSHS), Dr. B.W. Thomas (CSA) and Dr. Amit Jhala (CWSS). The goal when recruiting TE's is to ensure the representation of all three societies and corresponding disciplines/expertise. The Editor-in-Chief is Dr. Brian Beres.

CSA members are eligible for a deeply discounted rate for The Canadian Journal of Plant Science (CJPS) and the Canadian Journal of Soil Science (CJSS). The regular rate for CJPS or CJSS is $526 for the electronic version and $634 for print and electronic. CSA Members pay $50.00 for the electronic version and $125 for the print and electronic versions.

The CSA executive for 2018-2019 includes Dr. Helen Booker (Past President); Dr. Jaswinder Singh (President); Dr. Sheri Strydhorst (President-elect); Dr. Douglas Cattani (Secretary, Treasurer); Dr. Harpinder Randhawa and Laurel Thompson (Western Directors); Dr. Mumtaz Cheema and Dr. Andrew Burt (Eastern Directors) and Caleb Niemeyer (Student Representative). The CSA executive met via conference call 7 times over the year and released fall and spring newsletters to our membership.

In 2018, the CSA executive organized a joint ASA-CSSA-CSA conference ***Enhancing Productivity in a Changing Climate***, which took place in Baltimore, Maryland, USA from November 4 to 7, 2018. The CSA plant breeding committee hosted a symposium entitled *Germplasm exchange and the future of plant breeding*. The CSA awards and recognition luncheon and annual general meeting was held during the conference. 25 CSA members were in attendance. Outstanding scientific oral and poster presentations were recognized.

The CSA executive is organizing a joint CAPB-CBA-CPS-CSA-CSHS-CSPB-CWSS conference Communicating Innovation in Plant Science, which will take place in Guelph, Ontario from July 7-10, 2019. The CSA will host two sessions entitled Plant Breeding & Germplasm Exchange and Cropping Systems & Agronomy. The speakers for this session are being determined from the submitted abstracts which are due May 17, 2019. More details will be available after that.

The 2019 CSA awards recognition luncheon and annual general meeting will be held during Plant Canada 2019 on Wednesday, July 10th at 11:30 am – 1:00 pm. Outstanding scientific oral and poster presentations will be recognized by the CSA Graduate Student Oral and Poster Awards Program. There will also be a graduate student social event at Plant Canada on July 8th in the evening which is supported by CPS, CSHS and CSA.

Student travel to society meetings and conferences is sponsored in part by the Agricultural Institute of Canada (AIC). Canadian Science Publishing (CSP) also provides financial support to CSA for the awards and recognition program. The CSA is grateful to AIC and CSB for their support.

It is expected that the 2020 CSA Annual General Meeting will be held in conjunction with The International Crop Science Congress 2020 from June 21-25, 2020 in Saskatoon, Saskatchewan. An MOU is being drafted between CSA and ICS and this should be confirmed in the near future.

For more information on CSA Membership or our awards program contact Nancy Zubriski, PO Box 637, Pinawa, Manitoba, R0E 1L0, 204 299-2327, nzubriski@gmail.com or visit our website at agronomycanada.com and follow us on twitter @agronomycanada.

Canadian Society for Horticultural Science – Société Canadienne de Science Horticole

Founded in 1956, the Canadian Society for Horticultural Science – Société Canadienne de Science Horticole (CSHS-SCSH) is a professional society devoted to fostering, promoting and encouraging research and education in all branches of horticultural science in Canada. With a countrywide representation, our members are from a variety of horizons: scientists, educators, students, extension agents and industry personnel involved in research, teaching, information and technology related to all fields of horticulture.

Current Executive Board (2018-2019)

Due to the diversity of horticulture production in Canada, one of the priorities of the CSHS is to have a pan-Canadian representation on its board of directors. A new member representing Northern regions of Canada was added this year to the CSHS executive board. Therefore, the CSHS Executive board now includes members representing all regions of Canada.

While we practice a progression within the board, our members are encouraged to submit their candidacy to any position available. **In fact, we are currently recruiting for a representative from the Atlantic region.** Terms are for 2 years with the possibility of 2 consecutive terms at the

same position. Please contact the CSHS secretary (bourlaye.fofana@canada.ca) if you are interested in the position.

CSHS Annual Conferences

The CSHS also prioritizes travelling around the country for its annual meetings. Following a conference in Vancouver in 2017, this past year, the CSHS held its conference in Niagara Falls, Ontario on October 4th to 6th 2018. The conference was a huge success with 190 delegates. The conference was chaired by Dr. Karen Tanino and followed the Canadian Greenhouse Conference. A one-day symposium on Cannabis production, chaired by Dr. Youbin Zheng, attracted several participants and created a good platform for discussion on the subject. Delegates also had the opportunity to participate in a pre-conference tour highlighting horticulture production in the Niagara region as well as a Haskap Workshop.




In 2019, the CSHS is proud to be part of the Plant Canada 2019 Conference in Guelph, Ontario. The CSHS has organized 4 concurrent sessions targeting topics such as horticulture production under controlled environment, Pre and Post-harvest crop quality and horticultural field production.

In 2020, our annual meeting will be held in the Atlantic region, with Dr. Bourlaye Fofana as the chair. **If you are interested in participating in the organization of the conference, please contact the CSHS secretary** (bourlaye.fofana@canada.ca).

CSHS Student Committee

Students are an integral part of the CSHS and their involvement in the Society is important and valued. A Student board was implemented in 2016 within the Society to support students' initiatives and the Student Committee has been very busy this year.

Sara Stricker (CSHS Student Representative and Student Committee Chair) has organized the student social event for all societies attending the Plant Canada 2019 Conference. **We are encouraging all students to participate in this fun event, which will include motivational talks, time to network with other students and plant science trivia!**

In addition, this past year, Ariana Forand (Saskatchewan Representative) and Zahra Charkhzarrin (Quebec Representative) both visited elementary schools in their region to talk about horticulture and grow plants with the students. Varinder Sidhu (Vice-Chair of the student committee) held an information session at McGill University for CSHS and Plant Canada whereas Sarah Drury (Ontario Representative) hosted an event for Fascination of Plants Day at Wellington Woods Community Center in Guelph.




Other events are planned for the upcoming year so follow their activities on the CSHS on-line platforms, including the CSHS website, Facebook page and Instagram account!

We invite CSHS student members to become involved in the Committee. If you are interested, contact the Student Committee Chair, Sara Stricker (strickes@uoguelph.ca).

Becoming a member of the CSHS

Numerous benefits are offered to CSHS members including:

- Significantly reduced registration fees at the annual CSHS conferences and at the Plant Canada Conference
- Reduced page charges to publish in the Canadian Journal of Plant Science
- Timely direct mail alerts to jobs, grant opportunities, etc.
- Eligibility to the Best CJPS Paper award for horticulture (which comes with an invitation to be a conference speaker

In addition, for students, benefits also include:

- Eligibility for the Awards for oral and poster presentation
- Eligibility for Travel Awards to annual conference
- Community & Extension Funding, which supports student activities in introducing any form of Horticulture science in communities
- Network between members, sharing of experiences about studies and research

For more information and to become a member: www.CSHS.ca

Canadian Society of Plant Biologists Inc.

Société canadienne de biologie végétale inc.

About the CSPB-SCBV

The Canadian Society of Plant Biologists grew out of informal meetings and conferences in the 1950s and was founded in 1958 as the Canadian Society of Plant Physiologists. In 2012, the Society adopted its present name to represent the inclusion of all types of botanical research. CSPB-SCBV Inc. is a not-for-profit corporation and a registered charity. It is a founding member of both **Plant Canada** and the **Global Plant Council** and is a member of the **Partnership Group for Science and Engineering**.

Botany, published by NRC Press, is the official journal of both the CSPB-SCBV and the Canadian Botanical Association.

Our more than 400 members include undergraduate and graduate students, postdoctoral fellows and research associates, professional scientists and a few corporations. Members have interests in [alphabetical order] adaptations to biotic and abiotic stress, biochemistry, bioinformatics, biotechnology, cell and molecular biology, development of research techniques and equipment, education, genomics, metabolism, metabolomics, natural products, physiological ecology, physiology, plant development, and proteomics. Members of the CSPB are engaged in basic and applied research, undergraduate and graduate education, management, extension, and the design and manufacture of scientific equipment.

CSPB-SCBV Executive Committee

President:	Geoffrey Wasteneys (UBC, Vancouver)
Vice President:	Daphne Goring (U of T St. George)
Past President:	Anja Geitman (McGill)
Secretary:	Sherryl Bisgrove (Simon Fraser)
Treasurer:	Sheila Macfie (Western)
Eastern Regional Director:	Robert Mullen (Guelph)
Western Regional Director:	David Bird (Mount Royal)
Communications Director:	Ingo Ensminger (U of T Mississauga)
Education Director:	Steven Chatfield (U of T Mississauga)
Science Policy Director:	Owen Rowland (Carleton)
Senior Director:	Jean-Benoit Charron (McGill)
Student/PDF Representative:	Ryan Eng (Max Plank Institute)

Scientific meetings

The CSPB-SCBV holds its national meeting each summer, in a roughly four-year rotation of joint and solo meetings. Joint meetings include conferences organized by Plant Canada and those run by the American Society of Plant Biologists, as well as ad hoc co-sponsored meetings with other Canadian Societies as opportunities arise.

Eastern Regional Meetings are held in November or December of each year, and Western Regional Meetings are typically held every second or third fall.

Students and postdoctoral scientists feature prominently at our meetings and are known for their high quality oral and poster presentations.

Upcoming CSPB/SCBV Annual General Meetings:

2020 Annual General Meeting: Saskatoon

2021 Annual General Meeting: Dalhousie University, Halifax, Nova Scotia

2022: Plant Biology 2022 (Joint ASPB-CSPB/SCBV), Portland Oregon

Awards provided by the CSPB-SCBV

CSPB-SCBV Gold Medal: for outstanding contributions or service to plant biology
David Gifford Award: for outstanding and original contributions in tree biology
C.D. Nelson Award: for outstanding research contributions to plant biology
Mary E. Spencer Award: for outstanding research in plant biology and active public service engagement by a mid-career researcher
Gleb Krotkov Award: for outstanding service to the Society
Ragai Ibrahim Award: to recognize excellence in publication by graduate students
Carl Douglas Prize: for outstanding contributions to plant biology by a postdoctoral fellow, including originality, productivity and leadership
Ann Oaks Doctoral Scholarship: equivalent to an NSERC PGS-D award
George H. Duff Travel Bursaries: about $10,000 per year is given to students and postdoctoral fellows to support travel to the annual summer meeting.

Becoming a member of the CSPB-SCBV

New members from any discipline within plant biology are welcome to join the CSPB-SCBV. Benefits of membership include reduced registration fees at our conferences and meetings; access to the education, student/pdf funding links and employment pages of our website; eligibility for the various awards, scholarships and bursaries listed above; and above all, inclusion in a dynamic community engaged in research, education and social activities related to plant sciences.

At Plant Canada 2019:

As host society for Plant Canada 2019, CSPB-SCBV has been responsible for chairing the Scientific Program, Local Arrangements, and Fundraising Committees. Our student and post-doctoral representative, Dr. Ryan Eng, has organized the two careers workshops, which will run from 11:15 to 12:15 on Monday and Tuesday. The CSPB/SCBV Annual Business Meeting will be held on Wednesday at 11:15, at which we will announce our Presidents Awards. Our Society Social event will be held from 7 to 9 pm on Monday in the Bullring, and, along will other participating societies and associations, we are supporting the student social event, also on Monday evening. Two of our 2018 Awardees feature in the plenary talks; our C.D. Nelson Award winner Jaswinder Singh (McGill) will speak in the Tuesday morning session, while our Society Medal winner Bill Plaxton (Queen's) gives the final plenary lecture of the meeting on Wednesday afternoon. We will announce our 2019 major award winners at Sunday evening's awards ceremony.

For more information, please visit http://cspb-scbv.ca/

Canadian Weed Science Society
Société canadienne de malherbologie

The CWSS-SCM is a non-profit professional society for scientists, agronomists, economists, and students interested in weed science. The society is widely recognized in Canada and beyond for its national leadership in bringing together research and information on science and management related to plants potentially impacting the environment, economy and society. The three major goals of the CWSS-SCM are to: (1) be the Canadian scientific authority representing professionals working in weed science; (2) expand the CWSS-SCM network of members and partners; and (3) ensure good governance.
Some highlights of 2018-2019:

The CWSS-SCM held its 72nd annual meeting in Niagara Falls, ON in November 2018. The full-day plenary session focused on "New Frontiers in Weed Management", with a range of national and international speakers covering topics such as hyperspectral technologies, big data, advances in mechanical weed control, and ethics. Additionally, a fascinating session on Molecular Biology was added to the program for the first time. The graduate student presentations were again a highlight of the meeting, and we had 14 such speakers with best talk award going to Lauren Benoit from the University of Guelph for a presentation on multiple resistant waterhemp. For more details, see the meeting archive at https://weedscience.ca/wp-content/uploads/2018/11/CWSS-SCM-2018-Niagara-Meeting-Package-Nov-15.pdf.

The CWSS-SCM proudly awarded Dr. Linda Hall a Fellow Award at the 2018 annual meeting. Linda is a professor in the Faculty of Agriculture Life and Environmental Science at the University of Alberta. She has enjoyed a productive and distinguished career in weed science and transgenic crop biosafety. After spending 12 years as a Research Scientist with Alberta Agriculture, Linda joined the University of Alberta in 2006. Linda is a world-renowned weed scientist and pioneer of research on the environmental impacts of transgenic crops and gene flow via and pollen and seeds. She has also contributed to the development of the next generation of weed scientists through teaching, mentoring and training of undergraduates and graduate students. Linda has been an active member of the CWSS-SCM for many years and served as president from 2016-2017.

The CWSS-SCM will host its 73rd annual meeting from November 18-21, 2019 at the Grand Okanagan Resort in Kelowna, British Columbia. An exciting scientific agenda is taking shape for this meeting and all weed science professionals, consultants and stakeholders should mark the dates on their calendar. The 74th annual meeting will be in Gatineau, Quebec in November of 2020. Details can be found at https://weedscience.ca/meeting-home/.

Current Board of the CWSS-SCM is below:

President: Rory Degenhardt, Integrated Field Sciences Research Leader – Canada, Corteva Agriscience, Edmonton, AB
Past-President: Eric R. Page, Research Scientist, Agriculture and Agri-Food Canada, Harrow, ON
1st Vice-President: François Tardif, Professor, Department of Plant Agriculture, University of Guelph, Guelph, ON
2nd Vice-President: Marie-Josée Simard, Research Scientist, Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu, QC
Treasurer: Allison Hayward, Field Development Representative, FMC, Kitchener, ON
Secretary: Breanne Tidemann, Research Scientist, Agriculture and Agri-Food Canada, Lacombe, AB
Regulatory Representative: Wendy Asbil, Plant Health and Biosecurity Directorate, Canadian Food Inspection Agency, Ottawa ON
Regulatory Representative: Michael Downs, Herbicides and Plant Growth Regulators Efficacy and Sustainability Assessment Division, Pest Management Regulatory Agency, Ottawa ON
Webmaster and Publications Director: Robert Nurse, Research Scientist, Weed Science, Agriculture and Agri-Food Canada, Harrow ON
Research Representative: Scott White, Assistant Professor, Faculty of Agriculture, Agricultural Campus, Truro, NS
Croplife Canada Representative (East): Matt Underwood, Field Biologist, Syngenta Canada, Cambridge, ON
Croplife Canada Representative (West): Colleen Redlick, Technical Service Specialist – Northern Saskatchewan, BASF Canada Inc, Saskatoon, SK
Member-At-Large (East): Andrew McKenzie-Gopsill, Research Scientist – Weed Science, Agriculture and Agri-Food Canada, Charlottetown PE
Member-At-Large (West): Jessica Weber, General Manager, Western Applied Research Corporation (WARC), Scott, SK
Graduate Student Representative: Jonathon Rosset, Department of Plant Science, University of Manitoba, Winnipeg, MB
2019 Local Arrangements Chairs: Ken Sapsford and David Clements

PROGRAM SCHEDULE OVERVIEW FOR SATURDAY JULY 6, 2019

CPS Financial Advisory Committee ***5:00pm-9:00pm*** Delta Inn Hotel

EXHIBITOR SET-UP: Starting from Noon until 6:00pm

POSTER SET-UP: Early Poster Set-up available from 3:00pm – 6:00pm

PROGRAM SCHEDULE OVERVIEW FOR SUNDAY JULY 7, 2019

8:00 am – 4:00 pm Registration in the Rozanski Concourse

	POSTER VIEWING AND EXHIBITS AT PETER CLARK HALL FROM 8:00am – 5:00pm
Time/ Departure	**TOURS DEPARTURE from Rozanski Hall** (please wait at back entrance facing Trent Lane).
8:00am	**TOUR 4**: Niagara Area Plant Pathology Field Tour
9:30am	**TOUR 3**: Cambridge Area Field Tour and Hike
1:45pm	**TOUR 6**: University of Guelph Arboretum Tour
8:00am-1:00pm	**CPS Outgoing Board Meeting** Delta Inn Hotel
11:00 – 1:00pm	**CSPB Outgoing Executive Meeting** Rozanski r. 106
2:00 – 4:00pm	**Plant Canada Outgoing Board and Annual General Meetings** Rozanski r. 106
4:00 – 5:30pm	**CAPB Executive Meeting** Rozanski r. 106
4:00 – 5:30pm	**CBA Outgoing Executive Meeting** Rozanski r. 108
4:15 – 5:15pm	**Workshop 1** *Sponsor Introduction Workshop* Rozanski r. 104
5:30 – 5:45pm	Opening Remarks in Rozanski room 104 • Dr. Deena Errampalli, President of Plant Canada • Dr. Malcolm Campbell, University of Guelph Vice-president (Research) • Dr. Geoffrey Wasteneys, Chair of the Scientific Program Organizing Committee for Plant Canada 2019
5:45 – 6:45pm	Keynote Address by Dan Riskin, Rozanski room 104
6:45 – 7:30pm	Presentation of Major Society Awards, Rozanski room 104
7:30 – 10:00pm	*Plant Canada Welcoming Reception Mixer at the Atrium

*You are welcome to visit, relax or talk with others at the PC Welcoming Reception Mixer at the Summerlee Science Complex Atrium. Enjoy the sounds of Guitar player Juneyt Yetkiner and the sights of the Cellscapes exhibition.

PROGRAM SCHEDULE OVERVIEW FOR MONDAY JULY 8, 2019

time	POSTER VIEWING AND EXHIBITS AT PETER CLARK HALL (PCH) FROM 8:00am – 7:00pm
8:00 – 8:30am	Coffee Break in concourse sponsored by Canadian Science Publishing
Loading talks at 8am	**Plenary Session 1-Plant Biotechnology** Rozanski room 104 *Chairs: Rima Menassa & Abdelali Hannoufa (Agriculture and Agri-Food Canada)*
8:30 – 9:20 **PS1**	**Dr. Maureen Hanson, Cornell University, NY** ***Improving photosynthesis in C3 plants***
9:20 – 10:10 **PS2**	**Dr. Bing Yang, University of Missouri, MO** ***Genome editing enables disease resistance in rice***
10:10 – 11:00 **PS3**	**Dr. Leslie Sieburth, University of Utah, UT** ***Beyond transcription factors: A degrading story of gene expression control***
11:00 – 1:00	**LUNCH at Creelman Hall 11:00 am – 1:00 pm**
11:15 – 11:50	**Workshop 2**: ***Careers Outside of Academia*** Rozanski r. 101
11:15 – 12:15	**Workshop 3**: ***Towards developing a plant health science vision for Canada*** Rozanski r. 103
12:00 – 12:50	**Workshop 4**: ***NSERC Seminar*** Rozanski r. 101
11:15 – 1:00	**CAPB Annual General Meeting** Rozanski r. 105 - *lunch tickets*
11:30 – 1:00	**CBA Section Meeting: Ecology** Rozanski r. 106 - *lunch tickets*
11:30 – 1:00	**CBA Section Meeting: Systematics & Phytogeography** Rozanski r. 107 - *lunch tickets*
11:30 – 1:00	**CBA Section Meeting: Development** Rozanski r. 108 - *lunch tickets*
11:30 – 1:00	**CBA Section Meeting: Mycology** Rozanski r. 109 - *lunch tickets*

Rooms→	101	102	103	104	105	106	107	108	109
Loading talks will be inside corresponding rooms at 1:00-1:15pm for CS1 and at 3:00-3:15pm for CS2									
Concurrent Session 1	**SDG**	**AGR1**	**ABS1**	**MHPI1**	**BPP**	**EEP1**	**PPHQ**	**DM CPS-S1**	**PSDM**
1:15 - 1:30	**S1**	**S7**	**S12**	**S18**	**S23**	**S29**	**S35**	**S40**	**S45**
1:30 - 1:45	**S2**		**S13**		**S24**	**S30**	**S36**	**S41**	**S46**
1:45 - 2:00	**S3**	**S8**	**S14**	**S19**	**S25**	**S31**		**S42**	**S47**
2:00 - 2:15	**S4**	**S9**	**S15**	**S20**	**S26**	**S32**	**S37**	**S43**	**S48**
2:15 - 2:30	**S5**	**S10**	**S16**	**S21**	**S27**	**S33**	**S38**	**S44**	**S49**
2:30 - 2:45	**S6**	**S11**	**S17**	**S22**	**S28**	**S34**	**S39**	**S102**	**Panel disc.***
2:45 - 3:15	Coffee Break in concourse sponsored by Environ								**MACN r.113**
Concurrent Session 2	**MPI**	**AGR2**	**ABS2**	**BSB**	**BG1**	**EEP2**	**HFP**	**MHPI2 CPS-S2**	**FMW**	**CPDM**
3:15 - 3:30	**S50**	**S58**	**S62**	**S69**	**S75**	**S80**	**S86**	**S92**	**S97**	**S168**
3:30 - 3:45	**S51**	**S56**	**S63**	**S70**	**S76**	**S81**	**S87**	**S93**	**S98**	
3:45 - 4:00	**S52**	**S60**	**S64**	**S71**	**S77**	**S82**	**S89**	**S94**	**S99**	**S169**
4:00 - 4:15	**S53**	**S61**	**S65**	**S72**	**S78**	**S83**	**S90**	**S95**	**S100**	**S170**
4:15 - 4:30	**S54**	**S57**	**S66**	**S73**	**S79**	**S84**	**S88**	**S96**	**S101**	
4:30 - 4:45	**S55**	**S59**	**S67**	**S74**		**S85**	**S91**	**Panel disc.***		**S171**
5:00pm – 7:00pm	POSTER SESSION 1 (odd #'s) @ PCH Sponsored by **LI-COR Biosciences**									
5:30 – 7:30	PC President Reception @ University Center Club (invitation only)									
7:00 – 8:30	**CBA Workshop: Gender in Ecology** Rozanski r. 105									
7:00 – 9:00	CPS President Reception @ Delta Inn				CSPB Mixer @ Bullring -round bldg. (members only)					
8:30 – 10:30	**ALL SOCIETY Student Social** @ Grad Lounge-The Fifth at the Univ. Center in UofG									

8:00 am – 4:00 pm Registration in the Rozanski Concourse

PROGRAM SCHEDULE OVERVIEW FOR TUESDAY JULY 9, 2019

8:00 am – 4:00 pm Registration in the Rozanski Concourse

time	POSTER VIEWING AND EXHIBITS AT PETER CLARK HALL (PCH) FROM 8:00am – 7:00pm
8:00 – 8:30	Coffee Break in concourse sponsored by Western Grain Research Foundation
Loading talks at 8am	**Plenary Session 2-Agronomy** Rozanski room 104 *Chair: Helen Booker (University of Saskatchewan)*
8:30 – 9:20 **PS4**	**Dr. D. Brian Fowler, University of Saskatchewan, SK** ***Winter wheat production in the high winter stress climate of western Canada – An experiment in crop adaptation***
9:20 – 10:10 **PS5**	**Dr. Clarence J Swanton, University of Guelph** ***Plant competition and the physiology of fear***
10:10 – 11:00 **PS6**	**Dr. Jaswinder Singh, McGill University, QC** **CD Nelson Award Winner for 2018** ***New paradigms in the genetic regulation of pre- and post- harvest grain germination in cereals***
11:00 - 1:00	LUNCH at Creelman Hall 11:00 am – 1:00 pm / loading talks 12:30-1:00pm
11:15 – 12:15	**Workshop 5: *Beyond Grad School: A guide for PDF and PI positions*** Rozanski r. 101
12:00 – 1:00	**Workshop 6**: CAPB Genome editing workshop Rozanski r. 102
11:15 – 1:00	**CPS Annual Business Meeting** Rozanski r. 103 - *lunch tickets*
11:30 – 12:30	**CSA Executive Meeting** Rozanski r. 107 - *lunch tickets*

Rooms→	101	102	103	104	105	106	107	108	109
Loading talks will be inside corresponding rooms at 1:00-1:15pm for CS3 and at 3:00-3:15pm for CS4									
Concurrent Session 3	**ABS3**	**SM**	**CB**	**MHPI3**	**CE1**	**EEP3**	**SBGP**	**IPP1 CPS-S3**	**WHP**
1:15 - 1:30	S103	S109	S118	S121	S127	S133	S139	S145	S150
1:30 - 1:45	S105	S110	S117	S122	S128	S134	S140	S146	S151
1:45 - 2:00	S106	S111	S116	S123	S129	S135	S141	S147	S152
2:00 - 2:15	S107	S112	S120	S124	S130	S136	S142	S148	S153
2:15 - 2:30	S104	S113	S119	S125	S131	S137	S143	S149	S154
2:30 - 2:45	S108	S114	S115	S126	S132	S138	S144	Panel disc.*	S155
2:45 - 3:15	Coffee Break in concourse sponsored by Biochambers Incorporated								
Concurrent Session 4	**DR**	**CE2**	**BCM**	**BASP**	**BG2**	**TXS**	**BI**	**IPP2 CPS-S4**	**NBEI**
3:15 - 3:30	S156	S162	S207	S176	S178	S183	S190	S196	S201
3:30 - 3:45	S157	S163	S208	S172	S179	S184	S191	S197	S202
3:45 - 4:00	S158	S164	S209	S173	S180	S185	S192	S198	S203
4:00 - 4:15	S159	S165	S210	S174	S181	S186	S193	S199	S204
4:15 - 4:30	S160	S166	S211	S175	S182	S187	S194	S200	S205
4:30 - 4:45	S161	S167	S212	S177		S188	S195	Panel disc.*	S206
4:45 - 5:00						S189			
5:00pm – 7:00pm	POSTER SESSION 2 (even #'s) @ PCH Sponsored by **Hoskin Scientific**								
7:00 – 11:00	CPS Awards Dinner and 90th Celebration @ Delta Hotel, Royal Ballroom A 7:00pm – 11:00pm								

PROGRAM SCHEDULE OVERVIEW FOR WEDNESDAY JULY 10, 2019

8:00 am until noon Registration in the Rozanski Concourse

time	POSTER VIEWING AND EXHIBITS AT PCH FROM 8:00am – 11:00 am	
8:00 – 8:30	Coffee Break in concourse sponsored by BASF	
Loading talks at 8am	**Plenary Session 3-Managing Plant Disease in Horticulture** Rozanski room 104 *Chairs:* Lone Buchwaldt (Agriculture and Agri-Food Canada) and Valerie Gravel (McGill University)	
8:30 – 9:20 **PS7**	**Dr. Mary Ruth McDonald, University of Guelph, ON** ***Billions, trillions and quadrillions: The challenge of managing clubroot on canola and vegetables***	
9:20 – 10:10 **PS8**	**Dr. Richard Bélanger, Université Laval, Québec, QC** ***A unique interaction with a biocontrol agent alters the parasitic activity of powdery mildews on plants***	
10:10 – 11:00 **PS9**	**Dr. Diane G.O. Saunders, John Innes Centre, UK** ***The wheat-rust conflict: Shifty enemies and the long reach of genomics***	
Before Noon	Please pick-up posters @ Peter Clark Hall	
11:00 - 1:30	LUNCH at Creelman Hall 11:00 am – 1:30 pm / loading talks 1:00-1:30pm	
11:15 – 1:15	**CSHS Annual Business Meeting**	Rozanski r. 106 - *lunch tickets*
11:15 – 1:30	**CSPB Annual Business Meeting**	Rozanski r. 103 - *lunch tickets*
11:30 – 1:30	**CBA Annual General Meeting and Awards**	Rozanski r. 102 - *lunch tickets*
11:30 – 1:00	**CSA Annual General Meeting and Awards**	Rozanski r. 104 - *lunch tickets*
11:30 – 12:30	**CAPB Award Deliberations**	Rozanski r. 105 - *lunch tickets*
12:30 – 1:30	**CAPB Student Presentation Awards**	Rozanski r. 105
5:30 – 6:30	**Plant Canada Incoming Board**	Rozanski r. 106
Loading talks at 1pm	**Plenary Session 4-Root Evolution, Development and Function** Rozanski room 104 *Chair: Geoffrey Wasteneys (University of British Columbia)*	
1:30- 2:20 **PS10**	**Dr. Liam Dolan, University of Oxford, UK** ***Evolution and development of the earliest land plant rooting systems***	
2:20 – 3:10 **PS11**	**Dr. Siobhan Brady, UC Davis, CA** ***Regulation of root development – a systems biology perspective***	
3:10 – 3:40	Coffee Break in concourse sponsored by Regent Instruments Inc	
3:40 – 4:30 **PS12**	**Dr. William Plaxton, Queen's University, Kingston, ON** ***Feeding hungry plants: purple acid phosphatases play a pivotal role in phosphorous nutrition***	
4:30 – 5:00pm	AWARDS CEREMONY and CLOSING REMARKS	
7:00 – 11:00pm	ALL SOCIETY FINAL BANQUET DINNER AND STARPOWER ENTERTAINMENT	

*** Panel disc.** A Panel discussion will follow in the same room after all speakers' have completed their presentations.

Keynote Speaker

Effective science communication requires listening to what your audience wants

Sunday, July 7th @ 5:30pm

Rozanski Hall, room 104

University of Guelph, ON

There are many incentives for scientists to communicate their work to people outside their own field. It can help new ideas spread across disciplines, help scientists advocate for funding, and help build public trust and support for science itself. Plant scientists do some of the most important work in the world today, connected with basic issues such as food security, sustainability, and human adaptation to climate change. But despite the importance of their fields, plant scientists often have a difficult time wrestling public attention away from stories in other scientific disciplines, including zoology, medicine, and space science. In this keynote, I'll talk about my experience working in science communication, and offer some informed suggestions about how to get the attention of news journalists, or people in other popular media. Ultimately, I will argue that audiences are most interested in the big, unsolved questions that scientists go after, and that focusing on those, along with stories of human experience, can make science communication more effective than simply focusing on the discoveries we've most recently made.

Dan Riskin, PhD, is a scientist, author, and television personality. He is best known in Canada for his seven-year tenure as the co-host of Discovery's flagship Science Program, *Daily Planet*. In the US and elsewhere, he is recognized as the host of Animal Planet's hugely successful show about parasites, *Monsters Inside Me*. Dan has published more than 20 papers in scientific journals, including *Nature*, mostly about the biomechanics of bats. To make science accessible and interesting to wide audiences, Dan has appeared as a guest on *The Tonight Show with Jay Leno*, *The Late Late Show with Craig Ferguson*, *The Dr. Oz Show*, *The Doctors*, *CNN Tonight with Don Lemon*, *CBS This Morning*, *The CTV National News with Lisa LaFlamme*, Global's *Morning Show*, CTV NewsChannel, and CP24. His first popular book, *Mother Nature is Trying to Kill You* was a Canadian bestseller.

SCHEDULE OF PLENARY SPEAKERS FOR PLANT CANADA 2019

Time	Monday July 8th	Tuesday July 9th	Wednesday July 10th
Place	**Room: Rozanski 104**	**Room: Rozanski 104**	**Room: Rozanski 104**
8-8:30	Coffee-break (concourse)	Coffee-break (concourse)	Coffee-break (concourse)
Session	Plant Biotechnology	Agronomy	Managing Plant Disease in Horticulture
Chairs	Dr. Rima Menassa & Dr. Abdelali Hannoufa	Dr. Helen Booker	Dr. Lone Buchwaldt & Dr. Valerie Gravel
8:30am	**Dr. Maureen Hanson** Cornell University, NY *Improving photosynthesis in C3 plants*	**Dr. D. Brian Fowler** University of Saskatchewan, SK *Winter wheat production in the high winter stress climate of western Canada* *– An experiment in crop adaptation*	**Dr. Mary Ruth McDonald** University of Guelph, ON *Billions, trillions and quadrillions: The challenge of managing clubroot on canola and vegetables*
9:20am	**Dr. Bing Yang** University of Missouri, MO *Genome editing enables disease resistance in rice*	**Dr. Clarence J Swanton** University of Guelph, ON *Plant competition and the physiology of fear*	**Dr. Richard Bélanger** Université Laval, Québec, QC *A unique interaction with a biocontrol agent alters the parasitic activity of powdery mildews on plants*
10:10am	**Dr. Leslie Sieburth** University of Utah, UT *Beyond transcription factors: A degrading story of gene expression control*	**Dr. Jaswinder Singh** McGill University, QC *CSPB C.D. Nelson Award Address: New paradigms in the genetic regulation of pre- and post- harvest grain germination in cereals*	**Dr. Diane G.O. Saunders** John Innes Centre, UK *The wheat-rust conflict: Shifty enemies and the long reach of genomics*
11:00am	Lunch at Creelman Hall	Lunch at Creelman Hall	Lunch at Creelman Hall
Session	**Schedule of Plenary Talks at Plant Canada 2019**		Root evolution, Development and Function
Chairs			Dr. Geoffrey Wasteneys
1:30 pm			**Dr. Liam Dolan** University of Oxford, UK *Evolution and development of the earliest land plant rooting systems*
2:20 pm			**Dr. Siobhan Brady** U of California-Davis, CA *Systems biology of root development*
3:10 pm			Coffee-break (concourse)
3:40 pm			**Dr. William Plaxton** Queen's University, Kingston, ON *CSPB Gold Medal Address: Feeding hungry plants: purple acid phosphatases play a pivotal role in phosphorous nutrition*
4:30 pm			CLOSING REMARKS

ALL PLENARY TALKS WILL BE IN ROZANSKI HALL room 104

Dr. Richard Bélanger **Université Laval, QC**	**PS8**	A unique interaction with a biocontrol agent alters the parasitic activity of powdery mildews on plants
Dr. Siobhan Brady **UC Davis, CA**	**PS11**	Systems biology of root development
Dr. Liam Dolan **University of Oxford, UK**	**PS10**	Evolution and development of the earliest land plant rooting systems
Dr. Brian Fowler **University of Saskatchewan, SK**	**PS4**	Winter wheat production in the high winter stress climate of western Canada – An experiment in crop adaptation
Dr. Maureen Hanson **Cornell University, NY**	**PS1**	Improving photosynthesis in C3 plants
Dr. Mary Ruth MacDonald **University of Guelph, ON**	**PS7**	Billions, trillions and quadrillions: The challenge of managing clubroot on canola and vegetables
Dr. William Plaxton **Queen's University, ON**	**PS12**	CSPB Gold Medal Address-Feeding hungry plants: Purple acid phosphatases play a pivotal role in phosphorous nutrition
Dr. Diane G.O. Saunders **Norwich Research Park, UK**	**PS9**	The wheat-rust conflict: Shifty enemies and the long reach of genomics
Dr. Leslie Sieburth **University of Utah, UT**	**PS3**	Beyond transcription factors: A degrading story of gene expression control
Dr. Jaswinder Singh **McGill University, QC**	**PS6**	CSPB C.D. Nelson Award Address-New paradigms in the genetic regulation of pre- and post-harvest grain germination in cereals
Dr. Clarence Swanton **University of Guelph, ON**	**PS5**	Plant competition and the physiology of fear
Dr. Bing Yang **University of Missouri, MO**	**PS2**	Genome editing enables disease resistance in rice

PS1. Monday, July 8, morning session at 8:30 am

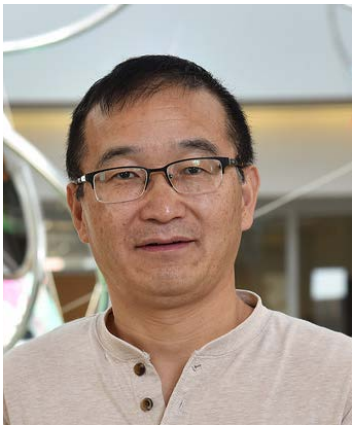
Dr. Maureen Hanson and Myat T. Lin
Cornell University, NY

Improving photosynthesis in C3 plants

Abstract: Rubisco, which catalyzes the first step in carbon fixation, is a target for efforts to improve photosynthetic efficiency. Modifying the cellular environment surrounding Rubisco to enhance the CO_2 concentration, in order to prevent photorespiration, is one strategy underway in our lab. Another strategy is to alter the properties of Rubisco itself to increase its enzymatic efficiency and/or to increase its affinity for CO_2. Manajit Hayer-Hartl's group recently demonstrated assembly of active Rubisco in *E. coli*, where the effects of mutagenesis can be quickly examined. Assembly of Rubisco requires multiple chaperones: Cpn60α, Cpn60β and Cpn20, as well as RbcX, Raf1, Raf2 and BSD2, for assembly of large and small subunits into L_8S_8 holoenzymes. We modified Hayer-Hartl's Arabidopsis vectors to express tobacco Rubisco by replacing the Arabidopsis assembly factor genes with tobacco ones. We used this system to survey the activity of enzymes comprised of individual members of the tobacco Rubisco small subunit family, by co-expressing each one with the single large subunit gene in *E. coli*. These novel *E. coli*-expressed Rubisco enzymes have carboxylation kinetics very similar to that of the native tobacco Rubisco. We also produced tobacco Rubisco with a recently discovered trichome small subunit in *E. coli* and found that it has a higher catalytic rate and a lower CO_2 affinity compared to the enzymes with other small subunits.

Bio:

Dr. Maureen Hanson is Liberty Hyde Bailey Professor in the Department of Molecular Biology and Genetics at Cornell University in Ithaca, NY. She previously was on the Biology faculty at the University of Virginia, Charlottesville. She holds a Ph.D. in Cell and Developmental Biology from Harvard University, where she subsequently held an NIH NRSA postdoctoral fellowship. She is a Fellow and recipient of the Lawrence Bogorad Award of the American Society of Plant Biologists and a Fellow of the American Association for the Advancement of Science. She received the SUNY Chancellor's Award for Faculty Service and the Cornell Award for Outstanding Accomplishments in Basic Research. Her lab is known for identifying the first single dominant fertility restorer (*Rf*) gene that suppresses the expression of a toxic mitochondrial gene encoding cytoplasmic male sterility, the rediscovery of stromules and the demonstration that molecules pass through them between chloroplasts, and identification of several gene families previously unknown to comprise plant organelle RNA editing machinery. Her group has ongoing projects concerning improving photosynthetic efficiency through synthesizing the cyanobacterial carbon-concentrating mechanism in chloroplasts or through engineering of the carbon-fixing enzyme Rubisco. https://hansonlab.org/



PS2. Monday, July 8, morning session at 9:20 am

Dr. Bing Yang
University of Missouri, USA

Genome editing enables disease resistance in rice

Abstract: Engineered CRISPR (clustered regularly interspaced short palindromic repeats) systems have emerged as potent biotechnological tools for both basic and applied research. The most promising utilization of CRISPR/Cas9 is for targeted genome editing, leading to precise genetic alterations within any genome of interest, as demonstrated in a plethora of organisms including several important crop plants. Bacterial blight is an important disease of rice in Asia and Africa. The causal agent *Xanthomonas oryzae* pv. *oryzae* (Xoo) uses secreted TAL effectors (TALes) to ectopically activate host SWEET sucrose transporter genes, enabling disease. *Xoo* uses a limited set of TALes to target promoters of three SWEET (*SWEET11*, 1*3*, and *14*) genes in rice. Naturally occurring variant *SWEET* genes act as recessive resistance genes by interfering with TALe targeting. We used CRISPR/Cas9 to engineer rice lines that carry multiple mutations in three *SWEET* gene promoters. The *SWEET* promoter mutations were introduced into different rice varieties, and the disease evaluation showed that editing SWEET promoters generated robust, broad-spectrum BB resistance. We also created rice lines that carry knockout mutations individually or in combination in three SWEET (*SWEET11*, *13*, and *14*) genes. The knockout lines are useful diagnostic tools to determine SWEET-inducing TALes in field Xoo isolates and guide the deployment of resistance genes derived from the naturally occurring or genome edited SWEET promoter mutations.

Bio:

Dr. Bing Yang is professor in the Division of Plant Sciences at the University of Missouri – Columbia and member at Donald Danforth Plant Science Center. He received PhD degree in plant pathology at Kansas State University in 2000, joined Iowa State University as an assistant professor in 2007, and moved to the University of Missouri – Columbia and Danforth Plant Science Center in 2018.

Yang works on development and application of TALEN- and CRISPR-based genome editing technologies in crops such as rice, maize, wheat, sorghum and soybean. His research also focuses on basic understanding of host susceptibility/resistance to bacterial infection and using genome editing tools to engineer disease resistance in crop plants.

https://cafnr.missouri.edu/person/bing-yang/

https://www.danforthcenter.org/scientists-research/principal-investigators/bing-yang

PS3. Monday, July 8, morning session at 10:10 am

Dr. Leslie Sieburth
University of Utah, USA

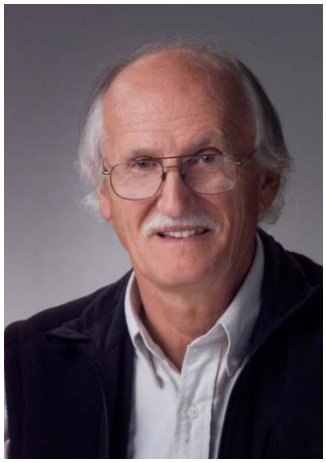
Beyond transcription factors: A degrading story of gene expression control

Abstract: Gene expression is a common component of many studies, and typically is quantified as mRNA abundance. mRNA abundances, however, are controlled by both rates of synthesis (transcription) and rates of decay, and yet roles of mRNA decay in regulating RNA abundances are largely unknown. To address this problem, my lab uses genetic and genomic approaches to identify mRNA substrates of the decay pathways in Arabidopsis. Mutants are used to link mRNA substrates with decay pathways, and our work focuses on *varicose* (*vcs*), which is required for the mRNA decapping step that initiates 5'-->3' decay, and *suppressor of varicose* (*sov*), which encodes a 3'-->5' exoribonuclease. The *vcs* mutant was initially identified because its phenotype includes thick and misshapen veins, especially in cotyledons and leaves. By contrast, the *sov* mutant has no obvious developmental defects. Genome-wide measurements of mRNA decay revealed that mRNA decapping carries out a majority of the fast-decaying mRNAs, and the fast-decaying mRNAs include those encoding transcription factors, components of signal transduction pathways, and genes annotated as responding to stress or developmental signals. Analysis of mRNA substrates of *sov*, by contrast, led to identification of an mRNA decay feedback pathway. In *sov* mutants, an over-compensating feedback mechanism reorganizes patterns of mRNA decay, decay rates, and also affects transcription. The profoundly altered gene expression dynamics in *sov* mutants maintains mRNA abundance at near wild-type levels. The implications of mRNA decay rates and feedback pathways for regulation of gene expression will be discussed.

Bio:

Dr. Leslie Sieburth is a Professor and the Associate Director of the School of Biological Sciences at the University of Utah. Dr. Sieburth's research uses genetic, genomic, and cell biological approaches to dissect fundamental processes in plants. A major project focuses on gene expression, and regulatory roles of mRNA decay in controlling mRNA abundance. Her lab was the first to identify VARICOSE (VCS), a scaffold protein that is essential for functional assembly of the mRNA decapping complex, and also discovered *SUPPRESSOR OF VARICOSE (SOV)*, another cytoplasmic mRNA decay pathway. Recent studies using genome-wide approaches identified the mRNA substrates of mRNA decapping and SOV, which also revealed overcompensating feedback pathways in mRNA decay mutants. A second project examines root-to-shoot signaling, and identified the *BYPASS1* gene as encoding a negative regulator of a root-derived signaling molecule that causes strong physiological and developmental responses in the shoot. This pathway appears to coordinate shoot physiology with perception of rhizosphere conditions, and because *BYPASS1*-like genes are present in genomes of all land plants, this work suggests that inter-organ communication mediated by BPS1 was vital as plants colonized land. Leslie began her independent academic career in the Biology Department at McGill University.

https://faculty.utah.edu/u0143322-LESLIE_E_SIEBURTH/research/index.hml



PS4. Tuesday, July 9, morning session at 8:30 am

Dr. Brian Fowler
University of Saskatchewan, Saskatoon, SK

Winter wheat production in the high winter stress climate of western Canada – An experiment in crop adaptation.

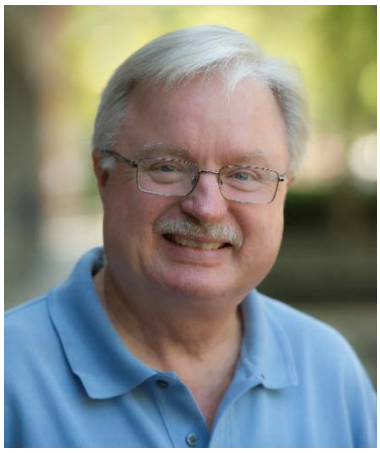
Abstract: The winter wheat production area on the North American Great Plains only extended as far north as southern Alberta in the 1970's. At that time, a research and development program was initiated with the objective of expanding production north and east into higher winter stress areas of the Canadian prairies. Winter survival was considered the main limitation in this region while market access, diseases and agronomic problems also restricted its acceptance as a viable cropping option. Intensive plant breeding efforts to increase cultivar winter hardiness were unsuccessful. However, research and development work started in the 1970's demonstrated that no-till seeding into standing stubble for snow trapping could successfully overwinter winter wheat if available cold hardy cultivars were grown using recommended management practices. Subsequent plant breeding improvements increased yield potential, straw strength, and rust resistance and winter wheat became one of the most environmentally sustainable cropping options. Commercial grain yield ranged from 125 to 149% of spring wheat and production increased to a high of 1.2 million ha in 2007 in Saskatchewan and Manitoba. In light of recent environmental concerns, changing weather patterns, diminishing world wheat reserves, and an ever increasing global population to feed, one would assume that winter wheat production in western Canada would continue to expand. However, marketing obstacles and difficulties inserting winter wheat into spring crop rotations, both of which have a direct influence on farmers' net returns, remain to be overcome before the full potential of this cropping option will be realized.

Bio:

Brian Fowler is a Professor in the Department of Plant Sciences at the University of Saskatchewan where his primary responsibilities have been in the areas of winter wheat plant breeding, genetics, drought, and mineral stresses, with special emphasis on cold hardiness and conservation farming systems. He has been a leader in winter cereal variety development and no-till research in the Great Plains region of North America. These efforts involved close co-operation with farmer and environmental groups that has been recognized by awards from the Manitoba-North Dakota Zero Tillage Farmers Association, the Saskatchewan Soil Conservation Association, the Alberta and Saskatchewan Winter Wheat Commissions and Winter Cereals Manitoba. In 2011, he was presented a Ducks Unlimited North American Recognition Award "for his passion of preserving the natural landscape across Canada". He was made a Fellow of both the Canadian and American Societies of Agronomy in recognition of his "significant contributions to the development of winter cereal production and conservation farming systems on the Canadian Prairies and the Northern Great Plains". In 2018, he was inducted into the Saskatchewan Agriculture Hall of Fame.

https://www.researchgate.net/profile/David_Fowler6;

https://www.wheatworkers.ca/wcsm.php



PS5. Tuesday, July 9, morning session at 9:20 am

Dr. Clarence J. Swanton, N. Berardi and S. Amirsadeghi
University of Guelph, ON

Plant Competition and the Physiology of Fear

Abstract: Plant competition is recognised as one of the most important biological interactions that influences plant community structure and individual plant fitness. The competitive interactions for limited resources of light, water and nutrients are thought to be the primary mechanisms by which plants are harmed. This presentation will explore an alternative view, a view that suggests that the primary mechanism of plant competition is the creation of a cellular imbalance. Experimental evidence will be presented to show that under resource independent competition, far red enriched light reflected from neighbouring weedy plants can alter the balance between the production of reactive oxygen species and the plant's ability to detoxify through antioxidant defence mechanisms. Specifically, the determination of singlet oxygen involvement in early responses of crop plants to neighbouring weeds changes everything that we know about plant competition. It also provides a unique opportunity to compare physiological responses of mammals and plants to competition, hence the "physiology of fear".

Bio:

Dr. Swanton obtained his BSc in Botany from the University of Toronto, His MSc in Agrometerology from the University of Guelph, and a PhD in Plant Ecology from the University of Western Ontario. During the years between earning his MSc and his PhD, he was employed as a field agronomist with the Campbell Soup Company of Canada and later as a weed biologist with the Ontario Ministry of Agriculture and Food. In 1985 he joined the University of Guelph as a faculty member in the Department of Crop Science. In 1996 he was promoted to full professor. From 1998 to 2004, Clarence served as the first Chair of the Department of Plant Agriculture which included the Departments of Crop Science, Horticulture and the Horticulture Research Institute of Ontario. From 2007 to 2008 he served as President of the Canadian Weed Science Society. He has won numerous awards for his research. In 2013 he received the Outstanding Canadian Award in the area of Crop Protection from Bayer CropScience for exceptional contributions to science and innovation. His research is focused on weed ecology and the development of integrated weed management systems for field and horticultural crops. https://www.plant.uoguelph.ca/cswanton

PS6. Tuesday, July 9, morning session at 10:10 am

Dr. Jaswinder Singh
McGill University, Montreal, QC

CSPB C.D. Nelson Award Address:

New paradigms in the genetic regulation of pre- and post-harvest grain germination in cereals

Abstract: In small grain cereals, it is an important goal to breed for the right balance of resistance to pre-harvest sprouting on one hand and reduced seed dormancy for rapid and uniform germination on the other, especially in many post-harvest processes. The antagonistic action of gibberellin and abscisic acid has been intensively investigated in recent years leading to an improved understanding of mechanisms underlying seed dormancy/germination. There is also emerging evidence for role of epigenetic mechanisms in seed dormancy which could be an alternate hormone independent genetic mechanism for seed dormancy. A key gene of RdDM pathway, *ARGONAUTE4_9* has been found to be associated with pre-harvest sprouting in barley and wheat. Significant variation in the expression of *AGO4_9* class genes in dormant and non-dormant barley and wheat genotypes was observed. Post-harvest seed germination commences after imbibition of dry seed activating many metabolic activities involving different carbohydrate reserves. During this process, we identified a specific Thaumatin- Like Protein, TLP8 which regulates the amount of β-glucan in germinating barley grains. β-glucan is one of the major bioactive components of endosperm cell walls for dietary fibers, excessive amount of which causes major hindrance during the malting process. Currently, we are employing CRISPR-based gene editing approaches to understand novel biological network during pre- and post-germination in barley. Overall, our efforts shed new light on the genetics of pre-harvest sprouting and on the protein-carbohaydrate interaction during post-harvest germination, which could be potentially valuable for the development of future generation of healthy, and productive cereals.

Bio:

Dr. Jaswinder Singh is currently an Associate Professor in the Department of Plant Science, McGill University, Canada. After completing his PhD from CSIRO Plant Industry, Canberra Australia, he did his postdoctoral studies at the University of California Berkeley. His research focuses on the enhancement of quality traits, and stress tolerance in crop plants using functional genomics tools. His laboratory is actively researching precocious germination from a unique perspective. His group has recently discovered a novel barley gene, which regulates the β-glucan activity during germination. His findings have shown for the first time the reversal of epigenetic silencing in plants. He has published over 50 research articles and delivered over 50 invited talks in international meetings and renowned academic institutes. He served in various executive positions in different plant science societies, notably as Eastern Director of Canadian Society of Agronomy (2010-12), International Committee member of the American Society of Plant Biologists (2012-15), is the current President of the Canadian Society of Agronomy and a Board Member, Plant Canada. The Canadian Society of Plant Biologists recognized his research with prestigious C. D. Nelson award in 2018 for his outstanding contribution to plant science. https://www.mcgill.ca/plant/faculty/singh

PS7. Wednesday, July 10, morning session at 8:30 am

Dr. Mary Ruth McDonald and Bruce D. Gossen
University of Guelph, ON; AAFC-Saskatoon

Billions, trillions and quadrillions: The challenge of managing clubroot on canola and Brassica vegetables

Abstract: Clubroot, caused by *Plasmodiophora brassicae* Wor., is a problem wherev er brassica crops are grown. The pathogen produces enormous numbers of long-lived resting spores, so keeping resting spore numbers low is key to effective clubroot management. One infected canola plant can produce 5 to 23 billion resting spores, and concentrations of 10^6 to 10^9 resting spores per gram of soil are common. Host resistance is often effective but not durable because intense selection for virulent pathotypes occurs on quadrillions of spores in each heavily infested field. As a result, there is renewed interest in physical and cultural controls to reduce disease pressure and protect genetic resistance. This has led to some unexpected findings. For example, a 2-year break from canola reduced spore numbers in soil by 99%, but this still left enough spores to cause 100% disease in a susceptible host. Also, spore survival was consistent with a Type III survival curve; spores that survive the initial two years can live a very long time. Other studies showed that no symptoms developed in infected plants at temperatures below 12 °C, so planting time can play a role in disease avoidance, especially for vegetable crops. Increasing soil pH to 7.2 or above can reduce severity, but is not fool-proof when temperature and soil moisture are optimum. Application of lime, calcium cyanamide, boron, solarisation or even fumigation can supress clubroot. One or more of these soil treatments can be combined with grass cover crops to manage small patches of clubroot in canola fields.

Bio:

Mary Ruth McDonald is a professor in the Department of Plant Agriculture, University of Guelph and she is also a Research Program Director at the university. Her research focuses on plant diseases, pathogen biology and integrated pest management for vegetable crops and canola, and also some aspects of sustainable vegetable production and adaptation to climate change. Mary Ruth teaches portions of undergraduate agriculture course and a graduate course on plant disease epidemiology. Prof. McDonald has published over 70 peer reviewed papers and has been an invited keynote speaker at regional, national and international conferences, including recent presentations in the U.K., Sweden and Mexico. She is the recipient of local, national and international awards for excellence in research, extension education, and integrated pest management. https://www.plant.uoguelph.ca/mrmcdona

PS8. Wednesday, July 10, morning session at 9:20 am

Dr. Richard R. Bélanger
Université Laval, Québec, QC

A unique interaction with a biocontrol agent alters the parasitic activity of powdery mildews on plants

Abstract: The phyllosphere harbors a diverse microbial community in which fungi occupy a predominant space. In the course of evolution, all leaf surface fungi have acquired specific properties that enable them to compete and survive in this restricted ecological niche in spite of the apparent limited resources on the leaf. While we, as scientists, have been trying to ascribe a certain hierarchy among the fungi inhabiting the phylloplane, it is nonetheless important to remember that in a balanced environment, each of these fungi manages successfully to acquire the resources necessary for its establishment and reproduction on the leaf surface. For instance, recent observations have highlighted that closely related organisms co-habit in this environment with albeit quite different lifestyles. Among them, the Ustilaginaceae, including the genera *Ustilago* and *Pseudozyma*, comprise members that can be plant pathogens, biocontrol agents, or simple epiphytes. Comparative genomic analyses among different members of the Ustilaginaceae have revealed that these opposite lifestyles in similar environments are seemingly associated with the presence/absence of a very limited number of genes coding mostly for effector proteins. In the same manner, the members lacking the effector proteins to be a plant pathogen, for example, seem to have acquired specific features, including their own unique set of effectors, to adopt a different lifestyle. These complex and subtle evolutive processes appear to play key roles in the adaption of fungi occupying specific ecological niches, and in their ability to extract resources necessary for their survival in a given environment.

Bio:

Dr. Richard Bélanger is full professor in plant pathology and holder of a Canada Research Chair in plant protection at Laval University. His research endeavors concentrate on the development of biological and non-chemical approaches to control plant diseases. Along those lines, sustained efforts have been devoted toward biological control of powdery mildews with natural antagonists. Belanger's lab has pioneered the exploitation of the fungus *Pseudozyma flocculosa* and its unique properties to attack powdery mildews. This research has led the way to the development of a commercial product and to the elucidation of an unusual tritrophic interaction where the plant, the pathogen and the biocontrol fungus each contributes coordinated factors leading to the collapse of the pathogen.

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PS9. Wednesday, July 10, morning session at 10:10 am

Dr. Diane G. O. Saunders
John Innes Centre, Norwich Research Park, UK

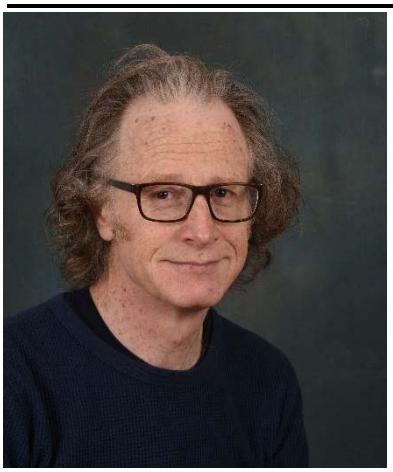
The wheat-rust conflict:

Shifty enemies and the long reach of genomics

Abstract: Wheat rusts have been associated with crop failures and famine throughout history. Recent outbreaks of yellow (stripe) and stem rust in Europe have been linked to expansions in pathogen geographic distribution, exotic incursions and increased virulence. Our rapid "field pathogenomics" strategy, that uses transcriptome sequencing of infected wheat leaves taken directly from the field, has enabled us to gain insight into the population structure of the yellow rust pathogen over successive seasons and track the recent re-emergence of wheat stem rust in western Europe. Whilst effectively capturing pathogen diversity, transcriptome sequencing of infected host tissue can also be leveraged to assess the genotype and expression profiles of the host in its natural environment. Through analysis from the host side of the interaction we also identified changes in the expression of primary metabolic pathways including photosynthesis through comparative differential gene expression analysis of wheat varieties with differing levels of susceptibility. Analysis of independent wheat mutants for several of these genes has shown that they play a key function in enabling disease progression, with mutants displaying a severe reduction in disease symptoms. Developing and applying a genomics-driven approach to pathogen surveillance, we have generated valuable new knowledge on both the pathogen and host sides of the interaction that could be extremely useful for disease management.

Bio:

Dr. Diane Saunders is a Project Leader at the John Innes Centre, Norwich Research Park, Norwich, UK. Dr.Saunders received her BSc from Exeter University where she continued her PhD in the laboratory of Prof. Nick Talbot studying the genetic mechanisms that regulate plant pathogen development. After receiving her PhD in 2009, she joined Prof. Sophien Kamoun's group at The Sainsbury laboratory to continue to study the molecular mechanisms that underpin plant-pathogen interactions. In 2014, Diane became a computational biology fellow at the JIC and Earlham Institute, and moved to a Project Leader in 2017. Diane's research focuses on (re-)emerging plant pathogens that pose a significant threat to agriculture, and particularly wheat rust pathogens that are known as the "polio of agriculture". She uses an array of approaches to improve our understanding of how plant pathogens cause disease. To gain insight into the population dynamics of the wheat rust pathogens, Diane pioneered a revolutionary genomics-based pathogen surveillance technique called "field pathogenomics" to generate high-resolution data directly from infected field samples. This information is essential to help breeders to develop wheat varieties that are resistant to the wider range of yellow rust isolates that they now find in the field. https://www.jic.ac.uk/people/diane-saunders/



PS10. Wednesday, July 10, afternoon session at 1:30 pm

Dr. Liam Dolan
University of Oxford, UK

Evolution and development of the earliest land plant rooting systems

Abstract: The evolution of the first rooting systems some time before 400 million years was a key innovation that occurred when the first complex multicellular eukaryotic photosynthetic organisms – plants – colonized the land. The rooting systems of the earliest diverging group of extant land plants comprised unicellular tip-growing filaments called rhizoids and are morphologically similar to cells that develop at the interface between the plant and the soil in vascular plants – root hairs. Subsequently specialized axes – multicellular structures that develop from self-renewing populations of cells called meristems – with evolved that carry out rooting function. A major aim of our research is to use fossils and genes to understand key events in the evolution of land plant rooting systems. Fossils demonstrate the variety of forms that existed and how these forms developed. We have identified the oldest rooting structures with meristems. Genetics has allowed us to define the regulatory mechanisms that controlled the development of the first land plant root system and demonstrate how these mechanisms changed during the course of evolution. This positive regulatory mechanism is preserved in most land extant plant lineages. By contrast, negative regulatory components of the mechanism evolved independently in different lineages and some are more than 300 million years old. By combining evidence from paleontology, genetics and development we can construct a picture for the evolution of rooting systems in the 100 million years after plants colonized the land and radiated across the continental surfaces.

Bio:

Liam Dolan graduated with a degree in Botany at University College, Dublin. He carried out PhD research on plant developmental genetics in cotton and Arabidopsis at the University of Pennsylvania with Scott Poethig and a post doc with Keith Roberts at the John Innes Centre in Norwich. After 13 years running his own research group at the John Innes Centre, he moved to the University of Oxford as the Sherardian Professor of Botany in 2009. He was Head of the Department of Plant Sciences between 2012 and 2017.

His research uses fossils and genes to understand how roots develop and evolved in the 470-500 million years since plants colonized the land. Fossils reveal the structure of ancient rooting systems. Genetics identifies developmental mechanisms controlling cellular development of rooting structures. Comparative developmental genetics illustrates how these mechanisms evolved in the course of plant evolution. A major discovery was the demonstration that the same genetic mechanism controlled the development of the simple rooting structures on the first land plants and the development of root hairs on the surface of extant vascular plant roots. https://www.plants.ox.ac.uk/people/liam-dolan

PS11. Wednesday, July 10, afternoon session at 2:20 pm

Dr. Siobhan Brady
University of California-Davis, USA

Systems biology of root development

Abstract: The plant vascular system supports the transport of water and nutrients throughout the plant body. Xylem cells contained within this tissue allow for long distance transport from the plant root to the shoot. Although the majority of plant cells are totipotent, xylem cells are unusual in that they undergo terminal differentiation. While the genes regulating this process are well characterized, much less is known regarding the dynamic behavior underlying the transition to xylem cell differentiation.

I will highlight the use of high-throughput yeast one hybrid network mapping, automated phenotyping, mining of publically available gene expression data and single cell sequencing approaches. Collectively, these approaches have led to the identification of double the number of transcription factors and novel modes of regulation involved in nitrogen metabolic regulation, and a bistable switch that underlies xylem cell differentiation.

Nitrogen is essential for plant growth. Insufficient nitrogen leads to decreased agricultural yield while nitrogen application from fertilizers results in increased plant productivity but can have a negative impact on the environment. Changes in nitrogen availability are perceived by dual function nitrate transporters in the root resulting in a signaling cascade and subsequent changes in gene expression. Despite the importance of transcriptional regulation in this adaptive response, a minimal number of nitrogen metabolic transcriptional regulators have been identified.

Bio:

Siobhan Brady received her PhD at the University of Toronto in 2005, and she was a Natural Sciences and Engineering Research Council of Canada Postdoctoral Fellow at Duke University from 2005 – 2008. In 2009 she began an Assistant Professor Position and became an Associate Professor in 2015 at the University of California, Davis in the Department of Plant Biology and in the Genome Center. In 2016, she was named as a Howard Hughes Medical Institute Faculty Research Scholar. Research in the Brady lab focuses on the global regulation of gene expression and its contribution to root morphology and development in Arabidopsis thaliana, Solanum species, Sorghum bicolor and maize.

Homepage: http://www-plb.ucdavis.edu/labs/brady/

Linkedin: http://www.linkedin.com/pub/siobhan-brady/33/b42/71a/

Twitter: @bradylabs

PS12. Wednesday, July 10, afternoon session at 3:40 pm

Dr. William Plaxton
Queen's University, Kingston, ON

CSPB Gold Medal Address:
Feeding hungry plants: Purple acid phosphatases play a pivotal role in phosphorous nutrition

Abstract: Phosphorus is an environmentally-limiting macronutrient that roots can only assimilate from soil as soluble inorganic phosphate (Pi, $H_2PO_4^-$). The most abundant P fraction of many soils exists as organic Pi-monoesters (derived from decomposing biomaterial) unavailable for root uptake until hydrolyzed by secretory purple acid phosphatases (PAPs). Plant PAPs belong to a relatively large multigene family whose specific functions in P-metabolism are poorly understood. Purification, characterization, and identification via LC-MS/MS (peptide sequencing) of intracellular (vacuolar) and secreted (cell wall) PAP isozymes upregulated by Pi-starved suspension cell cultures of the model plant *Arabidopsis thaliana* have been complemented by studies of the corresponding loss-of-function mutants. This has allowed us to pinpoint the predominant Pi-starvation-inducible PAP isozymes *(i.e.,* AtPAP12, AtPAP17, AtPAP25, and AtPAP26) that facilitate *Arabidopsis* P-acquisition efficiency. AtPAP26 is of particular interest since it is: (i) the predominant PAP isozyme upregulated by Pi-deprived *Arabidopsis*, and (ii) also markedly upregulated during leaf senescence to remobilize Pi to developing seeds. Kinetic studies with purified vacuolar and secreted AtPAP26 glycoforms demonstrated that it effectively hydrolyzes Pi from a wide range of substrates with high catalytic efficiency. Furthermore, a Pi starvation- and senescence-inducible, tyrosine-phosphorylated and dual-targeted (*i.e.,* cell wall & vacuole) GNA-apple domain lectin (AtGAL1) interacts with, stabilizes, and activates a high-mannose glycoform of AtPAP26. AtPAP26 is emerging as a promising candidate for enhancing the P-acquisition and P-use efficiency of engineered crop plants. Achieving this goal is urgently required to reduce the massive overuse of non-renewable, inefficient, and polluting Pi-containing fertilizers in agricultural production.

Bio:

William Plaxton received BSc (in 1980) and PhD (in 1984) degrees in Biochemistry from Carleton University (Ottawa). His PhD dissertation was under the supervision of Ken Storey and focussed on the metabolic adaptations of intertidal marine molluscs to anoxia stress. Plaxton was awarded an NSERC Post-doctoral Fellowship to conduct research on plant starch metabolism with Jack Preiss at the Dept. of Biochemistry, Michigan State University. In 1986 he was appointed to the faculty in the Dept. of Biology at Queen's University (Kingston). Plaxton's research program has been funded by NSERC and the Queen's Research Chair Program to conduct studies of the organization and control of plant (especially oilseed) glycolysis and respiratory metabolism, and the metabolic adaptations of phosphorus-starved plants. This research has integrated various biochemical, proteomic, genetic, and cell biology tools to characterize the molecular and functional properties of key enzyme proteins (with a particular interest in the crucial post-translational enzyme modifications such as phosphorylation and glycosylation). He has served as the President of the CSPB, and he is the recipient of both the CSPB C.D. Nelson Award and The Society Medal. Plaxton also enjoys Canada's magnificent outdoors and natural beauty, keeping fit, and playing upright and electric bass. https://biology.queensu.ca/people/department/professors/plaxton/

Concurrent Speaker Sessions-Overview

Rooms	Monday 1:15-2:45pm	Monday 3:15-4:45pm	Tuesday 1:15-2:45pm	Tuesday 3:15-4:45pm
101	**SDG** **Seed Development and Germination**	**MPI** **Molecular Plant Improvement**	**ABS3** **Abiotic Stress #3 Abiotic Stress Response Mechanisms**	**DR** **Development and Reproduction**
102	**AGR1** **Agronomy I – N and P Fertility**	**AGR2** **Agronomy II – Cropping Systems**	**SM** **Specialized Metabolism**	**CE2** **Controlled Environment 2**
103	**ABS1** **Abiotic Stress #1 Resilience to Temperature Extremes**	**ABS2** **Abiotic Stress #2 Oxidative and Nutrient Stress**	**CB** **Cell Biology**	**BCM** **Biochemistry and Metabolism**
104	**MHPI1** **Molecular Host-Pathogen Interaction**	**BSB** **Bioinformatics and Systems Biology**	**MHPI3** **Molecular Host-Pathogen Interaction**	**BASP** **Innovations in Biotic and Abiotic Stress in Potato**
105	**BPP** **Bioproducts Production in Plants-** **Sponsored by Medicago**	**BG1** **Breeding and Genetics**	**CEI** **Controlled Environment 1**	**BG2** **Breeding and Genetics**
106	**EEP1** **Ecology and Ecophysiology 1**	**EEP2** **Ecology and Ecophysiology 2**	**EEP3** **Ecology and Ecophysiology3**	**TXS** **Taxonomy and Systematics**
107	**PPHQ** **Horticulture: Pre and Post-Harvest Quality**	**CSHS-II** **Horticulture: Field Production**	**SBGP** **Soybean Breeding, Genetics, and Physiology**	**BI** **Biotic Interactions**
108	**DM** **Disease Management** **(CPS-S1 student competition)**	**HFP** **Molecular Host-Pathogen Interactions** **(CPS-S2 student competition)**	**IPP1** **Innovations in Plant Pathology P1** **(CPS-S3 student competition)**	**MHPI2** **Innovations in Plant Pathology P2** **(CPS-S4 student competition)**
109	**PSDM** **Innovations in Plant Pathology Surveillance and Diagnostic Methods**	**FMW** **Innovations in Fusarium Management in Wheat**	**WHP** **Weeds, Herbivores and Parasites**	**NBEI** **Nutrients, Biotic and Environmental Interactions**
MACN **r. 113**		**CPDM** **Cannabis Production and Disease Management-** **Sponsored by Innotech Alberta**		

MACN = MacNaughton Building (just to the north of the University Centre)

Details on Concurrent Speaker Sessions

Oral presentations are not numbered according to the ID# assigned during abstract submission; use the Concurrent Sessions below as a guide to find your new abstract number. The presenter's name is underlined, and student presenters being considered for speaker awards are shown by an asterisk (*). Within Adobe Acrobat, use 'Edit' → 'Find' to locate authors etc.

MONDAY AFTERNOON – Concurrent Session 1–

Room 101		**SDG – Seed Development and Germination** *Chair:* ***Mark Belmonte*** *(University of Manitoba)*
1:15	**S1**	**Transcriptome landscape of the early *Brassica napus* seed** **Zeigler, D; D. Khan; J.L. Kalichuck; M.G. Becker; M.F. Belmonte** (*University of Manitoba*)
1:30	**S2**	**Arabidopsis seed stored mRNAs are degraded constantly over aging time, as revealed by new quantification methods** **Zhao, L.[*1]; S. Wang[1]; Y-B. Fu[2]; H. Wang[1]** ([1]*University of Saskatchewan;* [2]*Agriculture and Agri-Food Canada*)
1:45	**S3**	**Strigolactone receptors from striga activate a latent Arabidopsis signaling pathway to bypass the gibberellin requirement for germination** **Bunsick, M.[*]; K. Nemrish; P. Sung; G. Ly; S. Lumba** (*University of Toronto*)
2:00	**S4**	**Early chemical priming persistently attenuates induced anthocyanin accumulation with broader metabolic and possible systems-level impact** **Hiiback, K.[*1]; M. Campbell[2]** ([1]*University of Toronto;* [2]*University of Guelph*)
2:15	**S5**	**Functional characterization of gibberellic acid signalling components in *Striga hermonthica*** **Wong, C.[*]; K. Meteleva; H. McIlwraith; A. Caragea; S. Lumba** (*University of Toronto*)
2:30	**S6**	**Two hallmarks of plant adaptation viewed through the embryonic lens** **Venglat, P.; K. Tanino** (*University of Saskatchewan*)
Room 102		**AGR1 – Agronomy I – N and P Fertility** *Chairs:* ***Jaswinder Singh*** *(McGill University)* and ***Amarjit Basra*** *(OCP North America)*
1:15	**S7**	**Fall and spring placement of nitrogen fertilizers. Where do enhanced efficiency fertilizers fit?** **Karamanos, R.** (Koch Fertilizer Canada, ULC)
1:45	**S8**	**Nitrogen and phosphorus nutrition in oat: nutrient uptake and interactive effect on crop lodging and yield** **Ma, B-L.[1]; Z. Zheng[2]; D. Pageau[2]; C. Vera[2]; J. Fregeau-Reid[2]; A. Xue[2]; W. Yan[2]** [1]*Agriculture and Agri-Food Canada;* [2]*AAFC*
2:00	**S9**	**Nitrogen fertilizer management for inbred seed corn** **Sayem, S.M.[*1]; L. Van Eerd[2]** ([1]*University of Guelph;* [2]*University of Guelph Ridgetown Campus*)
2:15	**S10**	**Evaluating the effects of organic and inorganic phosphorus amendment on soil biochemical and microbial characteristic in podzol following silage corn cultivation under boreal climate** **Cheema, M.[1]; W. Ali[1]; M. Nadeem[1]; W. Ashiq[1]; M. Zaeem[1]; S. Gillani[1]; S. Khamseh[2]; V. Kavanagh[3]; R. Thomas[1]** ([1]*Grenfell Campus, Memorial University of Newfoundland, Canada;* [2]*Shahrekord University;* [3]*Government of Newfoundland and Labrador*)

2:30	S11	**Evaluation of optical sensors in predicting yield and nitrogen application in sugarbeet (*Beta vulgaris*)** **MacFarlane, J.; L. Van Eerd** (*University of Guelph Ridgetown Campus*)
Room 103		**ABS1 – Abiotic Stress #1 Resilience to Temperature Extremes** *Chair:* ***Jean-Benoit Charron*** *(McGill University)*
1:15	S12	**Simulating natural environmental cues redefines winter hardiness of *Brachypodium distachyon* by connecting cold acclimation, vernalization, and development** **Charron, J-B.[1]; B.F. Mayer[1]; A. Bertrand[2]** ([1]*McGill University;* [2]*Agriculture and Agri-Food Canada*)
1:30	S13	**Dimerization of Vitis ICE with Vitis FAMA enables activation via a specific MYC element in the Vitis CBF4 promoter sequence** **Alibabai, L.; A. Edge; M. Rahman; Nassuth, A.** (*University of Guelph*)
1:45	S14	**Using global metabolomic and transcriptomic analysis to assess heat-shock-response functionality in the Antarctic alga Chlamydomonas sp. UWO241** **Possmayer, M.[1]; M. Cvetkovska[1]; N. Malczewski[2]; B. Szyszka[2]; N. Hüner[2]** ([1]*University of Ottawa;* [2]*UWO*)
2:00	S15	**Tissue-specific changes in the apoplastic and intracellular proteome during sub-zero acclimation of winter wheat and rye crowns** **Willick, I.[1]; M. Uemura[2]; B. Fowler[1]; K. Tanino[1]** ([1]*University of Saskatchewan;* [2]*Iwate University*)
2:15	S16	**Thriving or barely surviving: examining heat-stress induced mortality of tamarack under extreme climate conditions** **Murphy, B.[*]; D. Way** (*University of Western Ontario*)
2:30	S17	**Multigenerational heat stress induces phenotypic resilience as well as genetic and epigenetic variations in Arabidopsis thaliana offspring** **Yadav, N.[*]; V. Titov; I. Ayemere; B. Byeon; Y. Ilnytskyy; I. Kovalchuk** *(The University of Lethbridge*)
Room 104		**CHPI1 – Molecular Host-Pathogen Interaction** *Chair:* ***Jacqueline Monaghan*** *(Queen's University)*
1:15	S18	**Root damage and immune responses at cellular resolution** **Geldner, N.** (*University of Lausanne*)
1:45	S19	**The MACPF protein CAD1 is guarded by the plant immune system** **Sementchoukova, I.[*1]; D. Holmes[1]; M. Bredow[1]; K. Siegal[1]; K. Thor[2]; S. Pascetta[1]; C. Zipfel[2]; J. Monaghan[1]** ([1]*Queen's University;* [2]*University of East Anglia*)
2:00	S20	**Sub-functionalization of the calcium-dependent protein kinase CPK28 by site-specific phosphorylation** **Bredow, M.[*1]; K. Bender[2]; D. Holmes[1]; A. Thomson[1]; A. Johnson-Dingee[1]; S. Huber[3]; J. Monaghan[1]** ([1]*Queen's University;* [2]*University of Zurich;* [3]*University of Illinois-Urbana-Champaign*)
2:15	S21	**Biofilm formation contributes to *Pseudomonas syringae* pv. tomato success and suppression of biofilm formation is important for PAMP-triggered immunity in Arabidopsis** **Nunn, G.[*]; A. Fufeng; N. Xiao; A. Halim; R. Cameron** (*McMaster University*)
2:30	S22	**Regulation of plant immune signaling by receptor kinase phosphorylation** **Bender, K.[1]; D. Couto[2]; Y. Kadota[3]; A. Macho[4]; L. Stransfeld[1]; C. Zipfel[1]** ([1]*University of Zurich;* [2]*University of Geneva;* [3]*RIKEN;* [4]*Chinese Academy of Sciences*)
Room 105		**BPP1 – Bioproducts Production in Plants-Sponsored by Medicago** *Chair:* ***Dominique Michaud*** *(* Université Laval*)*
1:15	S23	**Plant proteases: a continuous battle in molecular farming** **Varennes-Jutras, P.; I. Dodds; R. van der Hoorn** (*University of Oxford*)

1:30	S24	**Development of LED light quality to optimise recombinant protein expression in Nicotiana benthamiana** **Ratcliffe, S.*** (*University of Guelph*)
1:45	S25	**Production of recombinant subunit vaccine candidates against Bovine Respiratory Disease pathogen *Mannheimia haemolytica* as an alternative to antimicrobials** **Kaldis, A.; M. Uddin; T. Alexander; R. Menassa;** (*Government of Canada*)
2:00	S26	**Controlling the accumulation of secondary metabolites by plants using antisense oligonucleotides** **Oberemok, V.*[1]; K. Laikova[1]; I. Novikov*[2]; N. Galchinsky[1]; R. Useinov[1]** [1]*V.I. Vernadsky Crimean Federal University;* [2]*Research Institute of Agriculture of Crimea*
2:15	S27	**Parallel branch pathways have evolved for assembly of major monoterpenoid indole alkaloids with opposite optical rotations in Catharanthus roseus** **Williams, D.*[1]; Y. Qu[2] ; V. De Luca[1]** ([1]*Brock University;* [2]*University of New Brunswick*)
2:30	S28	**Towards understanding the basis of substrate specificity in a newly characterized class of plant acyl-ACP thioesterases that produce high-value medium-chain fatty acids** **Kalinger, R.*; I. Pulsifer; O. Rowland** (*Carleton University*)
Room 106		**EEP1 – Ecology and Ecophysiology 1** *Chair:* ***John Markham*** *(University of Manitoba)*
1:15	S29	**Nutrient deposition modifies how arbuscular mycorrhizal fungi influences competitive interactions in plants** **Hicks, K.; H. Maherali** (*University of Guelph*)
1:30	S30	**Nitrogen fixing plant evolution: the interactive effect of elevating CO2 and herbivores on nitrogen fixing plants** **Chen, H.*; J. Markham** (*University of Manitoba*)
1:45	S31	**Spring into action: How warm air and cool soil temperatures influence nitrogen fixation and physiological performance in green alder** **Anderson, P.*; J. Markham** (*University of Manitoba*)
2:00	S32	**Influence of mycorrhizal mutualism and plant life history on the diversification of plant root morphology and function** **Shao, J.*; H. Maherali** (*University of Guelph*)
2:15	S33	**Rhizosphere temperature, tree species and ectomycorrhizae affect nitrogen uptake** **Hawkins, B.; S. Robbins** (*University of Victoria*)
2:30	S34	**Soil moisture and nitrogen, but not phosphorus and light, limit nitrogen fixation in alders in the south western boreal forest** **Markham, J.; P. Anderson** (*University of Manitoba*)
Room 107		**PPHQ – Horticulture: Pre and Post Harvest Quality** *Chair:* ***Jayasankar Subramanian*** *(University of Guelph)*
1:15	S35	**Mutational genetics in diploid potatoes and pre/post-harvest control of toxicants** **Fofana, B.[1]; A. Somalraju[1]; K. Ghose[2]; D. Main[1]; J. McCallum[1]** ([1]*Charlottetown research and development centre;* [2]*Texas Tech University*)
1:30	S36	**Recent advances in hexanal based packaging technologies to enhance shelf life of fruits** **Subramanian, J.[1]; G. Paliyath[1]; L-T. Lim[1]; K. Subramanian[2]** ([1]*University of Guelph;* [2]*Tamil Nadu Agricultural University*)
2:00	S37	**Mitigation of fruit drop and prolonging of postharvest shelf life in 'Honeycrisp' apples using hexanal** **DeBrouwer, E.J.*[1]; J.A. Sullivan[1]; G. Paliyath[1]; J. Subramanian[2]** *([1]University of Guelph;* [2]*University of Guelph, Vineland)*

2:15	S38	**The pollen tube growth model for precision blossom thinning of apples** **Sherif, S.; C. Allen; K. Yoder** (*Virginia Tech*)
2:30	S39	**Challenges of cultivating saffron under cold climate** **Ayari, M-A.*; L. Lapointe** ([1]*Université Laval*)
Room 108		**DM – Disease Management (CPS-S1 student competition)** *Chairs:* ***Vikram Bisht*** *(Manitoba Agriculture)* and ***Tom Fetch*** *(Agriculture and Agri-Food Canada)*
1:15	S40	**Does spraying paraquat increase in-field inoculum of *Colletotrichum fioriniae* in celery production?** **Reynolds, S.*[1]; L. Droste[1]; M. Celetti[2]; M.R. McDonald[1]** ([1]*University of Guelph;* [2]*Ontario Ministry of Agriculture, Food and Rural Affairs*)
1:30	S41	**Ferrous sulfate reduces dollar spot disease on different cultivars of creeping bentgrass** **Rudland, M.*; T. Hsiang; V. Forte-Perri** (*University of Guelph*)
1:45	S42	***In vitro* and in-field response of *Stemphylium vesicarium* to foliar fungicides** **S. Stricker*[1];Pethybridge, S.J.[2]; B. Gossen[3]; M.R. McDonald[1]** ([1]*University of Guelph;* [2]*Cornell University;* [3]*Agriculture and Agri-Food Canada)*
2:00	S43	**Evaluation of yield losses and pyraclostrobin sensitivity in *Leptosphaeria maculans*, cause of blackleg of canola** **Wang, Y.*; S-F. Hwang; A. Akhavan; S. Strelkov** (*University of Alberta*)
2:15	S44	**Effects of solarization, anaerobic soil disinfestation and mustard biofumigation on ginseng replant disease** **Shi, A.*[1]; S. Westerveld[2]** ([1]*University of Guelph;* [2]*Ontario Ministry of Agriculture, Food and Rural Affairs*)
2:30	S102	**Development of *Simplicillium lamellicola* as a biocontrol agent against the wheat pathogen *Fusarium graminearum*** **Abaya, A.*; T. Hsiang** (*University of Guelph)*
2:45		**Speakers participate in a panel discussion**
Room 109		**PSDM – Innovations in Plant Pathology Surveillance and Diagnostic Methods** *Chair:* ***Xuechan (Shannon) Shan*** *(University of Guelph)*
1:15	S45	**Diagnostic metagenomics in the context of molecular plant pathology** **Chen, W.[1]; S. Hambleton[1]; K. Seifert[1]; D. Radford[1]; C.A. Levesque[2]** ([1]*Agriculture and Agri-Food Canada;* [2]*Canadian Food Inspection Agency)*
1:30	S46	**Genome-enhanced detection and identification of regulated plant pathogens** **Bilodeau, G.J.[1]; E. Giroux[1]; N. Feau[2]; R.C. Hamelin[2]** ([1]*Canadian Food Inspection Agency;* [2]*University of British Columbia*)
1:45	S47	**Molecular surveillance of Fusarium species and chemotypes of wheat across western Canada** **Oghenekaro, A.[1]; P. Cholango-Martinez[2]; M. Oviedo-Ludena[2]; M. Harding[3]; X. Wang[4]; R. Kutcher[2]; D. Fernando[1]** ([1]*University of Manitoba;* [2]*University of Saskatchewan;* [3]*Agriculture and Forestry;* [4]*AAFC*)
2:00	S48	**Race dynamic, diversity and virulence in *Puccinia striiformis* f. sp. *tritici* in Canada over the last three decades** **Ghanbarnia[1], K.; R. Gourlie[1]; E. Amundsen[1];X. Chen[2]; Aboukhaddour, R.[1]** ([1]*AAFC;* [2]*USDA*)
2:15	S49	**Comparative study of grapevine red blotch virus (GRBV) pcr detection methods and their application to a general lab practice** **Kim, W-S.** (Norgen Biotek Corp.)
2:30		**Speakers participate in a panel discussion**

MONDAY AFTERNOON – Concurrent Session 2–

Room 101		**MPI – Molecular Plant Improvement** *Chair:* ***Yafan Huang*** *(Performance Plants Inc.)*
3:15	S50	**Improvement of biomass digestibility through the manipulation of tricin biosynthesis pathway in rice** **Lo, C[1] ; P. Ying[2]; A.C.W. Lui[1]; L. Wang[1]; T. Umezawa[2]; Y. Tobimatsu[2]** ([1]*The University of Hong Kong;* [2]*Kyoto University*)
3:30	S51	**mRNA long-distance transport of osmotic responsive genes in tomato/potato heterograft** **Hezema, Y.[*1]; S. Sherif[2]; M. Shukla[1]; P. Saxena[1]** ([1]*University of Guelph;* [2]*Virginia Tech*)
3:45	S52	**Complex Regulation of Condensed Tannin Biosynthesis in Poplar by R2R3 MYB Activators and Repressors** **Constabel, P.** (University of Victoria)
4:00	S53	**Genome-wide association analysis reveals the genetic basis of root system architecture in soybean** **Seck, W.[*]; D. Torkamaneh; F. Belzile** (*Université Laval*)
4:15	S54	**Metabolomics-assisted applications in nutritional genomics and crop improvement** **Wijekoon, C.[1]; S. Singer[1]; R. Weselake[2] S. Acharya[1] ;** ([1]*Agriculture and Agri-Food Canada;* [2]*University of Alberta)*
4:30	S55	**A unified DNA assembly platform for plant research and genome editing** **Bircheneder, M.[1] ; M. Parniske[1]; D. Chiasson[2]** ([1]*LMU Munich;* [2]*Saint Mary's University)*
Room 102		**AGR2 – Agronomy II – Cropping Systems** *Chair:* ***Mumtaz Cheema*** *(Memorial University)*
3:15	S58	**New long-term platforms to investigate agro-ecological services of cover crops across various grain cropping systems in Ontario** **Chapagain, T.[1]; M. Stewart[1]; G. Chu[1]; M. Raizada[1]; L. Van Eerd[2]; B. Deen[1]; D. Hooker[1]** ([1]*University of Guelph;* [2]*University of Guelph Ridgetown Campus*)
3:30	S56	**Integrating perennial forage seed crops in the cropping systems in western Canada: An agroecological and economic assessment** **Khanal, N.[1]; R. Azooz[1]; N. Lupwayi[1]; J. Otani[1]; C. Yoder[2]** ([1]*Agriculture and Agri-Food Canada;* [2]*Government of Alberta*)
3:45	S60	**The effect of micronutrients and macronutrients on the development and grain yield of annual canarygrass (*Phalaris canariensis* L.)** **May, W.** (Agriculture and Agri-Food Canada)
4:00	S61	**Maximizing canola yield by application of N, S, Micronutrients, Fungicide and Growth Regulator in Northwestern Ontario** **Sahota, T.** (LUARS Lakehead University Thunder Bay)
4:15	S57	**Responses of various cover crop species to agro-mineral soil amendment over time** **VanVolkenburg, H.[1*]; F. Guinel[2]; L. Vasseur[1]** ([1] *Brock University;* [2] *Wilfrid Laurier University)*
4:30	S59	**Sustainable agriculture kits (SAKs) for subsistence farmers** **Raizada, M.[1]; T. Chapagain[1]; P. Roshan[2]; B. Ghimire[2]; M. Thilakarathna[1]; L. Smith[1]; R. Devkota[1]; M. Sharma[3]; B. Thapa[2]** ([1]*University of Guelph;* [2]*Local Initiatives for Biodiversity, Research and Development;* [3]*Anamolbiu Prvt Limited*)

Room 103		**ABS2 – Abiotic Stress #2 Oxidative and Nutrient Stress** *Chair:* ***Mike Deyholos*** *(University of British Columbia-Okanagan)*
3:15	S62	**The Antarctic alga Chlamydomonas sp. UWO241 as an emerging model photosynthetic adaptation to extreme conditions: perspectives and challenges** **Cvetkovska, M.** (University of Ottawa)
3:30	S63	**Resource independent plant competition alters ROS levels, antioxidant status and susceptibility to cell death in Arabidopsis thaliana** **Berardi, N.[*]; S. Amirsadeghi; C. Swanton** (*University of Guelph*)
3:45	S64	**Metabolism of reactive oxygen and nitrogen species during anoxic stress and reaeration in tobacco plants differentially expressing alternative oxidase** **Jayawardhane, J.[*1]; A. Igamberdiev[1]; G.C. Vanlerberghe[2]** ([1]*Memorial University of Newfoundland;* [2]*University of Toronto Scarborough*)
4:00	S65	**An inverse correlation between surface temperature and nitrogen rate predicted by a thermodynamic theory** **Alzaben, H[*1]; R. Fraser[1] ; C. Swanton[2]** ([1]*University of Waterloo;* [2]*University of Guelph*)
4:15	S67	**High condensed tannin levels protect poplar against oxidative damage generated by UV-B exposure or drought stress** **Gourlay, G.[*1]; B. Hawkins[1]; J-P. Schnitzler[2]; I. Zimmer[2]; A. Albert[2]; P. Constabel[1]** ([1]*University of Victoria;* [2]*Helmholtz Zentrum*)
4:30	S68	**Impact of phosphate or phosphite resupply on the proteome and phosphoproteome of phosphate-deprived Arabidopsis thaliana suspension-cell cultures** **Ghahremani, M.[1]; D. Mehta[2]; M. Pérez-Fernández[3]; T. Barber-Cross[2]; R.G. Uhrig[2]; W. Plaxton[1]** ([1]*Queen's University;* [2]*University of Alberta;* [3]*University Pablo de Olavide*)
Room 104		**BSB – Bioinformatics and Systems Biology** *Chair:* ***R Glen Uhrig*** *(University of Alberta)*
3:15	S69	**Global insights into duplicated gene expression and alternative splicing in polyploid Brassica napus (canola) in response abiotic stress by transcriptome sequencing** **Adams, K.** (University of British Columbia)
3:30	S70	**Linking RNA processing and kinase signaling in the Arabidopsis stress response** **Mehta, D.** (University of Alberta)
3:45	S71	**RNA-Seq estimated gene abundance differences between Zea mays genotypes are strongly affected by read mapping bias** **Zhan, S.; J. Tosh; C. Griswold; L. Lukens** (*University of Guelph*)
4:00	S72	**A Tale of Two Genomes: Methylome and transcriptome profiling of Brassica napus seed development** **Khan, D.[*]; D. Ziegler; M. Belmonte** (*University of Manitoba*)
4:15	S73	**De novo assembly of the pokeweed genome provides insight into pokeweed antiviral protein (PAP) gene expression** **Neller, K.[*1]; C. Diaz[1]; A. Platts[2]; K. Hudak[1]** ([1]*York University;* [2]*New York University*)
4:30	S74	**The long story of small RNA: sRNA architecture of Brassica napus seed development** **Ziegler, D.[*]; D. Khan; M. Belmonte** (*University of Manitoba*)
Room 105		**BG1 – Breeding and Genetics** *Chair:* ***Joe Colasanti*** *(University of Guelph)*
3:15	S75	**Can phloem derived small RNA modify gene regulation in shoot stem cells?** **Minow, M.[*]; V. Coneva; V. Lesy; M. Misyura; J. Colasanti** (*University of Guelph*)
3:30	S76	**Characterization of B-genome specific high copy hAT MITE families in Brassica genome** **Perumal, S.[*]; I. Parkin** ([1]*Agriculture and Agri-Food Canada (AAFC)*)

3:45	S77	**Age of divergence among subgenomes determines gene expression between paralogs in Camelina species** **Chaudhary, R.[*1]; S. Kagale[2]; C.S. Koh[3]; E.E. Higgins[4]; A.G. Sharpe[3]; I.A.P. Parkin[4]** ([1]*University of Saskatchewan;* [2]*National Research Council Canada;* [3]*Global Institute for Food Security;* [4]*Agriculture and Agri-Food Canada*)
4:00	S78	**Transcriptome changes associated with phytoglobin expression during germination of barley seeds** **Zafari, S.[*1]; K.H. Hebelstrup[2]; A. Igamberdiev[1]** ([1]*Memorial University of Newfoundland;* [2]*Aarhus University*)
4:15	S79	**Genome-wide analysis of the SPL/miR156 unit in small grain cereals** **Tripathi, R.[*]; J. Singh** (*McGill University*)
Room 106		**EEP2 – Ecology and Ecophysiology 2** *Chair:* ***Art Fredeen*** *(University of Northern British Columbia)*
3:15	S80	**Influence of epiphyllous bryophytes on the water cycle in a tropical sub montane cloud forest in Costa Rica** **Fenton, N.** (Université du Québec en Abitibi-Témiscamingue (UQAT))
3:30	S81	**Fourteen-year impacts of partial and total forest harvest on epixylic bryophyte species in boreal black spruce –feathermoss forests** **Opoku-Nyame, J.[*1]; A. Leduc[2]; N. Fenton[1]** ([1]*Université du Québec en Abitibi-Témiscamingue (UQAT);* [2]*University of Quebec in Montreal)*
3:45	S82	**Modelling successional dynamics of Canadian boreal mixed woods prior to and following the Spruce Budworm outbreak** **Maleki, K.[*1]; M. Gueye[1]; B. Lafleur[1]; A. Leduc[2]; Y. Bergeron[1]** ([1]*University of Quebec in Abitibi-Temiscamingue (UQAT);* [2]*University of Quebec in Montreal*)
4:00	S83	**How is the understory vegetation influenced by changes in tree canopy dominance in black spruce and trembling aspen in a Canadian boreal forest?** **Rodríguez, J.[*1]; É. Mestre[2]; N. Fenton[1]; S. Kembel[2]; Y. Bergeron[1]** ([1]*Université du Québec en Abitibi-Témiscamingue (UQAT);* [2]*Université du Québec à Montréal (UQAM)*)
4:15	S84	**Compensatory growth release in surviving lodgepole pine in Northern BC after Mountain Pine Beetle attack** **McEwen, J**. (*University of Northern BC*)
4:30	S85	**Finding and re-measuring forest carbon plots after fifteen years: Why, how and so what?** **Fredeen, A.; L. Gan; C. Elkin** (*University of Northern BC*)
Room 107		**HFP – Horticulture: Field Production** *Chair:* ***Bourlaye Fofana*** *(Agriculture and Agri-Food Canada)*
3:15	S86	**Distribution and management of the carrot cyst nematode (*Heterodera carotae*) in Ontario, Canada** **Blauel, T.[1]; D. Van Dyk[2]; K. Vander Kooi[1]; Q. Yu[3]; M.R. McDonald[1]** ([1]*University of Guelph;* [2]*Ontario Ministry of Agriculture, Food and Rural Affairs;* [3]*Agriculture and Agri-Food Canada)*
3:30	S87	**Mycorrhizal fungi in the roots of onion and carrot in relation to mycorrhizal fungal inoculant and soil phosphorus** **Ilyas, U.[*1]; M. Raizada[1]; L. du Toit[2]; M.R. McDonald[1]** ([1]*University of Guelph;* [2]*Washington State University*)
3:45	S89	**Analyzing the effects of nitrogen fertilizer source on flower bud induction in day-neutral strawberry** **Paul, A.[*]; V. Gravel** (*McGill University*)

4:00	S90	**Light quality and night interruption controls morphogenesis and flowering time in day neutral strawberry** **Sidhu, V.*; V. Gravel; S. Jabaji** (*McGill University*)
4:15	S88	**Evidence for a recent re-expansion of market gardening in Ontario through organic field fruit and vegetable production** **Chappell, E; E. Deboer; B.J. Micallef (*University of Guelph)***
4:30	S91	**Microhazels: A novel industry for Ontario agriculture** **Shukla, M.; P. Saxena** (*University of Guelph*)
Room 108		**MHPI2 – Molecular Host-Pathogen Interactions (CPS-S2 student competition)** *Chairs: **Barry Saville** (Trent University)* and ***Tom Fetch** (Agriculture and Agri-Food Canada)*
3:15	S92	**Transcriptomic analysis of the response of *Brassica napus* to *Plasmodiophora brassicae*** **Zhou, Q.*; Galindo-González, L.; S-F. Hwang; S. Strelkov** (*University of Alberta*)
3:30	S93	**Transcriptome profiling of incompatible and compatible interactions between *Brassica napus* and *Leptosphaeria maculans*** **Padmathilake, R.*[1]; H. Sonah[2]; S. Jia[1]; Z. Zou[1]; J. Tucker[1]; A. Carter[3]; M-E. Balesdent[4]; P. Hu[1] ; R. Bélanger[2]; D. Fernando[1]** ([1]*University of Manitoba;* [2]*Université Laval;* [3]*Agriculture & Agri-Food Canada;* [4]*UMR INRA AgroParisTech BIOGER*)
3:45	S94	**Tissue specific RNA sequencing of *Brassica napus* in response to *Sclerotinia sclerotiorum* infection** **Walker, P.*** (University of Manitoba)
4:00	S95	**Boost your yield, harness the forcefield: advancing RNAi-based biocontrols against agronomic pathogens.** **Wytinck, N.*; A. McLoughlin; D. Ziegler; D. Khan; D. Sullivan; S. Whyard; M. Belmonte** *(University of Manitoba*)
4:15	S96	**Gene editing to enhance pathogen-induced cell wall reinforcement resistance to late blight in Russet Burbank potato** **Hegde, N.*[1]; D. Doddamani[2]; Y. Kalenahalli[3]; N. Soni[1]** ([1]*McGill University;* [2]*The Roslin Institute, The University of Edinburgh;* [3]*University of Adelaide*)
4:30		**Speakers participate in a panel discussion**
Room 109		**FMW – Innovations in Fusarium Management in Wheat** *Chair: **Denis Gaudet** (CPS Board Member, Lethbridge, Alberta)*
3:15	S97	**Assessing the impact of fungicides on FHB caused by Fusarium spp. on two wheat cultivars in Alberta** **Asif, M.*[1]; S. Strydhorst[2]; S. Strelkov[1]; A. Terry[3]; M. Harding[4]; D. Pauly[2]; J. Feng[2]** ([1]*University of Alberta;* [2]*Alberta Agriculture and Forestry;* [3]*Syngenta;* [4]*Agriculture and Forestry)*
3:30	S98	**Genetic factors affecting Fusarium head blight resistance improvement and linkage drag from introgression of exotic Sumai 3 alleles (including Fhb1, Fhb2, and Fhb5) in hard red spring wheat** **Brar, G.S.[1]; A. Brûlé-Babel[2]; Y. Ruan[3]; M.A. Henriquez[;] C.J. Pozniak[1]; R. Kutcher[1]; P.J. Hucl[1]** ([1]*University of Saskatchewan;* [2]*University of Manitoba;* [3]*Agriculture and Agri-Food Canada*)
3:45	S99	**Control of plant fungal pathogens using exogenous RNA** **E. Liu; U. Hemraz; S. Dodard; Y. Liu; S. Hrapovic; Clark, S.** (*National Research Council Canada*)

4:00	S100	**Multi-omic studies reveal the insertion of new mycotoxin virulence factors in Fusarium poae.** **Overy, D.[1]; T. Witte[1]; A. Sproule[2]; A. Hermans[1]; A. Johnston[1]; A. Xue[3]; J. Dettman[1]; H. Nguyen[1]; L. Harris[1]** (*[1]Ottawa Research and Development Centre; [2]Ottawa Research and Development Centre; [3]AAFC)*
4:15	S101	**Targeted mutation of multiple putative effectors in *Fusarium graminearum* utilizing CRISPR/Cas9** **Foster, A; R. Subramaniam** (*Agriculture and Agri-Food Canada*)
MacNaughton **MACN** Room 113		**CPDM – Cannabis Production and Disease Management** **-Sponsored by Innotech Alberta** *Chair:* ***Albert Tenuta*** *(OMAFRA)*
3:15	S168	**Indoor *Cannabis sativa* L. production: current practices and research directions** **Zheng, Y.** (University of Guelph)
3:45	S169	**Variation in rootzone environment influences growth and yield of drug-type cannabis cultivars during the flowering stage** **Yep, B.[*1]; N.V. Gale[2]; Y. Zheng[1]** (*[1]University of Guelph; [2]Green Relief*)
4:00	S170	**Diseases that can devastate *Cannabis sativa* production – bud rots, powdery mildew and root and crown rots.** **Punja, Z.** (Simon Fraser University)
4:30	S171	**Effect of methyl jasmonate on terpene/cannabinoid biosynthesis and suppression of gray mold in *Cannabis sativa* L.** **Cormier, C.; C. Balthazar; A. Cull; D. Joly** (*Université de Moncton*)

5:00 – 7:00 Poster Session 1 at Peter Clark Hall,
Located downstairs in the University Center.

Students that have a poster with an ODD number are to remain by their posters until they are judged.

Beverages will be served.

TUESDAY AFTERNOON – Concurrent Session 3–

Room 101		**ABS3 – Abiotic Stress #3 Abiotic Stress Response Mechanisms** *Chair:* ***Sophia Stone*** *(Dalhousie University)*
1:15	S103	**Flooding tolerance is regulated through the MiR156/SPL module in *Medicago sativa*** **Feyissa, B.A.[*1]; Y. Papadopoulos[2]; S. Kohalmi[3]; A. Hannoufa[4]** ([1]*University of Western Ontario;* [2]*Agriculture and Agri-Food Canada;* [3]*The University of Western Ontario;* [4]*Agriculture and Agri-Food Canada)*
1:30	S105	**Physiological and biochemical responses of alfalfa (*Medicago sativa* L.) to salt stress** **Bhattarai, S.[*1]; C. Karunakaran[2]; K. Tanino[1]; Y-B. Fu[3]; B. Coulman[1]; B. Biligetu[1]** ([1]*University of Saskatchewan;* [2]*Canadian Light Source;* [3]*Agriculture and Agri-Food Canada*)
1:45	S106	**The ABA-responsive SnRK1 kinase interaction network in *Arabidopsis thaliana*** **Carianopol, C.[*]; A. Chan; S. Lumba; S. Gazzarrini** (*University of Toronto*)
2:00	S107	**Characterizing the role of *Arabidopsis thaliana* RING-type E3 Ligase XBAT35.2 and its substrates in abiotic stress tolerance** **Li, Q.[*]; S. Stone** (*Dalhousie University*)
2:15	S104	**Identifying *Brachypodium distachyon* proteins interacting with histone deacetylase BdHD1** **Torrez, A.[*1]; H.A.L. Henry[1] ; L. Tian[2]** ([1]*The University of Western Ontario;* [2]*Agriculture and Agri-Food Canada*)
2:30	S108	**Overexpression of de novo DNA methyltransferase BdDRM2 alters *Brachypodium distachyon* development and abiotic stress response** **Ouellette, L.[*]; B.F. Mayer; J-B. Charron** (*McGill University*)
Room 102		**SM – Specialized Metabolism** *Chair:* ***Jake Stout*** *(University of Manitoba)*
1:15	S109	**Molecular regulation of monoterpene metabolism in Lavandula** **Mahmoud, S.** (UBC Okanagan)
1:30	S110	**Functional study of Lavandula prenyl diphosphate synthase genes** **Adal, A.M.[*1]; S. Mahmoud[2]** ([1]*UBC;* [2]*UBC Okanagan*)
1:45	S111	**Investigating transport of seco-iridoids in Catharanthus roseus** **Dastmalchi, M.[1]; Y. Qu[2]; V. De Luca[1]** ([1]*Brock University;* [2]*University of New Brunswick)*
2:00	S112	**Mitragyna speciosa – a promising player in the opioid crisis** **Moeller, E.; L. Virta; K. Theriault; J. Manduca; M. Perreault; T. Akhtar** (*University of Guelph*)
2:15	S113	**Distinct metabolic modes drive monoterpenoid biosynthesis in a natural population of Pelargonium graveolens (rose scented geranium)** **Bergman, M.; M. Phillips[*]**(*University of Toronto – Mississauga*)
2:30	S114	**Profiling anthocyanin species involved in developmentally regulated programmed cell death in lace plant (*Aponogeton madagascariensis*) leaf development** **Denbigh, G.[*1]; S. MacKinnon[2]; G. Pitcher[2]; H. Wright[2]; C. Lacroix[3]; A. Gunawardena[1]** ([1]*Dalhousie University;* [2]*Agriculture and Agri-food Canada;* [3]*University of Prince Edward Island)*

Room 103		**CB – Cell Biology** *Chair:* ***Jaideep Mathur*** *(University of Guelph)*
1:15	S118	**Make or break? Microtubule growth and shrinkage are controlled by dynamic turnover of plus-end proteins** **Halat, L.[*1]; R. Eng[2]; D. Coombs[1]; G. Wasteneys[1]** ([1]*University of British Columbia;* [2]*Max Planck Institute of Molecular Plant Physiology*)
1:30	S117	**Identification and characterization of novel targets for a subfamily of Arabidopsis calmodulin-like (CML) proteins** **Teresinski, H.[*]; W. Snedden** (*Queen's University*)
1:45	S116	**An Arabidopsis G-protein-coupled receptor-like module regulates cellulose synthase enzyme secretion** **McFarlane, H.** (University of Toronto)
2:00	S120	**DONGLE and DAD-LIKE LIPASE2 enriched sites create organelle interaction hubs** **Lobbezoo, M.[*]; N. Mathur; J. Mathur** (*University of Guelph*)
2:15	S119	**Mechanical role of callose plugs in pollen tubes** **Kapoor, K.[*]; A. Geitmann** (*McGill University*)
2:30	S115	**Hsp70 mediates programmed cell death during the remodeling of lace plant leaves (*Aponogeton madagascariensis*)** **Rowarth, N.[*1]; A. Dauphinee[2]; G. Denbigh[1]; A. Gunawardena[1]** ([1]*Dalhousie;* [2]*Swedish University of Agricultural Sciences*)
Room 104		**MHPI3 – Molecular Host-Pathogen Interaction** *Chair:* ***Dilantha Fernando*** *(University of Manitoba)*
1:15	S121	**Transcriptomic response of multiple Brassica species to *Sclerotinia sclerotiorum* infection** **de Jong, G.; K. Adams** (*University of British Columbia*)
1:30	S122	**Lectin genes in Brassica napus enhance resistance to the fungal pathogen *Sclerotinia sclerotiorum*** **Buchwaldt, L.; D. Hegedus; D. Bekkaoui; J. Durkin; J. Nettleton; E. Dzanaovic** *(Agriculture and Agri-Food Canada)*
1:45	S123	**Investigating the function of the APSES protein encoding gene apu2 (nlt1) during U. maydis biotrophic growth** **Saville, B.[1]; E. Storfie[1]; M. Seegobin[1]; J. Meade[2]; P. Mukondiwa[1]; L. Branch[1]; M. Donaldson[1]** ([1]*Trent University;* [2]*University of Toronto*)
2:00	S124	**Characterization of the Pyrenophora tritici-repentis-barley interaction** **Wei, B.[1]; M. Moscou[2]; K. Sato[3]; S. Strelkov[1]; Aboukhaddour, R.[4]** [1]*University of Alberta;* [2]*The Sainsbury Laboratory*; [3]*Institute of Plant Science and Resources, , 710-0046, Japan;* [4]*AAFC*
2:15	S125	**Relationship between foliar symptoms and gene expression induced by Pear Decline phytoplasma** **Kaviani, M.; P.H. Goodwin; D. Hunter** (*University of Guelph)*
2:30	S126	**Update on Manitoba potato and horticultural crops disease and insect pests in 2018.** **Bisht, V.** (Manitoba Agriculture)
Room 105		**CE1 – Controlled Environment I** *Chair:* ***Youbin Zheng*** *(University of Guelph)*
1:15	S127	**Comparative analysis between conventional and novel water treatment technologies in recirculating hydroponics** **Levesque, S.[*1]; T. Graham[1]; D. Bejan[2]; P. Zhang[1]; J. Lawson[1]; M. Dixon[1]** ([1]*University of Guelph;* [2]*Environmental Technology Consultant*)
1:30	S128	**Focusing on natural changes in solar spectrum to better understand plant light responses** **Marie, T.R.J.G.[*]; B.J. Micallef; B. Grodzinski** (*University of Guelph)*

1:45	S129	**Enhancing plant growth using light emitting diode (LED) technology** **Scandola, S.; Uhrig, R.G** (*University of Alberta*)
2:00	S130	**Optimizing spectral quality of light emitting diodes light for controlled-environment microgreen production** **Ying, Q.[*]; Y. Kong; G.G. Bozzo; Y. Zheng** (*University of Guelph*)
2:15	S131	**Optimizing growing conditions for romaine lettuce (Lactuca Sativa L. var. Longifolia) production in a plant factory** **Bayley, D.[*]; T. Graham; M. Dixon** (*University of Guelph*)
2:30	S132	**Monitoring of functional state of in vitro preserved plants in Lavandula angustifolia Mill.** **Brailko, V.[1]; I. Mitrofanova[2]; N. Ivanova[1]; O. Mitrofanova[1]; I. Novikov[3]** ([1]*FSFIS "The Nikita Botanical Gardens – National Scientific Center of the RAS, Yalta;* [2]*FSFIS "The Nikita Botanical Gardens - National Scientific Center of the RAS"* [3]*Research Institute of Agriculture of Crimea*)
Room 106		**EEP3 – Ecology and Ecophysiology 3** *Chair:* ***Tammy Elliot*** *(*Université de Montréal*)*
1:15	S133	**Precarity of American Water Willow (*Justicia americana*) in Ontario** **Vasseur, L.[1]; O. Groff[2]** ([1]*Brock University;* [2]*Land Care Niagara*)
1:30	S134	**Integrated metabolic strategy: a framework for predicting the evolution of carbon-water tradeoffs within plant clades** **Goud, E.[*1]; J. Sparks[1]; M. Fishbein[2]; A. Agrawal[1]** ([1]*Cornell University;* [2]*Oklahoma State University*)
1:45	S135	**Cryopreservation and reintroduction of Hill's thistle (*Cirsum hillii*) to its natural habitat** **Bi, W.; A. Saxena; M. Shukla; P. Saxena** (*University of Guelph*)
2:00	S136	**A comparison of the vascularization and morphology of floral nectaries in North American asters and goldenrods of tribe Astereae** **Braun, K.[*]; A. Davis** (*University of Saskatchewan*)
2:15	S137	**Impact of perimeter plantings on vineyard ecology** **Hughes, M.[*]; L. Vasseur** (*Brock University*)
2:30	S138	**The changing flora of a UNESCO Biosphere Reserve: a phylogenetic perspective** **Elliott, T.[*1]; J. Davies[2]** ([1]*Institut de recherche en biologie végétale;* [2]*University of British Columbia*)
Room 107		**SBGP – Soybean Breeding, Genetics, and Physiology** *Chair:* ***Istvan Rajcan*** *(University of Guelph)*
1:15	S139	**Genetic diversity in public soybean breeding programs** **Bruce, R.[1]; D. Torkamaneh[2]; A. Ficht[1]; C. Grainger[1]; F. Belzile[2]; M. Eskandari[1] ; I. Rajcan[1]** ([1]*University of Guelph;* [2]*Université Laval)*
1:30	S140	**Identification of a potential candidate gene for the E8 maturity locus in soybean (Glycine max)** **Sadowski, M.[*1]; B. Samanfar[2]; E. Cober[3]; M. Charette[3]; F. Dehne[1]; J. Green[1]; A. Golshani[1]** ([1]*Carleton University;* [2]*Agriculture and Agri-Food Canada;* [3]*AAFC Ottawa-RDC*)
1:45	S141	**Increasing soybean oil yield through targeted gene silencing and overexpression** **Fedosejevs, E.; Y. Ye; E. Myers; J. Thelen** (*University of Missouri*)
2:00	S142	**A compensatory mutation in the GmNFR5α gene restores soybean-rhizobia symbiosis fitness** **Torkamaneh, D.; F. Chalifour; C. Beauchamp; H. Maaroufi; F. Belzile** (*Université Laval*)
2:15	S143	**Identification of differentially-expressed genes involved in seed protein content in soybean (*Glycine Max*) grown In Western Vs. Eastern Canada** **Jahid, B.[*1]; B. Samanfar[2]; E. Cober[3]; L. Tan[2]; D. Luckert[2]; A. Golshani[1]** ([1]*Carleton University;* [2]*Agriculture and Agri-Food Canada;* [3]*AAFC Ottawa-RDC*)

2:30	S144	**Climate and daylength influence on soybean phenology in Manitoba and Ontario** **Ort, N.[*1]; M. Morrison[2]; E. Cober[3]; D. McAndrew[2]; Y. Lawley[1]** ([1]*University of Manitoba;* [2]*Agriculture and Agri-Food Canada;* [3]*AAFC Ottawa-RDC*)
Room 108		**IPP1 – Innovations in Plant Pathology Part 1 (CPS-S3 student competition)** *Chairs:* ***David Joly*** *(Université de Moncton)* and ***Tom Fetch*** *(Agriculture and Agri-Food Canada)*
1:15	S145	**Genomic and virulence differences between two sibling Clarireedia species causing dollar spot on grasses** **Valliani, M.[*]; M. Nasr-Sharif; J. Wang; P. Goodwin; T. Hsiang** (*University of Guelph*)
1:30	S146	**The first report of a culturable microbiome from pollinated style tissue** **Thompson, M.[*1]; A. Shrestha[1]; J. Rinne[1]; C. Shearer[1]; V. Limay-Rios[1]; L. Reid[2]; M. Raizada[1]** ([1]*University of Guelph;* [2]*Agriculture and Agrifood Canada)*
1:45	S147	**Developing a model for investigating pathogenesis by fungal hybrids using *Ustilago maydis* and *Sporisorium reilianum*** **Storfie, E.[*]; B. Saville** (*Trent University*)
2:00	S148	**Genome-wide-association studies on the resistance of rutabaga accessions to *Plasmodiophora brassicae* isolates from Alberta, Canada** **Yu, Z.[*]; R. Fredua-Agyeman; S. Hwang; S. Strelkov** (*University of Alberta*)
2:15	S149	**Molecular characterization and quantification of mycotoxins produced by Fusarium spp** **Durrani, P.[*]; B.M. Pillai** (*Mahidol University*)
2:30		**Speakers participate in a panel discussion**
Room 109		**WHP– Weeds, Herbivores and Parasites** *Chair:* ***François Tardif*** *(University of Guelph)*
1:15	S150	**Evaluation of acetolactate synthase inhibitors in Chenopodium album L. populations in Ontario** **Mo, C.[*1]; F. Tardif[1]; I. Rajcan[1]; M. Cowbrough[2]** ([1]*University of Guelph;* [2]*Government of Ontario*)
1:30	S151	**The use of cereal rye (*Secale cereale* L.) cover crops to control Canada fleabane (*Conyza canadensis* (L.) Cronq.)** **Vanhie, T.[*1]; F. Tardif[1]; C. Swanton[1]; M. Cowbrough[2]** ([1]*University of Guelph;* [2]*Government of Ontario*)
1:45	S152	**Evolution of three herbicide defence strategies: Fitness costs of glyphosate resistance, escape, and tolerance in an agricultural weed** **Teitel, Z.[*]; C. Caruso** (*University of Guelph*)
2:00	S153	**Evaluating seed treatments for the management of soybean cyst nematode (*Heterodera glycines* Ichinohe) in dry bean (*Phaseolus vulgaris* L.).** **Katsande, T.[*1]; K. Jordan[1]; A. Schaafsma[2]; C. Trueman[2]; C. Gillard[2]** ([1]*University of Guelph;* [2]*University of Guelph - Ridgetown Campus)*
2:15	S154	**Red alder defense mechanisms against western tent caterpillar defoliation** **Boateng, K.[*1]; B. Hawkins[1]; P. Constabel[1]; A. Yanchuk[2]** ([1]*University of Victoria;* [2]*BC Ministry of Forests, Lands, Natural Resource Operations and Rural Development*)
2:30	S155	**Investigating the basis of strigolactone perception by HYPOSENSITIVE TO LIGHT/KARRIKIN INSENSITIVE 2** **Toh, S.[1]; S. Schuetz[*2]; A. Arellano Saab[2]; H. Al Galib[2]; P. Stogios[2]; P. McCourt[2]; S. Lumba[2];** ([1]*Meiji University;* [2]*University of Toronto)*

TUESDAY AFTERNOON – Concurrent Session 4–

Room 101		**DR – Development and Reproduction** *Chair:* ***Daphne Goring*** *(University of Toronto)*
3:15	S156	**Arabidopsis clade I TGACG-motif binding basic leucine-zipper transcription factors mediate BLADE-ON-PETIOLE-dependent activities in development and defense** **Wang, Y.[*1]; C. Bergin[1]; B. Salasini[1]; M. Khan[1]; B. Devi[1]; M. Bush[1]; B. Oyetoran[1]; M.L. Smith[1]; R. Subramaniam[2]; S.R. Hepworth[1]** ([1]*Carleton University;* [2]*Agriculture and Agri-Food Canada*)
3:30	S157	**A role for receptor kinases in regulating compatible pollen responses in the Brassicaceae stigma** **Lee, H.K.[*]; D. Goring** (*University of Toronto*)
3:45	S158	**The E3 ubiquitin ligase XERICO modulates stomatal development in *Arabidopsis thaliana*** **Mohamed, D.[*]; E. Vonapartis; C. Carianopol; S. Gazzarrini** (*University of Toronto*)
4:00	S159	**A mechanical feedback loop regulates morphogenesis of pavement cell shapes in Arabidopsis** **Eng, R.[*]; A. Sampathkumar; R. Schneider** (*Max Planck Institute of Molecular Plant Physiology*)
4:15	S160	**Molecules in Action: Quantum dot enabled studies of plant growth regulation** **Erland, L.A.E.[1]; S.J. Murch[1]; P.K. Saxena[2]** ([1]*UBC;* [2]*University of Guelph*)
4:30	S161	**Family Ties: the expression of AROGENATE DEHYDRATASES** **Van Brenk, J.[*]; E. Cornelius; S. Kohalmi** (*The University of Western Ontario*)
Room 102		**CE2 – Controlled Environment 2** *Chair:* ***Karen Tanino*** *(University of Saskatchewan)*
3:15	S162	**Magic blue light: A versatile mediator of plant elongation** **Kong, Y.; K. Schiestel; D. Kamath; R, Johnson; Y. Zheng** (*University of Guelph*)
3:30	S163	**Adapted crops for the low light indoor environment: a concept for year round sustainable gardening in the home with potential for commercial greenhouse production** **Tanino, K.[1]; E. Benic[1]; M. Nair[2]** ([1]*University of Saskatchewan;* [2]*LLT Plants Inc.*)
3:45	S164	**Cultural and genetic approaches for improving the response of greenhouse vegetables to extended photoperiod and supplemental lighting** **Orozco, M.E.; T.R.J.G. Marie; M.C. Micallef; B.J. Micallef** (University of Guelph)
4:00	S165	**Comparison of a supplemental lighting control algorithm and conventional threshold control for greenhouse tomato production** **Poel, B.[1]; X. Hao[2]; M. Yelton[1]; E. Weissman[1]** ([1]*LumiGrow Inc.;* [2]*Agriculture and Agri-Food Canada*)
4:15	S166	**Evaluating the impact of Inter-canopy LED Lighting on the production of Bush Beans within a Controlled Environment** **Stoochnoff, J.[*]; T. Graham; M. Dixon** (*University of Guelph*)
4:30	S167	**Canopy growth manipulation and adventitious root development in Kalanchoe blossfeldiana cuttings using targeted LED lighting spectra** **Rasool, A.[*]** (University of Guelph)
Room 103		**BCM– Biochemistry and Metabolism** *Chair:* ***Wayne Sneddon*** *(Queen's University)*
3:15	S207	**Arabidopsis CTP:phosphocholine cytidylyltransferase is phosphorylated and inactivated by SnRK1** **Caldo, K.; Y. Xu; L. Falarz; K. Jayawardana; J. Acedo; G. Chen** (*University of Alberta*)

3:30	S208	**Identifying sequences required to piggyback AtADT5 into the nucleus** **Clayton, E.*; S. Abolhassani Rad; M. Smith-Uffen; S. Kohalmi** *(The University of Western Ontario)*
3:45	S209	**Evolutionary insights into the role of shikimate kinase-like 1 in chloroplast biogenesis** **Kanaris, M.*; D. Christendat; J. Lee** (*University of Toronto*)
4:00	S210	**Investigating quinate metabolism** **Gritsunov, A.*; D. Christendat** (*University of Toronto*)
4:15	S211	**Autophosphorylation inhibits the Ca2+-dependent protein kinase RcCDPK1 from developing castor oil seeds** **Kilburn, R.*; W. Snedden; W. Plaxton** (*Queen's University*)
4:30	S212	**Recent advances in plant ubiquinone (Coenzyme Q) biosynthesis and engineering** **Soubeyrand, E.[1]; T. Johnson[1]; S. Latimer[1]; A. Bernert[1]; M. Kelly[1]; J. Kim[1]; T. Colquhoun[1]; A. Block[2]; G. Basset[1]** ([1]*University of Florida;* [2]*USDA*)
Room 104		**BASP – Innovations in Biotic and Abiotic Stress in Potato** *Chair:* ***Nathalie Beaudoin*** *(University of Sherbrooke)*
3:15	S176	**Tuber-specific expression of a heterologous host defense peptide reduces post-harvest diseases in potato** **Yevtushenko, D.** (University of Lethbridge)
3:30	S172	**Increased resistance to potato common scab is associated with changes in the tuber periderm** **Turcotte, M.A.*; S. Labidi; S. Lerat; N. Beaudoin** (*University of Sherbrooke*)
3:45	S173	**Implication of major tuber flesh proteins in common scab resistance in Russet Burbank somaclonal variant adapted to thaxtomin A** **Isayenka, I.*; N. Beaudoin** (*University of Sherbrooke*)
4:00	S174	**Biosynthesis of the thaxtomin A phytotoxin in the potato common scab pathogen Streptomyces scabies: role of the MbtH-like protein TxtH** **Li, Y.; J. Liu; D. Adekunle; L. Bown; K. Tahlan; Bignell, D.** *(Memorial University of Newfoundland)*
4:15	S175	**Transcription regulatory map reveals important transcription factors regulating late blight resistance, leading to a higher accumulation of resistance related metabolites** **Joshi, S.*[1]; R. Singh Heikham[1]; A. Gagnon[2]; A. Kushalappa[1]** ([1]*McGill University;* [2]*Progest 2001 Inc.*)
4:30	S177	**The implications of drought stress on the nutritional quality of potato** **Da Ros, L.[1]; R. Elferjani[2]; R. Soolanayakanahally[2]; S. Kagale[3]; J. Wahab[2]; B. Bizimungu[2]** ([1]*University of British Columbia;* [2]*Agriculture and Agri-Food Canada;* [3]*National Research Council Canada*)
Room 105		**BG2 – Breeding and Genetics** *Chair:* ***Andrew Burt*** *(Agriculture and Agri-Food Canada)*
3:15	S178	**Whole genome comparisons of commercial *Phaseolus vulgaris* varieties and interspecific hybrids** **Perry, G.[1]; S. Munholland[2]; Y. Reinprecht[1]; E. Morneau[1]; W. Xie[1]; P.K. Pauls[1]; B. Crosby[2]** ([1]*University of Guelph;* [2]*University of Windsor*)
3:30	S179	**Cultivar classification, major genes, and chromosomal position explain the distribution of genetic diversity in a sample of Canadian bread wheat** **Hargreaves, W.*[1]; C. Pozniak[2]; L. Lukens[1]; A. N'Daiye[2]** [1]*University of Guelph;* [2]*University of Saskatchewan*
3:45	S180	**Tackling pre-harvest sprouting in small grain cereals** **Chen, W-Y*; S.K. Kadoll; J. Singh** (*McGill University*)

4:00	S181	**Identification of founding accessions and patterns of relatedness and inbreeding derived from historical pedigree data in a white clover (*Trifolium repens* L.) and red clover (*Trifolium pratense* L.) germplasm collection in New Zealand.** **Egan, L.[*1]; R. Hofmann[1]; B. Barrett[2]; K. Ghamkhar[2]; V. Hoyos-Villegas[3]** ([1]*Lincoln University;* [2]*AgResearch;* [3]*McGill University*)
4:15	S182	**Early flowering epi-mutants of 'Royal' flax.** **Booker, H.[1]; M. House[1]; L. Young[1]; A. Vasudevan[1]; R. Ragupathy[2]; S. Robinson[2]** [1]*University of Saskatchewan;* [2]*Agriculture and Agri-Food Canada*
Room 106		**TXS – Taxonomy and Systematics** *Chair:* ***Anne Bruneau*** *(McGill University)*
3:15	S183	**In praise of larger genera: looking at the Amelanchier-Hesperomeles-Crataegus clade (Rosaceae tribe Maleae)** **Dickinson, T.[1]; R. Ufimov[2]; D. Metsger[1]** ([1]*Royal Ontario Museum;* [2]*Komarov Botanical Institute RAS*)
3:30	S184	**Molecular and morphological data reveal hidden diversity in common North American Frustulia species (Amphipleuraceae)** **Bouchard, A.[1]; P. Hamilton[2]; J. Starr[1]** ([1]*University of Ottawa;* [2]*Canadian Museum of Nature*)
3:45	S185	**Systematics and biogeography in the ecologically conserved pantropical rainforest genus Crudia (Leguminosae)** **Domenech, B.[1]; M. de la Estrella[2]; L. Paganucci de Queiroz[3]; R. Barbosa Pinto[4]; C. Snak[3]; R. Steeves[5]; Bruneau, A.[1]** ([1]*Université de Montréal;* [2]*Universidad de Córdoba*; [3]*Universidade Estadual de Feira de Santana;* [4]*Universidade Federal de Goiás*; [5]*Department of Fisheries and Oceans Canada*)
4:00	S186	**Botany and textiles: The Indian Ocean connection** **Metsger, D.** (Royal Ontario Museum)
4:15	S187	**Rapid radiation and complex genome size evolution in a clade of holocentric sedges** **Elliott, T.[*1]; P. Bures[2]; S. Joly[3]; A. Muasya[4]** ([1]*Institut de recherche en biologie végétale;* [2]*Masaryk University;* [3]*Institut de recherche en biologie végétale, Université de Montréal;* [4]*Department of Biological Sciences*)
4:30	S188	**Diversity and evolution of seeds in Cuscuta (dodders, Convolvulaceae): morphology and structure** **Olszewski, M.[*]; M. Costea; H.A. El Miari** (*Wilfrid Laurier University*)
4:45	S189	**Canadensys: what's new and future directions in biodiversity data publication** **Bruneau, A.; C. Sinou; J. Goimard; L. Brouillet** (*Université de Montréal*)
Room 107		**BI – Biotic Interactions** *Chair:* ***Daya Dayanandan*** *(Concordia University)*
3:15	S190	**Herbivory induced Decadienal deferentially regulates light harvesting complex mRNAs at the level of transcription and mRNA stability in the marine diatom *Phaeodactylum tricornutum*** **Islam, S.[*]; T. Sabharwal; T. Bullock; M. Mehdy** *(University of Texas, Austin*)
3:30	S191	**An antisense oligoRIBO-11 fragment (contact DNA insecticide) penetrates through the integuments into the cells of gypsy moth larvae (*Lymantria dispar* L.)** **Oberemok, V.[1*]; K. Laikova[1]; I. Novikov[2]; N. Galchinsky[1]; R. Useinov[1], Y. Plugatar[3]** ([1]*V.I. Vernadsky Crimean Federal University*; [2]*Research Institute of Agriculture of Crimea;* [3]*Nikita Botanical Gardens—National Scientific Centre RAS*)
3:45	S192	**Transcriptomic analysis of red-berried grapevine infected with Grapevine leafroll-associated virus 3** **Song, Y.[*]; R. Hanner; B. Meng** (*University of Guelph)*

4:00	S193	**Isolation and characterization of endophytic microbes in poplar trees antagonistic to stem canker causative pathogenic fungus *Sphaerulina musiva*** **S. Naik[*1]; S. Palys[1]; A. Tsang[1]; P. Perinet[2]; R. UmaShaanker[3]; D. Dayanandan[1]** ([1]*Concordia University;* [2]*Ministère des Forêts, de la Faune et des Parcs;* [3]*University of Agricultural Sciences)*
4:15	S194	**A biosensor assay (GlnLux) for visualizing symbiotic nitrogen fixation output in root systems involved in the legume–rhizobia symbiosis** **Thilakarathna, M.[*]; M. Raizada** (*University of Guelph*)
4:30	S195	**The effect of urbanization on the evolution of floral traits in the wildflower *Linaria vulgaris*** **Longley, A.[*]; C. Caruso** (*University of Guelph*)
Room 108		**IPP2 – Innovations in Plant Pathology Part 2 (CPS-S4 student competition)** *Chairs:* ***Kenneth Conn*** *(Queen's University)* and ***Tom Fetch*** *(Queen's University)*
3:15	S196	**Monitoring airborne ascospores for the management of white mould (*Sclerotinia sclerotiroum*) in dry bean across Canada** **Reich, J.[*1]; U. Karerwa[2]; S. Chatterton[2]; M. Harding[3]** ([1]*University of British Columbia;* [2]*Agriculture and Agri-Food Canada;* [3]*Agriculture and Forestry*)
3:30	S197	**The prevalence and diversity of Fusarium species causing Fusarium Head Blight on oat in Manitoba** **Tabassum, M.[*1]; M. Banik[2]; M. Beyene[2]; F. Daayf[1]; X. Wang[3]** ([1]*University of Manitoba;* [2]*Agriculture and Agri-Food Canada;* [3]*Morden Research and Development Centre*)
3:45	S198	**'New' pathotypes of *Plasmodiophora brassicae* in Canada are not new** **Sedaghatkish, A.[*1]; B. Gossen[2]; M.R. McDonald[1]** ([1]*University of Guelph;* [2]*Agriculture and Agri-Food Canada*)
4:00	S199	**Assessment of fruit and foliage resistance to bacterial spot (*Xanthomonas gardneri*) in commercial processing tomatoes (Solanum lycopersicum L)** **Simonton, T.[*1]; C. Trueman[1]; D. Robinson[1]; C. Gillard[1]; K. Jordan[2]** ([1]*University of Guelph, Ridgetown Campus;* [2]*University of Guelph*)
4:15	S200	**Management of crown and root rot, caused by *Fusarium oxysporum*, and powdery mildew, caused by *Golovinomyces cichoracearum* on *Cannabis sativa*** **Scott, C.[*]; Z. Punja** (*Simon Fraser University*)
4:30		**Speakers participate in a panel discussion**
Room 109		**NBEI – Nutrients, Biotic and Environmental Interactions** *Chair:* ***Frederique Guinel*** *(Wilfred Laurier University)*
h3:15	S201	**Nutrients requirements of flax** **Sahota, T.** (LUARS Lakehead University Thunder Bay)
3:30	S202	**Quantifying the effects of a carbonatite rock fertilizer on wheat (*Triticum aestivum* L.)** **Jones, J.[*1]; P. Antunes[2]; F. Guinel[1]** ([1]*Wilfrid Laurier University;* [2]*Algoma University*)
3:45	S203	**The effects of nutrient enrichment on the community composition of arbuscular mycorrhizal fungi: a meta-analysis of fertilization studies** **MacColl, K.; H. Maherali** (*University of Guelph*)
4:00	S204	**Endophytic bacteria: nitrogen-source for lodgepole pine trees on disturbed sites?** **Padda, K.P.[*]; A. Puri; C. Chanway** (*University of British Columbia*)
4:15	S205	**Cucurbit seeds: Reservoirs of functional and antagonistic microbiomes** **Khalaf, E.; M. Raizada** (*University of Guelph)*

4:30	S206	**Environmental factors and polyketide synthase gene expression in an usnic acid producing lichen-fungus** **Gunawardana, D.[*]; N. Sveshnikova[2]; M.D. Piercey-Normore[2]** ([1]*Memorial University;* [2]*Grenfell Campus, Memorial University*)

5:00 – 7:00 Poster Session 2 at Peter Clark Hall,
Located downstairs in the University Center.

Students that have a poster with an EVEN number are to remain by their posters until judged.

Beverages will be served.

POSTER ABSTRACTS divided into topics

Poster Program-In Peter Clark Hall

Odd-numbered & even-numbered posters are presented Monday & Tuesday evening, respectively. Posters are not numbered according to the ID# assigned during abstract submission; use Topics 1-25 below as a guide to find your new poster number. The presenter's name is underlined, and student presenters being considered for poster awards are shown by an asterisk (*). Students being considered for poster awards will be interviewed during the evening poster sessions that begin at 5:00 pm in **Peter Clark Hall (PCH)**. Within Adobe Acrobat, use 'Edit' → 'Find' to locate authors etc.

TOPIC 1: Abiotic Stress (Posters P1-P24)

P1	**Photoperiodic injury in tomato involves opposing short-term and long-term acclimation of photosystem II operating efficiency and chlorophyll levels** Marie T.R.J.G.*; B. Grodzinski; B.J. Micallef (*University of Guelph)*
P2	**Superoxide is diurnally rhythmic and dampens under continuous light in tomato** Marie T.R.J.G.*; M.C. Micallef; B. Grodzinski; B.J. Micallef (*University of Guelph)*
P3	**Effects of exogenous melatonin on improving the drought resistance of oat seedlings** Chen, S. (Southwest Minzu University)
P4	**Wounding induces tomato Ve1 R-gene expression** Nazar, R.[1]; C. Castroverde[1]; X. Xu[1]; A. Kurosky[2]; E. Robb[1] ([1]*University of Guelph;* [2]*University of Texas Medical Branch*)
P5	**High temperature and ovule failure in field pea (*Pisum sativum* L.)** Osorio, E*; A. Davis; R. Bueckert *(University of Saskatchewan)*
P6	**Expression of the RING-type ubiquitin ligase, XBAT35, is regulated by ABA and abiotic stress** Serio, R.*; Q. Li; A. Schofield; S. Stone *(Dalhousie University*)
P7	**Unravelling the aspects of PGPR-mediated modulation of antioxidative defense expression and secondary metabolic profiling in *Solanum lycopersicum* under Cd stress** Khanna, K.*; P. Ohri; R. Bhardwaj (*Guru Nanak Dev University, Amritsar*)
P8	***Brassica rapa* Serine/Arginine-rich protein-like 3 (BrSR-like 3) regulates drought tolerance via alternative splicing of target genes in a concentration-dependent pathway** Lee, S.; M. Muthusamy; J. Kim; M. Jeong (*National Institute of Agricultural Sciences*)
S9	**Bioactive compounds in salt-stressed *Hypericum perforatum*: role of proline, salicylic acid and ascorbic acid pretreatments** Renault, S.[1]; S. Alinian Joozdani[2]; J. Razmjoo[2]; F. Daayf[1]; L. Adam[1] ([1]*University of Manitoba;* [2]*Shakhekord University*)
P10	**Conditioning of nursery plants using irrigation scheduling and mycorrhizae for improving post-transplant success rates** Keary, K.*; T. Graham; M. Dixon (*University of Guelph*)
P11	**Addition of sulfur decreases total cadmium uptake but increases cadmium translocation in soybean** Matt, S.; P. Boersma; Macfie, S. (*University of Western Ontario*)
P12	**Impacts of root-associated fungi on tree growth under elevated temperature and CO_2** Frank, J.*[1]; D. Way[2]; T. Ramsfield[3]; M. Abou-Zaid[1] ([1]*Western University;*[2]*University of Western Ontario;*[3]*National Resources Canada*)
P13	**Characterization of the role of SPL9 in drought stress tolerance in *Medicago sativa*** Hanly, A.*[1]; L. Amyot[2]; J. Karagiannis[1]; A. Hannoufa[2] ([1]*University of Western Ontario;* [2]*Agriculture and Agri-Food Canada)*

P14	**Exposure to low phosphate and salinity differentiate root systems for two ecotypes of the extremophyte crucifer *Eutrema salsugineum*** Irani, S.; P. Summers; E. Weretilnyk (*McMaster University*)
P15	**Molecular and biochemical assessment of mechanisms driving abiotic stress tolerance in *Medicago sativa* subsp. falcata** Singer, S.[1]; R. Orlando[1]; G. Dhariwal[1]; K. Burton Hughes[1]; A. Hannoufa[2]; E. Schultz[3]; S. Acharya[1] ([1]*Agriculture and Agri-Food Canada;* [2]*Agriculture and Agri-Food Canada;* [3]*University of Lethbridge*)
P16	**RNAi-mediated down-regulation of stress-response regulators in alfalfa for the improvement of abiotic stress tolerance** Singer, S.[1]; U. Subedi[1]; G. Dhariwal[1]; K. Burton Hughes[1]; G. Chen[2]; S. Acharya[1] ([1]*Agriculture and Agri-Food Canada;* [2]*University of Alberta*)
P17	**Investigating the relationship of HD2 family histone deacetylases in response to drought stress in Arabidopsis thaliana** Tahir, M.[*1]; J. Karagiannis[1]; L. Tian[2] ([1]*University of Western Ontario;* [2]*Agriculture and Agri-Food Canada*)
P18	**Genetic variation for yield formation traits affecting drought tolerance in commercial soybean [*Glycine max* (L.) Merr.] varieties adapted to Ontario** Gebre, M.G.[*]; H. Earl (*University of Guelph*)
P19	**Temporal shifts in oxidative stress and fermentative metabolites are associated with physiological injuries in postharvest pear fruit** Flaherty, E.[1]; G. Lum[1]; J. DeEll[2]; S. Subedi[3]; B. Shelp[1]; Bozzo, G.[1] ([1]*University of Guelph;* [2]*Ontario Ministry of Agriculture, Food and Rural Affairs* [3]*Binghamton University-State University of New York*)
P20	**A novel method for irrigating plants, tracking plant water use and imposing water deficits on plants grown in artificial environments** Bruch, A.[*]; H. Earl (*University of Guelph*)
P21	**Screening for heat stress resistant genotypes and evaluating heat stress effect on yield in hard red spring wheat when exposed to heat stress during flowering** Abeysingha, D.[*]; J. Ozga; D. Spaner; D. Reinecke (*University of Alberta*)
P22	**Expression and localization of the Arabidopsis thaliana HOTHEAD protein in response to stress.** Francom, T.[*]; S. Lolle (*University of Waterloo*)
P23	**Analysis of Abscisic acid (ABA) accumulation stressed and non stressed Brassicaceae plants** Hussain, S.[*]; E. Nambara; Z. Xu; F. Nguyen (*University of Toronto)*
P24	**The Drought Response Syndrome: A complex response mediated by water deficit severity and time** Chen, R.[*]; J. Sangiovanni; O. Wilkins (*McGill University*)

TOPIC 2: Agronomic Crop Production (Posters P25-P29)

P25	**Performances of early and late maturing oat varieties in cold regions, China** Zhou, Q. (Southwest Minzu University)
P26	**Yield stability of Canada Western Spring wheat under organically managed systems** Kubota, H.[1]; D. Spaner[2]; M. Iqbal[2] ([1]*Government of Canada;* [2]*University of Alberta*)
P27	**What are the critical phenological periods in the annual development of intermediate wheatgrass for sustainable perennial grain production?** Cattani, D.[1]; O. Duchene[2]; F. Celette[2]; C. David[2] ([1]*The University of Manitoba;* [2]*Agropole-ISARA*)

P28	**Effect of different colour rays on germination and mycoflora associated with maize caryopses** Niaz, I. (Pakistan Agriculture Research Council)
P29	**Phosphorus (P) and potassium (K) management in corn-soybean-winter wheat crop rotation in a long term experiment** Hanzra, H.[*1]; D. Hooker[1]; L. Van Eerd[2]; I. O'Halloran[1]; H. Bohner[3] ([1]*University of Guelph;* [2]*University of Guelph Ridgetown Campus;* [3]*OMAFRA*)

TOPIC 3: Agronomic Cropping Systems & Soil Management (Posters P30-P40)

P30	**Lentil enhances the productivity and stability of oilseed-cereal cropping systems** Liu, K.[1]; E. Johnson[2]; R. Blackshaw[1]; Y. Gan[1] ([1]*Agriculture and Agri-Food Canada;* [2]*University of Saskatchewan*)
P31	**Pulse-cereal rotation affects soil carbon and the stability of system productivity** Liu, K.[1]; M. Bandara[2]; Y. Gan[1] ([1]*Agriculture and Agri-Food Canada;* [2]*Alberta Agriculture and Forestry*)
P32	**Soil N gain from fall harvest to spring planting in soils under pulses, mustard and wheat** Luan, L.[1]; M. Bandara[2]; M. St.Luce[1]; Y. Gan[1] ([1]*Agriculture and Agri-Food Canada;* [2]*Alberta Agriculture and Forestry*)
P33	**Improving corn N fertilizer recommendations using rainfall effects on crop N demand** Niemeyer, C.[*]; J. Nasielski; K. Janovicek; B. Deen (*University of Guelph*)
P34	**Abiotic and biotic responses to cover crops and soil amendments in a vineyard** VanVolkenburg, H.[1*]; F. Guinel[2]; L. Vasseur[1] ([1]*Brock University;* [2]*Wilfrid Laurier University)*
P35	**Using species and genetic diversity to address stand establishment issues in red clover (*Trifolium pratense*) as a Cover Crop** Hilker, B.[*]; E. Lee; B. Deen; F. Tardif (*University of Guelph*)
P36	**Common bean cultivar mixtures and crop productivity** Reinprecht, Y.; L. Schram; T. Smith; P. Pauls (*University of Guelph*)
P37	**Exploring the potential of implementing pollinator friendly cover crop species in Southern Ontario.** Radcliffe, K.[*]; E. Lee; M. Raizada; B. Deen; N. Raine (*University of Guelph*)
P38	**Stubble affects genetic potential for inorganic nitrogen cycling by root associated microbiomes of oilseed crops** Wang, L.[1]; Y. Gan[2]; L. Bainard[3]; C. Hamel[2]; M. St-Arnaud[4]; M. Hijri[1] ([1]*Université de Montréal and Jardin botanique de Montréal* [2]*Agriculture and Agri-Food Canada;* [3]*Swift Current Research and Development Centre* [4]*Université de Montréal and Jardin botanique de Montréal, Montréal*)
P39	**Testing amendments and cover crops for improving soil health in vineyards** Christie, R.[1]; R. Honor[1]; L. Vasseur[2]; Guinel, F.[1] ([1]*Wilfrid Laurier University;* [2]*Brock University*)
P40	**Strike against Pseudomonas syringae: rye cover crop promotes a shift in squash phyllosphere bacterial abundance and plant gene expression** Maglione, R.[*1]; M. Ciotola[2]; M. Cadieux[2]; V. Toussaint[2]; M. Laforest[2]; S. Kembel[3] ([1]*UQAM;* [2]*Agriculture and Agrifood Canada;* [3]*Université du Québec à Montréal (UQAM)*)

TOPIC 4: Biochemistry, Metabolism, Photosynthesis (Posters P41-P68)

P41	**A central role for polyprenol reductase in plant dolichol biosynthesis** Van Gelder, K.*; L. Virta; T. Akhtar (*University of Guelph*)
P42	**Cytochrome P450 and O-methyltransferase catalyze the final steps in the biosynthesis of the anti-addictive alkaloid ibogaine from Tabernanthe iboga** Farrow, S.; M. Kamileen; S. O'Connor (*The John Innes Centre*)
P43	**Do r2r3-myb transcription factors directly regulate suberin biosynthesis?** Garant, T.*; O. Rowland; J. Murmu (*Carleton University*)
P44	**Processing strategies to reduce the level of acrylamide formation in potato chips, and their influence on reducing sugar and asparagine concentrations** Liyanage, D.[1]; D. Yevtushenko[1]; M. Konschuh[2]; B. Bizimungu[3]; Z. Lu[3] ([1]*University of Lethbridge;* [2]*Alberta Agriculture and Forestry;* [3]*Agriculture and Agri-Food Canada*)
P45	**Roadmap to potato suberin: an RNAseq approach** Bernards, M.; K. Woolfson (*The University of Western, Ontario*)
P46	**Roadmap to potato suberin: an RNAseq approach** Bernards, M.; K. Woolfson (*The University of Western Ontario*)
P47	**Post-translational modification in the regulation of starch branching enzyme 2.2 from *Arabidopsis thaliana*** MacNeill, G.*; I. Tetlow; M. Emes (*University of Guelph*)
P48	**Natural variation in glucosinolate profiles in *Camelina sativa* and its wild relative** Amyot, L.; A. Hannoufa; T. McDowell; J. Renaud (*Agriculture and Agri-Food Canada*)
P49	**Quality aspects of cooked early potatoes in relation to polyphenols/antioxidant content using a new LC-MS/MS technique (method development and application)** Varilla, C[1, 2]*, R.G. Pinhero[1], R.Y. Yada[3] and M.F. Marcone[1] ([1]Department of Food Science, University of Guelph [2]AFL – Laboratory Services Division-University of Guelph [3]Faculty of Land and Food Systems, University of British Columbia)
P50	**Are sensory attributes of potatoes affected by the polyphenol contents?** Varilla, C[1,2]*, R.G. Pinhero[1], M.F. Marcone[1] and R.Y. Yada[3] [1]Department of Food Science, University of Guelph [2]AFL – Laboratory Services Division-University of Guelph [3]Faculty of Land and Food Systems, University of British Columbia
P51	**Isoflavonoid metabolon and arogenate dehydratases in soybean (*Glycine max*): Identification and Functional Characterization** Sirjani, R.*[1]; K. Pannunzio[1]; S. Kohalmi[1]; S. Dhaubhadel[2] [1]*The University of Western Ontario;* [2]*Agriculture and Agri-Food Canada*
P52	**Photoacclimation to high-light in *Chlamydomonas reinhardtii* during senescence relies on generating high-quenching centres at detached antenna** Meagher, E.; P. Rangsrikitphoti; B. Faridi; D. Durnford (*UNB*)
P53	**Investigating high acetate as a regulator of senescence in *Chlamydomonas reinhardtii*** Lee, C.*[1]; D. Durnford[2] ([1]*University of New Brunswick;* [2]*UNB)*
P54	**Establishing a link between flavonol catabolism and auxin-mediated stem growth** Roepke, J.; G. Bozzo (*University of Guelph*)
P55	**Interactions between starch biosynthetic enzymes and 14-3-3 adaptor proteins in maize endosperm** Carswell, M.*; I. Tetlow; M. Emes (*University of Guelph*)

P56	**Functional characterization of *Arabidopsis thaliana* HXXXD-motif (BAHD) acyltransferases involved in suberin metabolism** Queralta Castillo, I.[*1]; M. Bernards[1] ; I. Molina[2] ([1]*The University of Western Ontario;* [2]*Algoma University*)
P57	**Understanding the regulatory role of rbcL RNA S1-Binding domain (RLSB) protein in the single-cell C4 species *Bienertia sinuspersici*** Yogadasan, N.[*]; S. Chuong (*University of Waterloo*)
P58	**Biochemical evidence for flavonol α-rhamnosidase activity in plants** Unterlander, N.[*]; H. Gordon; L. McGary; G. Bozzo (*University of Guelph*)
P59	**Genomic, chemical and functional analysis of adult leaf cuticle development in maize** Molina, I.[1]; R. Bourgault[1]; P. Qiao[2]; S. Matschi[3]; M. Vasquez[3]; A. Sonntag[1]; C. Charlebois[1]; M. Mohammadi[1]; M. Gore[2]; M. Scanlon[2]; L. Smith[3] ([1]*Algoma University;* [2]*Cornell University;* [3]*University of California San Diego*)
P60	**The role of starch in the development, physiology, and reproduction of *Arabidopsis thaliana*** Costain, C.[*]; M. Emes; I. Tetlow (*University of Guelph*)
P61	**Characterizing a novel protein targeting mechanism to the outer envelope of chloroplasts** Overton, A.[*1]; S. Chuong[1]; M. Smith[2] ([1]*University of Waterloo;* [2]*Wilfrid Laurier University*)
P62	**Exploring the role of the purple acid phosphatase AtPAP17 in Arabidopsis phosphate and ROS metabolism** O'Gallagher, B.[*] (Queen's University)
P63	**Investigating post-translational regulation of UDP-Glucose pyrophosphorylase in maize endosperm** Butler, V.; I. Tetlow (*University of Guelph*)
P64	**Investigating the functional evolution of plant shikimate kinase-like 1 (SKL1) in *Marchantia polymorpha*** Lee, J.[*]; M. Kanaris; D. Christendat (*University of Toronto*)
P65	**Distinct metabolic modes drive variation in cyclic and acyclic monoterpenoid biosynthesis in *Pelargonium graveolens* chemotypes** Bergman, M.[*]; M. Phillips (*University of Toronto – Mississauga*)
P66	**Mapping metabolic carbon partitioning in Arabidopsis rosette tissue using $^{13}CO_2$ labeling and ammonia chemical ionization mass spectrometry** Phillips, M.; B. Davis[*] (*University of Toronto – Mississauga*)
P67	**Enhancing yield and biomass in canola by modifying carbohydrate metabolism** Wang, L.; Y. Wang; A. Makhmoudova; I. Tetlow; M. Emes (*University of Guelph*)
P68	**Recent advances in plant ubiquinone (Coenzyme Q) biosynthesis and engineering** Soubeyrand, E.[1]; T. Johnson[1]; S. Latimer[1]; A. Bernert[1]; M. Kelly[1]; J. Kim[1]; T. Colquhoun[1]; A. Block[2]; G. Basset[1] ([1]*University of Florida;* [2]*USDA*)

TOPIC 5: Bioinformatics and Systems Biology (Posters P69-P73)

P69	**Custom selected reference genes outperform pre-defined reference genes in transcriptomic analysis** Goncalves dos Santos, K.[*]; I. Desgagné-Penix; H. Germain (*Université du Québec à Trois-Rivières*)
P70	**Redundancy removal in de novo transcriptomes of Piper nigrum (black pepper)** Doering, M.[*]; J. Stout (*University of Manitoba*)

P71	**Using interactome and ubiquitinome datasets to identify substrates for Arabidopsis RING-type ubiquitin ligases (E3s) and the ubiquitin system** Alotaibi, D.; J. Yang; L. Hongxia; Stone, S. (*Dalhousie University*)
P72	**Transcriptional control of bacterial cell division in a nitrogen fixing symbiosis** D'Alessio, M.; J. Cheng; A. Doxey; Charles, T. (*University of Waterloo*)
P73	**Expansion and diversification of the CCA1-LHY-RVE transcription factor family in monocots** Gélinas Bélanger, J.*; J. Sangiovanni; J. Singh; O. Wilkins (*McGill University*)

TOPIC 6: Bioproduct Production in Plants (Posters P74-P80)

P74	**Seed yield and oil and protein contents of main oilseed crops on the Canadian prairie** Hossain, Z.[1]; E. Johnson[2]; R. Blackshaw[3]; Gan, Y.*[3] ([1]*Swift Current Research and Development Centre;* [2]*University of Saskatchewan;* [3]*Agriculture and Agri-Food Canada)*
P75	**Plant-made virus-like particles for protection of piglets against porcine epidemic diarrhea virus** Zhu, H.[1]; Z. Khamis[2]; R. Menassa[3] [1]*Agriculture and Agri-Food Canada;* [2]*University of Western Ontario;* [3]*Government of Canada*
P76	**A rationally designed plant-produced IgA has improved yield and exhibits cross serotype protection against enterohemorrhagic Escherichia coli** Chin-Fatt, A.*[1]; R. Menassa[2] ([1]*Western University;* [2]*Government of Canada*)
P77	**Expression of malaria antigens in the chloroplast of *Chlamydomonas reinhardtii*; the first step towards developing malaria algae-based oral vaccine candidates** Shamriz, S.*[1]; H. Ofoghi[2] ([1]*University of Western Ontario;* [2]*Iranian Research Organization for Science and Technology*)
P78	**The effects of nutrient solution pH on protein expression and morphology of Agrobacterium-infiltrated Nicotiana benthamiana in hydroponic growth conditions** Bennett, L. (University of Guelph)
P79	**Recombinant protein expression in plants: The key influence of basic growth conditions** Shang, L.; M-C. Goulet; D. Michaud (*Université Laval*)
P80	**Identification of candidate cinnamyl alcohol dehydrogenases in Tabernanthe iboga root** McDonald, K.*; M. Kapasi; J. Stout (*University of Manitoba)*

TOPIC 7: Breeding and Genetics (Posters P81-P98)

P81	**Peduncle Strength: a potential selection criterion to improve lodging tolerance in Oat** Nakhforoosh, A.; S. Kumar; J. Mitchell Fetch (*Government of Canada*)
P82	**Soybean protein content variation among genotypes grown in Morden, MB and Ottawa, ON** Hou, A.[1]; E. Cober[2] ([1]*Agriculture and Agri-Food Canada;* [2]*AAFC Ottawa-RDC*)
P83	**Spring wheat breeding for eastern canada – challenges and opportunities** Burt, A.; X. Wang; A. Cummiskey; D. MacEachern; H. Voldeng *(Agriculture and Agri-Food Canada)*
P84	**Assessment of genetic structure of coleoptile length in spring wheat (Triticum aestivum L.) using a genome-wide association study** Khadka, K.*; M. Kaviani; A. Navabi (*University of Guelph*)

P85	**Identification and mapping of an unknown resistant locus in *Brassica napus* against Leptosphaeria maculans** Liu, F.; Z. Zou; D. Fernando (*University of Manitoba*)
P86	**Validation and discovery of genetic markers associated with loose smut resistance genes in a durum wheat (*Triticum durum* L.) doubled haploid population DT676/DT802** Bokore, F.[1];R. Knox[1]; Y. Ruan[1]; R. Cuthbert[1]; H. Campbell[2]; A. Sharpe[3]; E. Sari[4]; K. Boyle[4]; I. Piche[1]; B. Meyer[1] ([1]*AAFC;* [2]heather.campbell3@canada.ca*;* [3]*Global Institute for Food Security;* [4]*National Research Council of Canada*)
P87	**Leaf rust resistance genes in Canadian wheat cultivars Red Fife, Stettler, Vesper, Lillian, Carberry and AC Cadillac** McCallum, B.[1]; F. Bokore[2]; R. Cuthbert[2]; R. Knox[2] ([1]*Agriculture and Agri-Food Canada;* [2]*AAFC*)
P88	**Genetic analysis and molecular mapping of the oat crown rust seedling resistance gene Pc39** Zhao, J.[1]; A. Kebede[1]; Menzies, J.[2]; N. Tinker[3]; C. McCartney[1] [1]*Morden Research and Development Centre;* [2]*Agriculture and Agri-Food Canada;* [3]*Ottawa Research and Development Centre*
P89	**Genetic diversity of grain fatty acid composition in 295 accessions of Korean Rice Core Set** Yang, J.[1]; B. Ha[1]; S. Noh[1]; S Eom[1]; S. Chu[2]; K. Kim[2]; Y. Park[2]; Lee, Y.[3] ([1]*Soochunhyang University;* [2]*Kongju National University;* [3]*Soonchunhyang University*)
P90	**Regression data driven models on canopy hyperspectral reflectance for soybean yield prediction** Yoosefzadeh Najafabadi, M.[*]; M. Eskandari (*University of Guelph*)
P91	**Major genomic regions underlying seed size, protein and sucrose in food-grade soybeans** Torabi, S.[*]; R. Whaley; M. Eskandari (*University of Guelph*)
P92	**Mapping cold hardiness in tetraploid garden roses (Rosa x hybrida)** Rouet, C.[*1]; E. Lee[1]; K. Tanino[2]; D. Somers[3] ([1]*University of Guelph;* [2]*University of Saskatchewan;* [3]*Vineland Research and Innovation Centre*)
P93	**Genome-wide analysis of thaumatin-like proteins in cereals** Iqbal, I.[*]; R. Tripathi; O. Wilkins; J. Singh (*McGill University*)
P94	**Agronomic performance and nitrogen fixation of heirloom and conventional dry bean varieties under low-nitrogen field conditions** Wilker, J[*1]; A. Navabi[1]; I. Rajcan[1]; F. Marsolais[2]; B. Hill[2]; D. Torkamaneh[3]; P. Pauls[1] ([1]*University of Guelph;* [2]*Agriculture Agri-food Canada;* [3]*Université Laval*)
P95	**Genetic transformation of oat to elucidate a gene associated with beta-glucan** Fatmawati, A.[*1]; M. Mahmoud; T. Donoso; W. Chen[1]; R. Kaur; N. Tinker[2]; J. Singh[1] ([1]*McGill University;* [2]*Agriculture and Agri-food Canada)*
P96	**Identification of five QTLs for clubroot resistance to three novel pathotypes of Plasmodiophora brassicae in *Brassica oleracea* through genotyping-by-sequencing** Karim, M.[1]; F. Fuyou[1]; A. Dakouri[1]; S. Strelkov[2]; B. Gossen[1]; G. Peng[1]; F. Yu[1] ([1]*Agriculture and Agri-Food Canada;* [2]*University of Alberta)*
P97	**Evaluation of tissue culture and cloning propagation efficiencies of three industrial hemp varieties** El-Mezawy, A.; J. Slaski (*InnoTech Alberta*)
P98	**Characterization of nested association mapping population in dry bean** Vazin, M.[*]; T. Smith; K.P. Pauls (University of Guelph)

TOPIC 8: Cell Biology (Posters P99-P109)

P99	**Characterization of the pokeweed antiviral protein (PAP) interactome by proximity-dependent biotin identification** Chivers, J.*; K. Hudak (*York University*)
P100	**Understanding differential development and behaviour of plastids using the Arabidopsis immutans mutant** Burnside, M.*; K. Barton; N. Mathur; J. Mathur (*University of Guelph*)
P101	**Investigating the systematic regulation and function of cyclic nucleotide-gated channels in arabidopsis** Miraples, A.*; W. Moeder; Y. Keiko (*University of Toronto*)
P102	**Identification and characterization of new lipid droplet proteins in Arabidopsis thaliana** Doner, N.*[1]; F. Kretzschmar[2]; T. Ischebeck[2]; K. Chapman[3]; J. Dyer[4]; R. Mullen[1] ([1]*University of Guelph;* [2]*University of Goettingen;* [3]*University of North Texas;* [4]*U.S. Department of Agriculture–Agricultural Research Service*)
P103	**Regulation of cell size in *A. thaliana* shoot apical meristem** Echevin, E.*; A. Routier-Kierzkowska; P. Belska; D. Kierzkowski *(Institut de Recherche en Biologie Végétale - Université de Montréal*)
P104	**A feedback loop modulates root apical meristem development** Halat, L.; J. Rever; M. Law; Wasteneys, G. (*The University of British Columbia*)
P105	**Investigating the role of e3 ubiquitin ligases in the Brassicaceae self-incompatible pollen response** Beronilla, P.*; D. Goring (*University of Toronto*)
P106	**Characterization of *Camelina sativa* germination: The effect of gibberellins on vacuolation** Gomes, M.*; E. Nambara (*University of Toronto*)
P107	**A novel method of producing the putative c-terminal transit peptide of attoc159 for characterization of its targeting to the chloroplast outer membrane** Fish, M.*[1]; M. Jelokhani-Niaraki[1]; S. Chuong[2]; M. Smith[1] ([1]*Wilfrid Laurier University;* [2]*University of Waterloo*)
P108	**Investigating protein localization to the outer membrane of chloroplasts** Nash, D.*[1]; M. Smith[2]; S. Chuong[1] ([1]*University of Waterloo;* [2]*Wilfrid Laurier University*)
P109	**Characterizing the role of *Striga hermonthica* gibberellic acid receptors** Adityani, C.*; T. Pender; S. Lumba; P. McCourt (*University of Toronto*)

TOPIC 9: Controlled-Environment Crop Production (Posters P110-P113)

PS110	**Elongation and flowering promoted by blue light are independent of photoperiod: a comparison with red light in four bedding plant species** Zheng, Y.; Y. Kong; D. Kamath *(University of Guelph)*
P111	**Blue light can promote flowering of bedding plants when associated with low phytochrome activity** Kong, Y.; K. Schiestel; Y. Zheng (*University of Guelph*)
P112	**NLOS-OG: A nitrogen simulation tool for managing organic greenhouses** Dion, P.*[1]; M. Thériault[2]; D. Hunt[2]; S. Bittman[2]; S. Pepin[1]; M. Dorais[1] ([1]*Laval University;* [2]*Agriculture and Agrifood Canada*)
P113	**Minimizing unwanted callus during *in vitro* multiplication of daylilies** Callaghan, J.*; M. Jones (*University of Guelph*)

TOPIC 10: Crop Physiology (Poster P114)

P114	**Investigation of the critical growth period for yield component determination in quinoa** McCabe, J.; H. Earl (*University of Guelph*)

TOPIC 11: Development and Reproduction (Posters P115-P119)

P115	**The effect of hermaphroditism versus cross-pollination on sex ratios and genetic variation in *Cannabis sativa* L.** Holmes, J.[*]; Z. Punja (*Simon Fraser University*)
P116	**Characterizing and understanding the underlying molecular mechanism of the sugarcane anti-florigen ScFT2** Lesy, V.[*1]; M. Minow[1]; C. Coelho[1]; Z. Xu[1]; Z. Leblanc[1]; S. Rothstein[1]; A. Chalfun Junior[2]; J. Colasanti[1] ([1]*University of Guelph;* [2]*Universidade Federal de Lavras*)
P117	**Investigating the role of secretion in the *Arabidopsis thaliana* compatible pollen response pathway** Macgregor, S.[*]; D. Goring (*University of Toronto*)
P118	**POPCORN modulates auxin flow and polarity to define adaxial-abaxial cell fate in Arabidopsis leaf development** Quilichini, T.; P. Gao; R. Datla; D. Xiang (*National Research Council Canada*)
P119	**Investigating the role of BKNs in pollen-stigma interactions** Geng, B.[*1]; J. Doucet[2]; D. Goring[1] ([1]*University of Toronto;* [2]*U of T*)

TOPIC 12: Diagnostic Tools Applied to Crop Production (Poster P120)

P120	**Laboratory testing of qPCR assays designed in silico reveal promising results to rapidly identify phytopathogenic Tilletia species.** Tremblay, E.[*1]; D. Shearlaw[2]; H. Nguyen[1]; G. Bilodeau[2]; S. Hambleton[1] ([1]*Agriculture and Agri-Food Canada;* [2]*Canadian Food Inspection Agency*)

TOPIC 13: Ecology and Ecophysiology (Posters P121-P133)

P121	**Short-term effects of partial and clearcuttings on woody debris and understory vegetation in mixed-wood stands** Maleki, K.[*1]; B. Lafleur[1]; B.D. Harvey[1]; M. Mazerolle[2]; N. Fenton[3] ([1]*University of Quebec in Abitibi-Temiscamingue;* [2]*Université Laval* [3]*Université du Québec en Abitibi-Témiscamingue (UQAT)*)

P122	**Competition or facilitation: Examination of interactions between endangered *Sida hermaphrodita* and invasive *Phragmites australis*** Mulholland, S.*; M. Costea; K. Stevens (*Wilfrid Laurier University*)
P123	**The interaction of marine phytoplankton cell size with capacities for reactive oxygen detoxification** Rehman, A.*; D. Campbell (*Mount Allison University*)
P124	**Assessing threats and mitigation for Scarlet Ammannia (*Ammannia robusta*) in Southwestern Ontario** Salive, K.*; M. Costea; K. Stevens (*Wilfrid Laurier University*)
P125	**Assisted migration of whitebark pine to higher latitudes and elevations in the Canadian Cordillera** Haeussler, S.; L. Tackaberry; Massicotte, H. (*University of Northern British Columbia*)
P126	**Below-ground facilitation between tree species in the re-vegetalization of a degraded site** Pawuluwage, S.*[1]; P. Marchand[1]; N. Fenton[1]; M. Roy[2]; B. Lafleur[1] ([1]*Université du Québec en Abitibi-Témiscamingue (UQAT);* [2]*Université Paul Sabatier – CNRS*)
P127	**Is it possible to predict precipitation with readily available precipitation records?** Schellenberg, M.; H. Cutforth; J. Nimegeers (*Swift Current Research and Development Centre)*
P128	**Exogenous ethylene increases methane emissions from canola** Martel, A.[1]; M. Qaderi[1,2] ([1]*Saint Mary's University;* [2]*Mount Saint Vincent University*)
P129	**An analysis of invasive species management in the Niagara region of Ontario, Canada: establishment of a database to improve knowledge sharing** Vasseur, L.; L. Brown (*Brock University*)
P130	**Performance of Eastern white pine (*Pinus strobus* L.) at the limits of its distribution range in Western Newfoundland.** Sveshnikov, D.[1]; A. Arsenault[2]; N. Lake[1]; V. Valdez[1]; P. Baines[2]; R. LeBlanc[2]; K. Beals[1]; R. Skinner[1] ([1]*Grenfell Campus, Memorial University of Newfoundland;* [2]*Canadian Forest Service*)
P131	**Cold spring delays autumn senescence, elongates nutrient uptake period, but reduces nitrogen storage for winter in *Rhynchospora alba* (Cyperaceae)** Byne, K.; P. Ryser (*Laurentian University*)
P132	**Effects of drought, plant hormones and arbuscular mycorrhizal fungi on photosynthesis, transpiration and plant growth in corn (*Zea mays*)** Singh, S.; M. Fu (*University of British Columbia, Canada)*
P133	**Seasonal changes in photosynthesis, transpiration and chlorophyll levels in American Sweetgum (*Liquidambar styraciflua*) and Hungarian Oak (*Quercus frainetto*) and Japanese Katsura (*Cercidiphyllum japonicum*)** Singh, S.; G. Bhatt; A. Jimenez (*University of British Columbia, Canada*)

TOPIC 14: Entomology and Pest Management (Posters P134-P135)

P134	**Plastid transformation of Micro-tom tomato for RNAi interference in insects** Kaplanoglu, E.[1]; I. Kolotilin[2]; R. Menassa[3]; C. Donly[1] ([1]*Agriculture and Agri-Food Canada;* [2]*Scattered Gold Biotechnology Inc.;* [3]*Government of Canada*)

P135	**Modulation of lipopeptides production by Bacillus subtilis PTB185 in response to different plant pathogens** Cossus, L.[*1]; F. Roux-Dalvai[2]; I. Kelly[2]; T. Nguyen[2]; H. Antoun[2]; A. Droit[2]; R. Tweddell[2] ([1]*Laval university;* [2]*Université Laval*)

TOPIC 15: Growth Regulators (Posters P136-P137)

P136	**Karrikins: important regulators of seed germination in wildfire-prone regions** Monthony, A.[*1]; K. Baethke[2]; L. Erland[2]; S. Murch[2] ([1]*University of Guelph;* [2]*UBC*)
P137	**Indoleamine plant growth regulators perceive and initiate plant responses to specific light spectra in Scutellaria species** Forsyth, J.[*1]; L. Erland[2]; S. Murch[2] ([1]*University of British Columbia;* [2]*UBC*)

TOPIC 16: Horticultural Field Production (Posters P138-P139)

P138	**Remote assessment of phenological and phenotypic variability in wild blueberry fields** Anku, K.; D. Percival (*Dalhousie University*)
P139	**Evaluation of bottle and luffa gourds for commercial production in Canadian greenhouses** Arif, M.; P. Pauls (*University of Guelph*)

TOPIC 17: Mineral Nutrition (Posters P140-P142)

P140	**Towards low-input production of subirrigated chrysanthemums: Phosphorus acquisition and internal utilization efficiencies in two contrasting cultivars** Flaherty, E.; B. Shelp (*University of Guelph*)
P141	**A single amino-acid substitution in the Lsi1 aquaporin of tobacco confers elevated Si transport and plasma-membrane localization** Coskun, D.[1]; R. Deshmukh[1]; H. Sonah[1]; S. Matha[1]; R. Frenette-Cotton[1]; L. Tremblay[1]; P. Isenring[1]; R. Bélanger[2] ([1]*Laval University;* [2]*Université Laval*)
P142	**Towards low-input production of sub-irrigated chrysanthemums: optimizing calcium and magnesium usage** Duncan Stephens, S.[*1]; E. Flaherty[1]; W. Sutton[1]; W. MacDonald[2]; G. Bozzo[1]; B. Shelp[1] ([1]*University of Guelph;* [2]*Niagara College*)

TOPIC 18: Molecular Host-Pathogen Interactions (Posters P143-P154)

P143	**Creation of pokeweed mosaic virus infectious clone to study host-pathogen interactions** Klenov, A.*; K. Hudak (*York University*)
P144	**Monaghan Lab: Plant immunology and immune homeostasis** Monaghan, J. (Queen's University)
P145	**Variation between Ilyonectria mors-panacis and I. robusta isolates causing root rot in Panax quinquefolius** Behdarvandi, B*; M. Valliani; P. Goodwin (*University of Guelph*)
P146	**Para-aminobenzoic acid (PABA) reducing *Botrytis cinerea* disease in leaves of Nicotiana benthamiana plants** Costa, L.; A. Munawar; P. Goodwin (*University of Guelph*)
P147	**Development of a Grapevine rupestris stem pitting-associated virus strain Syrah clone and expression/VIGS vectors for *Vitis vinifera*** Roscow, O.; B. Meng (*University of Guelph*)
P148	**Molecular characterization of plasmodesmata-located protein Osmotin34 from Arabidopsis and its association with Turnip Mosaic Virus Infection** He, R.*[1]; M. Bernards[2]; A. Wang[3] ([1]*Western University;* [2]*The University of Western Ontario;* [3]*Agriculture and Agri-Food Canada; University of Western Ontario*)
P149	**Investigating the role of a family of receptor-like-cytoplasmic kinases in immune signaling** Gonzalez-Ferrer, C.*; K. Siegal; J. Monaghan (*Queen's University*)
P150	**Identification of determinants in the turnip mosaic virus coat protein that are critical for viral cell-to-cell movement and virion assembly** Dai, Z.*[1]; M. Bernards[2]; A. Wang[3] ([1]*Western University;* [2]*The University of Western Ontario;* [3]*Agriculture and Agri-Food Canada; University of Western Ontario*)
P151	**The Ve-resistance locus in tomato, a plant signalling intercept** Robb, E.[1]; R. Nazar[1]; C. Castroverde[1]; A. Kurosky[2]; H. Shittu[3]; X. Xu[1] ([1]*University of Guelph;* [2]*University of Texas Medical Branch;* [3]*University of Benin)*
P152	**Subcellular localization of prune dwarf virus coat and movement proteins** Simkovich, A.*[1]; S. Kohalmi[1]; A. Wang[2] ([1]*The University of Western Ontario;* [2]*Agriculture and Agri-Food Canada; University of Western Ontario*)
P153	**Control of Fusarium head blight using the Next-generation of fungicides** Djavaheri, M.[1]; T. Bender[1]; H. Borhan[1]; S. Clark[2]; R. Kutcher[3]; R. Subramaniam[1]; S. Robinson[1] ([1]*Agriculture and Agri-Food Canada AAFC;* [2]*National Research Council Canada;* [3]*University of Saskatchewan)*
P154	**Comparative transcriptomics of root responses to pathogenic (*Fusarium oxysporum* f. sp. lini) and non-pathogenic (*Rhizoglomus irregulare*) fungi** Quintans, I.; E. Packard; V. Kokkoris; E. Vukicevich; D. Adhikary; M. Deyholos *(University of British Columbia, Okanagan*)

TOPIC 19: Molecular Plant Improvement and Genome Editing (Posters P155-P158)

P155	**Characterization of *Arabidopsis thaliana* MYB transcription factor complexes and their roles in the regulation of suberin biosynthetic genes** Tapp, K.*; S. Khalil; O. Rowland (*Carleton University*)
P156	**Targeted mutagenesis in soybean using CRISPR-Cas9 system** Lu, M.; L. Tian (*Agriculture and Agri-Food Canada*)
P157	**Characterization of the EPF family of signalling peptides controlling stomatal development in Monocots** Jangra, R.*[1]; S. Brunetti[1]; N. Foroud[2]; P. Gulick[1]; J.S. Lee[1] ([1]*Concordia University;* [2]*Agriculture and Agri-Food Canada*)
P158	**The Global Industry Coalition (GIC) contributions to the work of Implementing the Cartagena Protocol on Biosafety** Luque, L. (CropLife Canada)

TOPIC 20: Mycology (Posters P159-P161)

P159	**Genetic diversity of *Fusarium poae* field populations affecting small grain cereals in western Canada.** Tabassum, M.[1]; A. Oghenekaro[1]; D. Fernando[1]; R. Kutcher[2]; D. Overy[3]; J. Tucker[1]; K. Turkington[4]; L. Harris[3]; W. Xu[5]; Wang, X.[5] ([1]*University of Manitoba;* [2]*University of Saskatchewan;* [3]*Ottawa Research and Development Centre;* [4]*AAFC;* [5]*Morden Research and Development Centre)*
P160	**Over-expression of a constitutively active MAP kinase kinase, MKK2, in *Fusarium graminearum* reduces its vegetative growth and disease progression in wheat** Gonzalez-Peña Fundora, D.*[1]; A. Eranthodi[1]; C. Rampitsch[2]; R. Subramaniam; N. Thakor[1]; N. Foroud ([1]*University of Lethbridge;* [2]*Agriculture and Agri-food Canada*)
P161	**The Canadian Collection of Fungal Cultures: What we have for you and what you have for us.** Robleh Djama, Z.; C. Robidas; B. Goulet; T. Rintoul (*Agriculture and Agri-Food Canada*)

TOPIC 21: Pathology, Epidemiology and Disease Management (Posters P162-P196)

P162	**Buckwheat rhizosphere as a host for unique bacterial species** Fofana, B.[1]; A. Alkhnajari[1]; K. Ghose[2]; A. Somalraju[1] ([1]*Charlottetown research and development centre;* [3]*Texas Tech University*)
P163	**A mycovirus cause hypovirulence in rice pathogen *Microdochium albescens*** Murcia, J.*[1]; R. Cascardo[2]; F. Souza[2]; M. Souza[2]; C. Farias[1]; D. Barros[1]; P. Alfenas[2] ([1]*Universidade Federal de Pelotas;* [2]*Universidade Federal de Viçosa*)
P164	**Development of a novel, eco-friendly plant defense activator against Botrytis blight** Seifi, S.; A. Zarei; T. Hsiang; B. Shelp (*University of Guelph*)

P165	**A potential QTL on Chromosome 3BS with major effect on adult plant resistance to stripe rust in a Canadian winter wheat diversity panel** Serajazari, M.[1]; H. Sidhu[1]; J. Follings[2]; N. Wilker[1]; P. Pauls[1]; A. Navabi[1] ([1]*University of Guelph;* [2]*Ontario Ministry of Agriculture, Food and Rural Affairs*)
P166	**Several grass crops reduce resting spores of *Plasmodiophora brassicae* in soil** Sedaghatkish, A.[*1]; B. Gossen[2,]; M.R. McDonald[1] ([1]*University of Guelph;* [2]*Agriculture and Agri-Food Canada*)
P167	**Development of an Immuno-PCR for the detection of pea root rot causal agent, Aphanomyces euteiches** Kaphle, S.[*1]; C. Sheedy[2]; S. Chatterton[2] ([1]*University of Lethbridge;* [2]*Agriculture and Agri-Food Canada)*
P168	**Fusarium head blight of wheat in Alberta: species complex and related trichothecene genotypes.** M. Hafiz; N. Schatz; M. Telfer; R. Gourlie; K. Turkington; Aboukhaddour, R. (*AAFC*)
P169	**A Brevibacillus fortis isolate produces extracellular antibiotics that inhibit the growth of the onion pathogen Fusarium oxysporum f. sp. cepae and other Fusarium species** Johnson, E.; M. Bowma; C. Dunlap (*USDA ARS*)
P170	**Post-harvest root decay of American ginseng (*Panax quinquefolious*) and the relationship with ginseng replant disease** Samur, I.[*]; P. Goodwin (*University of Guelph*)
P171	**Validation of antagonistic activity against fungal pathogens and the presence of antifungal genes in Pseudomonas chlororaphis strain S1Bt23** Xu, R.; J. Tambong; V. Plante (*Agriculture and Agri-Food Canada*)
P172	**Growth inhibition of the plant pathogen, Streptomyces scabies, using plant tinctures** Bakke, A.[*]; M. Vatta; R. Merrill (*University of Guelph*)
P173	**Reactions of Eastern Canada oat genotypes to crown rust** Xue, A.[1]; J. Menzies[2]; Y. Chen[2]; W. Yan[1]; B. Ma[2]; W. Guo[3]; F. Gao[2]; J. Liu[4]; C. Ren[5] ([1]*AAFC;* [2]*Agriculture and Agri-Food Canada;* [3]*Heilongjiang Bayi Agricultural University;* [4]*Inner Mongolia Agricultural University;* [5]*Baicheng Academy of Agricultural Sciences*)
P174	**Diversity in virulence frequencies and race structure of extensively and intensively sampled populations of *Puccinia coronata* Corda var avenae f.sp. avenae.** Menzies, J.[1]; J. Zhao[2]; S. Deceuninck[2]; H. Derksen[2]; Z. Popovic[2] ([1]*Agriculture and Agri-Food Canada;* [2]*Morden Research and Development Centre*)
P175	**Effect of host type on the virulence of Pyrenophora tritici-repentis (Ptr) in Canada** Wei, B.[*1]; S. Strelkov[1]; R. Aboukhaddour[2]; T. Despins[3]; M. Fernandez[4] ([1]*University of Alberta;* [2]*AAFC;* [3]*Agriculture and Agri-Food Canada, Lethbridge Research and Development Center;* [4]*Agriculture and Agri-Food Canada, Swift Current Research and Development Centre*)
P176	**Emerging diseases of new hazelnut varieties grown in the Fraser Valley, British Columbia.** Drugmand, B.; V. Vasile; S. Sabaratnam (*Ministry of Agriculture*)
P177	**In the footsteps of Dr. Margaret Newton: women plant pathologists leading the Canadian Phytopathological Society** Kora, C.[1]; D. Gaudet[2] ([1]*Pest Management Centre;* [2]*Retired*)
P178	**Integrated management of Cucumber Downey Mildew: a strategic approach** Kora, C.[1]; C. Gagnon[1]; C. Trueman[2]; G. Marchand[3]; A. Munawar[4] ([1]*Pest Management Centre;* [2]*University of Guelph, Ridgetown Campus;* [3]*Agriculture and Agri-Food Canada;* [4]*University of Guelph*)
P179	**Effect of Miravis Neo on Gibberella ear rot and related mycotoxins in corn grain** Eli, K.[*1]; D. Hooker[1]; V. Limay-Rios[1]; A. Schaafsma[2] [1]*University of Guelph;* [2]*University of Guelph - Ridgetown Campus*

P180	**A rapid molecular assay to identify *Plasmodiophora brassicae* pathotypes from plant, soil and water samples** Tso, H.[*1]; L. Galindo-González[1]; H. Askarian[1]; M. Holtz[2]; S. Strelkov[1] ([1]*University of Alberta;* [2]*Alberta Agriculture and Forestry*)
P181	**Potential use of *Acer saccharum* leaf extract for the control of lettuce bacterial leaf spot and varnish spot** Delisle-Houde, M.[*]; R. Tweddell (*Université Laval*)
P182	**Genetic mapping of adult plant leaf rust resistance in spring wheat line BW278** Lewarne, M.[*1]; B. McCallum[2]; C. Hiebert[2]; C. McCartney[3] ([1]*University of Manitoba;* [2]*Agriculture and Agri-Food Canada;* [3]*Morden Research and Development Centre*)
P183	**Resting spores of *Plasmodiophora brassicae* continue to develop after death of their host.** Al-Daoud, F.[1]; Gossen, B.[2]; M.R. McDonald[1] ([1]*University of Guelph;* [2]*Agriculture and Agri-Food Canada*)
P184	**Identifying clubroot resistance in canola and Brassica vegetable cultivars for Ontario, 2018** Drury, S.[*1]; B. Gossen[2]; M.R. McDonald[1] ([1]*University of Guelph;* [2]*Agriculture and Agri-Food Canada*)
P185	**Chitosan inhibits growth and development of *Phytophthora nicotianae* and induces tomato resistance against this pathogen** Falcón-Rodríguez, A.[1]; D. Csotales Menéndez[1]; Gonzalez-Peña Fundora, D.[*2]; D. Vaillant Flores[3]; M. Ochoa-Villarreal[4]; M. Martínez-Téllez[4] ([1]*National Institute of Agricultural Sciences (INCA);* [2]*University of Lethbridge;* [3]*Instituto de Investigaciones de Sanidad Vegetal;* [4]*Centro de Investigación en Alimentación y Desarrollo (CIAD)*)
P186	**Rotation with Aphanomyces-resistant pulse crops or intercropping with Brassicas to reduce impact of Aphanomyces root rot on field pea** Chatterton, S.[1]; S. Banniza[2]; R. Bowness[3]; M. Harding[4]; M. Hubbard[5]; L. Shaw[6]; S. Shirtliffe[2] ([1]*Agriculture and Agri-Food Canada;* [2]*University of Saskatchewan;* [3]*Alberta Agriculture and Forestry;* [4]*Agriculture and Forestry;* [5]*Swift Current Research and Development Centre;*[6]*South East Research Farm*)
P187	**Enniatin production does not influence *Fusarium avenaceum* pathogenicity on durum wheat or peas** Foroud, N.[1]; A. Eranthodi[2]; D. Overy[3]; D. Schneiderman[1]; L. Harris[3]; S. Chatterton[1]; D. Gonzalez-Peña Fundora[2]; W. Zhao[4] ([1]*Agriculture and Agri-Food Canada;* [2]*University of Lethbridge;* [3]*Ottawa Research and Development Centre;* [4]*Agricultural University of Hebei*)
P188	**SaltroTM: a SDHI seed applied fungicide for early control of blackleg in canola** Padmathilake, R.[*]; P. Parks; J. Rosset; R. Gulden; D. Fernando (*University of Manitoba*)
P189	**A novel approach to blackleg management in canola: Combining a new fungicide seed treatment with improved flea beetle control** Huang, S.[1]; D. Fernando[1]; D. McLaren[2]; G. Peng[2] ([1]*University of Manitoba;* [2]*Agriculture and Agri-Food Canada (AAFC)*)
P190	**Sensitivity of *Pseudoperonospora humuli* to the systemic fungicides, metalaxyl and fosetyl-Al.** Munawar, A.[1]; M. Filatos[2]; C. Bakker[1]; M. McDonald[1]; K. Jordan[1] ([1]*University of Guelph;* [2]*Ontario Ministry of Agriculture, Food and Rural Affair*)
P191	**Effect of biochar, vermicompost, micronutrient, and biofungicides for suppression of Sclerotinia rot of cabbage** Burlakoti, R.; S. Warhaft; C. Koch (*Agriculture and Agri-food Canada*)

P192	**Effects of temperature, light quality and nutrients on spore germination and growth rate of *Colletotrichum acutatum*** Charkhzarrin, Z.*; V. Gravel (*McGill University*)
P193	**Screening disinfectants for those effective against *Plasmodiophora brassicae* resting spores** Harding, M.[1]; B. Hill[2]; G. Daniels[2]; D. Burke[2]; R. Howard[3]; Chatterton, S.[4] ([1]*Agriculture and Forestry;* [2]*Alberta Agriculture and Forestry;* [3]*RJH Ag Research Solutions Ltd.;* [4]*Agriculture and Agri-Food Canada*)
P194	**Apple and apricot decline in Ontario** Griffiths, J.[1]; A. Lofano[1]; O. Ellouz[1]; A. Wang[2] ([1]*Agriculture and Agri-food Canada;* [2]*Agriculture and Agri-Food Canada; University of Western Ontario*)
P195	**Exobasidium diseases of *Vaccinium* spp. in Newfoundland** Jewell, L.; K. Compton; D. Wiseman (*AAFC*)
P196	**Revysol ® a new fungicide for horticulture crops and turf** Martens, G.; S. MacDonald; K. Dufton (*BASF Canada*)
P197	**Efficacy of registered fungicides to control cucurbit downy mildew isolates collected in 2017 and 2018 from Québec and Ontario** Marchand, G.[1]; C. Trueman[2]; O. Carisse[1] ([1]*Agriculture and Agri-Food Canada;* [2]*University of Guelph, Ridgetown Campus*)

TOPIC 22: Plant Physiology (Posters P198-P204)

P198	**Characterization of a novel Arabidopsis protein kinase involved in flowering** Wang, L.*; R.G. Uhrig (*University of Alberta*)
P199	**Pathogens and molds affecting quality of medical cannabis (*Cannabis sativa* L.) inflorescences.** Punja, Z.; D. Sutton; C. Scott (*Simon Fraser University*)
P200	**Role of aquaporins in root water transport of canola (*Brassica napus*) plants following waterlogging** Liu, M.*; J. Zwiazek (*University of Alberta*)
P201	**Identification and characterization of a photosynthesis-related phosphatidylinositide transfer protein in Arabidopsis** Kim, E.[1]; H. Yu[1]; Y. Lee[2]; H. Kim[3]; K. Lee[1] ([1]*National Institute of Agricultural Sciences;* [2]*Pohang University of Science and Technology;* [3]*Sejong University*)
P202	**What would you do if you had more days before shedding your leaves? Not much, said the sink-limited plant *E. americanum*** Bertrand, H.*; L. Lapointe (*Université Laval*)
P203	**Nitrogen isotope composition and content varied along xylem transport pathway of black cottonwood (Populus trichocarpa) under near steady-state hydroponics** Hu, Y.* (*University of British Columbia*)
P204	**Development of an efficient temporary immersion system for the micropropagation of American chestnut (*Castanea dentata* (Marsh.) Borkh.)** Liu, Z.*; M. Shukla; P. Saxena (*University of Guelph*)

TOPIC 23: Plant-Biotic Interactions (Posters P205-P211)

P205	**Foliar selenium application for controlling fungal diseases in greenhouse** Fofana, B.; A. Somalraju; J. McCallum; R. Peters; D. Main *(Charlottetown research and development centre)*
P206	**Diversity of rhizosphere microbiomes in pea plant with and without root rot** Hossain, Z.[1]; M. Hubbard[1]; L. Bainard[1]; Y. Gan[2] ([1]*Swift Current Research and Development Centre;* [2]*Agriculture and Agri-Food Canada*)
P207	**Cucurbit seed biogels antagonize major plant pathogens** Khalaf, E.; M. Raizada (*University of Guelph*)
P208	**Evaluating the ability of endophytic bacteria to support boreal forest tree growth** Puri, A.[*]; K. Padda; C. Chanway (*University of British Columbia*)
P209	**Investigating the Role of *Brachypodium distachyon* Cellulose Synthase 8 in *Gluconacetobacter diazotrophicus* Colonization** Yang, X.[*1]; K. Hill[1]; R. Austin[2]; K. Vessey[3]; L. Tian[2] ([1]*The University of Western Ontario;* [2]*Agriculture and Agri-Food Canada;* [3]*Saint Mary's University*)
P210	**Interaction of Arabidopsis calmodulin-like proteins with the protein 2b, an RNA silencing suppressor of cucumber mosaic virus** Nakahara, K.[1]; H. Teresinski[2]; M. Suto[1]; S. Jin[1]; W. Snedden[2] ([1]*Hokkaido University;* [2]*Queen's University*)
P211	**Context is everything: benefits of carbonatite rock fertilizers depend strongly on growing conditions and plant type** Jones, J.[1]; P. Antunes[2]; F. Guinel[1] ([1]*Wilfrid Laurier University;* [2]*Algoma University*)

TOPIC 24: Post-Harvest Physiology and Management (Posters P212-213)

P212	**Effect of pre-harvest hexanal spray on the quality of 'Honeycrisp' apples during post-harvest storage** Sriskantharajah, K.[*]; A. Sullivan; G. Paliyath; J. Subramanian (*University of Guelph*)
P213	**Smart delivery of hexanal from nanomatrix for extending the shelf life of fruits** Ranjan, S.[*]; L. Lim; A. Sullivan; G. Paliyath; J. Subramanian (*University of Guelph*)

TOPIC 25: Teaching in the Plant Sciences (Posters P214-215)

P214	**Environmental issues, concerns and education in rural districts** Elawana Mudiyanselage, N. (*Central Environmental Authority in Sri Lanka*)
P215	**The power of pi: using raspberry pis to photograph actively growing plants** Meyer, C.; K. Raymond (*University of Guelph*)

WORKSHOPS IN PLANT CANADA 2019

Plant Canada 2019 brings an exciting program of workshops for your benefit that are led by both professional and academic scientists.

WORKSHOPS

Workshops are open to all registered attendees of Plant Canada 2019.
Workshops are **free** with **no reservations** required.

The times and locations for each Workshop are provided in the table below.

#	Date	Times	Location	Title
W1	Sunday July 7th	4:15 – 5:15 pm	ROZ 104	**Sponsor Introductions (Lightning Round)**
W2	Monday July 8th	11:15 – 11:50 am	ROZ 101	**Careers Outside of Academia**
W3	Monday July 8th	11:15 – 12:15 pm	ROZ 103	**Towards Developing a Plant Health Science Vision for Canada**
W4	Monday July 8th	12:00 – 12:50 pm	ROZ 101	**NSERC Information Session**
W5	Tuesday July 9th	11:15 – 12:15 pm	ROZ 101	**Beyond Grad School: A Guide for PDF and PI Positions**
W6	Tuesday July 9th	12:00 – 1:00 pm	ROZ 102	**CAPB-Sponsored Genome Editing**
W7	Monday July 8th	7:00 – 8:30 pm	ROZ 105	**CBA Workshop: Gender in Ecology**

WORKSHOP #1- SPONSOR INTRODUCTIONS

Sunday July 7th - **4:15 - 5:15 pm ROZ r.104**

Sponsor Introductions

The purpose of this workshop is to focus your attention on our Silver and Gold sponsors that have exhibits in Peter Clark Hall (Poster area). This opportunity will be presented in a lightning round format to give you a chance to listen to details on their company and products for 3-4 minutes and 1-2 minutes for questions. The companies in this workshop include our Gold Sponsor Innotech Alberta, and our Silver Sponsors BASF, Biochambers Inc., Canada Science Publishing, Conviron, Hoskin Scientific, LI-COR Biosciences Inc., and Western Grains Research Foundation.

WORKSHOP #2 -CAREERS OUTSIDE OF ACADEMIA

Monday July 8th - **11:15 - 11:50 am ROZ r.101**

Careers outside of Academia

Goal: The goal of this workshop is to show career paths outside of academic research. The workshop will examine the differences between industry, government, and academia and any benefits, experiences, or drawbacks faced in a non-academic research setting. The workshop will be led by Dr. Teagen Quilichini who has valuable experience in academic (as a PhD/post-doc at UBC), industry (as a post-doc with Annandia Labs), and government (as a research associate with the NRC) research settings.

Speaker:

Dr. Teagen Quilichini (NRC Saskatoon) – Research Associate

WORKSHOP #3 -TOWARDS DEVELOPING A PLANT HEALTH SCIENCE VISION FOR CANADA

Monday July 8th - **11:15 - 12:15 pm ROZ r.103**

Towards developing a plant health science vision for Canada

The intent of this workshop is to foster discussion within the plant health community and act as a catalyst for imagining a common vision for plant health science that is unifying, relevant and aspirational. With increasing trade, the changing climate, the evolving policy/program landscape, and advancing science & technology capabilities, Canada is at a critical juncture. Due to these drivers, plant health threats will continue to intensify in number, range, and diversity posing potentially catastrophic consequences to Canada`s economic, environmental and sustainable development. Endorsed in 2017, the Plant and Animal Health Strategy directed that our current situation demands effective and urgent proactive collaborative action to ensure Canada's bio-economy sector, including agriculture and forestry, climbs to the cutting-edge; capitalizing on novel and disruptive discoveries and having the instruments (e.g. legislation, policy, surveillance, programs, research funds, etc.) in the most effective and efficient manner to maintain a clean environment and a strong economy. Plant health science will be a key component in implementing the Strategy, and there is a need to galvanize research scientists and organizations to unite their efforts under a common vision.

Agenda

Time	Presentations
11h15-11h20	**Introduction** Dr. Rene Van Acker, Dean, Ontario Agricultural College, University of Guelph
11h20-11h30	**Implementing the Plant piece of the Plant and Animal Health Strategy; progress to today** Deborah Lorenzin, Secretariat Canadian Plant Health Council
11h30-11h40	**Plant Canada : Recent efforts/successes in advocating for plant science in Canada** Dr. Deena Errampalli, President, Plant Canada
11h40-11h50	**Why is a plant health science vision needed?** Dr. Michele Marcotte, Director Ottawa Research & Development Centre, AAFC
11h50-12h00	**Establishing a Plant Health Vision for Canada** Dr. Pierre Bilodeau, Executive Director, Plant Health Science, CFIA
12h00-12h15	**Discussion/Conclusion**

WORKSHOP #4 -NSERC INFORMATION SESSION
Monday July 8th - 12:00 - 12:50 pm ROZ r.101

NSERC Information Session

The NSERC presentation will be delivered by Stéphanie Lanoix, Program Officer, Research Grants and Scholarships, NSERC, and it will focus on the recent results of the Discovery Grants competition with an emphasis on those from the Biological Systems and Functions Evaluation group. Success rates of plant sciences within the discovery and RTI programs, and the distribution of the 2018 federal investment for fundamental research, will be addressed. NSERC news and updates will also be presented. Relevant data will be provided in more detail than is provided by NSERC on their relevant websites.

WORKSHOP #5 -BEYOND GRAD SCHOOL: A GUIDE FOR PDF AND PI POSITIONS
Tuesday July 9th - 11:15 - 12:15 pm ROZ r.101

Beyond grad school: A guide for PDF and PI positions

The goal of the workshop is to help junior scientists apply for careers following graduate school. The workshop will address what qualities in an application (CV, cover letter) that potential employers are looking for. The speakers will also share tips and experiences that they have gained during their time as a PDF and Junior PI. The workshop will be led by Dr. Jacqueline Monaghan and Dr. Heather McFarlane. Both are junior PIs and have done their PhDs in Canada and post-doctoral work abroad.

Speakers:

Dr. Jacqueline Monaghan (Queen's U) – Asst. Professor

Dr. Heather McFarlane (U of Toronto) – Asst. Professor

WORKSHOP #6 -CAPB-SPONSORED GENOME EDITING

Tuesday July 9th - 12:00 - 1:00 pm ROZ r.102

CAPB-Sponsored Genome Editing Workshop

Genome editing tools have greatly accelerated the creation of new plant varieties. The implications with regards to economic profitability, governmental regulations and public acceptance of these technologies in Canada and in other countries will be discussed in this workshop. We have invited four panelists from government, academia and industry to describe the current status of this technology in Canada and in the rest of the world.

Agenda:

12:00 **Introduction**. Dr. Rima Menassa, President, Canadian Association for Plant Biotechnology – Research Scientist, Agriculture and Agri-Food Canada

12:05 **Genome editing: getting acquainted with the technology**. Dr. Bourlaye Fofana, Research Scientist, Agriculture and Agri-Food Canada

12:15 **Industry's perspective on genome editing**. Luis Luque, Science and Regulatory Affairs Officer, Crop Life Canada

12:25 **Clarifying Canada's Regulatory System: A focus on gene editing**. Amanda DeBruyn, Plant Biosafety Policy Analyst, Canadian Food Inspection Agency

12:35 **Canada's Position in the Global Regulation of Genome Editing**. Stuart Smyth, Assistant Professor, University of Saskatchewan

12:45 **Discussion**

WORKSHOP #7 -CBA WORKSHOP: GENDER IN ECOLOGY

Monday July 8th - 7:00 - 8:30 pm ROZ r.105

CBA Workshop: Gender in Ecology

Nicole Fenton (CBA President Elect) will host a CBA workshop to examine the influence of gender on ecological research.

Listing of Abstracts for the Speaker Program

S1. Transcriptome landscape of the early *Brassica napus* seed

Zeigler, D; D. Khan; J.L. Kalichuck; M.G. Becker; M.F. Belmonte
University of Manitoba

Brassica napus L. (canola) is one of the world's most economically important oilseeds. Despite our growing knowledge of Brassica genetics, we still know little about the genes and gene regulatory networks underlying early seed development. In this work, we use laser microdissection coupled with RNA sequencing to profile gene activity of both the maternal and filial subregions of the globular seed. We find subregions of the chalazal end including the chalazal endosperm, chalazal proliferating tissue, and chalazal seed coat, have unique transcriptome profiles associated with hormone biosynthesis and polysaccharide metabolism. We confirm that the chalazal seed coat is uniquely enriched for sucrose biosynthesis and transport, and that the chalazal endosperm may function as an important regulator of the maternal region through brassinosteroid synthesis. The chalazal proliferating tissue, a poorly understood subregion, was specifically enriched in transcripts associated with megasporogenesis and trehalose biosynthesis, suggesting this ephemeral structure plays an important role in both sporophytic development and carbon nutrient balance, respectively. Finally, compartmentalization of transcription factors and their regulatory circuits has uncovered previously unknown roles for the chalazal pole in early seed development.

Mark Belmonte (Mark.Belmonte@umanitoba.ca)

S2. Arabidopsis seed stored mRNAs are degraded constantly over aging time, as revealed by new quantification methods

Zhao, L.[*1]; S. Wang[1]; Y-B. Fu[2]; H. Wang[1]
[1]*University of Saskatchewan*
[2]*Agriculture and Agri-Food Canada*

How plant seeds age remains poorly understood and effective tools for monitoring seed aging are lacking. Dry seeds contain various stored mRNAs which are believed to be required for protein synthesis during early stages of seed germination. We reasoned that seed stored mRNAs would undergo degradation during seed aging, based on the propensity of mRNAs to degrade. We performed RT-PCR and qPCR analyses to study the changes in stored mRNA levels of Arabidopsis seeds. All stored mRNAs analyzed were gradually degraded in both naturally and artificially aged seeds. The difference in Ct values between aged and control seeds (ΔCt value) was highly correlated with the mRNA fragment size and seed aging time. We derived mathematical equations for estimating the relative amount of undamaged stored mRNAs and frequency of the breakdown at one nucleotide level for individual mRNAs. Our results suggest that stored mRNAs were broken down randomly. The frequency of breaks per nucleotide per day, which we named *b* value, remained fairly constant over aging time under the same aging conditions. Also, we showed that the change in stored mRNA levels could serve as a more precise biomarker for seed aging assessment compared to three existing methods. These findings have provided new insight on stored mRNA degradation and seed aging in plants, and the methods developed will advance studies on stored mRNAs.

Liang Zhao (liz704@usask.ca)

S3. Strigolactone receptors from striga activate a latent Arabidopsis signaling pathway to bypass the gibberellin requirement for germination

Bunsick, M.*; K. Nemrish; P. Sung; G. Ly; S. Lumba
University of Toronto

Parasitic plant infestations dramatically reduce the yield of major food crops in Sub-Saharan Africa and pose a serious threat to food security. The first step of a successful parasitic infestation is host-dependent germination. Seeds of the parasite *Striga hermonthica* detect hosts by sensing the plant hormone strigolactone, which nearby crops emit. Despite its importance, we do not know how host-derived strigolactones germinate parasitic plants. By expressing strigolactone receptors from *Striga* in different genetic backgrounds of the model plant *Arabidopsis thaliana*, we show *Striga* receptors co-opt the karrikin signaling pathway to germinate *Arabidopsis* seeds. Further, activation of this pathway circumvents *Arabidopsis's* requirement of the hormone gibberellin for seed germination. Our results suggest that parasitic plant species evolved a pathway, latent in non-parasitic plants, to become its dominant pathway for germination.

Michael Bunsick (michael.bunsick@mail.utoronto.ca)

S4. Early chemical priming persistently attenuates induced anthocyanin accumulation with broader metabolic and possible systems-level impact

Hiiback, K.*[1]; M. Campbell[2]
[1]*University of Toronto*
[2]*University of Guelph*

Priming is a general term for a phenomenon in which exposure to an early environmental stimulus results in more rapid or vigorous response when the plant is exposed to subsequent challenges. Various approaches to induce priming have been described including 'seed priming', a technique which traditionally involves application of nutrients or endogenous plant molecules to seeds to improve crop performance. Using a high-throughput approach, thousands of small molecules were screened to identify compounds capable of 'chemical priming', specifically producing an altered response to subsequent abiotic challenges when applied as seed priming treatments. Several novel molecules were identified in this screen that had the persistent ability to reduce total anthocyanin accumulation in 7-18-day old *Arabidopsis thaliana* seedlings induced by later chilling and low nitrogen treatments, even though chemical exposure was limited to the developmental windows of seed imbibition and germination. Untargeted metabolomic profiling revealed significant continued perturbations in the secondary metabolism of chemically-primed plants including but not limited to the expected changes in anthocyanins. Complementary transcriptional profiling of genes encoding flavonoid and anthocyanin biosynthetic enzymes was completed to examine another systems level possibly linked to the persistent effect. The presented research represents a proof-of-concept for the functional potential of seed priming with novel compounds, and underscores the complexity of secondary metabolism as a component of plant stress response.

Katrina Hiiback (k.hiiback@mail.utoronto.ca)

S5. Functional characterization of gibberellic acid signalling components in *Striga hermonthica*

Wong, C.*; K. Meteleva; H. McIlwraith; A. Caragea; S. Lumba
University of Toronto.

In the sub-Saharan farmlands of Africa, a devastating parasite, *Striga hermonthica* affects approximately $300 million worth of crops every year. *Striga* seeds germinate in response to strigolactones (SLs) emitted by host roots but do not germinate in response to gibberellic acid (GA). To investigate this difference between parasitic and non-parasitic plants, we will determine the function of various GA signalling components from *Striga* by expressing them in *Arabidopsis thaliana*. At the molecular level, the presence of GA causes DELLA proteins to be degraded in order to elicit a GA response. *Arabidopsis* has five partially redundant DELLA genes, all of which are additively involved in regulating important biological processes such as germination, cell expansion, and floral development. Our bioinformatics analyses revealed multiple DELLA homologues in *Striga* (*ShDELFA*s). To characterize the functions of these homologues, we generated a series of *Arabidopsis* transgenics over-expressing each *ShDELFA*. We found that these homologues are functional in *Arabidopsis*. One behaves similarly to *Arabidopsis* DELLAs, such that it suppresses germination and vegetative growth, and degrades upon the presence of GA. In contrast, the others showed several unique characteristics, such as resistance in GA-induced degradation, and no visible suppression in vegetative development. Further study on how the role of GA impacts *Striga* germination may contribute to a solution in eradicating *Striga* infestations.

Cynthia Wong (cynthia.wongcy@gmail.com)

S6. Two hallmarks of plant adaptation viewed through the embryonic lens

Venglat, P.; K. Tanino
University of Saskatchewan

During angiosperm embryogenesis, stem cell niches, viz., the shoot apical meristem (SAM), root apical meristem (RAM) and the pro-vascular initials are wired differently to their respective differentiation programs compared to animal embryogenesis where adult stem niches are nested within organs enabling their homeostasis. This plant-specific embryonic body plan facilitates an iterative process of differentiating shoot (phytomer) and root modules thus elaborating the plant body over time and providing an adaptive advantage. This iterative process, the first hallmark of plant adaptation, is developmentally timed and environmentally regulated giving rise to diverse architectures that is suited to their respective habitats. The second hallmark of plant adaptation is the regenerative potential, expressed as a greater degree of plasticity of their cells and tissues with regards to cell fate when compared to the animals. A wide range of plant tissues can reprogram their morphogenetic state and regenerate embryos, shoots and roots. These two hallmarks are generally viewed as two different genetic expressions of plant development. Using the genetic and molecular data from Arabidopsis embryogenesis that has been dissected and studied extensively, we present a model that explains the modular nature of development inherent in the plant embryonic body plan in the context of plant regenerative potential that transitions from totipotency to a gradient of reprogrammable pluripotent states.

Prakash Venglat (prakash.venglat@gmail.com)

S7. Fall and spring placement of nitrogen fertilizers. Where do enhanced efficiency fertilizers fit?

Karamanos, R.
Koch Fertilizer Canada, ULC

There are three major losses of nitrogen (N) from the soil-plant system, namely, volatilization, denitrification and leaching. There have been a number of practices recommended to reducing volatilization of urea-based fertilizers, e.g., use of urease inhibitors, slow-release forms, and, irrigation shortly after application. However, the most common practice in western Canada has been incorporation of the fertilizer into the soil, especially in bands. This practice now is under scrutiny as shallow banding of urea-based is proving to be less efficient in affording protection of urea-based fertilizers than deep banding. Further, denitrification losses have been shown to occur both during spring snowmelt and under wet conditions. This study summarizes the data from a three-year research conducted in the three prairie provinces that included deep-, shallow-banded and broadcast urea with or without the addition of stabilizers. Agrotain® stabilized urea (NBPT) and SuperU (NBPT and DCD) fertilizer were used (NBPT is a urease and DCD a nitrification inhibitor). There were no differences in yield when fertilizers were deep banded (6-8 cm); however, broadcasting or shallow banding (1-4 cm) non-stabilized urea resulted in significant yield reductions that were for the most part averted by using stabilizers.

Rigas Karamanos (rigas.karamanos@kochind.com)

S8. Nitrogen and phosphorus nutrition in oat: nutrient uptake and interactive effect on crop lodging and yield

Ma, B-L.[1]; Z. Zheng[2]; D. Pageau[2]; C. Vera[2]; J. Fregeau-Reid[2]; A. Xue[2]; W. Yan[2]
[1]*Agriculture and Agri-Food Canada*
[2]*AAFC*

Balanced plant nutrition is essential to achieve high productivity and get the best economic return from applied fertilizers. A field study was conducted across diverse locations in Canada to determine N and P uptake, agronomic traits and yield performance of oat cultivars under different fertilizer N rates. We found that yield components were altered to adapt to soil-environmental conditions, with panicles m^{-2} mostly accounted for yield variation at Melfort, seeds $panicle^{-1}$ and 1000-seed weight at Normandin, and lodging index was an additional yield-determining factor at Ottawa. Crop lodging displayed a strong correlation with straw P content, with a change-point of 13.6 kg P ha^{-1}, below which lodging rarely occurred. We speculate that high straw P content, induced by external N supply, may have exhibited similar behavior as N in weakening the strength of stem base and anchorage system, leading to crop lodging. Nutrient interaction is a complex issue, some other nutrient elements, such as K, may play an important role in stimulating crop lodging resistance. Taking multiple nutrients and their interaction and balances into considerations is beneficial in illustrating the mechanisms of lodging resistance in future studies.

Bao-Luo Ma (baoluo.ma@canada.ca)

S9. Nitrogen fertilizer management for inbred seed corn

Sayem, S.M.[*1]; **L. Van Eerd**[2]
[1]*University of Guelph*
[2]*University of Guelph Ridgetown Campus*

Seed corn (Zea mays L.), with an economic impact over $ 150 million, is expanding its acreage in Southwestern Ontario (est.9,100 ha). Optimization of the fertilizer N inputs to seed corn is necessary to sustain seed quality (e.i., marketable seed yield, 100 kernel weight, test weight, seed size) and yield, while maximizing economic returns and limiting N losses to the environment. Therefore, field split-block experiments were conducted in 2015-2017 using six fertilizer N rates (0 to 225 kg ha-1) to four inbreds of seed corn (11 site-years). At a given site-year, the optimum N rate to maximize seed yield (marketable and total expressed as Mg ha-1) depended on the inbred and varied from non-responsive to optimal of 120 to 175 kg N ha-1. This suggests the need for inbred-specific N applications in 9 of 11 site-years. Likewise, at a given site-year there were seed quality differences among the 4 tested inbreds (6 of 44 at 11 site-years). But there no inbred by applied N interaction for most quality parameters (38 of 44 at 11 site-years), which suggests that growers can adjust their N applications without compromising seed quality. To better understand the inbred-specific yield response to fertilizer N, an isotopic N field study is in process.

SM Sayem (ssayem@uoguelph.ca)

S10. Evaluating the effects of organic and inorganic phosphorus amendment on soil biochemical and microbial characteristic in podzol following silage corn cultivation under boreal climate

Cheema, M.[1]; **W. Ali**[1]; **M. Nadeem**[1]; **W. Ashiq**[1]; **M. Zaeem**[1]; **S. Gillani**[1]; **S. Khamseh**[2]; **V. Kavanagh**[3]; **R. Thomas**[1]
[1]*Grenfell Campus, Memorial University of Newfoundland, Canada*
[2]*Shahrekord University*
[3]*Government of Newfoundland and Labrador*

Inorganic phosphorus (IP) fertilizer application to soil is predominantly bound to aluminum and iron in acidic soils or with calcium in alkaline soils, thereby reducing its availability to crop plants. Dairy manure (DM) application can improve soil physiochemical properties, and nutrients cycling by enhancing biochemical and microbial attributes. A field experiment was conducted to investigate the effects of organic and inorganic P amendment on soil biochemical attributes and microbial community in silage corn mono-cropping systems in podzol under cool climate. Experimental treatments were: [P_0: control); P_1: DM with high P concentration; P_2: DM with low P concentration; P_3: IP and five silage corn genotypes (Fusion RR, Yukon R, A4177G3RIB, DKC 23-17RIB and DKC 26-28RIB). DM with high P manure increased 29% and 44% acid phosphatase activity (AP-ase) and 60% and 39% soil available (SAP), compared to control in 2016 and 2017. High gram negative bacteria, fungi, eukaryotes, total bacterial phospholipids fatty acids were also observed in high P manure. Yukon R and DKC 26-28RIB exhibited higher fungal biomass, total bacterial phospholipid fatty acid and total PLFA in the soil rhizospheres. Redundancy analysis showed significant and positive correlations between biochemical and microbial parameters with high P manure and Yukon R and DKC 26-28RIB. Results suggest that DM application could be a sustainable practice to enhance microbial population, and abundance and eventually, improve the AP-ase and SAP.

Mumtaz Cheema (mcheema@grenfell.mun.ca)

S11. Evaluation of optical sensors in predicting yield and nitrogen application in sugarbeet (*Beta vulgaris*)

MacFarlane, J.; L. Van Eerd
University of Guelph Ridgetown Campus

As farmers dependency on fertilizers to support sugarbeet (Beta vulgaris) nitrogen requirement grows, determining that requirement becomes important for maximizing the sugarbeet yield potential. Refinement companies such as Michigan Sugar pay growers based on root yield quantity and yield sucrose quality. Monitoring plant N levels in sugarbeet during the growing season is important for maximizing yield, as N fertility positively correlates with root yield but negatively with sucrose. Final yield sucrose is also impacted by harvest date as later dates have higher sucrose concentrations. Both having shown promise in monitoring nitrogen, the SPAD meter and GreenSeeker were compared in their ability to measure sugarbeet N content and predict yield quality mid growing season (2016/2017), and at two harvest dates (2015/2017). The design was a split-block with three replications, using eight cultivars of sugarbeet and five N rates (0, 44.84, 89.68, 156.94, 224.2 kg ha^{-}). Optical sensor observations taken in June and at harvest were compared with N rate, yield, and recoverable white sucrose per ton (RWST) at harvest. Throughout 2015/2016/2017, root yield (tonnes ha^{-}) did not have a significant relationship with optical sensors across cultivar. The optical sensors related better to N rate and RWST in September/October across majority of cultivar, when fertilizer adjustments would no longer be possible, making harvest date adjustments more viable to maximize profitable yield, based on sensor yield predictions.

John MacFarlane (jmacfa04@uoguelph.ca)

S12. Simulating natural environmental cues redefines winter hardiness of *Brachypodium distachyon* by connecting cold acclimation, vernalization, and development

Charron, J-B.[1]; B.F. Mayer[1]; A. Bertrand[2]
[1]*McGill University*
[2]*Agriculture and Agri-Food Canada*

With the dawning of climate change, it has become relevant to understand how plants respond to changing environmental conditions. Yet, temperate plants regularly face seasonal change and to persist in these conditions, have adapted by adjusting their stress tolerance, phenology and development. Understanding how temperate plants follow seasonal cues during their development can help elucidate adaptation mechanisms in plants. Cold acclimation (CA) and vernalization (VRN) are processes that ensure persistence in temperate climates by regulating freezing tolerance and flowering time. However, how these two processes are integrated into a coordinated developmental response remains poorly understood. The model grass *Brachypodium distachyon* has emerged as a model to study CA and VRN in temperate cereals. By identifying key seasonal cues that occur within the native range of the species, we designed a diurnal freezing treatment (DF) that combines prevailing summer-to-winter transition signals. Under DF, *B. distachyon* manifests coordinated cold acclimation, vernalization and developmental responses. Altogether, our results demonstrate a direct link between CA and VRN, and that typically used constant-temperature cold treatments induce an “over-vernalized” molecular state at the expense of freezing tolerance. This work also stresses the importance of reproducing natural signals in laboratory conditions.

Jean-Benoit Charron (jean-benoit.charron@mcgill.ca)

S13. Dimerization of Vitis ICE with Vitis FAMA enables activation via a specific MYC element in the Vitis CBF4 promoter sequence

Alibabai, L.; A. Edge; M. Rahman; Nassuth, A.
University of Guelph

Basic helix-loop-helix (bHLH) proteins dimerize with other bHLH proteins to form an active transcription factor complex, whereby different dimers bind to and activate via a specific MYC (CANNTG) promoter sequence and thus activate a specific regulon. ICE proteins have at least 2 functions: the activation of cold acclimation via the ICE-CBF pathway and the development mature stomata. ICE proteins are bHLH transcription factors that induce *CBF* expression but it is not known with what proteins they dimerize to do so. On the other hand, dimers of ICE with SPCH (speechless), MUTE and FAMA direct the three sequential steps in stomata development but it is not known which genes these dimers activate to direct this development. We investigated the dimer formation by *Vitis* ICE proteins using agroinfiltration-directed BiFC (Bimolecular fluorescence complementation), competitive BiFC and re-localization assays, and determined that many dimers can be formed. However, only ICE-FAMA combinations but not ICE-SPCH or ICE-MUTE combinations were found to activate expression from a specific MYC element in the *Vitis CBF4* promoter. The possible implications for the functions of *Vitis* FAMA or *Vitis* CBF4 will be discussed. This work was made possible due to an NSERC discovery grant to AN.

Annette Nassuth (anassuth@uoguelph.ca)

S14. Using global metabolomic and transcriptomic analysis to assess heat-shock-response functionality in the Antarctic alga Chlamydomonas sp. UWO241

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The psychrophilic green alga *Chlamydomonas* sp. UWO241 (hereafter UWO241) has been the subject of numerous studies, however these have mainly focused on adaptations which facilitate life at low temperature as opposed to restricting it from moderate ones. Here, we present the results of tandem experiments examining the changes to the transcriptome and metabolome of this Antarctic alga at steady-state growth temperatures and following temperature shifts, as compared to the model alga *Chlamydomonas reinhardtii*. Both these experimental approaches reveal that UWO241 has a distinctly more muted response to the temperature shift regime than does *C. reinhardtii*. This muted response reflects the inability of UWO241 to adjust its cellular metabolism in ways appropriate to growth at moderate temperatures. Furthermore, cell viability assays of UWO241 and *C. reinhardtii* subjected to the heat shock regimes used in the ‘omics experiments revealed that the mortality of UWO241, but not *C. reinhardtii*, was lowest when the heat shock regime was at its most extreme. These results challenge the notion that the optimal growth temperature for an organism is that at which it grows most quickly. In the case of UWO241, temperature stress resistance is greatest at the growth temperature eliciting the slowest growth, thus the optimal temperature for stress resistance differs from the optimal temperature for growth.

Marc Possmayer (mpossmay@uottawa.ca)

S15. Tissue-specific changes in the apoplastic and intracellular proteome during sub-zero acclimation of winter wheat and rye crowns

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[1]*University of Saskatchewan*
[2]*Iwate University*

Cold-acclimated winter cereals acquire an additional 2°C to 5°C increase in freezing survival when exposed to soil temperatures of -3°C for 3 d. This additional acquisition of cold hardiness is known as sub-zero acclimation. Previous crown studies have observed the vascular transition zone (VTZ) to have a higher freezing sensitivity than the shoot apical meristem (SAM). The mechanism behind the differential freezing response and how sub-zero acclimation enhances tissue-specific freezing survival is not fully understood. Using the current superior freeze resistant winter wheat (*Triticum aestivum* L.) 'Norstar' and more winter hardy 'Puma' rye (*Secale cereale* L.) as a model, freezing properties and proteome analysis of field grown sub-zero acclimated crown tissues were contrasted to identify species-specific mechanisms of freezing survival. In sub-zero acclimated crowns, patterns of injury were examined with tetrazolium chloride vital stain and compared to whole plant recovery. Cold and sub-zero acclimation resulted in distinct SAM and VTZ proteomes. In the sub-zero acclimated crowns, greater accumulation of anti-freeze proteins in the VTZ and proteins enhancing desiccation tolerance in the SAM improved resistance to freezing in rye compared to wheat. Differences in the intracellular and apoplastic proteomes will be discussed. Identification of protein markers associated with field acclimation will be useful to breeders' intent on selecting for and improving the freezing survival of winter wheat.

Ian Willick (ian.willick@usask.ca)

S16. Thriving or barely surviving: examining heat-stress induced mortality of tamarack under extreme climate conditions

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University of Western Ontario

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. We grew tamarack (*Larix laricina)* 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 to examine seedling carbon fluxes to investigate whether high growth temperatures may lead to carbon limitations and mortality. Growth at +8 °C warming led to considerable mortality in the ambient CO_2 treatment, but not the elevated CO_2 treatment. We first evaluated carbon balance parameters of healthy seedlings across all six treatments. There was no acclimation of photosynthesis, but respiration decreased with increasing growth temperature. Root respiration measured at a standard temperature did not differ across the treatments. We examined carbon balance parameters between healthy and dying seedlings in the ambient CO_2 /+8 ˚C treatment and found there was trend of a lower ratio of net CO_2 assimilation rate (A_{net}) to dark respiration rate (R_{dark}) in dying seedlings ($p=0.0931$). Further investigation should provide insight into whether carbon limitations are the cause of observed seedling mortality under high growth temperatures

Bridget Murphy (bmurph26@uwo.ca)

S17. Multigenerational heat stress induces phenotypic resilience as well as genetic and epigenetic variations in Arabidopsis thaliana offspring

Yadav, N.*; V. Titov; I. Ayemere; B. Byeon; Y. Ilnytskyy; I. Kovalchuk
The University of Lethbridge

The stress memory of plants has become a recent topic of interest as unpredictable weather patterns and widespread environmental changes through global warming are now quite commonplace. To that end, the current study intended to explore the effects of multigenerational heat stress memory in *Arabidopsis thaliana*. The 25 generations of *Arabidopsis* propagated in the presence of heat stress. The single (F1_H) and multigenerational (F25_H) stressed-progenies showed higher tolerance as compared to their parallel control. Both stressed-progenies also showed elevated homologous recombination frequency (HRF). Methylome analysis revealed that F25_H was different from parallel and parental control progenies by more than 66,000 cytosine methylations. Hierarchical clustering of these epimutations separated stressed- and parental-progenies plants into distinct groups suggesting directional changes. Genome analysis deciphered that F25_H showed 3-times more genetic variants (SNPs and INDELs) than control-progenies. Comparative analysis revealed that epigenetic-variations are more spontaneous and prevalent than genetic-variations. Further Gene Ontology analysis revealed that SNPs were enriched mostly at unknown biological processes in all lineages although processes such as response to stress and stimulus were enriched more in stressed-progenies. The DMRs (differentially methylated regions) were enriched mostly in processes such as transcription and DNA dependent processes, DNA or RNA metabolism. Overall our study highlighted the existence of multigenerational heat stress-induced genetic and epigenetic variations and the adaptability of genome and epigenome in plant phenotypic resilience to heat stress.

Narendra Yadav (narendra.yadav@uleth.ca)

S18. Root damage and immune responses at cellular resolution

Geldner, N.
University of Lausanne

Microbe-associated molecular pattern (MAMP) recognition is crucial to the plant's immune system, but how this sophisticated perception system can be usefully deployed in roots, continuously exposed to bacteria, remains unresolved. We have analyzed MAMP receptor expression and responses at cellular resolution in *Arabidopsis* and found that differentiated outer layers, exposed to bacteria, show low receptor levels and lack MAMP responsiveness. However, these cells can be locally "gated" to become responsive, by either neighbor cell damage or emerging lateral roots. Laser-induced localized damage also leads to immune responses to an otherwise non-immunogenic, beneficial bacterium and enhances responses to a root pathogenic bacterium. We find that single cell damage in differentiated roots leads to regional ROS and calcium waves, ethylene responses, but no detectable jasmonate responses. Treatment with DAMPs alone do not re-iterate laser-induced damage and, surprisingly, the highly local upregulation of MAMP responses by damage is independent of ethylene signalling. Our findings demonstrate that spatially restricted receptor expression is crucial for an appropriate MAMP response in roots and helps to conceptualize how MAMP perception can be used despite a continuous presence of microbial patterns in the soil.

Niko Geldner (Niko.Geldner@unil.ch)

S19. The MACPF protein CAD1 is guarded by the plant immune system

Sementchoukova, I.[*1]; D. Holmes[1]; M. Bredow[1]; K. Siegal[1]; K. Thor[2]; S. Pascetta[1]; C. Zipfel[2]; J. Monaghan[1]
[1]*Queen's University*
[2]*University of East Anglia*

Plant pathogens secrete effector proteins into host cells that target key components of immune signaling in order to shut down plant defenses. To protect against effector sabotage, intracellular NUCLEOTIDE BINDING AND LEUCINE RICH REPEAT RECEPTORS (NLRs) 'guard' the integrity of host immune proteins that are targeted during pathogenesis. NLR activation typically trig05/gers a form of localized programmed cell death known as the hypersensitive response (HR) that limits pathogen proliferation. Few NLRs have however been matched to their host or pathogen targets. Here, we investigate whether the *Arabidopsis thaliana* MEMBRANE ATTACK COMPLEX/PERFORIN (MACPF) protein CONSTITUTIVE ACTIVE DEFENSE 1 (CAD1) is guarded by plant NLRs as its loss of function leads to autoimmunity. We utilize a novel *cad1* allele that, similar to null alleles, results in enhanced EDS1-dependent immune signaling, and conducted a screen to identify NLRs that may be involved in *cad1* autoimmunity. Our analysis provides novel insight into the molecular aspects of host-pathogen recognition.

Irina Sementchoukova (17is12@queensu.ca)

S20. Sub-functionalization of the calcium-dependent protein kinase CPK28 by site-specific phosphorylation

Bredow, M.[*1]; K. Bender[2]; D. Holmes[1]; A. Thomson[1]; A. Johnson-Dingee[1]; S. Huber[3]; J. Monaghan[1]
[1]*Queen's University*
[2]*University of Zurich*
[3]*University of Illinois-Urbana-Champaign*

Plant innate immunity relies on the detection of pathogens at the cell surface which initiates intracellular signaling, culminating in broad-spectrum resistance. Immune signaling must be tightly regulated to safeguard against cellular damage. The *Arabidopsis thaliana* calcium-dependent protein kinase CPK28 negatively regulates early immune signaling by promoting degradation of the immune kinase BOTRYTIS-INDUCED KINASE 1 (BIK1). *cpk28* loss-of-function plants display enhanced immune function with no compromise to vegetative growth. However, CPK28 additionally functions in the transition to reproductive growth, as *cpk28* mutants display stunted stem elongation. Here, we explored site-specific phosphorylation as a mechanism for directing the activity of CPK28 in these two signaling pathways. Phosphoablative serine/threonine-to-alanine mutant lines were generated for previously identified *in vivo* autophosphorylation sites and BIK1 *in vitro* transphosphorylation sites identified on the rice ortholog of CPK28. We identified a single phosphorylation site that is uniquely required for CPK28-mediated immune homeostasis but is dispensable for CPK28-mediated reproductive stage transition. Ablation of this site resulted in higher calcium requirements for *in vitro* auto- and trans-phosphorylation activity. Our cumulative evidence suggests a role for phosphorylation at this site in "priming" CPK28 activation following immune-induced calcium influx. This work provides novel insight into the regulation of CPK28 which can be used for the biotechnological development of disease resistant crops without consequences to yield.

Melissa Bredow (11mb95@queensu.ca)

S21. Biofilm formation contributes to *Pseudomonas syringae* pv. tomato success and suppression of biofilm formation is important for PAMP-triggered immunity in Arabidopsis

Nunn, G.*; A. Fufeng; N. Xiao; A. Halim; R. Cameron
McMaster University

Biofilms consist of bacterial cells and associated extracellular poylsaccharides such as alginate, extracellular (e)DNA, lipids and proteins. Biofilms are thought to protect bacterial pathogens from plant defense responses. Using the bacterial pathogen *Pseudomonas syringae pv. tomato (Pst)* and *Arabidopsis*, we investigated the role of biofilms in bacterial pathogenicity by asking: Does biofilm formation contribute to *Pst* success and does the PAMP-Triggered Immunity (PTI) response limit biofilm formation in an SA-dependent manner? PTI was induced by flg22 treatment in wild-type Col-0, *fls2* (PTI mutant) and *sid2-2* (SA biosynthesis mutant). *In vivo* bacterial aggregate formation was monitored in leaves using *Pst* DC3000 pDSK-GFPuv and epifluorescence microscopy. *Pseudomonas* aggregate occurrence was positively correlated with bacterial success in *fls2* and *sid2-2*, while fewer and smaller aggregates were observed suggesting that *Pst* aggregate formation was suppressed in an SA-dependent manner during PTI. *In vivo* staining with DAPI for eDNA and calcofluor white for polysaccharides, combined with *in vitro* bacterial growth and biofilm formation assays with wild-type and *algD Pst* (alginate biosynthesis mutant), suggests that *Pst* aggregates are indeed biofilms (alginate is a common biofilm polysaccharide). Together these results provide compelling evidence that the ability to form biofilms contributes to *Pst* pathogenicity and suppression of biofilm formation is an important component of PTI.

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S22. Regulation of plant immune signaling by receptor kinase phosphorylation

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Several leucine-rich repeat receptor kinases (LRR-RKs) from the model plant *Arabidopsis thaliana* function as cell surface immune receptors which, upon perception of conserved pathogen associated molecular patterns (PAMPs), activate plant immune responses. The LRR-RK ELONGATION FACTOR Tu RECEPTOR (EFR) perceives bacterial elongation factor thermo unstable (or its derived peptide elf18) in concert with the co-receptor LRR-RK BRASSINOSTEROID INSENSITIVE 1-ASSOCIATED RECEPTOR KINASE 1 (BAK1). Phosphorylation of the EFR cytoplasmic domain is among the earliest detectable responses to elf18 perception, but the functional significance of receptor phosphorylation is largely unknown. We reveal that, while EFR is an active protein kinase *in vitro*, and is phosphorylated in a PAMP-dependent manner *in vivo*, kinase-inactive mutants of the receptor are fully functional for elf18-induced immune responses, indicating a non-catalytic role for the EFR cytoplasmic domain. Analysis of immuno-purified EFR from elf18-treated plants by LC-MS/MS revealed several Ser and Thr residues phosphorylated following PAMP perception. To understand the impact of these phosphorylation events on immune signaling, we generated transgenic plants expressing phospho-null and phospho-mimic site-directed mutants of EFR and characterized responses to elf18 elicitation. Collectively, our analysis reveals differential regulation of plant immune signaling by site-specific phosphorylation of EFR. We propose a model in which site-specific phosphorylation mediates receptor complex assembly/disassembly during immune signaling and are testing this hypothesis through a combination of quantitative biochemical and proteomics approaches.

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S23. Plant proteases: a continuous battle in molecular farming

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Over the past decade, clear evidence has uncovered the role of proteases in unwanted protein proteolysis in plant molecular farming. Proteolytic degradation remains a significant problem and restricts industrial viability of plant-based expression platforms. Controlling plant protease activity is an effective approach to improve the accumulation of recombinant proteins. However, the molecular functions of many proteases, including their regulators and their natural substrates, are mostly unknown. Hundreds of genes code for proteolytic enzymes of various classes involved in many biological processes in plants. Recombinant proteins are thus exposed to a large and complex proteolytic network. A better characterization of the plant protease repertoire is essential to identify the principal constituents of the recombinant protein degradation machinery. We here present the diversity of unrelated plant protease families and discuss the recent developments towards a solution to the proteolytic degradation problem. We exemplify the role of activity-based protein profiling to identify proteases and reveal candidate proteases for depletion strategies.

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S24. Development of LED light quality to optimise recombinant protein expression in Nicotiana benthamiana

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Valuable recombinant proteins such as those used in medical therapies can be mass produced in cost efficient plant-based systems. Plantform Corporation has developed a platform for expressing recombinant therapeutic antibodies based on transient expression of genes encoding therapeutic proteins introduced into *Nicotiana benthamiana* host plants by *Agrobacterium tumefaciens*. One therapeutic that the company has been developing production procedures for is trastuzumab, an IgG antibody used in breast cancer treatment and marketed under the name of Herceptin®. Environmental growth parameters can be manipulated to alter a plant's physiology. Among these, light quality is a key driver of metabolic pathways. Controlled environment chambers and tunable LED arrays were used to create eight separate spectral environments. The available LEDs used for this study were; (1) Red [655 nm], (2) Blue [448 nm] (3) Green [568 nm] (4) White [5650 K] and (5) Far-Red [735 nm]. Four visible mono-chromatic spectra and four mixed spectra were selected as the eight treatment groups. At the end of the plant production cycle, morphology was assessed, and biomass was analysed for total soluble protein and amount of IgG. Morphological parameters such as leaf biomass, leaf area and total biomass showed up to a 20% difference between treatments. The difference in IgG expression between treatment groups was shown to be up to 30%. Light quality can alter transient protein expression in plant-based systems.

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S25. Production of recombinant subunit vaccine candidates against Bovine Respiratory Disease pathogen *Mannheimia haemolytica* as an alternative to antimicrobials

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Bovine Respiratory Disease (BRD), or Shipping Fever, is a multifactorial disease which results in high economic loss for the North American beef industry. The goal of this project is to produce an oral vaccine in plants to protect cattle against infection with *Mannheimia haemolytica*, the predominant bacterial agent causing BRD, through mucosal immunity. Antigens were chosen and engineered to consist of important epitopes and immunogenic sites of proteins from *M. haemolytica*. Gene constructs were created with an N-terminal Cholera Toxin B element, as a mucosal adjuvant, fused to a modified virulence factor and a candidate antigen from *M. haemolytica*. These constructs were transiently expressed in *Nicotiana benthamiana* and targeted to various subcellular compartments to determine where the recombinant protein most abundantly accumulated and how structurally similar it was to the native protein components. These chimeric antigen fusions were also stably transformed into the *Nicotiana tabacum* chloroplast genome and analyzed. The immunogenicity of these candidate antigens is being tested in mice.

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S26. Controlling the accumulation of secondary metabolites by plants using antisense oligonucleotides

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The unmodified antisense oligonucleotides used for the first time in 2008 as contact DNA insecticides show great promise in the development of additional post-genomic approaches to problems in agriculture. The use of DNA oligonucleotides, some of which will act as insecticides against target insects, and others that will manage and improve the targeted biological parameters of cultivated plants, is a promising direction of research.

Successful management of the synthesis of secondary metabolites by plants was demonstrated in peppermint (*Mentha piperita*) using an unmodified antisense DNA fragment of oligoMEP-11 (5'-ACACTCTTTTG-3'), which is complementary to the mRNA of the menthon reductase that catalyzes the formation of menthol from menthon. Peppermint leaves were treated with DNA oligonucleotides at a concentration of 50 pmol/cm^2. Analysis of the composition of the essential oil was carried out 4 days after the treatment. The menthol content of the oligoMEP-11 group was 2.03 times less than content measured in the control group (13.12 ± 1.64% versus 6.47 ± 1.04%, respectively; $p<0.05$). The decrease in menthol content was accompanied by a significant increase in menthon content compared with control (61.2 ± 1.31% versus 53.5 ± 1.74%, respectively; $p<0.05$). The oligoYM-11 control fragment (5'-CGTACGTACGT-3') did not affect the accumulation of menthol or menthon.

The described approach can find its widest application in agriculture for growing essential oil and medicinal crops.

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S27. Parallel branch pathways have evolved for assembly of major monoterpenoid indole alkaloids with opposite optical rotations in Catharanthus roseus

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Investigations into the biosynthesis of monoterpenoid indole alkaloids (MIAs) in the medicinal plant, *Catharanthus roseus*, have led to discoveries of multiple branch pathways leading to their unique and diverse chemistries. MIAs have complex and unique ring structures that cannot be reproduced by chemical synthesis, and many have medicinally relevant biological activities. The aspidosperma MIAs are the most prevalent root-specific alkaloids in *C. roseus*, and it was previously thought that these MIAs were derived through various decorations of the tabersonine backbone. Recently, it was shown that separate hydrolases in *C. roseus*are responsible for the production of two aspidosperma-type MIAs with opposite optical rotations, (-)-tabersonine and (+)-vincadifformine, from a common intermediate (PNAS 2018, 115(12):3180-3185; Plant J 2019, 97(2):257-266). The present study shows that separate hydrolases, hydroxylases and O-acetytransferases catalyse parallel pathways in the formation of (-)-tabersonine and (+)-vincadifformine derivatives such as (-)-19-*O*-acetylhörhammericine and (+)-19-*O*-acetylvincadifformine, respectively (Plant J 2019, doi: 10.1111/tpj.14346). The enantiomeric-specificity of these enzymes for their respective (-)- and (+)-substrates sheds new light on the evolution of specialized metabolism and on the importance of taking stereochemistry into consideration in the discovery of new pathways.

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S28. Towards understanding the basis of substrate specificity in a newly characterized class of plant acyl-ACP thioesterases that produce high-value medium-chain fatty acids

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Acyl-ACP thioesterase enzymes, which cleave fatty acyl thioester bonds to release free fatty acids, contribute to much of the fatty acid diversity in plants. ACYL LIPID THIOESTERASES (ALTs), a novel class of plastid-localized thioesterases occurring in all plant taxa, generate medium-chain (C6-C14) fatty and β–keto fatty acids as secondary metabolites. Their volatile products likely serve to defend against predatory insects and pathogens. Medium-chain fatty acids are also used industrially to manufacture insecticides, pharmaceuticals, and biofuels. We investigated the catalytic diversity of ALT enzymes by expressing 15 ALTs from monocots, eudicots, a lycophyte, a green microalga, and *Ginkgo biloba* in *Escherichia coli*. Based on their substrate preferences in terms of chain length and oxidation state, the chosen ALTs could be classified into four catalytic groups comprising enzymes from diverse species and taxa. Structure-based phylogenetic analyses using three-dimensional models of ALTs revealed unique tertiary structural features of ALTs with preference for C6-10 or C12-14 acyl-ACP substrates. We performed domain-swapping experiments to determine whether these features influence ALT substrate specificity. Profiling the products of chimeric enzymes in *E. coli* led to the identification of amino acid sequence fragments that affect acyl-ACP chain length preference and enzyme activity, establishing the first links between ALT protein sequence and substrate specificity. Information from this study could be used to engineer recombinant ALTs with substrate specificities that suit particular industrial purposes.

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S29. Nutrient deposition modifies how arbuscular mycorrhizal fungi influences competitive interactions in plants

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Arbuscular mycorrhizal (AM) fungi increase plant access to phosphorous in exchange for sugars from photosynthesis and can provide a competitive advantage to highly responsive species in low nutrient soils. Increased phosphorus deposition may change the composition of AM fungal communities in soil, which in turn can influence competitive interactions among plant species. The aim of this study is to examine how phosphorous fertilizer and soil biota influence fungal effects on plant growth and competitive interactions between species that differ in their response to AM fungi using Andropogon gerardii, a highly responsive species native to tallgrass prairies, and Bromus inermis, a less responsive species that invades and competes with A. gerardii. Soil inoculum from three sites varying in phosphorous levels was applied along with low and high phosphorous fertilizer treatments in an additive replacement series competition experiment. Mycorrhizal fungi from soils with a history of low phosphorus inputs had more positive effects on plant growth than fungi from soils with high phosphorus input. For A. gerardii, we found that interspecific competition was either stronger or equal to intraspecific competition when grown with more beneficial soil biota. Our study can improve our understanding of how nutrient deposition can affect the mutualistic efficiency of AM fungal communities and imply the likelihood that non-native species could invade during the establishment phases of tallgrass prairie restoration efforts with A. gerardii.

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S30. Nitrogen fixing plant evolution: the interactive effect of elevating CO2 and herbivores on nitrogen fixing plants

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Nitrogen fixing plants evolved during the late Cretaceous period when atmospheric CO_2 was *ca.* 800-1600 ppm. The current CO_2 level is around 400 ppm and it is predicted to increase up to 800 ppm by 2100. Little is known about how nitrogen fixing and non-fixing plants respond to both changing CO_2 condition and herbivores. Speckled alder (*Alnus incana* ssp. *rugosa*) were grown in growth chambers and inoculated with the symbiont *Frankia* or not. Plants were grown at one of three atmospheric CO_2 levels: 400, 800, 1600 ppm, representing ambient, future and Cretaceous era atmospheric levels, respectively. After growing for three months, they were exposed to white-marked tussock caterpillar (*Orgyia leucostigma*) for 5 days. A choice experiment showed herbivores preferred nitrogen fixing plants. Nodulated plant biomass, leaf C:N ratio and plant total phenolic compounds were increased under elevated CO_2. Specific nodule activity and nodule allocation were decreased under elevated CO_2. Nodulated plants synthesized more total phenolic compounds to defend against herbivores damage. This suggests that nitrogen-fixing plants are likely to exhibit higher level of chemical defenses in the future in response to herbivore damage. Nitrogen fixing plants failed to balance C:N ratio suggesting increased carbon availability cannot be balanced by symbiotic nitrogen fixation.

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S31. Spring into action: How warm air and cool soil temperatures influence nitrogen fixation and physiological performance in green alder

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The short growing season and cold climate of the Canadian boreal forest can result in restricted amounts of available soil nitrogen, limited overall plant growth and low ecosystem productivity. Nitrogen fixing plants, which form symbiotic relationships with specialised bacteria, have an advantage in low nitrogen environments, but are not widespread in the boreal. The reason for this is not well understood. It has not been properly documented how nitrogen fixation and overall plant performance are impacted by seasonal temperatures changes in the soil and air, especially in the spring when soil temperatures remain cool as air temperatures increase. This study was conducted to examine how below ground (nitrogen fixation) and above ground (photosynthetic) processes are impacted when soil and air temperatures differ. A lab experiment using the woody, nitrogen fixing species *Alnus viridis* ssp. *crispa* (green alder) was conducted. Soil was cooled to 10˚C, 14˚C and 16˚C (control) independently of shoot temperature at 22˚C, over a period of 13 weeks. Cooler soil temperatures were found to inhibit nitrogen fixation and photosynthesis during the growing period. Decreasing soil temperatures also resulted in significantly lower chlorophyll content, growth rate, tissue weight and specific leaf area, compared to control plants at time of harvest. This research will help us to further understand the role of nitrogen fixing plants in the Canadian boreal and why their availability is restricted.

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S32. Influence of mycorrhizal mutualism and plant life history on the diversification of plant root morphology and function

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The root is an integral part of all vascular plants, which functions to anchor the plants, and to acquire and transport soil water and nutrients to ensure plant survival, growth and reproduction. There is significant variation in plant root functional traits such as plant root diameter, root hair density, and root branching intensity, but no consensus on the mechanisms causing the diversification of plant root traits. We hypothesized that plant arbuscular mycorrhizal (AM) fungal symbiosis, which has existed since early ancestral land plants, could have co-evolved with plant root systems to help overcome challenges like desiccation and nutrient limitation. One hypothesis is that plant responsiveness to AM fungi could covary with root morphological traits. Alternatively, plant economic spectrum (PES) hypothesized that plant roots could have evolved in a coordinated fashion with leaf functional traits, aligning with plant ecological strategies involving maximizing productivity or conservation of resources. To test these hypotheses, we examined the correlation between root traits, plant mycorrhizal responsiveness and leaf functional traits among 34 populations of legume *Medicago truncatula* under high and low Phosphorus environments. Plant shoot & root biomass, leaf chlorophyll, and root functional traits (root branching, average root diameter, specific root length) were measured and analyzed, the results and their implications will be discussed.

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S33. Rhizosphere temperature, tree species and ectomycorrhizae affect nitrogen uptake

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Temperature is a key determinant of the rate of biological processes. Rising global temperatures will profoundly affect ecosystems, potentially shifting existing species interactions. This study assessed the effect of rhizosphere temperature on nitrogen uptake by roots of two contrasting tree species colonized with two contrasting species of ectomycorrhizal fungi (EMF). Seedlings of *Pinus contorta* (from poor sites) and *Picea sitchensis* (from rich sites) were colonized by *Laccaria bicolor*, a common EMF, and *Thelephora terrestris*, an EMF common on rich sites. Seedlings were grown at 16^{o}C with root temperatures of 17^{o}C or 25^{o}C. Ammonium and nitrate uptake and proton net flux were measured with ion selective microelectrodes at 17^{o}C or 25^{o}C on seedling roots in a full factorial design. All EMF roots had higher rates of ammonium than nitrate uptake. Pine had higher rates of ammonium uptake than spruce, while spruce had higher nitrate uptake. Roots associated with *T. terrestris* had high ammonium uptake while roots associated with *L. bicolor* had high nitrate uptake. For roots associated with *T. terrestris*, measurement temperature had a greater effect on nitrogen uptake than growth temperature. Ammonium uptake was highest in roots grown at 17^{o}C and measured at 25^{o}C, while nitrate uptake was highest in roots grown and measured at 25^{o}C. Proton efflux was highest when roots were transferred from one temperature to another.

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S34. Soil moisture and nitrogen, but not phosphorus and light, limit nitrogen fixation in alders in the south western boreal forest

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Ironically, in areas of the globe where nitrogen limits productivity, nitrogen fixing plants are not dominant. A number of models have used the energy cost of nitrogen fixation to explain the paucity of nitrogen fixing plants, predicting both reduced light and increased nitrogen availability reduces the abundance of nitrogen fixing plants via competitive exclusion. Other hypotheses suggest nitrogen fixing plants have a greater need for phosphorus. Over 4 years we compared nitrogen fixation by *Alnus viridis*spp. *crispa*in a jack pine forest and adjacent open site, both amended with P and N fertilizer. Shrubs consistently got most of their nitrogen form fixation, showing a peak in years when growing season precipitation was 350mm. Contrary to expectation, shrubs in the forest derived more of their nitrogen from fixation than shrubs in the open, likely because open grown shrubs were more water limited. The addition of nitrogen caused a sharp decrease in nodule nitrogenase activity in both sites. In the forest site this was accompanied by a reduction in the proportion of cells in the nodules containing nitrogen fixing vesicles. Annually, nitrogenase activity remained low until mind June and peaked in late July. Nitrogenase activity was suppressed below 12oC. The highest levels of nitrogenase activity occurred at a soil water content of 10% suggesting plant water availability and soil aerobic conditions limit nitrogen fixation.

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S35. Mutational genetics in diploid potatoes and pre/post-harvest control of toxicants

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Cultivated potato (*Solanum tuberosum* L.) is the third most consumed food crop after rice and wheat. Potato is an auto tetraploid crop species having a highly heterozygous genetic base and a complex genome making its genetic studies tedious. Recently, diploid potato breeding has regained interest in the potato genetics community. Genetically, diploid potatoes are easy to work with and can be used in the cultivated potato breeding process as genetic resources and also they can be grown on their own as varieties. However, diploid breeding continuum faces many challenges including anti-nutritional factors and self-incompatibilities. Whereas conventional breeding strategies contributed to the releasing of varieties with low SGA, substantial resources are still required to minimizing these anti-nutritional factors. Recently, we developed and characterized an ethyl methane sulfonate mutagenized pre-breeding diploid potato population for identifying lines with low anti-nutritional factors. The data will be presented and discussed in relation to the high potential for diploid potatoes as a complement to tetraploid potatoes and in pre-and post-harvest management contexts.

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S36. Recent advances in hexanal based packaging technologies to enhance shelf life of fruits

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Hexanal, a natural volatile produced by plants, has been shown to enhance fruit retention and shelf life of several tropical and temperate fruits, when used as an emulsion for spraying or dipping (https://www.idrc.ca/en/project/enhanced-preservation-fruits-using-nanotechnology-cifsrf-phase-2). However, tender fruits such as berries are not benefited by this application due to excessive handling and related damage. Further regulatory issues are relatively easier to tackle when such product is applied as a post harvest treatment. To safely package hexanal and allow its release based on a natural trigger, we tested several approaches including some potentially nano-technology based methods to deliver hexanal precisely during packing and transit. Some of these approaches include the development of bio-degradable, nano-sachets, hexanal ‘pills’ and electro-spun fibers- all of which contained pre-determined doses of hexanal that will be released after packaging and during transit. Results of these ‘smart- delivery’ technologies will be discussed in this presentation.

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S37. Mitigation of fruit drop and prolonging of postharvest shelf life in 'Honeycrisp' apples using hexanal

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'Honeycrisp' apples are in high demand; however, the variety has a serious postharvest disorder known as bitter pit [BP] that renders apples unmarketable and can cause a yield loss of 50%. One technology to combat these challenges is hexanal, a natural compound that is currently being used to extend the postharvest shelf life of many fruits. Hexanal slows cell degradation through inhibition of phospholipase-D (PLD). PLD is an enzyme that initiates autocatalytic reactions, assisting in the degradation of lipids, leading to ripening and softening of the cell membrane. Hexanal was sprayed as a preharvest solution, known as the Enhanced Freshness Formulation [EFF], to 'Honeycrisp' apples. Quality characteristics such as colour, firmness, total soluble solids, titratable acidity, and BP progression were assessed. No significant differences were seen between treatments in quality characteristics, except for BP progression where the hexanal treated fruit had 5% decrease in BP compared to the control fruit. In assessing these components, we hope to increase the longevity, marketability and maintain palatability of 'Honeycrisp' apples.

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S38. The pollen tube growth model for precision blossom thinning of apples

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Management of apple crop load by chemical thinning is one of the most critical orchard practices that significantly affect the annual production and profitability of apple orchards. Although the majority of apple growers in the eastern USA tend to chemically thin their crop within the first four weeks after petal fall, crop loads not sufficiently thinned during this period could result in trees being thrown into the biennial bearing with little or no crop in the 'off' year. Thinning at bloom provides many advantages, e.g. better fruit size and return bloom, and it can be used as a supplemental and/or alternative practice to standard fruit thinning sprays. The application timing of bloom thinning sprays has been subjective until a group of researchers at Virginia Tech has developed a model known as "the pollen tube growth model" (PTGM) to precisely determine the day/time for the first thinning application and subsequent thinning sprays if required. Over the last 13 years, models have been developed for seven apple cultivars including Golden Delicious, Gala, Fuji, Cripps Pink, Honeycrisp, Granny Smith, and Red Delicious. A system whereby commercial apple growers in the eastern USA can now use these models has been created by a collaborative effort between researchers from Virginia Tech and Cornell universities and is now available on the Network for Environment and Weather Applications (NEWA) website.

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S39. Challenges of cultivating saffron under cold climate

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Saffron (*Crocus stivus*) is an autumn crocus that produces a highly valued spice. Most of the production of saffron comes from Iran and the Mediterranean basin. Its cultivation under more northern climates such as North Eastern Canada and US is quite recent. Much of what we know concerning its cultivation must thus be revisited. This leads us to test several aspects of crop production such as depth and period of planting, companionship, weed control, and fertilization. Furthermore, we addressed the issue of soil temperature during the summer, since high flowering yield requires that the corm be exposed to high soil temperatures (23 to 27 °C) for at least 50 days. Laying either mulch films or mini-tunnels over the beds during the summer moderately increased soil temperature at corm depth (20 cm) and strongly reduce the time of hand weeding. Date of planting (early August to early September) also markedly influence the rate of emergence and flowering in the autumn. Mineral fertilization at planting stimulated corm production and improved total corm mass and both nitrogen and magnesium absorption. Despite these improvements, saffron yield remains variable from year to year and strongly influenced by local meteorological conditions in autumn. Further essays are required to improve and stabilize saffron yield under temperate climates.

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S40. Does spraying paraquat increase in-field inoculum of *Colletotrichum fioriniae* in celery production?

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The fungal pathogen *Colletotrichum fioriniae* is the causal agent of celery leaf curl. The pathogen can survive as an epiphyte and endophyte on asymptomatic weeds and produce secondary conidia. Herbicides are commonly used to control weeds in celery fields, so it was important to determine if killing these asymptomatic weeds with herbicides results in sporulation of *C. fioriniae*. The non-selective herbicide paraquat was evaluated to determine effects on *C. fioriniae* sporulation on plant tissue and direct effects on the growth or sporulation of the fungus *in vitro*. Two common weed species, redroot pigweed and lamb's quarters, were inoculated with *C. fioriniae*. Two weeks post inoculation, leaves were detached, surface sterilized, and were either submerged in Gramoxone (500 ppm paraquat) or water and incubated in high humidity. Six days post treatment, abundant acervuli were only observed on paraquat treated leaves, with over 10,000 conidia per cm^2 of leaf tissue. When *C. fioriniae* was grown on potato dextrose agar amended with various concentrations of paraquat (0, 1, 5, 10, 50, 100 ppm), no significant differences were found for mycelial growth rate or the number of conidia produced. This suggests paraquat has an indirect effect on *C. fioriniae* sporulation, possibly through the release of nutrients from rapid plant cell death. Weed management strategies may need to be revised to reduce the inoculum of *C. fioriniae* in celery fields.

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S41. Ferrous sulfate reduces dollar spot disease on different cultivars of creeping bentgrass

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Clarireedia jacksonii is a destructive foliar pathogen that causes dollar spot disease on closely mown turfgrass around the world. The common method of managing dollar spot involves applying fungicides throughout the growing season, usually at 2-3 week intervals, but there are increasing societal concerns about pesticide use. Ferrous sulfate has been mentioned as a possible alternative to commercial fungicides, but its effects on different turfgrass cultivars and this fungus is not known. In this study, ferrous sulfate heptahydrate (FSH) was applied weekly at low 1x (250 g/100m^2) and high 5x (1250 g/100m^2) rates, and was compared to the commercial fungicide Banner Maxx on up to 10 cultivars of creeping bentgrass. Significant differences in the response of different cultivars to the low FSH rate were found (ranging from 47.5% to 85.9% disease suppression), and the high rate had similar disease suppression levels as the fungicide. However, darkening was evident, which led to discolouration trials at 1x to 15x rates. Increasing rates of FSH intensified darkening, which significantly decreased by two weeks later and almost completely dissipated by four week later. FSH also showed direct toxicity to fungal growth, but only significantly at higher rates. It did not significantly reduce grass height and biomass growth at low rates. FSH should be developed as a viable commercial control of dollar spot and other turfgrass diseases.

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S42. In vitro and in-field response of *Stemphylium vesicarium* to foliar fungicides

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Stemphylium leaf blight (SLB) of onion, caused by *Stemphylium vesicarium* (Wallr.) E.G. Simmons, can cause severe leaf necrosis resulting in small, unmarketable bulbs. To manage SLB, growers typically apply fungicides on calendar-based schedules that do not depend on weather conditions or pathogen biology. This can result in more applications than necessary, which increases the risk of fungicide insensitivity. Isolates of *S. vesicarium* were collected from onion and leek in southern Ontario to assesssensitivity to azoxystrobin (a strobilurin fungicide) and pyrimethanil (an anilinopyrimidine fungicide) comparedagainst an unexposed baseline isolate collected in 1995. The baseline isolate was sensitive to azoxystrobin at 0.5 µg ml^{-1}plus 100 µg ml^{-1}salicylhydroxamic acid (SHAM) and to pyrimethanil at 5.0 µg ml^{-1}, assessed as decreased mycelial growth and conidia germination on amended media. Of 10 isolates collected in 2018, 9 isolates exhibited decreased sensitivity to azoxystrobin and 7 isolates had decreased sensitivity to pyrimethanil. There were no differences in fitness (growth or sporulation) between insensitive and sensitive isolates. A field trial using a weekly foliar spray program of Quadris Top (difenoconazole and azoxystrobin) alternated with Luna Tranquility (fluopyram and pyrimethanil) reduced SLB symptoms by only 10%. This demonstrates that these fungicides no longer provide effective reduction of SLB on onion in southern Ontario, even with repeated application, due at least in part to fungicide insensitivity.

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S43. Evaluation of yield losses and pyraclostrobin sensitivity in *Leptosphaeria maculans*, cause of blackleg of canola

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Blackleg (*Brassica napus* L.), caused by *Leptosphaeria maculans* (Desm.) Ces. & de Not., is an important disease of canola worldwide. In Canada, blackleg is managed mainly by the cultivation of resistant or moderately resistant canola hybrids and the application of fungicides. Field experiments were conducted in central Alberta in 2017 and 2018 to determine the relationship between blackleg severity and yield in two moderately resistant hybrids '73-15RR' and '1950RR'. Seed yield per plant was found to decrease as a consequence of *L. maculans* infection, with regression analysis showing that the relationship between yield and disease severity was best explained by second degree quadratic equations. Sensitivity to the fungicide pyraclostrobin, a strobilurin that is commonly applied as a foliar and seed treatment for blackleg and other diseases, was compared in *L. maculans* collections made in Alberta in 2011 and 2016. The half-maximal effective concentration (EC_{50}) of pyraclostrobin was determined using agar and microtiter plate assays, and two discriminatory doses of the fungicide were selected to identify highly insensitive isolates in the collections. The mean EC_{50} was approximately 4× greater for the isolates collected in 2016 versus those collected in 2011. While almost all isolates were still sensitive to pyraclostrobin, this increase in the EC_{50} suggests that proper fungicide stewardship is warranted for the sustainable long-term management of *L. maculans*.

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S44. Effects of solarization, anaerobic soil disinfestation and mustard biofumigation on ginseng replant disease

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Ginseng replant disease (GRD) threatens the survival of the industry. Because of GRD, ginseng cannot be grown on the same land twice without considerable crop losses. To assess the effects of various soil treatments on GRD, a research trial was established in Ontario in 2016. The site was seeded eight years after harvest of a previous ginseng crop. The trial was arranged in a split-plot design with fumigant (metam-sodium) as the main-plot and treatment as the sub-plot with four replications. The treatments included solarization (tarped control), anaerobic soil disinfestation (ASD) (orchard grass), ASD (molasses), ASD (orchard grass + molasses), mustard seed meal (*Brassica juncea* + *Sinapis alba*) (6.7 ton/ha), mustard seed meal (3.35 ton/ha), mustard cover crop (*B. juncea* + *S. alba*) and untarped control. Plant stands were recorded during the growing season of 2017 and 2018 and roots were assessed each fall. Untarped control plots were nearly destroyed by GRD by 2018. Fumigated plots had much higher yield than unfumigated plots. When analyzing fumigated and unfumigated treatments together, mustard cover crop had the highest total and marketable yield. Solarization and ASD treatments also reduced disease compared to the control. The results suggest that fumigation does provide some control of GRD, but control is improved with mustard biofumigation, ASD and solarization. This trial will be monitored in 2019 to determine treatment efficacy at final harvest.

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S45. Diagnostic metagenomics in the context of molecular plant pathology

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To protect the food, agriculture and forestry sectors and the environment from biotic threats, effective diagnostic tools to support accurate surveillance and risk assessments of pathogens and pests are of great importance. High-throughput sequencing-based metagenomics (HTS) allows rapid, simultaneous detection of genetic material of a broad spectrum of known and unknown pathogens and pests. The dense ancillary information, e.g weather conditions and land use, associated with HTS data also allows modeling and inference of factors affecting their dispersal and spread. However, to enable HTS technologies as an effective diagnostic and decision-making tool, we must improve the identification accuracy of short HTS reads at species or subspecies levels, which regulatory programs and quarantine/trade regulations on pathogens and pests now emphasize. Caution must be taken when reporting classification at high taxonomic resolutions using off-the-shelf bioinformatics tools and public reference databases. We are introducing an improved bioinformatics solution for high-resolution pathogen/pest identification from metagenomics data. This bioinformatics tool, named Automated Oligonucleotide Design Pipeline (AODP, https://bitbucket.org/wenchen_aafc/aodp_v2.0_release), implements a novel sequence matching algorithm for superior performance of HTS taxonomic classification compared to other methods (e.g. BLAST, RDP classifier and USEARCH) [*BMC Bioinformatics* 19(1)**:**395]. The power of AODP coupled with curated and high-quality reference databases to detect known, new and potentially invasive/transboundary pathogens in commodities and agro-ecosystems has been tested using real data sets as test cases.

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S46. Genome-enhanced detection and identification of regulated plant pathogens

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Implementation of regulations to restrict the movement of plant pests on infected plant commodities rely heavily on accurate plant disease diagnostics; which can be challenging for organisms that are difficult to isolate and/or differentiate from closely-related, non-regulated species. Early detection of non-indigenous fungi is the key to manage regulated and invasive species. High-throughput sequencing technologies can process large numbers of samples and volumes of genomics data. We developed the Genome-Enhanced Detection and Identification (GEDI) approach which consists in by mining and comparing the genomes of pests and their closely-related pests to design species and lineage-specific molecular markers exploiting the genetic differences. These markers can be translated into real-time PCR, SNP markers, and AmpliSeq assays for the purpose of detecting and assessing the genetic diversity of pathogens in plant samples from the species to the intra-lineage. Genetic information from environmental samples can be obtained thereby allowing tracing the trajectory of plant diseases movement, i.e. population studies information linked with metadata. Proof-of-concept of an integrated method and bioinformatics pipeline was used to design some Fusarium and Phytophthora species, among others, organism-specific markers. Genomic approaches and bioinformatics pipelines help to quickly develop molecular tools to facilitate detection and identification of fungal pathogens

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S47. Molecular surveillance of Fusarium species and chemotypes of wheat across western Canada

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Fusarium head blight (FHB) is a disease that reduces both yield and quality of cereals. The dynamics and temporal changes of the Fusarium species and their chemotypes associated with this disease across western Canada have not been fully studied on a large scale. The objective of this study was to sample, collect and identify Fusarium species from FHB diseased wheat spikes across the three western provinces of Canada: Alberta, Saskatchewan and Manitoba. Diseased spikes were collected from all three provinces from 146 naturally infected wheat fields from 2015 - 2018. More than 500 single spore isolates were obtained so far. *Fusarium graminearum* was the most prevalent species (80%); other species identified were *F. culmorum, F. avenaceum, F. sporotrichiodes and F. proliferatum* in Alberta; *F. sporotrichiodes, F. poae*, and *F. incarnatum-equiseti* species complex in Saskatchewan; and *F. culmorum* and *F. avenaceum* in Manitoba. There was a continuous change in chemotypes across western Canada from 15ADON to 3ADON. The chemotype distribution for both Saskatchewan and Manitoba was 75% 3ADON and 25% 15ADON. The comparative fungal population structure based on years, previous crop and geographic location is being investigated to understand the reasons for this chemotype frequency. Additionally, a greenhouse experiment is being conducted to examine the aggressiveness of select isolates on multiple wheat cultivars that vary for resistance.

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S48. Race dynamic, diversity and virulence in *Puccinia striiformis* f. sp. *tritici* in Canada over the last three decades

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Stripe rust of wheat, caused by the fungal pathogen *Puccinia striiformis* f. sp. *tritici* (*Pst*), is one of the most important cereal diseases worldwide. In this study, the pathogen population in Canada, representing a time period from 1984 to 2017, was analysed for virulence diversity and geographical distribution. The results were compared with previously described races in the USA. in this study, the virulence of 141 isolates of *Pst* was evaluated on 18 wheat *Yr* single-gene lines in the Avocet background. The seedlings were inoculated with a spore/talc mixture (ratio 1:20) after 12 days of growth, and infection types (scale of 0–9) on the second leaves were evaluated 18–21 days post-inoculation. The experiment was repeated two independent times. In total, 85 different virulence patterns were observed. The dominant races in Canada were very similar to the main races previously reported in the USA (PSTv-41, PSTv-37, PSTv-52), which suggests long-distance migration of these races from the USA to Canada. However, the presence of a considerable number of unique low-frequency races in Canada supports the hypothesis that mutation of *Pst* also occurs in localized regions within Canada. Diversity analysis of the virulence spectra and comparison between Canadian isolates with races from the Pacific Northwest, the central, and the eastern regions of the USA are ongoing and will be presented.

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S49. Comparative study of grapevine red blotch virus (GRBV) pcr detection methods and their application to a general lab practice

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Grapevine Red Blotch Virus (GRBV) is a devastating DNA virus causing significant economic impacts on grape industries. GRBV infected vines result in reduction of sugar accumulation, uneven ripening and red color development. Only PCR based detection methods have been adapted as primary detection methods since no antibody has been available for ELISA detection. A comparative study between end-point PCR and Real-Time PCR (TaqMan®) methods indicated that Real-Time PCR could detect GRBV at a higher sensitivity level from different grape varieties. Along with the Real-Time PCR method, practical lab techniques for PCR control, robust and consistent GRBV isolation, sample collection strategy and quantification of GRBV infection were established. We also discovered a Real-Time PCR method as a screening tool for GRBV genetic variance found in Ontario.

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S50. Improvement of biomass digestibility through the manipulation of tricin biosynthesis pathway in rice

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Plant biomass is an abundant and sustainable raw material for biofuel ethanol production. However, the presence of lignin in cell wall impedes the release of sugar from cellulose for fermentation. Lignin is derived from oxidative couplings of monolignols. Interestingly, a wide range of monocots utilize tricin (a 3', 5'-dimethoxyflavone) as a natural co-monomer with monolignols for lignification. Following the characterization of two P450 enzymes CYP93G1 and CYP75B4, we finalized the tricin biosynthesis pathway in rice as naringenin → apigenin → luteolin → chrysoeriol → selgin → tricin. CYP93G1 is a flavone synthase II which introduces the C2=C3 double bond to naringenin to form apigenin. Meanwhile, CYP75B4 serves a dual functional enzyme with apigenin 3'-hydroxylase and chrysoeriol 5'-hydroxylase activities. Importantly, both CYP93G1 and CYP75B4 are indispensable for generating tricin monomer for lignification. The respective rice mutants showed wild-type growth phenotypes with intact vascular tissues while NMR analysis demonstrated the depletion of tricin in cell wall lignin. Furthermore, both mutants showed reduced lignin content, altered S/G ratio, and enhanced enzymatic saccharification efficiency in biomass. Hence, genetic manipulation of tricin biosynthesis represents an attractive strategy to engineer grass lignin for improved biomass utilization without severely compromising plant fitness. Given that CYP93G1 and CYP75B4 are highly conserved in Poaceae, there is a strong potential to extend the application to bioenergy grass crops and other cereal crop residues.

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S51. mRNA long-distance transport of osmotic responsive genes in tomato/potato heterograft

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The mechanisms underlying the effect of the rootstock on the scion properties are largely unknown. However, it has been established that the long-distance transport of mRNA through the graft union have a vital effect on the properties of the scion. In the present study, we hypothesized that transcripts of some, but not all, osmotic-responsive genes (ORGs) can be transported across the graft union, conferring tolerance to the scion tissues. To test this hypothesis, we used a heterograft system with *Solanum tuberosum* as the donor rootstock and *Solanum lycopersicum* as the recipient scion to identify transcripts of some ORGs that move across the graft union under osmotic stress conditions. Reverse transcription–PCR and quantitative real-time PCR analyses confirmed that among the studied ORGs, only *NPR1* transcripts have been detected in the scion under normal and osmotic stress conditions. Our results also indicated that the movement of mRNA is controlled by the need for the transported transcripts in the final destination, rather than their abundance in the scion. As a salicylic acid receptor, NPR1 plays a key role in abiotic and biotic stress tolerance, making it a plausible candidate for future transgrafting research. These results may help us to get a clear understanding of the mechanisms underlying the systematic acquired resistance in the tolerant grafted plants. Moreover, *NPR1* can be used to produce transgenic tolerant rootstocks.

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S52. Complex Regulation of Condensed Tannin Biosynthesis in Poplar by R2R3 MYB Activators and Repressors

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Condensed tannins are widespread plant secondary metabolites and highly abundant in woody plants. In poplar, condensed tannin biosynthesis responds to environmental stimuli, and is induced by wounding, pathogen infection, UV-B, high light stress, and nitrogen deficiency. CT synthesis is controlled by several R2R3 MYB transcription factor, including both positive and negative regulators. In particular, the MYB134 and MYB115 are key activators, and when overexpressed in transgenic poplars, lead to a strong over-accumulation of CTs. Surprisingly, these activator MYBs simultaneously induce expression of R2R3 MYB repressors, which we have shown can downregulate the CT pathway. Transcriptomic analysis of both MYB activator- and MYB repressor-overexpressing transgenics have provided new potential target genes and pathways. Our recent work attempts to determine how these regulators cooperate during stress induction of CTs. Promoter activation assays in poplar cells demonstrate that flavonoid genes are the targets of activator MYBs, and that this activation can be inhibited by the repressors. Furthermore, the MYB115 and MYB134 activators also regulate each other and a bHLH co-factor gene. Our data indicates that stress-induction of CTs in poplar depends on a complex network of positive and negative regulators, which act to fine-tune CT biosynthesis. How these genes are controlled by environmental stress will be investigated in future work.

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S53. Genome-wide association analysis reveals the genetic basis of root system architecture in soybean

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A better understanding of root system architecture (RSA), shape and spatial organization of the roots within the soil, is essential to improve resource-use efficiency in agricultural systems and to develop climate-resilient cultivars. Despite the importance of RSA, it remains an underexplored frontier in plant genetics. In this study, four RSA-related traits (total length of roots, average diameter of roots, depth of root system and total number of roots) were measured in a panel of 137 early soybean accessions (Canadian core collection) using rhizoboxes and 2D imaging. A significant phenotypic variation ($p<0.001$) was observed for these RSA-related traits. This panel was also genotyped using 243K genome-wide SNPs to conduct a genome-wide association study (GWAS). In total, we identified 19 QTLs for these RSA-related traits encompassing several putative candidate genes. This study performed on elite soybean lines provides fundamental insights into RSA and yielded a rich catalogue of QTLs and strong candidate RSA-related genes that will accelerate future efforts aimed to dissect genetic architecture of RSA and breed more resilient varieties.

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S54. Metabolomics-assisted applications in nutritional genomics and crop improvement

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Plants have potential for use in the treatment in obesity, hypertension, diabetes and cancer. Plants exhibiting a wide variety of medicinal properties can be improved for hypercholesterolemic, anti-diabetic, anti-inflammatory, antioxidant, anti-allergic, anti-nociceptive and antiulcer effects. Some plants are capable of regulating high blood pressure and the incidence of heart attacks and stroke. Beneficial effects of bio-active compounds of crops have driven a wide range of research activities including antimutagenic, anticarcinogenic, antioxidant activities, and their potential to decrease the risk of coronary diseases. This presentation explains about identifying plant metabolites important for human health and studying their underlying molecular mechanisms in plant biosynthetic pathways. New “omics” approaches, are being used to understand responses and constituents of crops and their wild plant relatives to develop them to the desired traits. Metabolomics and functional genomics are two of the “OMICS” strategies explained here using different crops. Gene silencing in various plants such as *Nicotiana benthamiana*, *Medicago truncatula*, *M. sativa*, *Onobrychis viciifolia* and *Trigonella foenum-graecum* showed a great potential in identifying the molecular basis of plant bioactive compounds and their biosynthesis. Improved health benefits can be achieved through enhanced bioactives such as polyphenols and antioxidants with desirable traits and associated crop production systems. This research would help to identify more nutritive and healthier crops to the consumer with value-added benefits to the producer.

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S55. A unified DNA assembly platform for plant research and genome editing

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Assembling composite DNA modules from custom DNA parts has become routine due to recent technological breakthroughs such as Golden Gate modular cloning. Using Golden Gate, one can efficiently assemble custom transcription units and piece units together to generate higher-order assemblies. Although Golden Gate cloning systems have been developed for experimental work in plants, they are not typically compatible with organisms from other kingdoms. Consequently, a plant molecular biology laboratory must use multiple cloning strategies to assemble DNA constructs for diverse experimental assays. To simplify the DNA assembly process and facilitate experiments across kingdoms, we built a modular cross-kingdom Golden Gate assembly platform. Plasmid backbones, parts, and cloning procedures are consistent across the platform, streamlining the assembly of complex DNA constructs. We are using the multi-kingdom (MK) system to characterize genes regulating the nitrogen-fixation symbiosis in legumes. Currently, we are focused on understanding the role of key transcription factors controlling rhizobial infection and nodule organogenesis. Modular DNA parts have also been developed to advance genome editing capabilities in legumes with Cas9 and Cas12a nucleases. Both nucleases have successfully generated new loss-of-function alleles for essential symbiosis genes. An overview of the modular cloning platform and its application for genome editing will be presented.

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S56. Integrating perennial forage seed crops in the cropping systems in western Canada: An agroecological and economic assessment

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Individual crops yield higher when alternated with unrelated species in cropping sequences than when grown continuously in the same field. Such yield benefits are attributed to various mechanisms including pest suppression, improved nutrient and water use efficiencies, changes in rhizosphere biology, allelopathy or soil structure. This presentation reports the results of a cropping sequence study involving perennial forage seed crops and annual food crops, conducted at Beaverlodge Research Farm in western Canada. Eight different crop sequences with three different levels of supplemental nitrogen were evaluated in terms of cropping systems productivity, relative profitability and changes in soil properties over four years. The results showed that forage seed crops can be integrated as profitable break crops in the annual cropping sequences with beneficial effects on soil properties. As the prices of forage seeds and food grains are major determinants of the profitability, prudent choice of cropping sequences can help stabilize farm income in the face of fluctuating market.

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S57. Responses of various cover crop species to agro-mineral soil amendment over time

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Cover cropping is a common technique used by farm managers to help improve or maintain the ecological integrity of an agroecosystem, particularly of the soil. Rock fertilizers or often called agrominerals, are rich in micronutrients and in some cases phosphorus and potassium. Combining cover crops with agromineral soil amendments may have further ecological benefits to a system including the potential to reduce reliance on synthetic soil amendments. This study aimed to determine, under greenhouse conditions, whether various cover crop species undergo similar growth patterns when planted in soil amended with agromineral Spanish River Carbonatite (SRC) as compared to synthetic fertilizer or water as a control, and with two continuous cropping periods. SRC was found to be especially effective for growth of *Medicago sativa* and *Trifolium pratense* while forb species, *Raphanus sativus* and *Cichorium intybus*, tended to grow better in synthetic fertilizer. *Raphanus sativus* grown for a second period of cropping in same soil without amendment addition showed greater growth in SRC, suggesting a long-term effect of SRC. The synergistic benefits incurred by some cover crop plants grown in agromineral demonstrate the potential for SRC in agroecosystem soil management.

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S58. New long-term platforms to investigate agro-ecological services of cover crops across various grain cropping systems in Ontario

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It is well-documented that cover crops have the potential to provide many services to growers and the environment, but the benefits are sometimes difficult to quantify across diverse cropping systems, especially in short-term studies. Thus in 2017, we established >1000 research plots of various cover crop intensities in two crop rotations (corn-soybean vs. corn-soybean-winter wheat) across two tillage systems (plowed vs. no-till) in two environments at Elora and Ridgetown, ON. These sites were designed to become a 20-30 year platform to investigate short- and long-term agronomic services (i.e., grain yield, yield stability, drought resilience, nutrient requirements, incidence of weeds/diseases/pests, and net economic returns), soil health services (i.e., organic matter, aggregate stability, rhizosphere and endophytic microbial diversity, soil water holding capacity, soil salinity), and environmental services (i.e., carbon sequestration through organic matter increases, reduced nitrogen losses, reduced susceptibility to soil erosion, reduced susceptibility to phosphorus losses, pollinator habitat). The most current objective at the outset of the study investigates the performance of sole vs. multiple cover crop species and whether the application of fertilizer nitrogen on cover crops is beneficial. We invite collaborators wishing to use this platform to address fundamental and applied agro-ecological research questions.

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S59. Sustainable agriculture kits (SAKs) for subsistence farmers

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Two billion people are involved in subsistence farming. How will we provide technical assistance to so many people, at a time of rapid climate change? The SAKNepal project was funded by a $2.3 million grant from the Canadian government. We tested a model to scale up a regional kit of seed packages, tools and agronomic innovations to reduce female hardship, help increase crop production/income, and/or enhance environmental sustainability for hillside terrace farm households in Nepal. We have now reached 62,000 households (272,000 people directly or indirectly), especially women farmers. The technologies are low cost and combined into a commercial menu of options known as sustainable agriculture kits (SAKs) from which households can purchase/adopt individual items. Forty-six products and agronomic practices were tested on-farm with 600 local farmers. Subsequently, consumer farmers began purchasing individual technologies from the menu. A graphical flyer accompanies each product to instruct illiterate farmers on how to use the products or consider novel practices. The products are sold via pre-existing commercial distribution networks including cigarette, snackfood and machinery dealers, reaching remote villages. At the end of the pipeline, cell phones are used to conduct feedback surveys with consumer farmers, using contact information collected from incentivized vendors. We propose that many SAK products/methodologies are transferrable to the world's 400 million subsistence farmer households, especially to improve the livelihoods of rural women and girls.

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S60. The effect of micronutrients and macronutrients on the development and grain yield of annual canarygrass (*Phalaris canariensis* L.)

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Annual canarygrass has a larger grain yield response to chloride (Cl) fertilizer (25%) than most cereals raising the question, is canaryseed more responsive to other micronutrients then other cereal crops**.** The objectives were to determine the effect of macro and micro nutrients on the yield and development of canaryseed in a side band or foliar application. Two experiments were conducted. In experiment 1 the first treatment received no fertilizer and followed by a series of 13 treatments with additional nutrients added or removed in a sideband at seeding. In experiment 2, a control received no fertilizer while the other treatments received nitrogen, phosphorus, potassium, Cl and sulfur in a sideband. The third treatment received a mixture of zinc, copper, manganese and boron in a sideband. The other treatments consisted of foliar applications of single nutrients, zinc, copper, manganese and boron at the 3-6 leaf and flag leaf stages. The results indicate that at sites with a Cl response the other macro and micro nutrients have very little impact on yield in the absence of Cl. Chloride impacted yield during or after anthesis. A surface application of chloride increased yield. Foliar application was inconsistent in increasing the concentration of the micronutrient in leaf tissue. Canaryseed is not more sensitive to micronutrients than other cereal crops. Currently, Cl is the only micronutrient of major importance in canaryseed.

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S61. Maximizing canola yield by application of N, S, Micronutrients, Fungicide and Growth Regulator in Northwestern Ontario

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Canola has fast become one of the main crops in the Northwestern Ontario. Newly released varieties have potential of producing very high seed yields, which are unlikely to be attained without proper application of fertilizer nutrients. A replicated field experiment with 12 treatments, including application of N, S, B, Zn, Mn (added one by one @ 150, 24, 1, 7 and 2 kg ha^{-1}, respectively), Proline spray, Manipulator 620 spray and a check, was conducted on canola at the Lakehead University Agricultural Research Station, Thunder Bay, Ontario, during 2016-'18. P and K were applied uniformly to all treatments on soil test basis. All nutrients were applied at seeding except Mn that was sprayed at 4-6 leaf stage. Manipulator @ 8 L ha^{-1} was sprayed just before bolting and Proline @ 315 ml ha^{-1} was sprayed at 25 % flowering. The data were subjected to the pooled analysis of variance. The results revealed that N application @ 150 kg ha^{-1} brought the biggest canola seed yield increase of 1.78 Mg ha^{-1}. Each additional nutrient (S, B, Zn and Mn) raised the seed yield further and the maximum seed yield of 5.34 Mg ha^{-1} was obtained with the combined application of N, S, B, Zn and Mn (as compared to 4.15 Mg ha^{-1} with N alone). Manipulator/or Proline spray didn't bring any yield improvement.

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S62. The Antarctic alga Chlamydomonas sp. UWO241 as an emerging model photosynthetic adaptation to extreme conditions: perspectives and challenges

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Permanently cold habitats, including the oceans, polar and alpine regions dominate our planet and are inhabited by a huge diversity of organisms, many of which are permanently adapted to the cold (psychrophiles). The environmental conditions in these habitats severely limit the spread of terrestrial plants, and primary production in perpetually cold environments is largely dependent on microbes. Green algae, including the most notable member of this group *Chlamydomonas reinhardtii*, have been used for decades as models for elucidating fundamental cellular processes such as photosynthesis, light perception and flagellar motion. Here we discuss the Antarctic green alga *Chlamydomonas* sp. UWO241, an emerging model for photosynthetic adaptation to extreme conditions. This polyextremophile originates from the Antarctic Lake Bonney where it thrives in a highly stable environment characterized by permanently low temperatures (4-6°C), low light irradiance (<50 μmol photons m^{-2} s^{-1}), prolonged darkness during the polar night, and high salinities (700 mM). Life at such conditions is particularly challenging for photosynthetic psychrophiles, due to the thermal imbalances between the rates of biophysical light absorption (temperature-insensitive) and enzyme-driven carbon fixation (temperature-sensitive). Here we report the sequencing of the genome, transcriptome and metabolome of UWO241 and the recent advances that have revealed some of the unique adaptive features of this organism. We discuss future opportunities and challenges in developing UWO241 as a model alga for photosynthetic adaptation to extreme conditions.

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S63. Resource independent plant competition alters ROS levels, antioxidant status and susceptibility to cell death in Arabidopsis thaliana

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Changes in light quality induced by the presence of neighbouring vegetation is an important mechanism of plant competition. Alteration of the light environment is recognized via changes in the red to far-red light ratio (R/FR), in which a reduction in R/FR is induced by light that is reflected horizontally off neighbouring vegetation. Recognition of a reduced R/FR elicits physiological stress responses within the plant characterized by increased reactive oxygen species (ROS) production and subsequent modification of antioxidant capacity to regulate ROS levels. Previous research suggests that as ROS levels rise, they may elicit a signalling event within the plant causing a distinct set of genes to be up- or down- regulated which is specific to each individual ROS. To further explore the mechanisms surrounding plant competition and ROS signalling, Arabidopsis thaliana was studied under two light environments: a high R/FR (weed-free) environment and a low R/FR (weedy) environment. Results indicate that ROS levels and subsequently, antioxidant status are altered in response to far-red enriched light. The results also suggest that key ROS are involved in the physiological stress response to low R/FR and that signalling events of various ROS may be competing. Further identification of these responses would not only provide important insights into the molecular basis of plant competition, but may also provide support for theories that suggest the competitive nature of ROS signalling.

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S64. Metabolism of reactive oxygen and nitrogen species during anoxic stress and reaeration in tobacco plants differentially expressing alternative oxidase

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Flooding and waterlogging create low oxygen conditions in plants limiting mitochondrial respiration and oxidative phosphorylation while reaeration after receding of water elevates the oxidative damage. Leaves of wild type and transgenic tobacco (*Nicotiana tabacum* L. cv Petit Havana SR1) plants differentially expressing alternative oxidase (AOX) were used to investigate the role of AOX during anoxia and post-anoxia in comparison to normal air conditions. ATP/ADP ratio decreased during anoxia and increased during reaeration. AOX overexpressing lines showed higher ATP/ADP ratio in each condition as compared to other plant lines. Nitric oxide production was higher in AOX overexpressing lines during anoxia. *S*-nitrosylation was higher in knockdown lines under each condition and the levels increased during reaeration in both lines. The levels of reactive oxygen species and lipid peroxidation were higher in anoxia and during post-anoxia. However, those levels were lower in AOX overexpressing lines. The activities of catalase and SOD increased during anoxia and reaeration. Levels of SOD were higher in AOX knockdown lines while catalase activity was higher in AOX overexpressing lines. Ascorbate peroxidase activity followed a similar pattern as catalase. Glutathione reductase activity decreased during anoxia and increased during reaeration. Other enzymes of the ascorbate-glutathione cycle varied differently during anoxia and post-anoxia depending on AOX expression. It is concluded that AOX has a protective effect on cellular energy level and oxidative damage during anoxia and reaeration.

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S65. An inverse correlation between surface temperature and nitrogen rate predicted by a thermodynamic theory

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Crop stress can affect a plant's ability to grow, develop and its ability to utilize and destroy solar exergy. Exergy measures the energy quality, and is defined as the maximum useful to-the-dead-state work. Consequently, exergy measures a system's distance from equilibrium with the dead-state or environment. Previous studies have utilized surface temperature as an ecological indicator for ecosystem development. The more developed the ecosystem the cooler its surface temperature. In this study we define our ecosystem as a corn field in which varying rates of nitrogen have been applied. It is hypothesized that nitrogen stressed corn plants would be less developed and have higher surface temperatures compared to non-stressed and more developed plants. The objective is to investigate whether surface temperature can be used to identify nitrogen stress at an early growth stage as predicted by the exergy destruction principle. Experimental trials were conducted at the University of Guelph Elora Research Station in 2016, 2017 and 2018. Three spatial scales were investigated; leaf, canopy, and over a plot area. Leaf and canopy temperatures were collected using an IR hand-held gun and a FLIR T620 thermal camera. A significant inverse correlation was observed between surface temperature and nitrogen stress at a 0.05 significant level. A significant difference of less than $1^{?}$C was consistently observed between stressed and non-stressed corn plants.

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S66. Photoperiodic injury in tomato is linked to circadian control of both nitrate assimilation and ROS metabolism

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Photoperiodic injury (PI) in tomato (*Solanum lycopersicum* L.) is characterized by chlorosis of vegetative tissues when grown in extended photoperiods. The tomato cultivar 'Micro-Tom' is tolerant to PI whereas the cultivar 'Basketvee' is PI-susceptible. A comparison of these two cultivars in photoperiods ranging from 12 to 24 h light demonstrates a correlation between PI and accumulation of nitrite in leaf tissue. Nitrite is a potentially toxic intermediary compound formed by nitrate reductase (NR) that is converted to ammonium by nitrite reductase (NiR) during nitrate assimilation. The PI-tolerant cultivar 'Micro-Tom' maintained normal circadian rhythms for NR and NiR activity even in 24-h light, whereas the enzyme activities became arrhythmic in the PI-susceptible cultivar 'Basketvee'. A reduced NiR/NR activity ratio correlated with increased nitrite and protein nitrosylation. We then hypothesized that a reduction in the NiR:NR ratio in leaves will cause the PI-tolerant 'Micro-Tom' to become susceptible to PI. To test this hypothesis, we generated several transgenic 'Micro-Tom' lines that contain an antisense construct for NiR. Transgenic lines with reduced NiR activity became more susceptible to PI. Genetic analysis showed that PI-tolerance in 'Micro-Tom' is controlled by two genes including CAB-13, which is a light-harvesting protein in photosystem II. Interestingly, circadian rhythms of ROS accumulation differed between 'Micro-Tom' and 'Basketvee'. A model showing the involvement of both nitrate assimilation and ROS metabolism in PI will be presented.

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S67. High condensed tannin levels protect poplar against oxidative damage generated by UV-B exposure or drought stress

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Condensed tannins (*syn.* proanthocyanidins) are polyphenolic compounds synthesised from the flavonoid pathway. Although condensed tannins are often considered to be plant defence compounds, they may have additional biological functions. In poplar (*Populus* spp.), condensed tannin biosynthesis is stimulated by multiple stresses including wounding, pathogens, UV-B, nitrogen deficiency, and high light stress, which all generate reactive oxygen species (ROS) and oxidative stress. Tannins have high antioxidant capacity *in vitro*, but whether they protect against oxidative stress *in planta* has not been demonstrated. This work tests the hypothesis that condensed tannins can act as *in vivo* antioxidants. Transgenic poplar saplings engineered to accumulate high concentrations of condensed tannins were challenged with two stresses that induce accumulation of ROS - drought and UV-B exposure. Drought stress was imposed by reducing water availability to saplings for three weeks, and UV-B treatments were carried out in specialized environmental chambers capable of simulating sunlight including UV-B. Chlorophyll fluorescence measurements in both the drought-stressed or UV-B stressed plants showed that high-tannin transgenic poplar retained greater photosystem II operating efficiency (*Fq'*/*Fm'*) compared to control plants. For both stresses, the high-tannin transgenics had lower hydrogen peroxide and malondialdehyde levels relative to controls. Since the protective effects of condensed tannins were observed with two distinct abiotic stresses, our data suggest that foliar condensed tannins can act as a general defense against stress-induced oxidative damage.

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S68. Impact of phosphate or phosphite resupply on the proteome and phosphoproteome of phosphate-deprived Arabidopsis thaliana suspension-cell cultures

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Despite the vital role of phosphate (Pi; HPO_4^{2-}) in growth and development, how plants signal changes in Pi supply to adjust its uptake and utilization remains poorly understood. Pi itself has been proposed to be the signaling molecule that controls plant Pi starvation responses (PSRs) because phosphite (Phi; HPO_3^{2-}) is a non-metabolizable Pi analog that suppresses most aspects of the PSR. Protein phosphorylation is an essential PTM that plays central roles in how plant cells perceive and respond to stress. Thus, the aim of this study was to profile (phospho)proteome alterations that occur when Pi-starved (-Pi) Arabidopsis suspension cells are resupplied with 2 mM Pi or Phi for 48 hours. LC-MS/MS of TiO_2-enriched phosphopeptides quantified a total of 3646 proteins and 1318 phosphoproteins (consisting of 5171 unique phosphopeptides) across all conditions. Consistent with earlier reports, phosphoenolpyruvate carboxylase was phosphorylated and more abundant in the –Pi cells, whereas several purple acid phosphatases such as AtPAP17 and AtPAP25 were detected only in the –Pi cells. Pi or Phi resupply to the –Pi cells triggered marked and mostly similar alterations to the total proteome and phosphoproteome, including proteins involved in transcription, translation, proteasome function, metabolism, and signaling. t

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S69. Global insights into duplicated gene expression and alternative splicing in polyploid Brassica napus (canola) in response abiotic stress by transcriptome sequencing

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Polyploidy has made a major impact on plant genomes and several crop plants are polyploids. There is considerable interest in characterizing expression of genes duplicated by polyploidy in various polyploid plants using RNA-sequencing approaches. In this study, we conducted comprehensive transcriptome analyses of *Brassica napus*, an allotetraploid derived from *B. rapa*(A_T) and *B. oleracea*(C_T), by transcriptome sequencing (RNA-Seq) of strand specific libraries made from plants subjected to drought, cold, and heat stress treatments. Analyses of 27,360 pairs of homoeologs (genes duplicated by polyploidy) revealed $A_T$subgenome biases in gene expression and $C_T$subgenome biases in the extent of alternative splicing under all four treatments. For all types of alternative splicing events, significant negative correlations were found between expression level and alternative splicing frequency. Cold stress resulted in the greatest changes in gene expression and alternative splicing changes when compared to the control. Cold-induced alternative splicing changes were more likely to be shared with those generated by drought than by heat stress. Our results indicate that divergence in gene expression and alternative splicing patterns among homoeologs may increase the flexibility of polyploids when responding to multiple abiotic stressors.

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S70. Linking RNA processing and kinase signaling in the Arabidopsis stress response

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Protein phosphorylation via protein kinases is the predominant post-translational protein modification in Eukaryotes, playing a major role in transmitting extracellular signals such as stress perception to the cell nucleus. Kinase signaling cascades thereby permit the transcriptional and post-transcriptional machinery of a cell to sense and respond to external stresses. However, recent proteomics studies in *Arabidopsis thaliana* in our lab as well as results in other organisms suggest a new mechanism by which protein kinase-mediated signaling is linked to RNA processing during cellular responses to stress. Using a combination of mass-spectrometry based proteomics, transcriptomics and biochemistry to study proteome, phospho-proteome and iso-transcriptome level changes in *Arabidopsis* cells, we describe how nuclear RNA processing machinery intersects with protein phosphorylation in the context of abiotic stress. The results presented aim to both advance our understanding of how plant cells can diversify their proteomes upon stress-perception and generate new targets for agricultural applications.

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S71. RNA-Seq estimated gene abundance differences between Zea mays genotypes are strongly affected by read mapping bias

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RNA sequencing has been used widely to quantify genetic variation of gene expression. A potential problem with this approach is that RNA-Seq reads carrying a reference allele of a polymorphic locus may map correctly to a reference genome, but RNA-Seq reads carrying a non-reference allele may not or incorrectly map. To test the effect of preferential alignment on transcript abundance estimates, we aligned RNA-Seq reads from 105 individuals derived from a biparental cross between inbred lines B73 and Mo17, to a B73 reference genome. There is strong evidence for transcript abundances estimates biased to B73. B73 alleles at 83% of the genes with transcript levels that differ between B73 and Mo17 alleles lead to higher gene expression estimates than do Mo17 alleles. The number of single nucleotide polymorphisms between alleles strongly correlates with the magnitude of the B73 allele's preferential expression. Reducing the stringency of RNA-Seq read/reference alignment criteria has little effect on the number of genes with higher B73 transcript abundances but reduces the magnitude of the B73- Mo17 difference for 80-85% of all genes. Finally, the frequency of B73 read alignment to genomic DNA encoding mRNA untranslated regions is notably higher than that of Mo17. Our results reveal that reduced read mapping due in part to SNPs and to differences in UTR regions contributes to strong differences in genetic estimates of gene expression.

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S72. A Tale of Two Genomes: Methylome and transcriptome profiling of Brassica napus seed development

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Canola (*Brassica napus*) is one of Canada's most economically valuable crops. *B. napus* is an allotetraploid comprised of two progenitor genomes (*B. oleracea* and *B. rapa*). We can take advantage of methylome and transcriptome sequencing to better understand how gene regulatory networks contribute to valuable seed traits such as vigor, size, and nutrient content. We profiled the methylome and transcriptome of canola seeds during morphogenesis and seed maturation. Significant subgenome bias is observed in leaves and seeds. Genes, promoters, and repetitive elements are all more heavily methylated in the *B. oleracea* subgenome than the *B. rapa* subgenome. Unique suites of promoters are differentially methylated in early and late seed development, targeting genes involved in development and carbon metabolism. Transcription factors are hypomethylated to other protein coding genes, possibly permitting fast transcriptional responses during seed development. We uncovered distinct transcriptional networks in the *B. oleracea* and *B. rapa* subgenomes of canola, indicative of unique regulatory mechanisms between the two subgenomes. Several bZIP transcription factors are identified as potential regulators of energy metabolism and development in canola seeds. Knockdown of *BnBZIP11* using RNA interference resulted in a seed-lethal phenotype and knockdown of target genes predicted to be activated by BZIP11. Our analysis provides new insight into the genomic architecture and mechanisms of regulation that underlie the complex processes of seed development.

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S73. De novo assembly of the pokeweed genome provides insight into pokeweed antiviral protein (PAP) gene expression

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Pokeweed antiviral protein (PAP) is a ribosome-inactivating protein synthesized by American pokeweed (Phytolacca americana). PAP inhibits virus infection when expressed in crop plants, yet little is known about the function of PAP in pokeweed due to a lack of genomic tools for this non-model species. We de novo assembled the pokeweed genome from short-read sequencing and annotated protein-coding genes. Our draft assembly (83X coverage, N50 = 42.5 Kb) accounted for 74% of the measured pokeweed genome size of 1.3 Gb. We obtained 29,773 genes, 73% of which contained known protein domains, and identified several PAP isoforms. Within the gene models of each PAP isoform, a long 5' UTR intron was discovered and validated by PCR and RT-PCR. Interestingly, the intron stimulated reporter gene expression in tobacco. We complemented this genomic resource with expression profiles of pokeweed plants subjected to stress treatments (JA, SA, PEG, and wounding; n=4). Cluster analysis revealed that some PAP isoforms were co-expressed with genes involved in terpenoid biosynthesis, JA-mediated signalling, and metabolism of amino acids and carbohydrates. Diverse, stress-responsive cis-regulatory elements were present in PAP isoform promoters, and we identified a region of PAP-I sufficient for JA response in tobacco, based on reporter constructs containing promoter truncations. This study generated the first draft genome for the Phytolaccaceae family and provided insight into the regulation and function of PAP in pokeweed.

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S74. The long story of small RNA: sRNA architecture of Brassica napus seed development

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Canola (*Brassica napus* L.) is a nascent allotetraploid and is Canada's most important oilseed crop, contributing $26.7 billion to the Canadian economy in 2016. Despite this, seed development in *B. napus* is not well understood, especially from an epigenetic perspective. Seed development in eudicots is preceded by the ovule stage (pre-fertilization) and followed by morphogenesis and maturation phases constituting embryo development. Morphogenesis is defined by cellular differentiation and tissue organization of the embryo, while elongation and deposition of lipids/proteins are characteristic of maturation in late seed development. Small RNAs (sRNA) act as important genetic switches in orchestrating developmental processes and are particularly important in regulating gene activity during precise developmental transitions. Broadly, small RNAs can be classified into two groups: micro RNA (miRNA) and small interfering RNA (siRNA). While siRNA and miRNAs both act as negative regulators of gene expression, their modes of biogenesis and loci encoding them vary drastically among subgroups. In this work, we predict the sRNA populations of five stages of seed development and dissect the different miRNA and siRNA profiles between them. We find siRNA populations to be much more diverse than that of miRNAs, and that subgenome dominance is evident throughout seed development. Lastly, we predict targets of the sRNAs to extrapolate biological function, and piece together the epigenetic machinery underpinning *B. napus* seed development.

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S75. Can phloem derived small RNA modify gene regulation in shoot stem cells?

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Plant small RNA (sRNA) can regulate genes by post transcriptional gene silencing (PTGS) through repressing mRNA, or transcriptional gene silencing (TGS) through RNA-directed DNA methylation (RdDM). The phloem contains sRNA; however, it is unknown if phloem derived sRNA can reach the shoot apical meristem (SAM). To test phloem-to-SAM sRNA transport, transgenic Arabidopsis plants were created with a phloem specific promoter driving an RNA interference cassette targeting the floral regulator *FLOWERINGLOCUS D* (*FD*), which is constitutively expressed in the SAM. These transgenic plants showed significantly delayed flowering through reduced *FD* transcript levels. Late flowering caused by the *FD* interference transgene was not observed in sRNA biogenesis mutants or *fd*$^{-}$ mutants. A parallel synthetic biology approach was devised to test whether phloem sRNA can move to the stem cell subdomain within the SAM, which is defined by *CLAVATA3* (*CLV3*) gene expression. A *clv3-2* deletion mutant was transformed with a *CLV3* transgene modified to include a synthetic sRNA target site and driven by its native promoter. These rescued plants were then transformed with an artificial microRNA (*aMIR*) targeting the synthetic *CLV3* site and driven by a phloem-specific promoter. Several independent *aMIR* lines showed strong *clv*$^{-}$ defects. These findings demonstrate that phloem-to-SAM sRNA trafficking occurs, which has implications for long distance signals altering stem cell activity. Potential epigenetic alterations that give rise to transgenerational effects will be discussed.

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S76. Characterization of B-genome specific high copy hAT MITE families in Brassica genome

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Miniature inverted-repeat transposable elements (MITEs) are non-autonomous class II transposon which has shown to influence the evolution of genomes. *Brassica nigra* (B-genome) is one of the three widely cultivated *Brassica* diploids primarily as an oil crop, which harbors important traits for Breeding value. However, limited genetic knowledge about the B-genome has hindered utilizing these agronomically important traits. Here, we characterized two new high copy hAT MITE families (BnHAT-1 and BnHAT-2) in the B-genome and comparatively analyzed with its related diploids, *B. rapa* (A) and *B. oleracea* (C). Both MITE families were present as high copy elements in B-genome as 420 and 329 copies of BnHAT-1 and BnHAT-2, respectively, while less than 20 elements were identified in A, and C -genomes, supporting the B-genome specific proliferation of both MITE families. In addition, 44% and 47% of the B-genome members were present in ≤ 2 kb flanking region in the vicinity of the genome speculating the MITEs influence to the gene structure and function. Insertion time analysis of MITEs has revealed that the major proliferation MITEs occurred ≤ 2 million years ago. Site-specific polymorphism analyses showed that 44% MITEs were actively amplified into the B-genome. Overall this study elucidates a comprehensive understanding of two B-genome specific high copy MITE families, and also role on the B-genome evolution also discussed.

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S77. Age of divergence among subgenomes determines gene expression between paralogs in Camelina species

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Camelina sativa, an oilseed crop, is a hexaploid and based on comparison of its genome structure with those of its wild relatives was formed through step-wise hybridization events. The subgenomes of *C. sativa* have undergone limited changes post-hybridization, irrespective of the age of divergence for these subgenomes. The underlying subtle variations in the subgenomes are important for subsequent hybridization success of the crop. This study determined the overall subgenome dominance observed in *Camelina* species and identified the relationship between the age of divergence of each subgenome and the expression pattern among the gene paralogs. A linear relationship between the age of divergence and the dominance of the subgenomes was discovered. We found the basal subgenome of *Camelina* had a lower number of expressed genes compared to an earlier diverged subgenome. The third subgenome shared by *C. sativa, C. alyssum* and *C. microcarpa* that resulted from the oldest divergence event was found to be dominant in comparison to the other two subgenomes. In contrast, in *C. neomicrocarpa*, a hexaploid with one unique subgenome compared to *C. sativa*, the second subgenome, which showed the earliest divergence age among the three subgenomes, was again dominant. This suggests irrespective of the species the subgenome dominance has a relationship with the age of the divergence of the subgenomes in *Camelina* species.

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S78. Transcriptome changes associated with phytoglobin expression during germination of barley seeds

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To understand how the class 1 phytoglobin (Pgb) manages the energy crisis and supports the embryo growth via nitric oxide (NO) metabolism modulation, we performed the analysis of physiological and molecular parameters in the embryos of transgenic barley (Hordeum vulgare L. cv Golden Promise) plants differing in expression levels of the Pgb gene (Pgb+ and Pgb–) during germination. The genes encoding the proteins involved in the Pgb-NO cycle (Pgb, nitrate reductase) and S-nitrosoglutathione reductase (GSNOR) were highly expressed to control the level of NO and generate growth potential in the Pgb+ embryos. Lactate and alcoholic fermentation were activated in all tested samples, but more significantly in Pgb– embryos, which indicated that lactate and alcohol dehydrogenase are involved in the anaerobic step of germination more actively when Pgb is underexpressed. The up-regulation of genes encoding the fermentative enzymes contributed to a higher ratio of ATP/ADP in the anaerobic step of germination. The overexpression of succinate dehydrogenase and pyruvate dehydrogenase in Pgb+ embryos after radicle protrusion highlighted a substantial role of the Pgb-NO cycle in enhancing TCA for provision of metabolic intermediates and ATP during germination. These results offer an invaluable picture of how the efficient Pgb-NO cycle affects the dynamic gene expression and protein turnover for the maintenance of redox and energy balance in germinating seeds.

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S79. Genome-wide analysis of the SPL/miR156 unit in small grain cereals

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The *SQUAMOSA-promoter binding like*(*SPL*) gene family encodes transcription factors that have been shown in many species to influence plant growth and development, but information about these genes in small grain cereals is limited. This study identified 17 *SPL*genes in barley within eight distinct groups, that are orthologs of *SPL*genes described in *Arabidopsis*, *Brachypodium*,wheat, and rice. Sixteen barley *SPLs*undergo alternative splicing. Seven SPLs contain a putative miR156 target site and the transcript levels of the miR156-targeted *HvSPLs* (*HvSPL3*,*13*and *23*) were lower in vegetative than in reproductive phase but this was true also for some *SPL*genes such as *HvSPL6*that were not regulated by miR156. An antagonistic expression pattern of miR156 and miR172b during the vegetative and the reproductive phases also signifies their apparent function in barley growth phase transition. Characterization of a barley *mir172*mutant having an abnormal, indeterminate spikelet phenotype suggests the possible feedback role of AP2/miR172 module on *HvSPL*genes. Overall, our results highlight the role of *SPL*genes in different phases of the plant development in small grain cereals.Currently, we are analyzing the available T-DNA mutants of *Brachypodium*for functional characterization of *SPL*genes. This will provide a basis to elucidate their roles in various biological processes, which could lead to develop future generation of cereal crops.

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S80. Influence of epiphyllous bryophytes on the water cycle in a tropical sub montane cloud forest in Costa Rica

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Globally bryophytes influence carbon, nitrogen and water cycles in areas where they cover ecosystem surfaces. Bryophytes (mosses and liverworts) are abundant in terms of both volume and species richness in humid tropical forests, such as tropical montane cloud forests or high montane forests (TMCF). While the role of epiphytic bryophytes (growing on branches and trunks of trees) in the water cycle of TMCF is starting to be explored, no work has been done on the role of epiphyllic bryophytes on the water cycle. I studied the influence of these small species on understory species on water absorption and retention in a tropical submontane forest in Costa Rica. Epiphyll cover increased significantly with host leaf age, and volume of water absorbed per cm^2 significantly increased with epiphyll cover, reaching a maximum of 0.06m per cm^2. Preliminary results indicate that the amount of epiphyll cover does not influence the rate of water loss, but rather the greater amount of water retained in leaves covered in epiphylls results in evaporation back to the atmosphere over a longer period. Going forward analyses on the influence of epiphyll community composition on water absorption and retention will help determine the importance of epiphyll diversity vs biomass on ecosystem function.

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S81. Fourteen-year impacts of partial and total forest harvest on epixylic bryophyte species in boreal black spruce –feathermoss forests

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Partial cut harvest has been hypothesized to have a lower impact on forest vegetation and to encourage old growth species assemblages compared to clear cut harvest. Fourteen years after harvest, we used epixylic bryophytes as indicator species to assess partial cut efficacy to attenuate harvest impacts on forest vegetation in the boreal black spruce forest of Quebec.We examined changes in the epixylic bryophyte community and their microhabitat in 30 permanent plots along an unharvested, partial cut and clear cut harvest gradient. Also, we compared our results to that of an initial post-harvest study to examine species changes overtime. The results showed that, epixylic species richness and composition were mainly influenced by canopy openness, deadwood decay and diameter size. Partial cut stands recorded a richer epixylic community compared to unharvested and clear cut stands. Species richness and frequency of occurrence doubled in partial and clear cut stands overtime compared to the initial study. Additionally, conditions in partial cut stands supported drought sensitive and old growth confined species which are threatened by conditions in clear cut stands. In conclusion, partial cut harvest provides a better option in achieving species and habitat conservation goals than clear cut harvest. However, deadwood input should be considered in implementation strategies to ensure continual persistence of epixylic bryophytes and deadwood living organisms in general.

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S82. Modelling successional dynamics of Canadian boreal mixed woods prior to and following the Spruce Budworm outbreak

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Forest simulators provide better understanding and predicting of the forest response to different silvicultural treatments or environmental stresses. Applying SORTIE-ND, we modelled short- and long-term successional dynamics in the boreal mixedwoods of eastern Canada. We used 431 quadrats (16×16m), distributed in seven stands originating from different fires (1760-1944) and representing a chronosequence of post-disturbance stand development. In each quadrat, all trees, including seedling, saplings and adults were sampled in both 1991 and 2009. Using the 1991 data, we calibrated SORTIE-ND through 18-year simulations to reconstruct the empirical data collected in 2009, in terms of stand composition and structure. When the model successfully parametrized, over long-term (100-year) simulations, we tested whether simulating young stands to reach to older ages resulted in structure and composition similar to those seen in old-growth stands. We also verified the influence of spruce budworm outbreak on post-fire stands by simulating stands prior to and following the outbreak. Results showed that due to possible differences in stand composition following wildfires and in stand disturbance histories, SORTIE-ND could not precisely estimate species dominance of old-growth stands, though it provided a decent estimation of species composition and diameter distribution of old-growth mixedwoods. Moreover, long-term simulations revealed that despite the impacts of the most recent spruce budworm outbreak on species dominance, in long term, forest composition turned to be similar for disturbed and undisturbed stands.

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S83. **How is the understory vegetation influenced by changes in tree canopy dominance in black spruce and trembling aspen in a Canadian boreal forest?**

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The Canadian boreal forest has globally significant ecosystem services related with nutrient and water cycles, as well as wood production. Canopy composition influences habitat conditions for plants in the understory of these forests and consequently affects ecosystem processes. In the clay belt of Québec, we manipulated understory conditions in adjacent black spruce (*Picea mariana*) and trembling aspen (*Populus tremuloides*) stands to understand the mechanism of impact on the understory community. We found that litter deposition from trembling aspen trees is the principal mechanism that significantly affects moss establishment though a physical rather than a chemical effect. In addition, understory plants from trembling aspen stands are more resilient to individual and global changes in canopy composition after 5 years of treatment, in contrast to the less resilient layer of mosses of black spruce stands. Black spruce stands are stable ecosystems that resist colonization by other herbaceous plants. However, once the system is disturbed and herbs and shrubs are established, the system is not resilient. In contrast, trembling aspen stands with an understory dominated by herbs and shrubs is much more resilient to disturbances as the native vegetation invaded the transplanted mosses. In these boreal forests, a feedback loop between overstory and understory creates microconditions affecting decomposition and nutrient cycling, in turn influencing tree regeneration and growth.

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S84. **Compensatory growth release in surviving lodgepole pine in Northern BC after Mountain Pine Beetle attack**

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The most recent Mountain Pine Beetle (MPB) epidemic in forests across western North America, beginning in the late 1990s, caused widespread mortality in BC pine forests with major consequences for present and future forest carbon (C) stocks. Early modeling had predicted these stands would transition from C-sinks to C-sources and remain in that state for decades. However, Eddy-Covariance (EC) measurements showed that these stands, when left unharvested, could recover to C-sinks in 3-5years following MPB attack. This was attributed to a growth release in the residual live trees and advanced regeneration in stands with 80-95% overstory mortality. At our northern BC site, attacked in 2006-2007, we measured growing season height and diameter changes in 160 residual trees in 2017 and 2018. Height growth of residual trees averaged ~10cm annually in these both years, while diameter growth was much greater in 2018 than 2017. The heights and diameters over the 2017 and 2018 growing seasons were used to determine annual C-storage in residual tree stems, contributing ~8 and ~17 g m-2 yr-1, respectively. Using dendrochronology approaches, we determined that our sample trees increased their annual wood volume by 295% in the decade following the outbreak when compared to the decade prior. There were strong positive linear relationships between stem C-storage and EC NEP (R2=0.657) as well as stem C-storage and % of downed trees (R^2=0.712).

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S85. Finding and re-measuring forest carbon plots after fifteen years: Why, how and so what?

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The growing urgency around rising CO_2 and climate change are demanding action. From a forest biologist's perspective, a similar urgency exists with respect to understanding how forest carbon sequestration and stocks are being impacted by climate change. While forests and forest products contain significant carbon, recent findings suggest that older boreal trees and forests have become much more vulnerable in recent decades. To help address this question, we decided to revisit a subset of 17 year-old forest carbon plots spread out across a 9,250 ha sub-boreal spruce and fir research forest in central British Columbia to re-measure live tree aboveground biomass (and carbon) in these plots. Twenty-six plots were ultimately located and re-measured; many of our intended plots had been harvested or could not be located. Diameters for all standing live trees were re-measured in these plots and their aboveground carbon contents evaluated and compared with initial values from 2003 and 2004. The results show how recent volume growth and carbon sequestration levels in live tree carbon stocks have changed in this common forest type in central BC, and how initial forest state (e.g. age, species composition) influences the growth or decline in aboveground forest carbon.

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S86. Distribution and management of the carrot cyst nematode (*Heterodera carotae*) in Ontario, Canada

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The carrot cyst nematode (CCN), *Heterodera carotae*, is a plant-parasitic nematode that parasitizes commercial and wild carrots, reducing yield and causing unmarketable forked and stunted roots. The nematode is present in many European countries, Cyprus, India, Mexico and in the state of Michigan, USA, and has recently been reported in Ontario, Canada. A survey, field trial and laboratory trial were conducted to better understand the distribution of, and control options for, this nematode. Between 2016 to 2018, the multi-year survey was conducted by soil sampling 68 carrot fields throughout Ontario. Carrot cyst nematodes were found in 72% of carrot fields and were only present in fields of muck (high organic matter) soil. A nematicide/fumigant field trial was conducted in a field naturally infested with CCN in the Holland Marsh, Ontario and efficacy laboratory trials were conducted at the University of Guelph Muck Crops Research Station. There were no differences in percent nematode damage and yield among chemical and biological nematicides and fumigants in the field trial. However, nematicides significantly reduced the number of living eggs inside CCN cysts by up to 30% compared to the water control in the laboratory trial. Managing this cyst nematode is complex due to its biology and life cycle. Further research is continuing to develop effective management options to deal with this new and persistent pest.

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S87. Mycorrhizal fungi in the roots of onion and carrot in relation to mycorrhizal fungal inoculant and soil phosphorus

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The use of arbuscular mycorrhizal fungal (AMF) inoculants is becoming popular for the commercial production of onions and carrots in Ontario. This study evaluated the effect of these inoculants on the diversity of native AMF communities in roots of onion and carrot, and how these AMF communities varied with soil phosphorus (P) concentration. Field trials were conducted on high organic matter soils (56% organic matter) with two levels of soil P concentrations: low P ~46ppm without application of P fertilizer and high P ~68 ppm with P application, at a site in the Holland Marsh. Treatments were seed pre-coated with AMF (3–5 propagules of *Rhizophagus intraradices* Walker and Schüßler per seed) and untreated seeds, grown on low and high P soil. The AMF communities in roots were identified by Illumina sequencing. Five genera of AMF were identified in roots of onion and four in carrot. The AMF community in onions from inoculated seed was richer and more diverse compared to the no AMF check, but there were no differences in carrots. The diversity of AMF in carrots was lower on high P soil, but there was no effect of soil P on richness or diversity of AMF in onions. Overall, both AMF inoculant and soil P concentrations affected the diversity of AMF communities in roots, but these effects varied with crop type.

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S88. Evidence for a recent re-expansion of market gardening in Ontario through organic field fruit and vegetable production

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Market gardening can be defined as the production of fruits and vegetables for the fresh-market by small- to medium-sized family operations that each grow multiple commodities close to urban centers. A brief history of the fruit and vegetable industry in Ontario over the last 100+ years will be presented, including field and greenhouse production in the Golden Horseshoe, Holland Marsh, Norfolk County and SW Ontario. The impact of both urbanization and the profitability of farming on market gardening are analyzed, including their role in the significant contraction of market gardening that occurred in Ontario starting in the late 1960's. Some myths or misconceptions regarding the fresh fruit and vegetable industry are examined, including myths related to greenhouse production, the impact of 'yield', operation size, and the role of corporate farming. This historical analysis will be used to put into context and to access the future of market gardening in Ontario, including evidence for a recent re-expansion of market gardening through organic fruit and vegetable production. Results from a survey of organic growers in Ontario will be presented in terms of challenges to expansion of organic fruit and vegetable production and their marketing channels. As a backdrop to these analyses, B. Micallef will share some experiences of his family, who have been market gardening in Ontario for 84 years.

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S89. Analyzing the effects of nitrogen fertilizer source on flower bud induction in day-neutral strawberry

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Day-neutral strawberry varieties have been developed apart from short-day and everbearing varieties to produce fruit irrespective of photoperiod, allowing for an extended harvest season and higher yields. The use of day-neutral strawberry in Canada, as an alternative to short-day, is a promising pursuit to increase annual strawberry yields and address increasing strawberry demands. However, research on the optimal environmental and fertilizer conditions of day-neutral strawberry is limited, particularly in the transplant stage of cultivation. It is the purpose of this study to further the understanding of day-neutral production in Quebec through observing different sources and concentrations of nitrogen and develop a treatment for optimal flower bud induction in developing transplants. The study was performed for six-weeks and considers nitrate, ammonium, and urea sources of nitrogen at 50g/L, 100g/L and 150g/L concentrations in solution. All other essential nutrients were balanced to deliver optimal concentrations, avoiding the combination of multiple nitrogen sources. During the six weeks, phenology data, rate of photosynthesis, relative growth rate, and soil microbial activity were observed to determine the nitrogen treatment that provides the most optimal results. Preliminary results have shown that the use of higher concentrations of urea has resulted in the greatest production of flower buds each week. A relationship was also established between the photosynthetic performance of plants and the source of nitrogen used.

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S90. Light quality and night interruption controls morphogenesis and flowering time in day neutral strawberry

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Light quality, referring to wavelength and photoperiod regulate strawberry flowering time, phenological growth and consequently, fruit production. While the light quality and photoperiodic control of flowering has been extensively studied in short day (SD) strawberry, little is known about day neutral (DN) cultivars, despite their rising popularity. This study determines the effect of light quality and night interruption (NI) on flower bud induction (FBI), morphogenesis and transcription of flowering gene, FLOWERING LOCUS (*FvFT1*), in *Fragaria vesca* cv 'Alexendria'. Seedlings were grown under far-red (760nm) and blue (450nm) light emitting diodes (LEDs) at a ratio of 5:1 and 1:5, supplied with long-day (LD) photoperiod (16h light/8h dark). LD photoperiod supplemented with higher blue light resulted in a significant ($p<0.05$) increase in leaf growth and flower bud induction compared to far-red light during transplant production. Additionally, it was observed that flowering time and expression of *FvFT1* can be stimulated by blue light quality. As a second step, seedlings were exposed to photoperiods of 10h (SD), 15h (LD), 10h (8h+2NI) and 15h (13h+2NI) using fluorescent lights in growth chambers under controlled conditions (25/20°C and 70% RH). Plants treated with 13h+2NI significantly induced flower bud differentiation compared to 8h+2NI. The study implies that flowering in DN strawberry can be accelerated with increased ratio of blue to far-red light supplemented during night interruption.

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S91. Microhazels: A novel industry for Ontario agriculture

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Hazelnut cultivation has a tremendous potential for bringing immediate and long-term benefits to Ontario agriculture due to the rapidly increasing demand for hazelnuts by Ferrero Canada and other food industries. Lack of disease-free plant materials coupled with time-consuming propagation technologies have restricted the introduction of new hazelnut cultivars. In vitro technologies such as micropropagation can be used to multiply plants from an existing population in large numbers to distribute plants with greater expediency. Micropropagation allows plants to be multiplied exponentially and since they are grown in aseptic culture conditions, plants are healthy and genetically uniform. We have developed efficient protocols for large-scale micropropagation using liquid based bioreactor systems. Cryopreservation, a process of maintaining tissues in liquid nitrogen at -196°C allows for disease elimination and conservation of genetic resources. A novel approach has been developed by shifting the emphasis on optimizing explant physiology and enabling them to withstand stresses of dehydration and temperature changes to improve cryopreservation. The Integrated Plant Production System (IPPS), which combines plant propagation in vitro, acclimation in the greenhouse, and field transplantation, would facilitate delivery of certified, clean plants that are adapted to Ontario climate to satisfy local demand as well as open new avenues of growth for the Canadian hazelnut industry.

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S92. Transcriptomic analysis of the response of *Brassica napus* to *Plasmodiophora brassicae*

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Clubroot, caused by the biotrophic parasite *Plasmodiophora brassicae* Wor., is an important disease of cruciferous crops worldwide. To improve understanding of the mechanisms of resistance and pathogenesis in the clubroot pathosystem, the transcriptomes of two rutabagas (*Brassica napus* var. *napobrassica* (L.) Rchb.) were compared by RNAseq analysis. We challenged the cultivars 'Wilhemsburger' (partially resistant) and 'Laurentian' (susceptible), with *P. brassicae* pathotype 3A, and harvested roots at 7, 14 and 21 days after inoculation (dai). Microscopy preparations showed reduced colonization of the host roots for 'Wilhemsburger' relative to 'Laurentian'. Differentially expressed genes (DEGs) were identified by comparing inoculated plants with non-inoculated controls. At 7 dai, a greater number of DEGs was detected in 'Wilhemsburger' vs. 'Laurentian', with a significant number of genes showing opposite expression patterns in the two hosts. At this stage, genes associated with ethylene-related pathways and transcriptional regulation were upregulated in 'Wilhemsburger'. At 14 dai, pathways related to the cell cycle and division, as well as organ development, were induced specifically in 'Laurentian'. However, these pathways were induced in both hosts at 21 dai. Also at 21 dai, some biotic stress related pathways were still active in 'Wilhemsburger' but inactive in 'Laurentian'. The results suggest that DEGs involved in early resistance pathways are important in limiting infection, and that resistance responses are weaker in the susceptible host at later stages of infection.

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S93. Transcriptome profiling of incompatible and compatible interactions between *Brassica napus* and *Leptosphaeria maculans*

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Canola (*Brassica napus*) is a 26-billion-dollar crop in Canada. *Leptosphaeria maculans* causes blackleg disease, the most economically significant disease of canola. *B. napus* genotype, '01-23-2-1' that contains only *Rlm7* was inoculated with a *L. maculans* isolate (UMAvr7) carrying *AvrLm7*, and with the CRISPR knockout *AvrLm7* mutant (umavr7) of the same isolate carrying *avrLm7* to represent incompatible and compatible interactions, respectively. A dual RNA-seq experiment was done to explore differential gene expressions during both interactions. Defense-related Gene Ontology analysis revealed calcium and iron ion binding, chitinase, glutathione peroxidase, oxidoreductase, hydrolase, and methyltransferase activities related genes expression started early at one dpi and significantly increased from seven dpi onwards in incompatible *Rlm7-AvrLm7* interaction. In contrast, compatible interaction showed no or very low-level expression of those genes at 1-dpi and 3-dpi but significantly very high expression levels at 7-dpi onwards compared to incompatible interaction. Westar with no R proteins showed compatible interactions with both isolates and the expression patterns of aforesaid genes were similar to the compatible interaction of *Rlm7* with *umavr7* giving disease. In the incompatible avirulence effector -R receptor interaction, early activation of defense genes protects the host from the invading blackleg pathogen. This is not the case when the host comprises no R protein or the pathogen possesses no avirulence protein clearly highlighting the importance of gene-for-gene interactions in plant defense.

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S94. Tissue specific RNA sequencing of *Brassica napus* in response to *Sclerotinia sclerotiorum* infection

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White mold in *Brassica napus* (canola) is caused by the fungal pathogen *Sclerotinia sclerotiorum* and is responsible for significant losses in crop yield across the globe. With advances in high-throughput transcriptomics and computational biology, our understanding of canola's defense response to *S. sclerotiorum* is becoming clearer; however, the response of individual tissue layers directly at the site of infection has yet to be explored. Using cutting edge laser-capture microdissection coupled with high-throughput RNA sequencing we have profiled epidermal, mesophyll and vascular leaf tissues in response to *S. sclerotiorum* infection. This strategy increases the number of genes detected compared to whole leaf assessment and provides information on tissue-specific gene expression directly at the site of infection. Our findings indicate distinct roles for each tissue layer in response to infection and our bioinformatics approach has identified multiple novel defense regulators predicted to guide plant immunity. These putative defense regulators were further characterized by challenging target knockout *A. thaliana* lines with multiple fungal and bacterial pathogens. Using *in planta* infection assays we have identified both broad spectrum and pathogen-specific target defense genes that are essential in reducing losses to pathogen attack. We further discuss how this information will play a role in protecting one of Canada's most important cash crops against pathogenic attack.

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S95. Boost your yield, harness the forcefield: advancing RNAi-based biocontrols against agronomic pathogens.

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Crop species such as canola (*Brassica napus*), Canada's most valuable oilseed, are under constant pressure from phytopathogens which greatly decreases yield potentials. The highly aggressive necrotroph, *Sclerotinia sclerotiorum* is an annual burden for producers. Despite continued efforts to protect canola, there remains a direct and immediate need to find novel, sustainable methods to specifically target single pathogens. RNA interference has emerged as a compelling control strategy to impart plant protection against attack from agricultural pathogens through foliar sprays. While applications of double stranded (ds) RNA molecules that specifically targets a single gene in *Sclerotinia* has proven effective, the timing of the spray application remains a limitation. Thus, we developed canola that constitutively expresses dsRNA that targets individual pathogenicity genes. *In planta* greenhouse experiments suggest substantial resistance and we are now working to resolve the physiological and molecular mechanisms occurring within these RNAi plants. In addition to the phenotypic differences in lesion progression and severity, we have observed differing plant defence responses including with hormone signalling during infection. Due to the dsRNA-mediated decrease in fungal pathogenicity, plants are able to mount more effective defences and therefore cellular differences are observed at infection sites. For example, tylose-composed 'forcefields' shield the inner stem tissue layers from further *Sclerotinia* penetration and prevent lodging and complete yield loss. Ultimately, with continued development, RNAi has the promise to be at the forefront of agricultural pest control as we move towards a more ecologically-sound future.

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S96. Gene editing to enhance pathogen-induced cell wall reinforcement resistance to late blight in Russet Burbank potato

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Potato late blight, caused by the oomycete *Phytophthora infestans*, remains the major threat to potato production. Pyramiding of leucine-rich-repeat (NB-LRR) receptor R genes and fungicide applications are commonly used to manage late blight. However, the receptor R genes are not stable, and the fungicide applications are often not adequate. Pathogen-induced metabolites can impart durable resistance to late blight through active cell wall reinforcement at the site of infection. Several resistance R genes were identified based on RNAseq of resistant and susceptible potato cultivars. A R gene, *StCCoAOMT*, with known cell wall reinforcement resistance function was found polymorphic in Russet Burbank. A CRISPR/Cas9-based genome editing was used to replace the polymorphic segment of this R gene in Russet Burbank with a functional segment from a resistant potato genotype. The enhanced late blight resistance of gene-edited Russet Burbank was confirmed under greenhouse conditions. Stacking of more R genes can further enhance resistance. This technology can be used to improve resistance in more than 200 cultivars of potato currently being cultivated in Canada and more around the world.

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S97. Assessing the impact of fungicides on FHB caused by Fusarium spp. on two wheat cultivars in Alberta

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Crop rotations in western Canada are becoming tighter, increasing the presence of wheat pathogens, including the *Fusarium* species, which increases the chance of yield and quality losses. Downgrading of grain due to fusarium damaged kernels (FDK) is becoming a bigger problem, resulting in an increase in the use of fungicide at BBCH61-63. One purpose of this research was to assess the impact of fungicide application on *Fusarium* spp., fusarium head blight (FHB), and deoxynivalenol (DON). In 2018, field trials were conducted at four locations in Alberta. Thirteen treatments evaluated the quality and yield benefits of: fungicide rates; application timing; and various fungicide modes of action. These were applied to two genetically different Canadian Western Red Spring wheat cultivars, 'AAC Brandon' and 'AAC Viewfield'. Grain samples were assessed visually for FDK and all sites were found to have low levels. PCR analyses and DNA barcoding at two sites revealed that most plots had traces of *Fusarium* species (*F. culmorum, F. avenaceum, F. poae and F. graminearum*). DON analysis on some samples found an average of 82.5 ppb. These low levels are not a significant problem for growers. Low levels of FDK/DON are attributed to the 2018 weather conditions being unfavorable for disease development. This research shows that BBCH61-63 fungicide applications were not needed in 2018. Trials will be repeated in 2019.

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S98. Genetic factors affecting Fusarium head blight resistance improvement and linkage drag from introgression of exotic Sumai 3 alleles (including Fhb1, Fhb2, and Fhb5) in hard red spring wheat

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Fusarium head blight (FHB) resistance genes, Fhb1, Fhb2, Fhb5, from Sumai-3, are among the most important in wheat. Near-isogenic lines (NILs), in CDC Alsask and CDC Go backgrounds, carrying these genes in all possible combinations were developed using MAS, evaluated for FHB and DON accumulation in eight environments, agronomic/end-use quality assessments, and haplotyped with wheat 90K-iSelect assay. Other than evaluating the effects of major genes, the study elucidated epistatic gene interactions as they influence FHB measurements; identified loci other than Fhb1, Fhb2, Fhb5, in both recurrent and donor parents and examined annotated genes. Genotyping revealed polymorphism on all chromosomes and that the NILs carried <3% alleles from the resistant donor. The phenotypic response of NILs suggested non-additive responses and Fhb5 was as good as Fhb1. In addition to Fhb1, Fhb2, Fhb5, 4-5 resistance improving alleles in both populations were identified and three of five in CDC Go were contributed by the susceptible parent. The introgressed chromosome regions carried genes encoding disease-resistance proteins, protein-kinases, NBS-LRR domains. Epistatic gene-gene interactions among marker-loci explained >20% variation. Introgressions resulted in lower TKW and increased plant height with Fhb5; SDS-sedimentation volume and grain protein content were also affected. In addition to Fhb1, Fhb2, Fhb5, we identified 10 loci in Alsask and 9 in Go NILs that affected the agronomic traits. Sumai-3 derivatives carry a number of resistance improving minor effect alleles, other than major genes and genetic background of the recipient line and epistatic interactions can have a strong influence on expression.

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S99. Control of plant fungal pathogens using exogenous RNA

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Fungal pathogens represent one of the greatest threats to the global food supply. While some pathogens can be effectively controlled through plant based resistance fungicides are required to control several prominent fungi. The wide spread use of fungicides has adverse environmental consequences and can lead to fungicide resistance. Plant RNAi expression can silence genes in closely associated pathogenic fungi in a phenomenon known as host induced gene silencing. While this strategy has been demonstrated for a wide range of fungi it requires the use of genetic modification that is not accepted in many important crop species. Here we explored the use of exogenous RNA applications to provide plant protection without the need for genetic modification. Data will be presented for the control of *Fusarium graminearum* and *Botrytis cinerea*. We have found that the targeting of essential chitin synthase genes can significantly reduce infection with quantitative real-time PCR confirming silencing of target fungal transcripts. The data for targeting additional fungal genes will also be presented. We are also evaluating the use of nanomaterials for the encapsulation of RNA to improve stability and uptake and progress in this area will be discussed. The development of RNA based fungicides will provide a new tool for the control fungi that would allow precise targeting of fungal pathogens.

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S100. Multi-omic studies reveal the insertion of new mycotoxin virulence factors in Fusarium poae.

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Fusarium poae (Peck) Wollenweber is cosmopolitan, occurring on a range of hosts and associated with Fusarium Head Blight (FHB) in cereals. Extensive sampling of oat, barley, and wheat heads infected with FHB from Ontario, Quebec and Saskatchewan fields (from 2006 – 2016) confirmed that *F. poae* and *F. graminearum* Schwabe are the main Fusaria isolated from barley while *F. poae* is predominant contaminating oats. Historically, mycotoxin production associated with *F. poae* in Europe is quite variable and little is known about the mycotoxigenic potential of Canadian isolates. Several researchers hypothesize that the variation in mycotoxin expression observed in *F. poae* results from the presence of supernumerary chromosomes and the abundance of transposable elements (TEs) within its genome. Supernumerary chromosomes act as evolutionary cradles for pathogen virulence factors and transposon facilitated translocations into core chromosomes can accelerate genome evolution and therefore present a considerable challenge towards a durable disease management strategy. In depth metabolomic profiling and genome sequencing was carried out on 46 monosporic Canadian *F. poae* isolates demonstrating a degree of chemotypic diversity. Metabolomic profiling revealed consistent production of multiple “core genome” associated metabolites including the emerging mycotoxins diacetoxyscirpenol and beauvericin. Of particular interest, strain specific production of new mycotoxins and potential virulence factors were also observed and linked with horizontal gene transfer through supernumerary insertions into the *F. poae* genome.

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S101. Targeted mutation of multiple putative effectors in *Fusarium graminearum* utilizing CRISPR/Cas9

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Fusarium graminearum, a causal agent of Fusarium head blight (FHB) in wheat, barley and oats, utilizes secreted cysteine-rich effector proteins to modulate host immunity. One method to characterize fungal effectors is gene disruption through homologous recombination, but this approach is limited as only one gene or gene cluster can be targeted per transformation and many effector proteins are suspected of having functional redundancy. CRISPR-Cas9 recently emerged as a powerful new tool for gene editing in molecular biology. Among the different uses of the CRISPR/Cas9 system is the ability to target multiple genes with a single transformation event. The main objective of this work was to develop a streamlined method to disrupt multiple effectors. Expression vectors were constructed using a dual ribozyme expression system for sgRNA with GFP as a marker and codon optimized Cas9. We targeted a group of three putative effectors by protoplast transformation that were not clustered together in the genome with five different sgRNAs. This approach successfully induced deletions from 200 bp to over 2000 bp in one or more target genes in approximately 20% of transformed isolates. Additional transformations were also performed to determine if the putative effectors are secreted during infection, by tagging genes with GFP. Pathology tests with the CRISPR edited lines on wheat and potato are ongoing and results will be discussed.

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S102. Development of *Simplicillium lamellicola* as a biocontrol agent against the wheat pathogen *Fusarium graminearum*

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The endophytic fungus *Simplicillium lamellicola* was isolated from tissues of moderately resistant cultivars (winter wheat ‘AC Morley’ and ‘25R34’, *Triticum aestivum*). This isolate was assayed for the ability to suppress disease caused by *Fusarium graminearum* under growth room and field conditions. Agar inoculum of *S. lamellicola* applied 3 days before an agar plug of *F. graminearum* on wheat leaves reduced disease by more than 80% in growth room tests. Spore suspensions of *S. lamellicola* which were applied at anthesis of lab grown plants at three hours before the pathogen inoculation, reduced disease by 41-58% for susceptible cultivar ‘Wilkin’ and moderately resistant ‘Glenn’. In field tests, the biocontrol agent reduced disease for three cultivars, susceptible ‘Wilkin’ (65%), moderately resistant ‘AAC Scotia’ (72%), and moderately resistant ‘Glenn’ (77%). The endophytic fungus *S. lamellicola* isolate AA2016 was effective against *F. graminearum* for reducing disease in lab and field tests and should be further developed as a biological control agent.

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S103. Flooding tolerance is regulated through the MiR156/SPL module in *Medicago sativa*

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Climate change is expected to increase the mean annual temperature and precipitation resulting in frequent flooding events. To select or generate flooding-tolerant plants, it is imperative to understand the underlying tolerance mechanisms. microRNA156 (miR156) is highly conserved across plant species and is reported to impart effects on plant development, chemical composition, and stress physiology. To investigate whether miR156 affects the response of Medicago sativa (alfalfa) to flooding stress, we used miR156 overexpressors, miR156-regulated SPL13RNAi, flooding- tolerant (AAC Trueman) and sensitive (AC-caribou) cultivars, exposed to two weeks of flooding. Physiological analysis, hormone profiling and global transcriptomic data illustrated the positive role of miR156 in flooding stress tolerance. During flooding, moderate miR156 over-expressers, SPL13RNAi, and AAC Trueman alfalfa plants maintained Vcmax and Jmax, maximum rate of rubisco carboxylase activity and photosynthetic electron transport rate, as well photosynthetic assimilation rate. Global transcriptomic-based pathway analysis revealed the enrichment of transcripts related to photosynthesis and secondary metabolites pathways. Moreover, hormone profiling showed an increase in the abundance of total ABA metabolites contributed mainly by increased ABAGE and Phaseic acid, a catabolite of ABA, in flooding tolerant alfalfa genotypes. Together, our results suggest that the role of a miR156/SPL13 module in regulating flooding response in alfalfa is mediated in part by ABA and other secondary metabolites.

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S104. Identifying *Brachypodium distachyon* proteins interacting with histone deacetylase BdHD1

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Gene expression of stress-responsive genes can be regulated through epigenetic mechanisms which include DNA methylation and histone modifications. Current evidence has elucidated the involvement of histone deacetylases (HDACs) in plant stress responses. HDACs facilitate the removal of acetyl groups from histone tails and cause a condense chromatin structure, thus leading to gene repression. In Arabidopsis thaliana, HDA19, belonging to the RPD3/HDA1 class, can interact with many transcription factors to form complexes to repress gene expression. HDAC research has mainly been conducted within dicotyledons and research within monocotyledons is limited. Brachypodium distachyon is used as a model plant to investigate questions unique to monocot crops. BdHD1, the closest homologous gene of HDA19, has been identified in B. distachyon. This study investigated potential protein-protein interactions between BdHD1 and each of BdMYB22, BdWRKY24 and BdHOS15. The interactions were investigated using yeast two-hybrid assays (Y2H) and bimolecular fluorescence complementation (BiFC). Y2H assay shows that BdHD1 strongly interacted with WRKY transcription factor member BdWRKY24. This interaction was further confirmed via BiFC. An interaction between BdHD1 and the SANT domain-containing protein BdMYB22 was identified via Y2H and confirmed via BiFC. The SANT domain is involved in chromatin remodeling. No interactions were observed with BdHOS15. This research provides an insight for further discovering BdHD1-complexes in B. distachyon.

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S105. Physiological and biochemical responses of alfalfa (*Medicago sativa* L.) to salt stress

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The objective of this study was to understand the effects of salt stress on alfalfa from the whole plant to sub-cellular levels. Five alfalfa cultivars were grown in five gradients of salt stress of 0, 4, 8, 12 and 16dSm^{-1} electrical conductivity (EC) in a sand-based hydroponic system for 12 weeks in the greenhouse. The elemental concentrations in leaf, stem and root tissues were determined by Inductively Coupled Plasma-Mass Spectroscopy. Biochemical compounds in tissues of two selected alfalfa cultivars with contrasting salinity tolerance were localized using Mid-infrared and VESPERS beamlines at Canadian Light Source.

Increasing salt stress significantly (P<0.001) reduced plant height and dry shoot yield of alfalfa, with 4.2% and 7.9% reduction for each 1dSm^{-1} increase, respectively. Alfalfa under high salt stress (8-16dSm^{-1}) showed high concentrations of sodium and chlorine in leaf tissues compared to stem and root. The *in-situ* study using the VESPERS showed accumulation of chlorine in the leaf lamina and leaf margin, which resembled necrosis symptoms in salt-stressed alfalfa, while calcium accumulated in leaf veins. Salt tolerant alfalfa accumulated higher amides at >4dSm^{-1}, which may be a key feature for its osmotic adjustment. We concluded that alfalfa showed ion exclusion at salinity levels of 4dSm^{-1} EC, and shoot tissue tolerance at high salt stress (>8dSm^{-1}EC) at the flowering stage. Taken together, these results provide new insights into salt resistance mechanisms in alfalfa.

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S106. The ABA-responsive SnRK1 kinase interaction network in *Arabidopsis thaliana*

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Environmental stress greatly affects plants growth, posing challenges to food security. The yeast Snf1 (Sucrose non-fermenting1), mammalian AMPK (5' AMP-activated protein kinase) and plant SnRK1 (Snf1-Related Kinase1) are highly conserved heterotrimeric kinase complexes, activated under metabolic stress to re-establish energy homeostasis in eukaryotes. In plants, the hormone abscisic acid (ABA) plays a crucial and well-known role in stress response. Activation of SnRK1 or ABA signaling results in overlapping transcriptional changes, suggesting these two important stress pathways share common targets. To investigate how SnRK1 and ABA interact to regulate stress responses in Arabidopsis thaliana, the six SnRK1 complex subunits were screened by yeast two-hybrid against 258 ABA-responsive proteins. A set of 125 unique SnRK1-complex interactors were uncovered, which included known and core ABA signaling components, suggesting that SnRK1 may modulate the ABA response pathway at multiple levels. Network analysis indicates that a subset of SnRK1 kinase interactors forms a signaling module in response to osmotic and salinity stress. Functional studies using T-DNA insertion mutants show the involvement of SnRK1 and five interacting partners in salinity stress responses. This targeted study uncovers the largest set of SnRK1 interactors, which can be used for further characterization of the role of SnRK1 and its ABA-responsive partners in plant survival under stress.

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S107. Characterizing the role of *Arabidopsis thaliana* RING-type E3 Ligase XBAT35.2 and its substrates in abiotic stress tolerance

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Ubiquitin ligases (or E3s) select specific proteins for ubiquitination, which involves the attachment of one or more ubiquitin molecules. The major outcome of ubiquitination is breakdown of modified proteins by the 26S Proteasome. In plants the ubiquitin-proteasome system is required for responses to environmental stresses such as pathogen, drought, and high salinity. Of interest is XBAT35, a RING-type ubiquitin ligase, whose transcript is alternatively spliced to produce two isoforms; *XBAT35.1* and *XBAT35.2*. XBAT35.2, but not XBAT35.1, can promote defense against pathogen attack by mediating the 26S Proteasomal turnover of Accelerated Cell Death11 (ACD11) [1]. The aim of this study is to determine whether XBAT35.2, and possibly ACD11, is also involved in abiotic stress tolerance. We found that seedlings overexpressing ACD11 and mutant *xbat35-1*, which lack expression of both E3 isoforms, are more tolerant to the inhibitory effects of ABA and salt on germination and early growth. Interestingly, under mild salt stress, XBAT35.2 abundance significantly decreases, while the level of ACD11 increases considerably. However, the abundance of ACD11 is reduced when exposed to severe salt stress, and this decrease is dependent on proteasome activity. The results and others suggest that mild abiotic stress stabilizes ACD11 through downregulating its negative regulator XBAT35.2, while severe stress may produce the opposite outcome. Further study is required, but our preliminary results suggest a role for XBAT35.2 in abiotic stress tolerance.

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S108. Overexpression of de novo DNA methyltransferase BdDRM2 alters *Brachypodium distachyon* development and abiotic stress response

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DNA methylation is a major epigenetic modification that can alter gene expression. Changes in DNA methylation are involved in many plant processes including growth, development, stress response and possibly adaptation. Genome-wide DNA methylation patterns depend on both *de novo* and maintenance methylation, as well as passive and active demethylation. DOMAINS REARRANGED METHYLTRANSFERASE 2 (DRM2) is the primary *de novo* DNA methyltransferase in plants, however, its involvement in temperate cereal development and stress response remains unclear. Therefore, to better understand the role of DRM2 and *de novo* DNA methylation in modulating gene expression as it relates to important agronomic outcomes, we have developed independent *BdDRM2*-overexpression lines of the model cereal *Brachypodium distachyon*. Results suggest that BdDRM2 also regulates DNA methylation and consequently plays a role in development and abiotic stress response in *B. distachyon*. When compared to control plants, *BdDRM2*-overexpression lines exhibit higher global DNA methylation, abnormal transcriptional responses to abiotic stress and altered vegetative and reproductive growth. Efforts to characterize the effects of these characteristics on the stress tolerance of the lines are ongoing. The findings of this research provide insights into cereal abiotic stress responses, breeding for stress-resistance in a changing climate, and the possibility of epigenome editing.

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S109. Molecular regulation of monoterpene metabolism in Lavandula

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Lavenders (*Lavandula*) are widely cultivated for their essential oils (EO), which are mainly constituted of monoterpenes. We have developed genomics resources to facilitate the discovery of structural and regulatory genes that control EO formation, secretion and storage in Lavandula. This presentation summarizes recent findings concerning the molecular aspects of EO metabolism in these plants. Specifically, recent progress in cloning and characterization of genes that control flower development, and those that encode terpene synthases, terpene synthase regulators (transcription factors) and prenyl transferases.

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S110. Functional study of Lavandula prenyl diphosphate synthase genes

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Lavandula essential oils are mainly composed of monoterpenes and a lesser amount of sesquiterpenes. The flux of these terpenoids can be regulated by expression of terpene synthases and the amount of supplied precursors, which are produced by short-chain isoprenyl diphosphate synthases (IDSs) from the pools of isoprene units (IPP and DMAPP). The IDSs include geranyl diphosphate synthase (GPPS), farnesyl diphosphate synthase (FPPS), and geranylgeranyl diphosphate synthase (GGPPS), which give rise to monoterpenes, sesquiterpenes, and diterpenes, respectively. Although several studies have focused on genes encoding terpene synthases, the biosynthesis of major terpenoid precursors has not been determined in *Lavandula*. Here, we report the cloning and functional characterization of GPPS, FPPS and GGPPS from *L. x intermedia.* The cloned *Lavandula* IDSs resemble those previously reported in mints. LiGPPS is a heteromeric protein, composed of a large and a small subunit, while FPPS and GGPPS are homomeric proteins. Recombinant GPPS, FPPS and GGPPS catalyzed the condensation of IPP with DMAPP to form GPP, FPP, and GGPP, respectively. The small subunit of LiGPPS also interacted with GGPPS, modifying this enzyme to produce GPP.

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S111. Investigating transport of seco-iridoids in Catharanthus roseus

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Decades of research has resolved the biosynthesis of monoterpenoid indole alkaloids (MIAs) and the anti-cancer drugs vincristine and vinblastine in *Catharanthus roseus*. Studies suggest that MIA biosynthesis is highly compartmentalized in organelles (e.g. plastids and vacuoles) and in, at least, three specialized tissue-types. Spatial separation of distinct metabolic branches requires the translocation of intermediates across organelle and cell boundaries. While components of the transport system, such as vacuolar efflux, have been isolated, an accurate model of the whole transit network has eluded researchers. We identified a transcript encoding a putative transporter from an EST database. Gene expression was suppressed in *C. roseus* using virus induced gene silencing (VIGS), resulting in reduction of the seco-iridoid, secologanin and the MIA, catharanthine in leaf extracts. Secologanin is coupled with tryptamine in the vacuole to form the MIA backbone, strictosidine. The reduction in secologanin and catharanthine levels, suggests a potential bottleneck early in the iridoid branch. To dissect this metabolic phenotype, we characterized the subcellular localization of the protein using fluorescence confocal microscopy. The transporter was heterologously expressed in yeast and assayed for substrate acceptance of iridoid intermediates. This novel transporter appears to work with other transporter families to orchestrate biosynthesis in the seco-iridoid pathway. The transporter could be deployed in the microbial reconstitution of MIA pathways to add a layer of control and complexity.

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S112. Mitragyna speciosa – a promising player in the opioid crisis

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Mitragyna speciosa, also known as ‘Kratom’, is a tropical tree species native to South East Asia where herbal preparations of Kratom leaves haves been used since antiquity to treat various ailments, including opioid addiction. Approximately twenty different alkaloids have been reported to accumulate within Kratom leaves, of which mitragynine shows the most promise as a potential opioid replacement. While Kratom continues to receive much world-wide attention, there is still a gap in our knowledge about the growth and propagation of the plant as well as how the accumulation of its various alkaloids changes throughout plant development. Moreover, almost nothing is known about how Kratom alkaloids impact areas of the brain that are associated with drug addiction and abuse liability. Accordingly, we report here the development of a method for vegetative propagation of Kratom with over a 90% rooting rate and define the peak accumulation times for the various therapeutic alkaloids during leaf development. Finally, it was demonstrated that acute mitragynine exposure (10 mg/kg, i.p.) to rats resulted in a moderate but significant suppression of theta and gamma neural oscillations selectively in cortical sub-regions of the brain, with no effects within the reward pathway that mediates addiction. These findings support a lack of abuse potential for mitragynine.

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S113. Distinct metabolic modes drive monoterpenoid biosynthesis in a natural population of Pelargonium graveolens (rose scented geranium)

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Pelargonium graveolens is a wild predecessor to rose-scented geraniums cultivated for their essential oils, which are useful in the cosmetics, fragrance and flavoring industries. Despite their economic uses, little is known about the biosynthesis of *Pelargonium* essential oil components. Untargeted volatile profiling of 22 seed-grown wild-type *P. graveolens* lines and whole plant isotopic labelling studies demonstrated the contribution of at least two distinct monoterpene biosynthetic pathways in these plants; namely, cyclic *p*-menthanes such as (-)-isomenthone and acyclic monoterpene alcohols such as geraniol and (-)-citronellol and their derivatives (referred to here as citronelloid monoterpenes). Three distinct chemotypic groups favoring either *p*-menthane or citronelloid biosynthesis were defined as a result of hierarchical clustering analysis. $^{13}CO_2$ isotopic labeling studies and targeted chiral GCMS analyses indicated that *p*-menthane monoterpenoids in *Pelargonium* are synthesized via (+)-piperitone. This whole plant isotopic labeling approach also permitted us to measure the rate of monoterpenoid biosynthesis under physiological conditions in intact plants. Labeling in the (-)-isomenthone-rich chemotype correlated with (+)-limonene but not its antipode, an effect absent in the citronelloid rich chemotypes, from which we conclude that (+)-limonene is most likely the precursor to *p*-menthane monoterpenoids in geraniums. The absence of (+)-pulegone in *Pelargonium* extracts and rapid labeling of (+)-piperitone provide evidence that *p*-menthane biosynthesis in rose-scented geranium is fundamentally distinct from the related *p*-menthane pathway in peppermint (*Mentha x piperita*) which yields (-)-menthol.

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S114. Profiling anthocyanin species involved in developmentally regulated programmed cell death in lace plant (*Aponogeton madagascariensis*) leaf development

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Programmed cell death (PCD) is a systematic method of cellular destruction and is required in plants for normal development and survival. Lace plant (*Aponogeton madagascariensis*) uses PCD to form perforations throughout its leaves and has emerged as a model organism in the study of developmentally regulated PCD in plants. The development of perforation formation in lace plant leaves is divided into five main stages: pre-perforation (prior to PCD initiation), window (PCD occurs), perforation formation, perforation expansion, and mature (PCD completed). Early stage leaves are pink in colour due to abundant anthocyanin pigmentation; the first visible sign of cell death is the disappearance of anthocyanin in window stage leaves. Due to this conspicuous pattern of anthocyanin loss, it is suspected that these pigments may play a role in lace plant PCD. The research objective is to profile anthocyanin species involved in developmental PCD during lace plant leaf development. Sterile cultures of lace plant were established, and tissues were excised for crude anthocyanin extraction. The extracts profiled via LC-DAD and LC-MS. LC-DAD results indicated that the anthocyanin species and their relative abundances varied with the stages of leaf development. LC-MS identified four abundant anthocyanin species present in lace plant leaves that are not found in common fruits and vegetables. The identity of these anthocyanin species are presently being determined.

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S115. Hsp70 mediates programmed cell death during the remodeling of lace plant leaves (*Aponogeton madagascariensis*)

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Leaves of the lace plant utilize programmed cell death (PCD) to form perforations during development. Heat shock proteins (Hsps) are essential for development and are known to be involved in plant PCD, however, have not been investigated in lace plants. Hsp70 levels were analyzed throughout lace plant leaf development and results indicate they are highest during early development before and during PCD. Basal Hsp70 synthesis correlates with raised anthocyanin levels and caspase-like protease activity (CLP), two hallmarks of lace plant PCD. We treated whole plants with known regulators of PCD (ROS and antioxidants) alongside an Hsp70 inhibitor, chlorophenylethynylsulfonamide (PES-Cl) to investigate the effects of Hsp70 on leaf development. ROS induced Hsp70 2-fold and CLP in early developing leaves, however, there was no change in anthocyanin levels and the number of perforations formed. Antioxidants significantly decreased Hsp70 and CLP in early leaves, resulting in significantly less anthocyanin and the fewest perforations. PES-Cl induced Hsp70 4-fold in early leaves, causing anthocyanin, superoxide and CLP to significantly decline, leading to fewer perforations. The departure from basal Hsp70 levels in young leaves alters anthocyanin and CLP, inhibiting PCD induction. Our results indicate Hsp70 plays a role in lace plant leaf development by mediating PCD.

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S116. An Arabidopsis G-protein-coupled receptor-like module regulates cellulose synthase enzyme secretion

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Cellulose is crucial for plant morphology and water transport and also provides raw material for fibre and fuel industries. Cellulose is produced at the plasma membrane by large Cellulose Synthase (CESA) protein complexes. These CESA complexes must be secreted from the Golgi apparatus to reach the plasma membrane; however, the regulatory framework for this secretion is not clear. We have identified several members of the seven transmembrane domain containing protein (7TM) family as important for cellulose production during cell wall integrity stress. Cell wall stress, such as cellulose synthesis inhibition, resulted in reduced growth, cell swelling, and reduced cellulose production in the *7tm* mutants compared to wild-type. 7TM proteins are often associated with G-protein signaling. Indeed, mutants for several of the canonical G-protein complex components were also hypersensitive to cell wall stress. Furthermore, the 7TM proteins could interact with the G-protein complex at the Golgi apparatus and trans-Golgi network. To understand the cellulose deficient phenotype of *7tm* mutants, we examined fluorescently tagged CESAs in the *7tm* mutants. While the CESAs at the plasma membrane were unaffected, CESA secretion was substantially reduced in mutant plants, compared to wild-type. By contrast, other secreted proteins appeared unaffected. We propose a model in which G-protein coupled 7TM proteins regulate CESA trafficking and defects in this process result in hypersensitivity to cell wall integrity stress.

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S117. Identification and characterization of novel targets for a subfamily of Arabidopsis calmodulin-like (CML) proteins

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Calcium ions serve as ubiquitous second messengers in eukaryotes. Calcium sensor proteins, such as calmodulin (CaM), detect and transduce calcium signals by regulating downstream target proteins. In plants, the largest family of calcium sensors are the CaM-like (CML) proteins: Arabidopsis has 7 CaMs and 50 CMLs. Some CMLs are known to function in development and stress-response but most remain unstudied. Whereas many downstream targets of CaM are well characterized, very few CML targets have been identified. Here, using a range of biochemical and molecular approaches, we have identified several target proteins that interact exclusively with a small subfamily of Arabidopsis CML paralogs. Our data indicate that these particular CMLs display unusual calcium-binding and structural properties relative to other members of the CML family. Using the yeast two-hybrid system, we identified putative targets of these CMLs, delineated the CML-target interaction domains, and corroborated the high specificity of this interaction using *in vitro* assays and the *in planta* split-ubiquitin system with *Nicotiana benthamiana*. Structural and biophysical analyses indicate the presence of both CaM and CML binding sites on the target proteins that we have identified. We will discuss proposed roles for these CMLs and their targets in cytoskeletal function based on our analyses using T-DNA insertion knockout-lines, subcellular localization analyses using GFP-CML fusion proteins, and promoter activity assays using CML promoter:GUS reporter transgenic plants.

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S118. Make or break? Microtubule growth and shrinkage are controlled by dynamic turnover of plus-end proteins

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Assembly and disassembly of microtubule (MT) polymers is critical for plant development and response to environmental signals. In *Arabidopsis thaliana*, MICROTUBULE ORGANIZATION 1 (MOR1) acts as a MT polymerase by rapidly adding tubulin dimers to the growing (plus) ends of MTs. By contrast, Armadillo Repeat Kinesins (ARKs) are motor proteins that act as catastrophe factors by promoting MT disassembly. The indispensable role of MOR1 is well established, but its mechanism of polymerase activity and association with catastrophe factors remains elusive. To investigate MOR1 kinetics *in vivo*,we used homologous recombination to engineer yellow fluorescent protein (YFP) tagged wild-type MOR1 and a mutant form of the protein (mor1-1) that has been shown to reduce MT polymerization rates. Using Total Internal Reflection Fluorescence microscopy, we performed fluorescence recovery after photobleaching (FRAP) on growing MTs. Compared to the wild-type MOR1-YFP, the mutant mor1-1-YFP protein recovered fluorescence very slowly, which indicated MOR1 normally has a transient association with the growing MT that is tightly coupled to MT growth. We next hypothesized that ARKs promote MT disassembly by interfering with MOR1's affinity for MTs. Using CRISPR/Cas9, we simultaneously knocked out expression of the functionally redundant *ARKs 1*and *2*, and assessed MOR1 dynamics by FRAP. Through these strategies and innovative techniques for live cell imaging, we have generated a new model on the fundamental process of MT dynamics.

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S119. Mechanical role of callose plugs in pollen tubes

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Pollen tube growth and gametic fusion are two fundamental processes that result in successful fertilization and are crucial determinants of seed yield. Pollen tubes are fast growing cellular protuberances that function to deliver sperm cells to female gametophyte. They are an ideal model to study plant cellular morphogenesis, polar growth and cellular signaling. A growing pollen tube is exposed to different types of stresses such as turgor induced tension stresses in the cell wall and compressive stresses exerted by the growth matrix. Pollen tubes display a characteristic deposition of callose in the form of plugs that separate the active portion of the pollen tube cytoplasm from the degenerating segments. Callose (ß-1,3 glucan) is a polysaccharide in plant cell walls that is synthesized and accumulated at the outer surface of the plasma membrane by callose synthase – a membrane localized enzyme. It is abundantly present in pollen grains, pollen tube cell walls and callose plugs and must therefore have an important role for their specific functions. My research explores the formation and the mechanical role of callose plugs. To understand the mechanical properties of callose as a material, I perform mechanical assays to determine the correlation between turgor pressure and callose abundance in the pollen tube cell wall. GFP tagging of callose synthase enzyme will also provide insight into the molecular mechanism governing callose plug formation

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S120. DONGLE and DAD-LIKE LIPASE2 enriched sites create organelle interaction hubs

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Lipases hydrolyze lipids and help maintain cellular homeostasis and defense responses in plants. Phospholipases A1 (PLA1) act on the sn-1 position of glycolipids to release lyso-lipids and free fatty acids (FFA) and trigger the jasmonic acid biosynthesis pathway. While biochemical activity in the pathway spans chloroplasts, peroxisomes, the endoplasmic reticulum (ER) and oil-bodies (OB) the physical interactions between these organelles have not been observed in living cells. We have investigated organelle interactions using fluorescent protein fusions of the phospholipases DONGLE (DGL) and DAD-LIKE LIPASE2 (DALL2). Both proteins localized to the chloroplast envelope as patches of variable size. While an earlier study had concluded additional localization of DGL on OB this was not confirmed. Nevertheless, OB numbers and their clustering around chloroplasts increased considerably in wounded leaf cells and under these conditions OB often localized to DGL enriched patches. OB also associated with DGL-rich vesicles released from injured chloroplasts. Further observations using ER-targeted fluorescent proteins showed the ER mesh interspersed with OB and OB-peroxisome clusters and also showed the convergence of ER tubules to the lipase-enriched regions on the chloroplasts. Our observations strongly suggest that during the early stages of plant defense response the generation of signaling molecules such as FFA and lyso-lipids at lipase enriched regions of chloroplasts creates subcellular hubs of increased physical interactions between the ER, OB and peroxisomes.

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S121. Transcriptomic response of multiple Brassica species to *Sclerotinia sclerotiorum* infection

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Whole-genome duplication (WGD; polyploidy) events have played an extensive role in the evolution of flowering plants. The sudden doubling of genetic material can expedite rapid novel changes to polyploid transcriptomes. For example, polyploids formed via an interspecific hybridization of closely related species, or allopolyploids, can exhibit expression patterns inconsistent with their parental species. Consequently, allopolyploidy could have profound effects on the stress responses of these hybrids; however, the extent to which the transcriptomic shock that follows WGD events plays a role in a biotic stress response remains a nascent topic in polyploidy research. To investigate the interplay between polyploid gene expression and biotic stress response, *Brassica napus*, *Brassica oleracea*, *Brassica rapa*, and a synthetic *Brassica napus* (formed directly from the aforementioned parental species of *B. napus*) were subjected to the economically devastating fungus *Sclerotinia sclerotiorum.* RNA-Seq analysis of these pathosystems revealed wide-spread transcriptomic changes involving both constitutive gene expression and alternative splicing. Cross-species comparisons showed a concerted response between all assayed *Brassica* species characterized by the up-regulation of jasmonic acid signalling pathways, cell-wall defense genes, chitinases, and pathogen responsive genes. Subgenome comparisons also showed considerable non-parental gene expression patterns in the synthetic *Brassica napus*, in addition to a C-subgenome expression bias, suggesting transcriptome reprogramming occurs relatively quickly following polyploidization.

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S122. Lectin genes in Brassica napus enhance resistance to the fungal pathogen *Sclerotinia sclerotiorum*

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Lectins are known to contribute to defense against fungi, virus, bacteria and insect pests. We have shown that certain lectin genes are up-regulated in canola (*Brassica napus*) after inoculation with the fungal pathogen *Sclerotinia sclerotiorum*. To investigate the effectiveness of lectin genes, a single allele of curculin, concanavalin and hevein, were cloned from the partially resistant cultivar Zhongyou 821 and each inserted in a susceptible line, DH12075, under the constitutive gene promoter, CaMV35S, using *Agrobacterium*-meditated transformation. Subsequently, five transformed lines showed 50-80% reduction in disease severity. The three lectins have a signal peptide (SP) that directs the protein into vacuoles destined for the cell's secretory system, and the remaining protein contains one or more carbohydrate recognition domains (CRD) with different substrate specificities. Both curculin and concanavalin CRDs have mannose specificity, while hevein has chitin specificity. Since both mannose and chitin are constituents of fungal cell walls they are targeted by these CRD. In *Arabidopsis* these lectin genes are induced by fungal pathogens or chitin treatment, and their proteins are prominent in both apoplast and xylem. The lectin genes cloned from Zhongyou 821 harbour amino acid substitutions in either CRD and SP domains, which could account for enhanced vacuolar secretion or higher affinity for fungal carbohydrate moieties leading to enhanced resistance to *S. sclerotiorum*. The genes or transformed lines might be used in future canola breeding.

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S123 Investigating the function of the APSES protein encoding gene apu2 (nlt1) during U. maydis biotrophic growth

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Ustilago maydis D.C. Corda is a model for investigating basidiomycete biotrophic pathogenesis. Recent transcriptome analyses of its disease development, by Lanver et al (2018), revealed that the protein encoded by *UMAG_04778*, which they called non-leaf tumor 1 (*nlt1*), had a controlling role in the third wave of effector expression. We previously identified this gene in a cDNA subtraction library and termed it APSES protein Ustilago maydis 2 (*apu2*) noting that it contained a previously unrecognized APSES domain. This helix-loop-helix DNA binding domain is highly conserved in a group of fungal-specific transcription factors described in the ascomycetes as being involved in the control of morphological transitions. Previously in *U. maydis*, another APSES protein, Ust1, was shown to regulate dimorphism, virulence, and sporulation. We discovered four other APSES proteins encoded in the *U. maydi*s genome, including apu2 which was the only family member with elevated transcript levels during pathogenic development. *Apu2* deletion did not inhibit plate mating or filamentous growth; however, it led to decreased leaf tumor formation, and virulence as well as dramatically reduced teliospore formation during solopathogenic haploid and dikaryon infections. Constitutive expression of *apu2* led to plate growth and pathogenesis phenotypes consistent with the hypothesis that Apu2 has a role in regulating morphological transitions leading to teliospore development in *U. maydis*. This, as well as expression data on potential downstream genes, will be presented.

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S124. Characterization of the Pyrenophora tritici-repentis-barley interaction

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Tan spot caused by the necrotrophic fungus *Pyrenophora tritici-repentis* (*Ptr*) is a major foliar disease of wheat worldwide. The fungus produces several necrotrophic effectors that trigger susceptibility in the wheat host. While the *Ptr*-wheat interaction has been the focus of in-depth research over the last 40 years, the nature of its interaction with various other gramineous hosts remain under-investigated. Here we provide evidence for a specific interaction between barley and *Ptr*, describe the infection process and highlight the genetics behind this interaction. A comprehensive genetic map composed of 381 SNP markers was used to map the locus conditioning this specific interaction in a population of 94 double haploid lines from a cross between Haruna Nijo and H602. Reaction to the race 5 isolate of the fungus, a Ptr ToxB-producer, was evaluated at the seedling stage in a greenhouse. The lines segregated 1:1 for susceptible: resistance phenotypes, indicating the involvement of a single locus. The locus was mapped to the distal region of the short arm of chromosome 2H in barley. The region encompassing the locus includes membrane receptor-like kinases (RLKs), intracellular nucleotide-binding, leucine-rich repeat receptors (NLRs), and ankyrin-repeat proteins. The underlying gene will be identified using high resolution mapping and transgenic complementation.

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S125. Relationship between foliar symptoms and gene expression induced by Pear Decline phytoplasma

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Pear tree selections developed at AAFC with PD phytoplasm infection show either leaf curling (selection 9328-1) or leaf reddening (selection 8824-1) indicating different responses to infection. PD populations in the two selections were not significantly different, except for ten time higher numbers in roots of selection 9328-1 than 8824-1 indicating greater susceptibilty. Gene expression between non-infected and PD-infected tissues of both selections was determined for sucrose synthase and acid invertase, which are affected by localized changes in sugars, and alcohol dehydrogenase, chitinase class III, phenylalanine ammonia-lyase and phloem protein2, which are affected during PAMP triggered immunity. Greater up-regulation of gene expression in PD-infected tissues was observed in selection 8824-1 for sucrose synthase in leaves, acid invertase in leaves and roots, alcohol dehydrogenase in shoots, chitinase in all tissues, and phloem protein2 in roots. In contrast, greater up-regulation in PD-infected selection 9328-1 was only observed for sucrose synthase, acid invertase and phenylalanine ammonia-lyase in shoots. The results indicate that leaf reddening may be due to an accumulation of anthocyanins as part of a greater PAMP triggered immunity response in selection 8824-1, while leaf curling in selection 9328-1 may be due to water stress because of more dysfunctional phloem.

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S126. Update on Manitoba potato and horticultural crops disease and insect pests in 2018.

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Potato and horticultural crops are high value and high input crops with significant disease and insect pest risks. The 2018 cropping season had normal spring planting. The growing season was generally dry with extended warm periods, and just prior to harvest a prolonged wet period, followed with freezing temperatures. The foliar diseases were generally lower than normal, but Verticillium wilt and black dot (*Colletrotrichum coccodes*) diseases were more extensive. In-vitro testing identified some fungicides effective against *C. coccodes*. Late blight was not found in 2018. Colorado potato beetles appeared in increasing numbers even after seed treatments. Aphid numbers in traps were significantly lower than normal, reducing risk of mosaic diseases in seed potato. European corn borer injury was noticeable in a few fields, but did not warrant insecticide application. Aster leafhopper (ALH) numbers in traps were also low on potato and carrots, resulting in lower ALH transmitted diseases. Cauliflower blackrot disease was not an issue in 2018. On strawberry and raspberry Botrytis grey mold was found at low levels; probably due to high temperatures near harvest time. Verticillium wilt/stripe was recorded in many crucifer vegetables in infested trial plots. End of the crop season was marked by severe frost damage to many crops. This resulted in nearly 6000 acres of potato and vegetables not being harvested, and soft rot issues in potato storages.

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S127. Comparative analysis between conventional and novel water treatment technologies in recirculating hydroponics

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Fertigation water, irrigation water with fertilizer dissolved in it, is commonly employed in hydroponic cropping systems. Capturing fertigation run-off and reapplying it to the crop conserves fertilizer and water resources while limiting the discharge of these nutrient rich solutions to the environment. Although an efficient use of resources, recirculating fertigation water does pose a risk in terms of pathogen proliferation. Pathogens can be picked up from infected plants and other sources and inadvertently directly applied to the crop during solution re-use. There are many conventional technologies, such as ozone (O_3) or Advanced Oxidation Processes (AOPs) that can eliminate pathogens and prevent their proliferation in fertigation water. There are also emerging electrochemical technologies, such as the use of Dimensionally Stable Anodes (DSA), that can inactivate pathogens using *in situ* regenerative hypochlorination. These emerging electrochemical chlorination processes are superior to conventional chlorination in that disinfectant does not need to be continually added, a process that can sour the solution making it unfit for crop production. The regenerative electrochemical chlorination technology is evaluated against ozone and AOP technologies for pathogen control during *Cyclamen persicum* production. Fertigation solutions spiked with *Fusarium oxysporum f. sp. cyclaminis* were treated with the three technologies and then allowed to recirculate through the crop. After 6 weeks of growth, plants were harvested and evaluated for disease symptoms. Results of the study will be presented.

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S128. Focusing on natural changes in solar spectrum to better understand plant light responses

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Portions of the solar spectrum are filtered out through the Earth's atmosphere. This filtering can be attributed to Rayleigh scattering, Mie scattering, and absorption by atmospheric gases. Rayleigh scattering preferentially diminishes short wavelength blue light while Mie scattering evenly dissipates PAR. The circular nature of the Earth's atmosphere makes solar radiation path-length through the air mass longer in lower solar elevations which enhances light scattering. Dusk/Dawn, winter solstice, and high latitudes each manifest a change in spectrum due to their inherent lower solar elevations. The presentation will discuss data on ratios, absolute irradiance, and rates of spectral changes in these situations. Furthermore, recommendations for the horticultural LED lighting industry and plant photobiological research community will be emphasized. The take home message is; when we assess plant physiological responses to light, we should factor and correlate light intensity, photoperiod duration, and spectral quality as it would naturally change in a day, season, and geographic latitude. Once natural lighting scenarios can be standardized artificially, then we can modify it for yield, morphology, and phytonutrient content. It is believed that fundamental responses to natural changes in solar spectrum is ubiquitous among land plants.

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S129. Enhancing plant growth using light emitting diode (LED) technology

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Light is essential to plant growth and development. It is required to drive CO_2 assimilation into the building blocks required by plants while also being a key trigger for important plant responses such as shade avoidance, developmental programs and seed / fruit production. In countries such as Canada, horticulture is an important component of the food production landscape. An important component of horticulture is the application of artificial light to facilitate plant growth. Typical light technologies currently deployed in horticultural plant growth involve high pressure sodium or fluorescent lights which are energetically and economically expensive, in addition to being technologically limited. Light emitting diode (LED) light technology represents an alternative to these standard approaches. Generally, LEDs are used to supplement these standard lighting technologies or glasshouse operations; however, there is limited knowledge of how plants respond to growth under an LED-only light regime. Advancing our understanding of LED impact on plant growth and development and how this can be harnessed for increased horticulture output, represents a timely opportunity given the increasing unpredictability of weather and climate. Using a programmable LED technology, in conjunction with multiple genetic resources, we have generated both a molecular and phenotypic understanding of how plants respond to growth under an exclusive LED-lighting regimen. Together, these findings demonstrate the utility of LED technologies in horticultural plant growth.

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S130. Optimizing spectral quality of light emitting diodes light for controlled-environment microgreen production

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Microgreens are becoming highly consumed due to their various colors, attractive flavours, tender textures, high nutritional values, as well as short growth period. For controlled-environment production, light is a major factor in controlling microgreens' morphological, physiological and biochemical processes. To determine optimal light-emitting diode (LED) spectral qualities for microgreen production, experiments were conducted in both growth chamber and greenhouse environments using arugula, cabbage, kale and mustard microgreens from the *Brassicaceae* family. Under blue and red LED combinations with the same photon flux density of ≈300 $\mu mol \cdot m^{-2} \cdot s^{-1}$, increasing blue light percentage (ranging between 5%-30%) proportionally decreased the hypocotyl length and cotyledon area of kale and mustard, whereas the fresh and dry weight were unaffected except for cabbage. However, the levels of ascorbate, anthocyanin and total phenolics were higher at blue light percentages of 15%-20%, although the magnitude of these responses varied with species. In another two experiments (one in growth chamber, one in greenhouse), low-level monochromatic blue with or without far-red light were applied throughout the night period. Although both blue and far-red light promoted hypocotyl elongation,blue light at 20 $\mu mol \cdot m^{-2} \cdot s^{-1}$ in the growth chamber and 14 $\mu mol \cdot m^{-2} \cdot s^{-1}$ in the greenhouse maximally increased fresh weight and improved the appearance of microgreens relative to similar levels of far-red light. These results can be used by growers to determine and manipulate their light quality for high quality and yield microgreen under controlled environment.

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S131. Optimizing growing conditions for romaine lettuce (Lactuca Sativa L. var. Longifolia) production in a plant factory

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Plant Factories (PF) are indoor crop production facilities utilizing high cropping densities and vertically integrated growing layers. These systems generally require less inputs (water, fertilizer, pesticides, etc.) compared to traditional farming and take advantage of volume use efficiencies via vertical integration. In order to realize the full potential of these production systems the correct complement of environmental conditions (e.g., light, CO2, humidity, nutrition, etc.) needs to be developed for each crop. There is ample research supporting the production of leaf lettuce cultivation in these facilities; however, there is no such body of information for romaine lettuce, a popular and economically significant type of lettuce. The presented study examines the response of romaine lettuce to variable planting densities, and its hydroponic nutrient requirements for PF production.

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S132. Monitoring of functional state of in vitro preserved plants in Lavandula angustifolia Mill.

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The resistance of chlorophyll-containing tissues to excess light is widely used in experimental biology as an integral criterion for the functional state of plants. The parameters of fluorescence induction of microshoots in lavender plants at different temperatures (4 to 12°C), duration of conservation and light intensity 1.25-3.75 μM m^{-2} $s^{-}1$ in genebank *in vitro* were investigated. The conservation was carried out on ¼ MS medium with sucrose and chlorocholin chloride. After 6 months of depositing, the indicator (F_m - F_{st}) / F_m in cultivars ‘Record’ and ‘Belyanka’ approached the suboptimal values (0.38 ... 0.53 a.u.). At this time photosystem of the plants not damaged and an active production processes are suspended. The temperature significantly affects the functional state of microshoots: optimal temperatures of 4°C and 6°C after 6 months and 12 months of conservation have been identified. Temperature going up was induced the increasing of (F_m - F_{st}) / F_m indicator (r = 0.23 ... 0.43; R^2 = 0.03 ... 0.68). This study was funded by the ST No. 0829-2019-0038 of the FSFIS “NBG-NSC”.

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S133. Precarity of American Water Willow (*Justicia americana*) in Ontario

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The American waterwillow (AWW) is an aquatic clonal plant, threatened in Canada. Two populations are found in Ontario and two others in Quebec. This plant grows along the waterbody shores, but habitat loss, water level fluctuations and presence of invasive species pose as threats. The Niagara populations have been monitored to understand the ecological factors that may limit its distribution. One priority of the recovery plan is to reintroduce the species in waterbodies where it was found prior to the construction of the Welland Canal. The 2014-2018 field surveys showed that, partly due to increased sampling effort, the number of individual stems has increased from about 20,000 to over 100,000. Seeds pods were collected for three years and, on average, 1 over 200 pods contained an assumed viable seed. Seed germination experiments, using direct seeding, cold treatment, and scarification, resulted in no seed germination. In controlled conditions, plants can survive but require to be maintained with a constant water level. Genomic analyses have been conducted on the Ontario and one Quebec populations and preliminary results suggest low polymorphism. As AWW is located at the northern limit of distribution, it is highly possible that it is affected by founder effect.

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S134 Integrated metabolic strategy: a framework for predicting the evolution of carbon-water tradeoffs within plant clades

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The fundamental tradeoff between carbon gain and water loss has long been predicted as an evolutionary driver of plant strategies across environments. Nonetheless, challenges in measuring carbon-water tradeoffs in ways that integrate over leaf lifetime have limited our understanding of the variation in and mechanistic bases of this tradeoff. Here we introduce the concept of 'integrated metabolic strategy' (IMS) to describe the ratio between carbon isotope composition ($\delta^{13}C$) and oxygen isotope composition above source water ($\Delta^{18}O$) of leaf cellulose. IMS is a measure of leaf-level conditions that integrate several mechanisms contributing to carbon gain ($\delta^{13}C$) and water loss ($\Delta^{18}O$) over leaf lifespan, with larger values reflecting higher metabolic efficiency and hence less of a tradeoff. We tested how IMS evolves among closely related yet ecologically diverse milkweed species. Larger IMS values were associated with species from dry habitats, with larger carboxylation capacity, smaller stomatal conductance and smaller leaves; smaller IMS was associated with wet habitats, smaller carboxylation capacity, larger stomatal conductance and larger leaves. The evolution of IMS was dominated by changes in species' demand for carbon more so than water conservation. IMS variation among and within species may shed light on unresolved questions relating to the evolution and ecology of plant ecophysiological strategies.

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S135. Cryopreservation and reintroduction of Hill's thistle (*Cirsum hillii*) to its natural habitat

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Hill's thistle (*Cirsum hillii*) is a perennial species native to North America which has been threatened in Canada since 2008. The aim of this study was to establish efficient protocols for cryopreservation and long-term conservation of in-vitro grown shoot tips of Hill's thistle using droplet-vitrification method, and reintroduction of regenerated plants to their natural habitat in Bruce Peninsula National Park. Shoot tips with 5-6 leaf primordia were successfully cryopreserved using a plant vitrification solution (PVS3, 50 % sucrose and 50 % glycerol; w/v) after keeping them for 20 mins in the loading solution containing 1.9 M glycerol and 0.5 M sucrose. Shoot tips were revived from the cryobank with a 96% survival efficiency. Frozen shoot tips were re-warmed in a solution of 0.8 M sucrose and cultured in the shoot multiplication medium. Currently, 200 shoot tips have been cryopreserved in the GRIPP cryobank for long-term storage. Of these cryopreserved shoot tips, 75 were recovered and fully developed into plants with well-formed roots and re-introduced into their habitat at the Bruce Peninsula National Park in the summer of 2018. The survival efficiency of these plants, evaluated after four months of field transplant, was more than 99%. Our results demonstrated that the droplet-vitrification procedure developed in this study is an efficient method of cryopreservation for long-term conservation and may also be used for recovery of other endangered plant species.

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S136. A comparison of the vascularization and morphology of floral nectaries in North American asters and goldenrods of tribe Astereae

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Representing over 25,000 species, it is of no surprise that members of Asteraceae can be found on all continents except Antarctica. Within subfamily Asteroideae, the tribe Astereae has a nearly cosmopolitan distribution, and is extremely diverse. This tribe is designated into clades based primarily on geographic regions, and the North American clade contains many common species such as asters (*Symphyotrichum* spp.) and goldenrods (*Solidago* spp.), among others. The inflorescences of these plants attract a large variety of insects, which feed on nectar produced deep within the florets by structures called nectaries. In Astereae, like most members of the family, these diminutive floral organs are of an annular shape, surrounding the base of the style atop the inferior ovary, where nectar is secreted through modified stomata. Although floral nectaries are thought to be ubiquitous in Asteraceae, they remain understudied. Here, the morphology of floral nectaries of disk and ray florets within the tribe's North American clade is being examined using scanning electron microscopy. Also, to determine how sugars are delivered into the nectary as a source for nectar production, we are using resin and paraffin sectioning to examine nectary anatomy and vascularization. The results of this work will contribute to a better phylogenetic understanding of the members within the largest tribe of this extremely diverse dicot family.

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S137. Impact of perimeter plantings on vineyard ecology

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Perimeter plantings may support local abundance of natural pest-enemies, through increased plant diversity. The impact of increased diversity within the margin of fields may be influenced by a number of landscape and management variables, and can be location or region specific. The study aims to examine the interaction between plant diversity in various types of perimeter plantings in eight vineyards of the Niagara region, and the potential impact on invertebrate communities, specifically natural pest enemies. Both plant and invertebrate communities were surveyed in the perimeter plantings and within the vineyards. Management practices were also recorded as a potential explanatory variable. Results showed that perimeter plant communities differed among vineyards and this was dependent on management. Diversity also varied within the vineyards and were not always related to the diversity in the perimeters. Plant functional diversity also varied among study sites. Through further investigation of the impact of plant species and functional diversity on invertebrate assemblages, best practices may be designed, increasing economic and environmental benefits through increasing the potential for biological pest control.

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S138. The changing flora of a UNESCO Biosphere Reserve: a phylogenetic perspective

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Global change has been occurring at unprecedented rates, with potential consequences for community composition and ecosystem functioning. Recent debate has focused on how global change will affect species richness, ecosystem functioning and the provisioning of ecosystem services. Growing scientific consensus suggests that more diverse communities support greater ecosystem functioning; however, species numbers often fluctuate over time, and ecosystem processes are shaped by both species richness and identities. In recent decades, land transformation due to suburban development on the edge of urban centres has been a significant contributor to habitat loss and biodiversity change. Comparing biological surveys conducted in the same location over time can capture changes in species numbers and identities, and allow us to quantify the impacts of habitat transformation. Here, I reveal changes in species richness, composition and phylogenetic structure between two surveys of vascular plants conducted over 50 years apart on Mont St. Hilaire, Québec, Canada. We recorded 198 more species in the more recent survey but failed to detect 70 species that had been previously documented. Introduced, non-native species comprised a significant number of species gains. Species losses were more frequently native species of special conservation status, which tended to be more evolutionary distinct than species gained. Our results show that there have been significant changes in species richness and composition over the last half-century in this protected UNESCO Biosphere Reserve.

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S139. Genetic diversity in public soybean breeding programs

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Studying crop breeding programs can provide important insight into the mechanisms of crop improvement from a historical context and identify strategies for future crop improvement. To study diversity in soybean breeding germplasm a panel of 296 pedigree-related accessions was characterized, representing decades of breeding in two programs at the University of Guelph – the Guelph Campus (maturity groups [MG] 0 and I) and the Ridgetown Campus (MG II). Field trials were carried out in multiple environments in Ontario to measure agronomic and seed composition traits. Within the soybean cultivars, significant yield increases of 17.1 $kg \cdot ha^{-1} \cdot year^{-1}$ and 15.7 $kg \cdot ha^{-1} \cdot year^{-1}$ were identified in Guelph and Ridgetown Campus programs, respectively. Protein and 100-seed weight were also significantly increasing in Ridgetown cultivars (0.76 $g \cdot kg^{-1}$ $year^{-1}$ and 0.1 $g \cdot year^{-1}$). Genotyping the accessions resulted in 76,549 SNPs. Structure analysis did not identify stratification between breeding program and historical accessions. Nucleotide diversity analysis revealed that historical accessions were the most diverse, however, breeding has significantly increased genetic diversity in recent years. Genome-wide association identified regions significantly associated with seed and agronomic traits and further haplotype analysis has uncovered trends in the genomic regions associated these traits. Comparison of the University of Guelph's breeding germplasm to the germplasm accessions in the USDA gene bank showed that only a portion of the available genetic diversity in soybean has been used for breeding at Guelph.

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S140. Identification of a potential candidate gene for the E8 maturity locus in soybean (Glycine max)

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Soybean is one of the largest sources of vegetable oil and protein in the world, and also an important legume crop to the Canadian economy. In order to expand soybean further north and west in Canada, the identification and characterization of genes involved in time of flowering and maturity are crucial. The E8 maturity locus was previously identified in our lab using classical breeding practices and a genome-wide SSR marker analysis, revealing a large, high confidence region. This region has been investigated by a functional genomics approach using a bioinformatics tool called Soybean-PIPE (Protein-Protein Interaction Prediction Engine) which predicts genome wide protein-protein interactions. To filter the ~1000 genes of the E8 region, each gene was ordered based on how many of its interacting partners (genes) were involved in development and flowering, shortlisting the candidate region down to ~25 genes. A likely candidate *Glyma.04G124300,* is annotated with FAR-RED ELONGATED HYPOCOTYLS 3 (FHY3) and FAR-RED-IMPAIRED RESPONSE 1 (FAR1) functions. These proteins are known to have multifaceted roles in light signaling and various physiological and developmental processes. Sequencing contrasting lines for E8 and e8 revealed a number of single nucleotide polymorphisms (SNPs) and insertion and deletion (INDELs), altogether suggesting that *Glyma.04G124300* is the likely candidate gene for maturity locus E8.

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S141. **Increasing soybean oil yield through targeted gene silencing and overexpression**

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Soybean oil content is lower than most oilseed crops at 16-22% of dry weight. We are developing soybean germplasm with improved oil content and seed yield through rational metabolic engineering. To do this, we are primarily targeting the enzyme acetyl-CoA carboxylase (ACCase), which catalyzes the entry point into fatty acid biosynthesis, carboxylating acetyl-CoA to malonyl-CoA. Increasing ACCase activity provides a "push" of fatty acids into FA biosynthesis, resulting in increased oil production. We have developed and are testing soybean lines 1) that incorporate a gene silencing cassette that reduces expression of a family of negative regulators of fatty acid biosynthesis called biotin/lipoyl attachment domain containing-proteins (BADCs) or 2) that overexpress a modified form of the limiting subunit of heteromeric ACCase, α-carboxyltransferase (α-CT). These strategies have demonstrably increased oil content in the model organisms *Arabidopsis thaliana* and *Camelina sativa*. We are also pursuing further strategies to improve soybean seed yield and oil content, including by repressing α-CT interactor protein (CTI), a new ACCase interactor that our lab recently discovered (Ye *et al.*, unpublished), and by boosting seed sink strength through overexpression of an engineered form of sucrose synthase (SUS). Additional novel regulators of FA biosynthesis are being identified through traditional biochemical techniques and via co-expression meta-analyses of massive RNA-seq data sets with a software tool that we are developing (RNA-see).

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S142. **A compensatory mutation in the GmNFR5α gene restores soybean-rhizobia symbiosis fitness**

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In soybean, NFR5α is a key regulator of root-hair curling in response to Nod factors (NFs) released by rhizobacteria and plays an essential role in the initiation of symbiosis. Sequencing of the entire transcribed region of NFR5α in 297 African soybean lines revealed two non-synonymous (E345K and M490V) mutations defining three alleles. Each of these exhibited a distinct phenotype, with one mutation (E345K) causing a severe decrease (35%) in symbiotic-nitrogen fixation (SNF) activity while the second mutation (M490V) partially compensated (60% restoration) for this decrease. As all three alleles are expressed equally (in terms of mRNA abundance), we hypothesized that the uncovered mutations have a structural impact on protein function. We found that the substitution E345K introduces a positively charged amino acid residue that would be expected to cause a repulsion between the NFR5α and ROP6 proteins, this interaction being essential for root-hair curling. The predicted NFR5α-ROP6 binding affinity was decreased in the E345K mutant allele while, in the double mutant (E345K + M490V), the predicted binding affinity was increased, a form of epistasis. However, although all three alleles were frequently present in wild soybeans (*G. soja*), we found evidence of purifying selection, during soybean domestication, against the unfavorable allele (E345K) in cultivated soybeans (*G. max*). This study provides fundamental insights into NFR5α and its essential role in the initiation of SNF in soybean.

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S143. Identification of differentially-expressed genes involved in seed protein content in soybean (*Glycine Max*) grown In Western Vs. Eastern Canada

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Soybean (*Glycine max*) is a legume grown for its protein-rich seeds and is the fourth largest crop in Canada. Soybean is widely grown in Eastern Canada, however, growing soybean in Western provinces has many issues mainly a lower seed protein content. Previous researches investigated the role of environmental stresses like drought and salt on gene expression, however, the role of the Western Canadian environment in regulating genes involved in economically important traits such as seed protein content is not well understood. Therefore, there is a need to develop high seed-protein varieties of soybean that are tailored for the different environments of Western/Northern Canada. Using RNA-Sequencing (transcriptome-wide approach) we will attempt to identify differentially-expressed genes involved in seed protein content in response to Western Canadian environment. RNA sequencing has been performed at an average of ~18-25 million base reads-depth for each of the 90 samples to detect genes with differential expression frequency

Our preliminary data analysis has identified a list of genes/isoforms expressed differently in Western Canada involved in seed protein content and seed oil content. Further follow-up experiments including co-expression network analysis, QTL mining for the candidate genes etc., are underway to shed more light into differential expression of the selected candidate genes and to develop allele-specific markers.

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S144. Climate and daylength influence on soybean phenology in Manitoba and Ontario

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The development of short season soybean [*Glycine max* (L.) Merr.] cultivars has allowed Manitoba soybean production to increase. In 2018, soybean occupied 19% of the province's cropland with over 1.8 million acres planted. Manitoba has longer summer days and lower average daily temperature than traditional soybean growing regions of North America. Paired field experiments in 2008-2010 were done to evaluate the influence of climate and daylength on the phenological development of ten soybean cultivars in Morden (49.2°N) and Ottawa (45.4°N). The experiment was then repeated in Carman (49.5°N) and Ottawa, in 2017 and 2018. Soybean cultivars were selected to represent maturity groups 000 to 1. Growth stages were recorded multiple times a week and paired with daily weather data. In Manitoba, longer days resulted in an 8% longer vegetative period which led to shorter reproductive and seed filling period compared to Ottawa. Furthermore, the same soybean cultivars required different amounts of crop heat units to reach critical growth stages, and ultimately harvest maturity between the two locations for all maturity groups tested. Phenology and climate data will be used to develop a growth stage predictive model for soybean in Manitoba.

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S145. Genomic and virulence differences between two sibling Clarireedia species causing dollar spot on grasses

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The most common disease of intensively managed turfgrass in the lower Great Lakes region is dollar spot caused by *Clarireedia jacksonii* on cool season grasses such as *Agrostis stolonifera* (creeping bentgrass). Recently, the causal agent of this disease on warm season grasses was split from the cool season grass pathogen and called *C. monteithiana*. The purpose of this research was to characterize these two sibling species in terms of virulence differences on different grasses and genomic differences. In this study, both species were found to be capable of attacking both cool season and warm season grasses, with *C. jacksonii* seemingly causing more disease on all hosts. Isolates that had originated from warm season grasses (all *C. monteithiana*) were ranked low-moderate for virulence on cool season grasses and the warm season *Cynodon dactylon*. Among more than 10,000 genes for each fungal species (15 *C. jacksonii*, 11 *C. monteithiana*), the average similarity within species was 95% for *C. jacksonii* and 91% for *C. monteithiana*, and between them it was 85%. This comparative genomic analysis supports the separation of these two taxa into separate species. As well, the only known case of *C. monteithiana* in Canada was on *Trichophorum cespitosum*, tufted bulrush, in Nova Scotia.

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S146. The first report of a culturable microbiome from pollinated style tissue

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The style tissue of plants has not previously been explored for a microbiome including endophytes. In plants, the style is the female reproductive tissue that transmits sperm nuclei from pollen to enable fertilization, but it is also susceptible to pathogen entry. In maize, the styles are the unusually long silks, which can be invaded by mycotoxin-producing pathogens such as *Fusarium graminearum* and *Aspergillus flavus* (causative agents of Gibberella ear rot and Aspergillus ear rot, respectiely). We hypothesized that maize genotypes that are partially resistant silk-invading pathogens house microbes in the silk to defend the entryway to the developing grain. Fourteen genotypes of maize were grown in 2017, open-pollinated, treated with and without *F. graminearum*, and the cobs were harvested at maturity. The exposed tips of the silks were discarded, and the portion of the silks protected by the husk were split into tip and base samples. Over 1000 microbes were isolated from these silks. Taxonomic identification of these strains revealed that silks do indeed host a diversity of culturable bacteria and fungi. The preliminary anti-*Fusarium* assays have discovered 3 candidate bacteria which suppress *F. graminearum* growth *in vitro*. These microbes may have coevolved with maize to protect the grain from mycotoxigenic fungi. They could potentially be used as a treatment to prevent toxins such as vomitoxin (Deoxynivalenol), zearalenone, or aflatoxins from contaminating food.

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S147. Developing a model for investigating pathogenesis by fungal hybrids using *Ustilago maydis* and *Sporisorium reilianum*

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We are developing a system to investigate fungal pathogen fusions using the model pathogen *Ustilago maydis* and a closely related species, *Sporisorium reilianum*. Both infect maize; however, *U. maydis* produces localized infections while *S. reilianum* infections are systemic. Preliminary RNA-seq analysis from the hybrid dikaryons, induced to develop on plates, revealed a transcript population more similar to *U. maydis* than to *S. reilianum*. Pathogenesis assays with the hybrid, *U. maydis*, and *S. reilianum* dikaryons were carried out in which symptoms and pathogenesis gene transcript levels, determined using species specific primers, were assessed during a time course of early disease development. The genes assessed included *U. maydis* pathogenesis related transcription factors, cell signalling proteins, and effectors as well as the orthologs of these genes in *S. reilianum*. The transcript levels were also compared to those in dikaryons formed on plates. The reduced level of disease symptoms observed for the hybrid was consistent with reductions in pathogenesis gene transcript levels. This suggests that experimentally modifying pathogenesis gene expression would improve pathogenic development of the hybrid and make it a viable model for investigating fungal hybrids and their pathogenesis. Modifying expression of select genes is underway. All results will be discussed in terms fungal hybridization and providing a framework for investigating hybrid formation and new pathogen emergence.

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S148. Genome-wide-association studies on the resistance of rutabaga accessions to *Plasmodiophora brassicae* isolates from Alberta, Canada

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Clubroot, caused by *Plasmodiophora brassicae* Wor., is a devastating soil-borne disease of *Brassica* crops worldwide. In this study, genomic regions associated with resistance to five single-spore isolates (classified as pathotypes 2F, 3H, 5I, 6M, and 8N) and 12 field isolates (classified as pathotypes 2B, 3A, 3O, 5C, 5G, 5K, 5L, 5X, 8E, 8J and 8P) were investigated using 125 *Brassica napus* L. spp. *napobrassica* (swede or rutabaga) accessions. The accessions were screened for resistance in greenhouse inoculation experiments, while genotyping was conducted with a 15K *Brassica* SNP array. The rutabaga accessions exhibited differential reactions towards the 17 isolates with 0.8 - 46.4% found to be resistant, 3.2 - 17.6% moderately resistant and 37.6 - 94.4% susceptible. About 50.0% of the 13714 SNP markers used for genotyping were included in the association studies, while those that did not meet specific filtering criteria were discarded. One-hundred and five SNPs (71 on A_{01}-A_{10} chromosomes and 34 on C genome scaffolds) were found to be significantly (p<1E-06) associated with resistance to the 17 *P. brassicae* isolates. Fifteen, nineteen and nine of SNPs associated with clubroot resistance was found respectively on A_{02}, A_{03} and A_{08}, which is consistent with the previous identification of at least eleven clubroot-resistance genes on these three chromosomes. The SNPs identified in this study will be important in the marker-assisted breeding of clubroot-resistant canola.

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S149. Molecular characterization and quantification of mycotoxins produced by Fusarium spp

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Fusaric acid is one of the important mycotoxin of the *Fusarium* species and is of concern to agro-economics. It is produced by *Fusarium oxysporum* and *Fusarium verticilloides* species. Fusaric acid aids to the pathogenecity of these strains. *Fusarium oxysporum* and *Fusarium moniliforme* are *Fusarium* wilt and Bakane disease that has been a reason to world pandemics. The vital gene involved in the production of the fusaric acid is *FUB1* gene. In order to detect the presence of *FUB1* gene in the strains available at PCMC laboratory of COMSATS Islamabad and designed the sets of primers against this conserved region of *FUB1* gene. DNA quantification was done and the concentration was observed through nano-drop with the range scale between 36.7 ng to 204ng. The *FUB1* region was amplified through PCR amplification and amplification with the product size of 375bp was achieved at 45ºC. Both *Fusarium* species i.e. *F.oxysporum* and *F.moniliforme* were detected with the presence of PKS encoding *FUB1* gene which is responsible for the synthesis of fusaric acid. This is an ongoing research towards structural remodeling of Fusaric acid into its antimicrobial effect.

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S150. Evaluation of acetolactate synthase inhibitors in Chenopodium album L. populations in Ontario

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Common lamb's-quarters (*Chenopodium album* L.) is an annual dicot plant that is highly adaptable and competitive with major global crops. Left uncontrolled, common lamb's-quarters can cause a 55-95% and 60-75% yield loss in Ontario corn and soybeans, respectively. Long seed dormancy and high fecundity make this species persistent and hard to manage. Historical uses of acetolactate synthase (ALS) inhibitors, a group of herbicides that inhibit branched-chain amino acid production, were efficacious in common lamb's-quarters control. However, common lamb's-quarters was documented to be resistant to two subclasses of ALS inhibitors in Canada. Differential response to the ALS herbicide subgroups were examined in this study. Four post-emergent ALS inhibitor classes were evaluated against two susceptible and two resistant biotypes of common lamb's-quarters at different biologically active rates. Above ground biomass was collected and dry weight was plotted as a dose response curve to generate a growth rate 50 (GR_{50}) value. Resistant biotypes displayed anywhere from 2 to 20 fold resistance to the ALS inhibitors used, suggesting cross-resistance between four of the five subclasses of this herbicide group, two more than previously documented. Thiencarbazone-methyl, a newer molecule was more effective at controlling common lamb's-quarters populations than historically used ALS inhibitors. The results suggest that an underlying mechanism or mutation is responsible for the rapid development of acetolactate synthase resistance in Ontario populations of common lamb's-quarters.

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S151. The use of cereal rye (*Secale cereale* L.) cover crops to control Canada fleabane (*Conyza canadensis* (L.) Cronq.)

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Glyphosate and group 2-resistant Canada fleabane (*Conyza canadensis* (L.) Cronq.) is a weed that is spreading rapidly and becoming a great concern for farmers across Canada and around the world. Managing herbicide-resistant Canada fleabane is proving difficult as farmers have a limited selection of management strategies available to control this weed. This is especially true for soybean growers, to whom Canada fleabane poses the greatest threat. In fields where this weed is left uncontrolled soybean yields can be decreased over 90%. The agricultural industry realizes that new management solutions are required to overcome herbicide-resistant Canada fleabane. This past summer, a trial in Delhi Ontario was conducted to evaluate if an integrated weed management strategy that included cereal rye cover crops alongside tillage and herbicide treatments improved the control of Canada fleabane. In some cases, when rye was added with one other management tactic control of Canada fleabane exceeded 90%. The results of this trial are promising, they show a new management strategy that can complement the control of Canada fleabane when paired with other management strategies, and help diversify the methods used to control this weed to prevent further resistance.

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S152. Evolution of three herbicide defence strategies: Fitness costs of glyphosate resistance, escape, and tolerance in an agricultural weed

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In response to the application of herbicides, agricultural weeds can evolve multiple defence strategies, including resistance, escape, and tolerance. Although each of these strategies are expected to incur fitness costs, such costs are often not detected. We studied the costs of resistance, escape, and tolerance to glyphosate herbicide in the agricultural weed *Amaranthus palmeri* grown in North Carolina soybean fields. To estimate fitness costs, we regressed estimates of resistance, escape, and tolerance on four components of female fitness measured in the absence of glyphosate. As to be expected if there is a cost of tolerance, increased tolerance was associated with lower fitness: more tolerant populations produced shorter inflorescences, fewer seeds per cm of inflorescence, and fewer seeds per plant. We also found some evidence for a cost of resistance: although there was no relationship between resistance and three of the fitness components measured, more resistant populations did produce shorter inflorescences. In contrast to tolerance and resistance, we found no evidence of a cost of escape: there was no relationship between escape and any component of fitness. Overall, our results suggest that the evolution of tolerance to herbicide application is more likely to be limited by fitness costs than the evolution of resistance and escape. However, more studies using other agricultural weed species are needed to determine how widespread fitness costs for glyphosate tolerance are.

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S153 Evaluating seed treatments for the management of soybean cyst nematode (*Heterodera glycines* Ichinohe) in dry bean (*Phaseolus vulgaris* L.).

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Dry bean is a high value crop grown worldwide. Canada is the fourth largest dry bean exporter, making it a producer of global importance. Soybean cyst nematode (SCN) infestation is a major cause of yield loss in soybean (*Glycine max* (L.) Merr.), and dry bean is an alternate host. In soybean, genetic resistance is the primary source for SCN control however there are no management measures currently available in dry bean. Seed treatments for soybean, including BAS576AAS, BAS79800F, BAS97474F, *Bacillus amyloliquefaciens*, *Pasteuria nishizawae*, *Bacillus firmus* and fluopyram were assessed for effects on SCN populations in black (cv. Zorro) and kidney (cv. Dynasty; Red Hawk) bean. Two field studies were conducted in 2018 on naturally infested soils near Highgate and Rodney, ON. In addition, two different growth cabinet studies, each repeated once, were completed. There was little treatment response in the field studies. In the first growth cabinet study, *B. amyloliquefaciens* and *B. firmus* reduced cysts by 24% and 10% in black bean and by 25% and 24% in kidney bean, respectively, while fluopyram only reduced cysts in Red Hawk by 25%. In the second study, fluopyram reduced cysts by 49% and 87% in Dynasty and Red Hawk, respectively while the other treatments had less effect. Results provide a better understanding of potential SCN management options for dry bean production in Ontario.

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S154. Red alder defense mechanisms against western tent caterpillar defoliation

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Red alder (*Alnus rubra*) is a tree species with high economic and ecological importance. It is subject to defoliation during unpredictable, episodic outbreaks of tent caterpillars (*Malacosoma spp*.) that result in reduced growth and mortality in severe cases. To identify *A. rubra* families or individuals that may be resistant to tent caterpillars, we evaluated the variation in tent caterpillar resistance among and within red alder populations, and investigated defense mechanisms of red alder against tent caterpillars. Bioassay feeding trials were conducted with western tent caterpillars (WTC) (*Malacosoma californicum*) on twenty red alder clones from ten provenances. Phenology and quality of red alder leaves as food for the defoliators were analyzed to determine if budburst, leaf chemical content, or physical traits are major determinants of WTC preference for red alder leaves. Seasonal variations in concentrations of oregonin and total phenolics in red alder leaves, and induction of these compounds in response to wounding were examined. Alder clones differed in percentage leaf area eaten by caterpillars and in leaf defense traits. The concentrations of foliar phenolic compounds negatively correlated with the percentage leaf area eaten by the caterpillars. Particularly, oregonin concentration above 20 % leaf dry weight consistently appeared to reduce feeding by caterpillars. The concentration of oregonin varied during the growing season and there were no significant responses of any of the measured compounds to wounding.

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S155. Investigating the basis of strigolactone perception by HYPOSENSITIVE TO LIGHT/KARRIKIN INSENSITIVE 2

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The HYPOSENSITIVE TO LIGHT/KARRIKIN INSENSITIVE 2 (HTL/KAI2) α/β hydrolases are known to play a critical role in the life cycle of parasitic plants of the genus *Striga*. These hydrolases serve as receptors for strigolactones (SLs), a class of compounds exuded by the roots of many plants. Upon perception of even minute concentrations of SLs, *Striga* seeds begin to germinate and parasitize the host. *Striga* poses a serious threat to farming in many regions of the developing world, including sub-Saharan Africa, where two thirds of arable land are estimated to be infested with *Striga* seeds. For scientists seeking to develop strategies to combat *Striga* infestation, the basis of the remarkable sensitivity of Striga's SL receptors represents a promising area of study. To this end, we have produced a series of mutant variants of the *Arabidopsis thaliana* homolog of HTL/KAI2, which is only weakly responsive to SL. By substituting certain key amino acids in the protein's active site, we have created a receptor conferring heightened *Arabidopsis* germination under inhibitory conditions, which is further enhanced by the addition of SL. Additional study of this mutant receptor may offer insight into the biochemical basis of *Striga'*s SL sensitivity.

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S156. Arabidopsis clade I TGACG-motif binding basic leucine-zipper transcription factors mediate BLADE-ON-PETIOLE-dependent activities in development and defense

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Lateral organs formed by the shoot apical meristem (SAM) are separated from surrounding stem cells by low-growth regions called boundaries. Boundaries also provide axillary meristems and regulate abscission to determine plant architecture. *Arabidopsis thaliana* (Arabidopsis) *BLADE-ON-PETIOLE1* and *2* (*BOP1/BOP2*) represent a class of genes important for boundary patterning in land plants. Members of this family encode transcriptional co-regulators that interact with TGACG-motif binding (TGA) basic leucine-zipper (bZIP) transcription factors for recruitment to DNA. Here, we show that clade I TGA bZIP transcription factors TGA1 and TGA4, previously associated with plant defense, are essential cofactors in BOP-dependent regulation of plant development. TGA1 and TGA4 are expressed at organ boundaries and function in the same genetic pathways as BOP1/BOP2 required for SAM maintenance, flowering, and inflorescence architecture. Further, we show that TGA1/TGA4 form complexes with BOP1/BOP2 *in vivo*, contributing to activation of *ARABIDOPSIS THALIANA HOMEOBOX GENE1*, which is needed for boundary establishment. Transcript profiling and chromatin immunoprecipitation assays were used to identify additional co-regulated target genes of TGA1/TGA4 and BOP1/BOP2 involved in plant immunity. This work reveals a role for clade I TGAs at boundaries and hints at possible additional roles for this module in plant defense.

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S157. A role for receptor kinases in regulating compatible pollen responses in the Brassicaceae stigma

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Brassicaceae flowers have evolved mechanisms to recognize their pollen grains as providing nutrients to the wrong mating partner would be disadvantageous. The dry stigmas lack surface secretion which normally enables automatic pollen germination, and this allows the stigma to tightly regulate pollen acceptance following pollen-stigma contact. The cellular processes in the stigma that facilitate pollen acceptance are becoming more clearly defined, but the initial upstream signalling components are yet to be identified. Previous work in the Goring lab identified a set of receptor-like cytoplasmic kinases, BRASSIKINS (BKNs), as candidate stigmatic signalling proteins in this pathway. We hypothesize that the BKNs mediate signal transduction by forming a complex with membrane-bound receptor kinases to facilitate pollen acceptance. To address this hypothesis, the BKNs were used to screen for putative protein interactors by testing pairwise combinations with kinase domains from stigma-expressed receptor kinases in the yeast two-hybrid system. Further characterization of the putative interactors identified two distinct clusters of receptor kinases, and so far, the loss-of-function mutants show mild compatible pollen response defects. Current work is focused on creating additional mutant combinations and testing whether these receptor kinases from different Brassicaceae species can rescue the mutant stigma phenotype. Overall, we aim to better understand how these stigma-expressed receptor kinases facilitate the early stages of compatible pollen acceptance and whether they represent a conserved signalling module across the Brassicaceae.

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S158. The E3 ubiquitin ligase XERICO modulates stomatal development in *Arabidopsis thaliana*

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Plants must alter their developmental module to effectively respond to a host of environmental stresses for survival. Stomata, which are epidermal pores that control gas and water exchange, are pivotal for ensuring plant survival and growth under stress. Consequently, stomatal aperture, density and patterning are tightly regulated by developmental and stress related signals, to ensure optimal gas and water exchange between plants and their environment. *Arabidopsis* XERICO (XER) is a putative RING E3 ubiquitin ligase that increases abscisic acid (ABA) levels and promotes drought tolerance when overexpressed. Analysis of *xer* T-DNA insertion and CRISPR-Cas9 mutants revealed that XER may function in regulating stomatal development. Therefore, I hypothesized that XER promotes drought tolerance by regulating stomatal development and distribution. To understand XER's role in development and stress response, a high throughput yeast-two-hybrid (Y2H) screen was conducted against a library of ABA responsive genes. A glycosyltransferase (GT) implicated in cell wall synthesis was shown to interact with XER in Y2H and *in planta*. Subcellular localization studies and phenotypic analysis of T-DNA insertion lines revealed the localization of the XER-GT interaction and demonstrated that GT also functions in stomatal development. We propose that XER may regulate stomatal development by affecting cell wall function, which may influence plant survival under stress.

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S159. **A mechanical feedback loop regulates morphogenesis of pavement cell shapes in Arabidopsis**

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Cotyledon surfaces are covered by pavement cells (PCs) with alternating lobe outgrowths and indenting neck regions. It is postulated that cellulose microfibrils alignment mediated by microtubules (MTs) determines the final shape of PCs by either restraining or promoting PC growth. Recent work demonstrated that lobes form in order to reduce the biomechanical stress of the PC; however, the relationship between MTs and biomechanical stress is unknown. Here, we demonstrate how MT ordering and biomechanical stress leads to PC morphogenesis. Upon dissecting cotyledons from the seed and imaging PCs for 96 hours post-dissection (hpd), we noted varying degrees of MT ordering over time. At 48 hpd, aligned MT arrays were highly correlated with necks, coinciding with peak PC growth rates and increased lobe formation, while this correlation was reduced at necks and earlier/later timepoints. Mutants lacking the MT-regulators, CLASP and KATANIN, had enhanced and reduced PC shape complexity, respectively, relative to wild-type PCs. While clasp PCs had increased MT bundling at necks at all timepoints, MT bundling at necks were absent in katanin PCs. In silico quantification of biophysical stress revealed that mutant PCs have increased mechanical stress, suggesting that MT ordering is essential for proper lobe formation thereby modulating mechanical stress. Taken together, we postulate a feedback model where MT ordering regulates growth and lobe formation which subsequently feedbacks in regulating mechanical forces and MT organization.

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S160 **Molecules in Action: Quantum dot enabled studies of plant growth regulation**

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Quantum dots (QD) are fluorescent and UV active nanoparticles which can be conjugated to diverse molecules of interest thereby allowing for direct visualization and single molecule tracking with an appropriate microscope. We developed a new technique to conjugate QD to plant growth regulators (PGRs) for in vivo visualization of molecules in action. In proof of concept experiments, we used QD conjugated indoleamines, melatonin (N-acetyl-5-methoxytryptamine) and serotonin (5-hydroxytryptamine) and followed the movement of the PGRs in living tissues. We were able to determine molecular location, transport patterns and redistribution in response to thermal stress in the model medicinal plant species, *Hypericum perforatum*(L.). In subsequent experiments, we also conjugated QD to other PGRs including auxins and cytokinins and visualized the action of the molecules in classic experiments. Our experiments provide proof of concept of the applicability and utility of QD technologies for studies of plant growth and development. In the future, studies of QD-labeled PGRs have the potential to directly demonstrate mechanisms of action and can greatly improve our understanding of the mechanisms, transport and localization of both traditional and emerging plant signaling molecules.

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S161. Family Ties: the expression of AROGENATE DEHYDRATASES

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Phenylalanine (Phe) is a precursor to many specialized metabolites in plants, including lignin and flavonoids. The last step of Phe synthesis is a decarboxylation/dehydration reaction performed by AROGENATE DEHYDRATASES (ADTs) named ADT1-ADT6 in Arabidopsis thaliana. In silico analyses of publicly available ADT expression data suggest differential tissue-specific ADT expression patterns. Unsurprisingly, we were able to identify individual compositions of promoter motifs associated with endogenous and exogenous responses for each ADT. To confirm and add more resolution to these in silico data, in vivo experiments using each ADT promoter were performed. Either the intergenic region or up to approximately 1 kb upstream of the translational start site was cloned into an EGFP/GUS expression vector and stably transformed into wild-type Arabidopsis. For ADTs with introns, the start of the promoter to the end of the first intron was also cloned. Expression of reporter genes under standard growth conditions was determined by confocal microscopy (EGFP) or light microscopy (GUS), for each ADT across all tissues and stages of development. Already, initial analyses show that each ADT has a unique expression pattern, and we propose that they are linked to metabolomic requirements of specific tissues. Most surprisingly for essential enzymes, not a single ADT is constitutively expressed. In the future, our catalogue of standard ADT expression patterns will be compared to those of plants grown under stress growth conditions.

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S162. Magic blue light: A versatile mediator of plant elongation

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It's commonly stated that "blue" light causes more compact plants than red light (R) in plant lighting related literatures. This is challenged by our recent studies on many species using light emitting diodes in growth chambers. We found that pure blue light (B), compared to R, promoted plant elongation at different growth stages under light intensities of 20–650 $\mu mol \cdot m^{-2} \cdot s^{-1}$, and photoperiods of either 24 or 16 h. However, unpure blue light, BR, by mixing B with 6% or 10% R, showed a similar or greater inhibition effect relative to R. Unpure blue light, BRF, by adding low-level far-red light (FR) to BR (with R/FR = 1), reversed the inhibition effect of BR, and showed a similar or greater promotion effect relative to B. Phytochrome photostationary state (PPS) values were around 0.89, 0.69, 0.60, and 0.50 for R, BR, BRF, and B, respectively. With the decreasing PPS, the plant elongation under "blue" (pure and unpure) light increased, and gradually became saturated once the PPS < 0.60. Furthermore, unpure blue light by mixing B with a low-level FR, UV-B, UV-A, or Green light resulted in PPS < 0.60, and showed a promotion effect similar to B. Therefore, our studies demonstrate that blue-light-mediated plant elongation is related to phytochrome activity; there is a promotion effect under lower PPS, but an inhibition effect under higher PPS.

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S163. Adapted crops for the low light indoor environment: a concept for year round sustainable gardening in the home with potential for commercial greenhouse production

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Commercial greenhouses can offset power costs by either growing crops which are low light adapted and do not require high irradiance conditions, or through double cropping. Vegetable and fruit cultivars have been traditionally bred and selected under high light conditions in the greenhouse or under full sun conditions in the field. Nevertheless, there appears to be a large genetic variation for adaptation to low irradiance conditions within existing commercial vegetable cultivars. Over 55 crops/cultivars were screened for potential commercial greenhouse production. Several crops show promise including a cool temperature adapted *Brassica japonica* cv. 'Kyoto Mizuna' examined in a commercial greenhouse environment. Furthermore, the limiting factor to producing plants year round indoors on home and school windowsills is not heat, but light. After 38 years of breeding, a Low Light Tolerant lemon and lime were developed: 'First Canadian' lemon and 'First Canadian Golden' lime, producing up to 12 – 15 commercial size lemon fruit/plant in a 15-cm pot on the windowsill. Microgreens are also an important first step introducing growing and consuming fresh greens to children in schools. Collectively, these plants have potential to introduce children to the idea of growing and eating tasty horticulture crops year-round since plants can be produced indoors in the classrooms during the school term.

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S164. Cultural and genetic approaches for improving the response of greenhouse vegetables to extended photoperiod and supplemental lighting

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The three major greenhouse vegetable crops, including tomatoes, peppers and cucumbers, all show some susceptibility to photoperiodic injury (PI). PI is characterized by chlorosis of vegetative tissues when grown in extended photoperiods or non-24 h light-dark cycles. This phenomenon can limit the efficiency in which greenhouse vegetable crops respond to supplemental lighting (SL) during the winter months, and particularly when photoperiod extension is required to make SL economically feasible, such as in Ontario. We have shown that PI in greenhouse vegetable crops is linked to nitrate uptake and assimilation and the circadian clock. By establishing the physiological basis for PI in greenhouse crops, we have developed cultural and genetic approaches to reduce PI and improve the response to supplemental lighting. Three cultural methods that will be discussed include the use of: (1) specific time-of-day patterns of SL; (2) time-of-fertigation techniques and altered nitrate fertilization; and (3) altered light spectrum. Some of these approaches have been tested in commercial greenhouse operations in Leamington, ON, including tomato and cucumber operations. Variation does exist in the severity of PI among existing cultivars of greenhouse and field tomato and greenhouse cucumber, and our group has shown that two genes affect PI in tomato. The potential and limitations in breeding greenhouse vegetables that show an improved response to supplemental lighting will also be discussed.

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S165. Comparison of a supplemental lighting control algorithm and conventional threshold control for greenhouse tomato production

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Recent advances in supplemental lighting technology such as light-emitting diodes (LEDs) and integrated control systems have the potential for significant yield increases and energy savings in vine crop production. Beyond the inherent energy savings LEDs have over HPS lighting systems in terms of efficacy (µmol/joule), LEDs can be implemented into lighting control systems that adjust output based on ambient light intensity in order to meet a specified daily light integral (DLI). The current standard for supplemental lighting control is the threshold method, where lighting is on or off based on measured outdoor radiation and a proving or refractory period, required to preserve HPS bulb life. Because LEDs can be powered on and off instantaneously as well as dimmed, there is tremendous potential to reduce over- and under-lighting to meet a target DLI and significantly improve production efficiency.

We compared the performance of a DLI control algorithm that adjusts LED fixture output intensity based on ambient conditions to meet a preset DLI to a conventional threshold program that turns LED fixtures on or off based on global radiation recorded by an outdoor pyranometer for winter production of high-wire tomatoes. Despite the threshold control consuming approximately 90% more energy compared to the DLI control method, yields were not significantly different suggesting current supplemental lighting strategies need to be re-examined in terms of set points and delivery methods.

Brian Poel (bpoel@lumigrow.com)

S166. Evaluating the impact of Inter-canopy LED Lighting on the production of Bush Beans within a Controlled Environment

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The challenge of high-density controlled environment agriculture is to maintain homogenous environment conditions throughout the plant's life cycle. As the crop matures, a dense canopy of leaves can challenge uniform light distribution. The upper leaves attenuate incident light from the primary overhead source and as a result, the lower leaves receive less light and photosynthesis in these leaves is reduced. Intercanopy LED lighting can supplement the amount of light available to lower canopy leaves, thereby maintaining photosynthetic activity and increasing net photosynthetic rate overall. Intercanopy LED lighting has been shown to increase yield of greenhouse vine crops such as tomato and cucumber. To date, the effect on LED intercanopy lighting has not been tested on bush bean (Phaseolus spp). This research project compared the productivity (fruit/shoot/agronomics) of bush bean grown under fluorescent lighting (300 µmol m^{-2} s^{-1}) with or without the presence of additional LED intercanopy lighting in a controlled environment growth chamber. Preliminary results of this study will be discussed during the presentation.

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S167. Canopy growth manipulation and adventitious root development in Kalanchoe blossfeldiana cuttings using targeted LED lighting spectra

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Light is a crucial environmental component needed in production of all crops grown in the commercial greenhouse industry and field environment alike. LED lighting is becoming a more prevalent technology over traditional irradiation sources due to its growing technical advances and impact on canopy crop production of ornamentals such as Kalanchoe blossfeldiana. Manipulating the lighting environment can lead to improved shoot growth and expedited production cycles. More specifically, light qualities involving high Red: Far-red ratios are shown to signal stem branching and cell elongation, whereas blue and UV light spectra are shown to decrease cell elongation, creating shorter plant morphology. The canopy environment is known to be heavily influenced by light quality, thereby manipulations of this factor can affect canopy development. Cuttings were established in a growth chamber equipped with 6 separate water cooled tuneable LED fixtures. Cuttings of a vigorous rooting variety (Ann) and slow rooting variety (Ingrid) were planted in a peat-based substrate and grown under an 18- hour photoperiod with a photosynthetic photon flux density of 300 µmol m−2 s−1. Four red: blue: white light ratios were evaluated: (1) 90R: 5B: 5W; (2) 70R: 25B: 5W; (3) 40R: 55B: 5W; and (4) 20R: 75B: 5W. Results for cultivar Ann and Ingrid showed no significant differences in canopy growth under the four light regimes.

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S168. Indoor *Cannabis sativa* L. production: current practices and research directions

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Cannabis sativa L. (cannabis) was legalized in Canada for medicinal and recreational use in 2002 and 2018, respectively. Since the legalizations, the number of licensed producers has been increasing rapidly. As of today, there are 177 cultivators, processors and sellers that hold a license issued by Health Canada under the Cannabis Regulations. Most of the licensed producers are expanding their growing facilities to meet the increasing demand of cannabis products. Based on a recent Deloitte report, it is estimated that the sales of recreational cannabis alone can have a potential annual economic impact as high as $23 billion in Canada. Currently, almost all legal cannabis in Canada is produced in controlled environments, such as greenhouses and warehouse type facilities where artificial lighting is used as the sole light source. To produce cannabis with high floral yield and quality (e.g., high and consistent cannabinoid and terpene concentrations), it is essential to understand how different environmental factors, such as lighting, carbon dioxide (CO_2), air temperature, and root zone environment affect the yield and quality of cannabis. This talk will provide an overview of the current commercial practices and research achievements in the aforementioned areas, as well as the knowledge gaps and challenges currently facing this industry. The discussions on these subjects will provide future research directions for the controlled environment plant production research community.

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S169. Variation in rootzone environment influences growth and yield of drug-type cannabis cultivars during the flowering stage

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Cannabis cultivators use diverse production systems and rootzone management strategies in indoor cannabis production. To investigate the impact of rootzone environments on the growth and yield of two drug-producing cultivars, three rootzone environments were applied to 60 cannabis plants during the flowering stage, using a randomized block design. The rootzone environments tested were: 1) an 11-litre pot containing a peat based growing substrate, top fertigated with a synthetic fertilizer solution ("hydroponic"); 2) an 11-litre pot containing a peat based growing substrate, top fertigated with aquaculture effluent solution ("aquaculture"); and 3) a 3-litre pot containing a custom made growing substrate, sub-irrigated with aquaculture effluent solution ("aquaponics"). The experiment was conducted at Green Relief, a licensed indoor cannabis facility in Puslinch Ontario. Cultivar 'Nordle' grown via hydroponic rootzone had 41% and 116% higher floral biomass (at 13% moisture content) than plants grown with aquaculture and aquaponics, respectively. Similarly, cultivar 'Sensistar' grown with hydroponics had 61% higher floral biomass than plants grown with the other two rootzones. In contrast, however, Nordle plants grown with aquaponics had significantly higher floral tissue concentrations of total THC and CBD compared to the other two rootzones investigated. Leaf tissue and rootzone nutrient analyses suggests that differences in nutrient supply was a primary factor causing the observed differences within cultivars. Differences in floral yield across cultivars can be attributed to phenotypic differences.

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S170. Diseases that can devastate *Cannabis sativa* production – bud rots, powdery mildew and root and crown rots.

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Cannabis (*Cannabis sativa* L.) is cultivated by licensed producers in Canada under greenhouse and indoor environments. With the increasingly large-scale production of cannabis, a number of pathogens and molds that reduce yield and quality have been identified within several facilities and are described here. Isolations were performed from diseased tissues and colonies were identified using PCR of the ITS1-5.8S-ITS2 region. Botrytis bud rot (*Botrytis cinerea*) affected inflorescences at the flowering stage and caused a post-harvest disease. Powdery mildew (*Golovinomyces chicoracearum*) infected the foliage and inflorescences. Root and crown rots on stock (mother) plants and on vegetative and flowering plants were caused by several species of *Fusarium* and *Pythium*, including *Fusarium oxysporum, F. solani, F. proliferatum, F. brachygibbosum, Pythium dissotocum, P. myriotylum, P. ultimum* and *P. aphanidermatum*. Symptoms included root browning, discoloration of crown and pith tissues, stunting and yellowing, and in some instances, plant death. The most prevalent pathogens were *F. oxysporum* and *P. myriotylum*, particularly on plants in the vegetative growth phase. Differences in disease severity were observed between cannabis strains (genotypes) for bud rot and powdery mildew, but not for root and crown rots. The epidemiology and management of these diseases will be discussed. They include sanitation practices, management of water regimes, application of biological control agents, and selection of cannabis strains.

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S171. Effect of methyl jasmonate on terpene/cannabinoid biosynthesis and suppression of gray mold in *Cannabis sativa* L.

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Supplying cannabis to a legalized market represents a major economic opportunity. Indeed, the retail market value in Canada is expected to reach $8.7 billion annually. However, cannabis being one of the most widely used illicit drugs excluded it from research programs that have led to massive increases in yields in other crops. Supply shortages are plaguing the industry, and cultivation often faces important phytosanitary problems due to diseases like powdery mildew and gray mold (*Botrytis cinerea* Pers.). Cannabinoids and terpenes are important secondary metabolites responsible for the psychoactive/medicinal effects and aromas of cannabis, respectively. As in other plants, terpenes (and possibly cannabinoids) also exhibit essential roles in defense against biotic and abiotic stresses. Methyl jasmonate (MeJA) is an endogenous volatile compound involved in plant defense and developmental pathways. Here we used RT-qPCR and GC-MS to explore whether MeJA directly impacts the biosynthesis of terpenes and cannabinoids. Results suggest that certain genes involved in their biosynthesis, including terpene or cannabinoid synthases, are induced following treatments with MeJA. We also aimed to determine whether MeJA induces resistance against *B. cinerea* and reduce disease incidence in cannabis. Further work is needed to confirm our results, but they suggest that application of MeJA could play two beneficial roles in cannabis cultivation: a control measure against *B. cinerea* and a catalyst to increase the production of cannabinoids and terpenes.

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S172. Increased resistance to potato common scab is associated with changes in the tuber periderm

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Potato common scab is a major disease affecting potato fields around the world. The disease is characterized by the formation of scab-like corky lesions on developing tubers. These lesions are mainly caused by *Streptomyces scabies* which synthesizes during the infection process the essential toxin thaxtomin A (TA). TA production is stimulated by suberin and cellobiose. Suberin is a component of the potato periderm where it plays a role in the protection of tubers against the invasion of microorganisms. In our laboratory, potato calli of the potato variety Yukon Gold were habituated to increasing concentrations of TA. Some of the somaclones regenerated from TA-habituated calli were more resistant to common scab. To identify the changes that contribute to the increased resistance to common scab in the tubers of these somaclones, we analysed the organisation of their periderm using fluorescence microscopy. The tuber phellem from resistant somaclones contained more distorted cells and a higher number of cell layers than the phellem from the original variety. Expression of genes involved in suberin synthesis and defense responses was analysed by RT-qPCR. Several of those genes showed a higher expression in the tubers from resistant somaclones compared to those from the original variety. We will discuss how these changes can contribute to the increased resistance to common scab in the TA-habituated somaclones.

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S173. Implication of major tuber flesh proteins in common scab resistance in Russet Burbank somaclonal variant adapted to thaxtomin A

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Potato common scab is a widely spread disease of potato tubers inducing significant economic losses. Mechanism of potato resistance to common scab is not understood. Common scab is caused by the actinobacterium *Streptomyces scabies*. Pathogenicity of *S. scabies* depends on its ability to produce a phytotoxin thaxtomin A (TA). TA mode of action remains unknown although it was described as a cellulose biosynthesis inhibitor that induces programmed cell death. The somaclone variant RB9, which was produced by the adaptation of the Russet Burbank cultivar to TA, is more resistant to common scab. LC-MS/MS analysis showed that increased resistance was associated with changes in the RB9 tuber proteome. Changes included increased accumulation of major tuber proteins: storage proteins (patatins), proteins implicated in lipid metabolism (9-lipoxygenases, 9-LOX) and serine protease inhibitors (Kunitz-type, KTI). Gene expression analysis (qPCR) showed significantly higher expression of the KTI coding DrTI-like gene in RB9. Higher abundance of patatin in RB9 was associated with enhanced expression of PATB1 gene and of different RB9 patatin coding loci. 9-LOX protein accumulation was not associated with increased 9-LOX gene expression, suggesting regulation at the protein level. During infection of RB and RB9 young developing tubers, we detected a significant decrease in patatin and KTI abundance in the parental cultivar comparing to RB9. At the same time, 9-LOX was highly accumulated in infected RB and RB9 tubers.

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S174. Biosynthesis of the thaxtomin A phytotoxin in the potato common scab pathogen Streptomyces scabies: role of the MbtH-like protein TxtH

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Common scab (CS) is a disease that negatively impacts the quality and market value of seed, processing and table stock potatoes. The disease is caused by *Streptomyces* soil bacteria, of which *Streptomyces scabies* is the first described and best characterized pathogenic species. The principle pathogenicity determinant produced by *S. scabies* is a phytotoxic metabolite called thaxtomin A (ThxA), which functions as a plant cellulose biosynthesis inhibitor. The enzymes requires for the biosynthesis of ThxA are all encoded within a biosynthetic gene cluster in *S. scabies*. In addition, the gene cluster encodes a small protein called TxtH, which belongs to the MbtH-like protein (MLP) family. The objective of this study was to investigate the role of TxtH in the biosynthesis of ThxA in *S. scabies*. Biochemical studies in *Escherichia coli* revealed that TxtH functions as a chaperone that is required for the proper function of the megasynthase enzymes which synthesize the ThxA backbone. Deletion of the *txtH* gene significantly reduced ThxA production in *S. scabies*, while deletion of two other MLP-encoding genes in the *S. scabies* genome abolished ThxA production completely. The *txtH* single mutant and the MLP triple mutant were reduced in virulence in a potato tuber bioassay compared to the wild-type strain. Overall, the results our study demonstrate that TxtH plays a key role in ThxA biosynthesis and plant pathogenicity in *S. scabies*.

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S175. Transcription regulatory map reveals important transcription factors regulating late blight resistance, leading to a higher accumulation of resistance related metabolites

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Late blight of potato caused by *Phytophthora infestans* causes up to 40% yield loss worldwide. Resistance to late blight is either qualitative or quantitative. Even though quantitative resistance is durable, its regulation is not well deciphered, which limits its applications. Based on RNA seq and semi-targeted metabolomics we identified several Resistance Related Induced (RRI) genes and metabolites upon pathogen inoculation, in resistant genotype (Libertas) compared to susceptible genotype (AG704.10). A total of 281 resistance related constitutive (RRC) and 160 RRI metabolites were detected, which belonged to different chemical groups. RNAseq and *de novo* assembly identified 611 RRI genes which were further categorized based on their biological functions. Promoter sequences of these RRI genes were identified, using in house script, which was used for transcription factor (TF) enrichment study to identify regulatory transcription factors. 134 transcription factors ($p < 0.05$) were found to have binding sites in the promoters of RRI genes. Among these, *bHLH66, MYB61, NAC56, WRKY51* and *MYB like HHO2* transcription factors were upregulated after pathogen inoculation. These TFs were further mapped to downstream genes, and these were mainly the resistance related metabolite biosynthetic genes. The RRI genes identified here can be exploited to enhance disease resistance in susceptible cultivars, following further characterization of their resistance functions.

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S176. Tuber-specific expression of a heterologous host defense peptide reduces post-harvest diseases in potato

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Development of control strategies to fight plant diseases effectively and with minimal impact on the environment is one of the greatest challenges for food security in this century. In the present study, evaluation of the spatiotemporal activities of various plant promoters in transgenic hosts using the *GUS* reporter gene system revealed that the *PmBiPPro1* promoter of the luminal binding protein (BiP) from Douglas-fir exhibited organ-specific, wound-inducible and developmental patterns of activity, with particularly high transcriptional activity in potato tubers. The latter suggests that this promoter likely contains important cis element(s) that interact with tuber-specific transcription factors required for promoter activation in the storage organs. The organ-specific activity of the *PmBiPPro1* promoter was examined for targeted expression of MsrA2 peptide in potato tubers. MsrA2 is a small membrane-active host defense peptide, containing the full-length amino acid sequence of naturally occurring dermaseptin B1 (31 residues) and exhibiting high antimicrobial activity against phytopathogenic fungi and bacteria. The nucleotide sequence encoding MsrA2 was transcriptionally fused to the *PmBiPPro1* promoter, and introduced into potato via *Agrobacterium*-mediated transformation. Western blot analysis showed high level of MsrA2 accumulation in tubers of transgenic plants. Moreover, *in vitro* bioassays revealed that the expression level of the MsrA2 peptide in tubers was sufficient to confer resistance to bacterial soft rot and Fusarium dry rot, two major potato diseases causing post-harvest losses of potatoes.

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S177. The implications of drought stress on the nutritional quality of potato

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Potato is among one of the most important food crops, yet maintaining plant productivity in this drought sensitive crop has become a challenge. Competition for scarce water resources and the continued effects of global warming exacerbate current constraints on crop production. While plant response to drought in above ground tissues and the corresponding effects on yield have been well documented, the regulatory cascades and the metabolic consequences in developing tubers have been largely unexplored. Using the commercial Canadian cultivar 'Vigor', plants were subjected to a drought treatment under high-tunnels in the field with demonstrated effects on plant physiology, as seen by a 4°C increase in canopy temperature and a 44% decrease in leaf *F*v/*F*m ratios when compared to the well-watered control. Tubers at the tuber bulking phase were sampled for RNAseq and metabolite analysis. 2600 genes and 5232 transcripts were differentially expressed by at least four-fold in drought-stressed potato tubers, with approximately 71–75 % of those being downregulated. A further 229 smRNA were implicated in gene regulation during drought. The comparison of protein homologues between *Solanum tuberosum* and *Arabidopsis thaliana* indicates that downregulated genes are associated with an array of metabolic pathways including phenylpropanoid, flavonoid, carotenoid, and amino acid biosynthesis. This suggests that there are both yield and dietary implications to drought stress occurring during the potato tuber bulking phase in sensitive cultivars.

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S178. Whole genome comparisons of commercial *Phaseolus vulgaris* varieties and interspecific hybrids

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Among *Phaseolus* species, *Phaseolus vulgaris* is the most widely cultivated member for direct human consumption. The dry bean breeding program at the University of Guelph has produced a wide range of varieties, including those derived from interspecific hybridization with *Phaseolus acutifolius* (PI440795 and PI319443), which brought over strong genetic resistance to CBB caused by *Xanthomonas spp*. OAC-Rex was the first commercial variety released to contain this resistant trait in 2001, and its genome was sequenced in 2015, with a formal V1.0 release occurring in 2019. As OAC-Rex has been extensively used in the bean breeding program to date, this has created an opportunity to leverage new bioinformatics techniques and directly compare the genetic diversity present in the population. A total of 10 dry bean varieties were each crossed with a single parental line, Ex Rico, and the genomes of each of these parental lines are being fully sequenced using a combination of PacBio, and Illumina sequencing platforms. Here we describe whole genome comparisons between the preliminary assemblies of Ex Rico, Rexeter, and Mist, along with the previously released *P. vulgaris* genomes, G19833, OAC-Rex, and Bat93. Overall gene order and orientation is highly conserved across all sequenced lines, and a sliding window analysis has shown that the individual pedigrees of these varieties can be distinguished, including conserved regions that are derived from interspecific hybridization.

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S179. Cultivar classification, major genes, and chromosomal position explain the distribution of genetic diversity in a sample of Canadian bread wheat

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Understanding the distribution of genetic diversity and linkage disequilibrium within Canadian bread wheat illuminates past effects of selection and enables an increased rate of improvement. Here, population structure and genetic diversity of a sample of Canadian bread wheat was investigated in a sample of 365 cultivars using 14,074 SNPs. Cultivars were classified by year of release, phenotypic group, market class, and breeding program. All classifications partitioned genetic diversity; phenotype captured the most at 22.7% with the other factors dividing more within phenotypes. A single dominant allele is sufficient to switch type for three phenotypic traits. Two of these, however, have homoeologous genes with dominant alleles leading to genetically heterogenous but phenotypically similar cultivars. Despite this, markers linked to a number of these genes are differentiated between contrasting trait groups. Finally, recombination is repressed in large chromosomal regions proximal to centromeres potentially resulting in highly reduced variation due to drift in effectively small breeding populations. Within chromosomes 1A, 2A, 6A, 6B and 7A large haplotypes 100s of Mb long were observed proximal to the centromeres. We potentially observed similar large haplotypes on 3A, 3B, 4A, 4B, 5A, 5B, and 7B based on sparse polymorphic markers usually in high LD. In conclusion, although attributes and major genes affect allelic diversity, we view that these very large, non-recombining, haplotypes is a major stumbling block for generating diversity within Canadian bread wheat.

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S180. Tackling pre-harvest sprouting in small grain cereals

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Pre-harvest sprouting (PHS) is the premature germination of grains while head is still maturing in the field. Breeding PHS resistance is challenging due to genetic complexity and phenotyping difficulties. We have recently discovered specific set of *Argonaute (AGO)* genes, which associates with PHS resistance in both wheat and barley. This novel *AGO/* PHS association could lead to provide efficient and reliable biomarkers for the development and selection of PHS tolerant wheat and barley varieties. Moreover, the *AGO4_9* is a member of RNA-directed DNA methylation (RdDM) pathway, which is involved in DNA methylation process. The current efforts are, first, identifying the RdDM pathway gene families and other genes associated with germination process such as pullulanases in small grain cereals. Data indicates that barley has 14 *AGO* related genes. In addition, 17 *Pol* subunit1 like, 10 methyltransferase, 7 *RDR*, 5 *DCL*, 1 pullulunase, 2 pullulunase inhibitors and only one *HEN1* genes were identified. Their spatiotemporal expression of key genes was also studied in barley. Efforts are being made to functionally characterize sprouting specific *AGO4_9* and pullulunase genes in barley. These results will allow us to devise new tools for improvement in grain quality and quantity, nutritional value and farm economy of cereal grains production in Canada.

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S181. Identification of founding accessions and patterns of relatedness and inbreeding derived from historical pedigree data in a white clover (*Trifolium repens* L.) and red clover (*Trifolium pratense* L.) germplasm collection in New Zealand.

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White clover (*Trifolium repens*) is the most common pasture legume in New Zealand, where it is usually grown with perennial ryegrass in swards and grazed *in situ*. Red clover (*Trifolium pratense*) is grown worldwide as a fodder crop and used as silage and hay. In a grazing system it is often mixed with white clover in pasture mixes. The objectives of this study were to identify patterns in *Trifolium* breeding programs and to produce an overview of these patterns across time. A pedigree map was used to visualise, and cluster analysis was used to describe population structure and genetic diversity in white and red clover germplasm stored in the Margot Forde Germplasm Centre in Palmerston North, New Zealand. Relatedness and inbreeding coefficients were derived for both species. The overall relatedness was k=0.002 and overall inbreeding was 0.39% for white clover, and k=0.005 and 0.56% for red clover, respectively. Relatedness and inbreeding coefficients revealed distinct germplasm pools formed across time that are of interest to pre-breeding efforts. Founding and influencing accessions were identified. A total of 34 founding accessions were found in the germplasm database from the year 1941, with three founders having distinct lineages with highly influential parents (C40, C43 and C63). The 'Type 1' class phenotype had a strong impact on the identification of influencing accessions, forming three sub-population clusters.

Lucy Egan (lucy.egan@agresearch.co.nz)

S182. Early flowering epi-mutants of 'Royal' flax.

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Canada is the largest producer and exporter of flaxseed and seeks to improve yields through greater adaptation to prairie climatic conditions. Target traits include cultivars that flower early regardless of day length and result in earlier maturity. Treatment with 5-azacytidine (which alters DNA methylation patterns) resulted in earlier flowering variants (RE) in the oilseed variety Royal (RC) that is stably inherited through meiosis. Short day/long day transfer studies demonstrate the RE lines are significantly less photosensitive than their progenitor RC line and commercial flax cultivars. Gene expression analysis in leaves indicates the RE lines express *FLOWERING LOCUS T* (FT) earlier and at higher levels than RC lines despite sharing the same genotype. To understand factors controlling the new variation, flowering time was scored in a population of recombinant inbred lines derived from a cross between the RC/RE2 parents. Whole genome resequencing and bisulfite sequencing of the parents and early and late flowering bulks revealed quantitative trait loci (QTL) and differentially methylated regions associated with the variation, with the largest QTL detected on chromosome 12. Transcriptome examination (RNASeq) in the RC and RE2 parents revealed differentially expressed flowering time genes as early as 10 days after planting, with many annotated in the vernalisation and photoperiod pathways. We will report on progress to identify the cause of the early flowering trait in RE2 and agronomic consequences.

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S183. In praise of larger genera: looking at the Amelanchier-Hesperomeles-Crataegus clade (Rosaceae tribe Maleae)

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The value of larger, more inclusive genera is apparent to us. While it can be argued that taxonomic ranks are arbitrary and need only map to monophyletic groups, large genera focus attention on relatively recent evolutionary radiations that appear to have followed on from major divergences. Based on DNA sequence data from several loci, the Rosaceae comprise three supertribes of which one, the Pyrodae, includes both some plants with dry dehiscent fruits and the berry- and drupe-bearing fruit trees in tribe Maleae. This tribe includes three major clades, of which the more basal one is made up of *Amelanchier* and its segregate genera, *Hesperomeles*, and *Crataegus*. Relative to *Amelanchier*, *Hesperomeles* and *Crataegus* share the synapomorphies of (1) a pattern of leaf secondary venation resembling but somewhat different from camptodromous; (2) producing determinate lateral shoots, the tips of which may become sclerified so that they form a thorn, variously leafy or leafless; and (3) producing polypyrenous drupes rather than berries. Likewise, both genera exhibit a trend toward producing fewer-seeded fruits. The possibility of treating *Hesperomeles* as a sixth subgenus in *Crataegus* (much as has been done with *Mespilus*) appeals to us because of the way doing so enforces a comprehensive interpretation of evolution in the *Hesperomeles*-*Crataegus* lineage (leaf venation, thorns, fruit type). A MorphoBank project supporting this research is accumulating images representing phenotypes of these genera.

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S184. Molecular and morphological data reveal hidden diversity in common North American Frustulia species (Amphipleuraceae)

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Frustulia is an established diatom genus that is common and widespread across North America. Like many diatom genera, *Frustulia* has been the subject of taxonomic confusion. Although recent studies have examined taxa from Europe and New Zealand, there exists no detailed genetic data for North American individuals. Using both molecular (*rbcL* and 18S rRNA sequences) and morphological (frustule characters and shape analysis) data, we investigated common taxa from the genus in North America. We recognized eight taxa in this study, including two unknowns. A new species, *F. gibsonea* sp. nov., is described. This species was found in previous studies and described as *F.* cf. *krammeri* based on morphology. The use of molecular characters demonstrates that the group is a distinct species. Despite differences in molecular sequences, *F. gibsonea* and *F. krammeri* are similar morphologically, showing overlap using traditional measurements and shape analysis. This suggests that the combination of molecular and morphological data can help in deciphering cryptic taxa. We were unable to separate *F. saxonica*, *F. crassinervia*, and *F. krammeri* based on molecular data alone, although they could be separated using morphology. The low sequence divergence values obtained between the three taxa indicate that they are very closely related. Future research, focusing on less conserved genes, will be necessary to resolve these taxonomic complexes. Alternatively, this morphological variation may be the result of phenotypic variation.

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S185. Systematics and biogeography in the ecologically conserved pantropical rainforest genus Crudia (Leguminosae)

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Studying the evolution of widely distributed lineages in conjunction with past geological events and climatic features leads to a better understanding of life's history on Earth. Here, we investigate the systematics and biogeography of the pantropical genus *Crudia* (Leguminosae, Detarioideae) using sequences from five nuclear loci (ETS, ITS, *AGT1, AIGP, CALTL*) and a broad taxonomic and geographic species sampling. We also characterise ecological niches of *Crudia* using bioclimatic variables to look at niche conservatism across continents. Our Bayesian inference phylogenetic analysis strongly supports *Crudia* as monophyletic and reveals a clade of Asian species sister to a clade of African and American species. While species assignments using both molecular phylogeny and traditional taxonomy are generally congruent, relationships among species within each clade remain mostly unresolved, particularly in the Asian clade. Biogeographical and divergence time analyses show the genus *Crudia* first evolved during the Eocene from an African ancestor, and subsequently migrated independently to South America and Southeastern Asia, either through terrestrial boreotropical migration or long distance oceanic dispersal, in the Miocene. Although occurring in superficially similar lowland rainforest habitats on the three continents, our analyses indicate that the ecological niches of *Crudia* species differ between continents suggesting local adaptations of species after migration in the Miocene.

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S186. Botany and textiles: The Indian Ocean connection

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Trade, exploration and empire building in the sixteenth, seventeenth and eighteenth centuries led to the movement of plants around the globe, revolutionary advances in the process of identifying and naming plants, a golden age of botanical art and illustration and a world-wide network of botanical gardens. The botanical renaissance and cross-cultural exchanges were manifest in the decorative arts of the period particularly those on Indian painted cottons – chintz – produced for the European market. Standard botanical identification techniques were combined with an aesthetic appraisal of recognized plant-based motifs to identify the elaborate flowers on eighteenth century chintz in the Royal Ontario Museum's Textile Collection. The suite of common species, including tulip, rose, carnation, poppy, peony and chrysanthemum reflect the influence art and culture of the Middle East, Asia and Europe carried through trade over time. The botanical assessments increased the number of recognizable taxa from what had previously been catalogued or described and linked motifs thought to be geometric patterns to real plant parts like fruits and filiform leaves. The botanical assessments also raised the question of how experience of the flora of the Indian subcontinent, both native and introduced, along with the countries rich artistic heritage might have inspired the creation of the seemingly fantastical flowers by local artists.

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S187. Rapid radiation and complex genome size evolution in a clade of holocentric sedges

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Genome sizes across land plants exhibit huge variation, with genome expansion events occurring predominately through polyploidy and the accumulation of repetitive DNA sequences. Another important factor determining evolution of genome size in plants is whether a species has monocentric or holocentric chromosomes. Whereas most plant species have monocentric chromosomes in which acentric fragments can be lost, holocentric species have chromosomal fragments that are regularly inherited. To date, holocentric chromosomes have only been reported in a few plant lineages, including the Cyperaceae family (sedges). Here, we examine genome size evolution in the southern African clade of *Schoenus*, a group of recently radiating sedges that are predominately restricted to nutrient-poor sandstone habitats in the temperate areas of the southern hemisphere. We will present the results of recent phylogenetic analyses based on paired-end genotyping-by-sequencing (GBS) data, which has been used to resolve species relationships in other plant radiations. Our results show that genomes within *Schoenus* are substantially larger than those of other closely-related groups, suggesting that polyploidy and the possible accumulation of repetitive sequences are important mechanisms in this genus. In addition, our results show complex clade-dependent patterns of phylogenetic resolution and genome size evolution, which suggests rapid radiation and probable allopolyploidy. Ongoing work is focusing on improving the sampling in this clade and further examining other aspects of genome size evolution in this lineage.

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S188. Diversity and evolution of seeds in Cuscuta (dodders, Convolvulaceae): morphology and structure

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Cuscuta is a genus of nearly 200 obligate stem parasites with subcosmopolitan distribution and considerable agricultural and ecological significance. Dodder seeds are considered unspecialized, with no morphological adaptations towards particular dispersal vectors; however, the seed coat anatomy has recently suggested structural features that enable endozoochory. This is the first attempt to provide a genus-wide overview of the diversity in morphology and anatomy of *Cuscuta*, together with an assessment of the water gap and exploration of functional relationships. Subsequently, 140 species belonging to all the four Cuscuta subgenera were surveyed. Species of the first infrageneric dodder lineage diverged, subg. *Monogynella*, retain epidermal cells that are elongated and puzzle-like, morphologically uninfluenced by dryness/wetness and an incomplete outer palisade layer. In contrast, seeds of the other subgenera, *Cuscuta*, *Pachystigma* and *Grammica*, are more or less isodiametric and have evolved the ability to alternate their morphology and physiology between two states: with deeply pitted epidermal surface when dry, and papillose through hydration. Majority of taxa of the three subg. excluding *Monogynella* have a complete outer palisade layer throughout the entirety of the seed. An embryo with a globose radicular end has evolved in sect. *Denticulatae* and sect. *Subulatae*, likely with a storage function. The water gap in numerous species was investigated and two mechanisms for initial dormancy break were described. Furthermore, functional relationships between seed characters were analyzed.

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S189. **Canadensys: what's new and future directions in biodiversity data publication**

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Since the development of the Global Biodiversity Information Facility (GBIF) more than a billion standardised occurrences have been made available, ranging widely in taxonomy, geography and history. The national and regional nodes structure developed by GBIF to facilitate publication of data is serving well its purpose, giving capacity to each country or network to take care of datasets linked to their own biodiversity and history. Canadensys has been publishing biodiversity data to GBIF since 2011 and became an official associate node for Canada in 2014. Canadensys has grown from 9 institutions to nearly 25, including Canadian universities, museums, as well as municipalities and non-governmental organisations, from which we aggregate curated datasets and publish over 5.5 million records. Keeping an established network alive while continuing to grow and to develop new methods and technologies is a challenge, especially in a context where institutions are separated across large distances and where funds are scarce. In 2017, we migrated from an in-house Explorer, to a Living Atlases framework, to improve visualisation and search functions, and to better respond to our growing data needs. Despite the universal accessibility to GBIF and its improved discovery and visualisation tools, Canadensys continues to play a crucial role by offering national expertise and garnering community involvement. We will continue to develop tools that allow data-usage fit for the needs of Canadian networks.

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S190. **Herbivory induced Decadienal deferentially regulates light harvesting complex mRNAs at the level of transcription and mRNA stability in the marine diatom *Phaeodactylum tricornutum***

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During herbivory, various diatom species release toxic polyunsaturated aldehydes (PUAs) as a defense response to impair grazers' reproduction as well as affect neighboring unwounded diatom cells. Diatoms exposed to low concentrations of PUA developed increased survival to toxic concentrations of PUA and maintained photosynthetic efficiency. The contribution of photosynthetic gene regulation as a survival strategy is poorly understood. This study investigated photosynthetic light harvesting complex (LHC) genes regulation in the marine diatom *Phaeodactylum tricornutum* in response to a model PUA, 2E, 4E-Decadienal (DD). Analysis of RNA-seq showed an overall suppression of LHC mRNA levels at 3 h compared to the solvent control. Two LHC mRNAs were selected for further study; significantly upregulated *Lhcf15*, and down-regulated *Lhcf2* mRNAs. Transcription rate of *Lhcf15* mRNA rapidly increased and its mRNA half-life was highly stabilized through 9 h. While, transcription rate of *Lhcf2* was strongly suppressed and its mRNA half-life decreased through 3 h then increased by 9 h. Thus, the differential effects of DD on the steady-state levels of *Lhcf2* and *Lhcf15* mRNAs involved regulation at the levels of transcription and mRNA stability. The significance of these gene regulatory mechanisms is unknown but may enhance the opportunity to survive under herbivory stress by adjusting resource allocation. Understanding this mechanism may enable enhancement of cell growth and photosynthetic efficiency in herbivory for commercially cultivated microalgae population.

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S191. An antisense oligoRIBO-11 fragment (contact DNA insecticide) penetrates through the integuments into the cells of gypsy moth larvae (*Lymantria dispar* L.)

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We developed the oligoRIBO-11 fragment (5'-TGCGTTCGAAA-3') (0.9 nmol/larva) and used it as an antisense DNA oligonucleotide (DNA insecticide) to penetrate through the integuments into the cells of gypsy moth larvae, a major insect pest of hardwood trees. Studies were then conducted using a variety of mass spectrometric method – matrix-activated laser desorption/ionization (MALDI).

After the oligoRIBO-11 fragment was applied to the larvae, MALDI registered the penetration of the fragment into the insect cells at 30 minutes post-treatment (peak at 3360.1 Da) and detected a significant response to the applied oligonucleotide 60 minutes post-treatment. In the control group, a peak characteristic of the oligoRIBO-11 fragment was not found. In addition, in the control group, the profile of the recorded peaks (peaks at 2558.2 Da, 2582.2 Da, and 2910.5 Da) differed noticeably from those of the experimental groups. This indicates that the oligonucleotide not only entered the insect cells, but also that the synthesis of new substances (many of them were oligonucleotides) in response to the applied DNA fragment occurred. Many new peaks were obtained in the diagram for samples 60 minutes post-treatment with the oligoRIBO-11 fragment (peaks at 3604 Da, 4267.2 Da, 5509 Da, 7151 Da, 7737.1 Da, 8568.5 Da, and 9389.9 Da).

This provides compelling evidence that DNA insecticides are able to penetrate the integuments of the gypsy moth larvae, triggering an active cell response.

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S192. Transcriptomic analysis of red-berried grapevine infected with Grapevine leafroll-associated virus 3

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Grapevine leafroll-associated virus-3 (GLRaV-3) is the major virus associated with grapevine leafroll complex and has a worldwide prevalence. The impact of GLRaV-3 infection on vine health, yield and fruit quality at the molecular level has yet to be characterized. It is believed that GLRaV-3 infection is associated with expressional changes of select genes in grapevine that are involved in biological pathways fundamental for grapevine growth, development, and fruity quality. Red-berried grapevines (*Vitis vinifera* cv. Cabernet franc) infected and uninfected with GLRaV-3 were identified using virus-specific primer with reverse transcription polymerase chain reaction (RT-PCR). Transcriptome analysis by RNA sequencing was carried out on leaves of identified grapevines at the harvest stage. Differentially expressed genes (DEGs) suggested repressed photosynthetic activity with enhanced sink activity in infected leaves, indicating source-to-sink transition in response to viral infection. Activation of defence mechanisms was suggested by DEGs including increased biosynthesis of flavonoids, lignin, amino acids, and differentially regulated biosynthesis and signalling of hormones. Our results from transcriptomic analysis on red-berried grapevine leaf at harvest suggest down-regulation of biological processes that are fundamental to plant growth and development while up-regulation of genes related to defense mechanisms in responses to GLRaV-3 infection. Our ultimate goal is to understand the impact of GLRaV-3 infection on global gene expression through transcriptome analysis of leaves and berries collected at different growth stages.

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S193. Isolation and characterization of endophytic microbes in poplar trees antagonistic to stem canker causative pathogenic fungus *Sphaerulina musiva*

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Species of the genus *Populus* commonly known as poplars are one of the most widely used groups of forest trees in North America and Europe, and play a significant ecological role as pioneer species in boreal forests, and as a dominant species in the riparian forests that serve as rich wildlife habitats and watersheds. Numerous natural and artificial hybrids of poplars with superior qualities are being widely used in commercial plantations. However, many hybrid poplars are susceptible to *Sphaerulina musiva*, the leaf spot and stem canker causative pathogenic fungal species and limits the utility hybrid poplar as a plantation tree. Endophytic microbes living inside host plant tissues without causing visible symptoms are known to produce antimicrobial compounds and emerging as important players in biocontrol of plant diseases. We isolated endophytic microbes from *Populus deltoides*, *P. balsamifera* and their hybrid, *P.* x *jackii* in Quebec and tested against *Sphaerulina musiva* cultured on Potato Dextrose Agar plates, and discovered one bacterial and several fungal species antagonistic to *S. musiva*. The whole genome sequencing and biochemical characterization of the bacterial species revealed it as a strain of *Bacillus amyloliquefaciens*, contains secondary metabolite production gene clusters and produces at least seven compounds with antifungal activities. Five of these compounds were identified as Iturins, and the remaining two compounds remain unidentified.

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S194. A biosensor assay (GlnLux) for visualizing symbiotic nitrogen fixation output in root systems involved in the legume–rhizobia symbiosis

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Inside legume root nodules, atmospheric nitrogen (N_2) is fixed into usable nitrogen (NH_4^+) by rhizobia bacteria which is then assimilated into amino acids including glutamine (Gln) for export to shoots. There is a need for new tools to image *in planta* nitrogen fixation, assimilation and transport across plant genotypes and rhizobia strain combinations. Here, we demonstrate the use of companion biosensor cells called *GlnLux* (*Escherichia coli* auxotrophic for Gln and constitutively expressing lux) to image Gln accumulation in nodulated root systems across a diversity of legume/rhizobia species. Companion *GlnLux* cells are embedded into agar (*GlnLux*-agar) upon which legume root systems are placed following freeze-thawing to cause Gln leakage. Photons released from nearby activated biosensor cells are captured using a photon capture camera. Using split root systems, we demonstrate that in diverse amide-exporting legumes (alfalfa, lentil, and green pea) that *GlnLux*-agar imaging is sufficiently sensitive to detect Gln release from individual nodules and can differentiate root systems with active *nif*+ from inactive *nif*− nodules. Using this technology, we show that defoliation of forage legumes leads to release of Gln as root exudates, but unexpectedly, this release is rapid (starting within 2 hours) and it originates from not only root tips but also nodules. *GlnLux*-agar-based imaging is thus a new research tool to localize the accumulation and transfer of a critical amino acid required for rhizobia symbionts.

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S195. The effect of urbanization on the evolution of floral traits in the wildflower *Linaria vulgaris*

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Urbanization-induced changes to the biotic environment may cause divergent evolution between urban and rural plant populations. One such environmental change is decreased pollinator activity, which can increase competition for visitation from pollinators, resulting in natural selection for more attractive floral traits. To test whether urbanization could affect floral evolution, we measured natural selection on floral traits of the wildflower *Linaria vulgaris* in urban and rural populations. We did not find evidence that urbanization intensified selection on floral traits: there was significant selection via seeds/fruit on landing pad width, landing pad length, and inflorescence size in at least one population, but selection did not differ between urban and rural *L. vulgaris* populations. However, we did find that mean floral traits differed between urban and rural populations. Relative to rural populations, plants from urban populations had 12.3% wider landing pads, 6.4% longer landing pads, and 11.8% longer nectar spurs. This suggests that urban populations have already evolved more attractive floral traits than rural populations in response to increased competition for pollination. However, considering the lack of studies looking at the effects of urbanization on phenotypic evolution, more research is required to determine whether his trend is consistent along other urban to rural gradients.

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S196. Monitoring airborne ascospores for the management of white mould (*Sclerotinia sclerotiroum*) in dry bean across Canada

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White mould, caused by the fungal pathogen *Sclerotinia sclerotiroum* Lib. (de Bary), is an economically important disease of dry bean (*Phaseolus vulgaris* L.) in the Canadian Prairies. Monitoring the daily aerial ascospore concentrations of *S. sclerotiorum* could provide better management of the disease. To determine the best sampling locations for capturing ascospores, nine Burkard 7-day volumetric spore samplers were placed in three bean fields in southern Alberta in 2018. In addition, air samples were collected from a potato late blight monitoring network in the same regions. Daily samples were deposited into 1.5 mL vials, from which DNA was extracted and ascospores were quantified using species-specific primers in a qPCR assay. Correlations of the ascospores quantified from samplers within the same field ranged from not significant to moderate ($r = 0.35$, $p < 0.01$), suggesting that a single sampler could suffice for sampling a single field. Disease incidence within the same fields ranged from very low (seasonal maximum of 3%) to moderate (seasonal maximum of 25%) under similar ascospore loads, which highlights the importance of management practices in the prevention of white mould. No ascospores were detected from the potato late blight monitoring stations. This project will continue for the next 3 years and will be extended to bean fields in ON and MB to develop a prediction model for white mould.

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S197. The prevalence and diversity of Fusarium species causing Fusarium Head Blight on oat in Manitoba

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Fusarium head blight (FHB), a devastating fungal disease caused by Fusarium spp., can lead to dramatic yield loss and mycotoxin contamination in commercial grain production. Trichothecenes of type-A (T-2 and HT-2) and type-B (DON and NIV) are the common mycotoxins produced by Fusarium pathogens affecting small grain cereals. Oat is a common crop grown for both feed and food in Canada. Recent research has indicated that FHB has become very common on oat in western Canada. Nevertheless, the impact and severity of FHB on Canadian oat production is not very clear. In this study, we investigated the prevalence and diversity of Fusarium species in 168 oat samples collected from commercial fields in Manitoba from 2016 to 2018 through morphological, conventional PCR and qPCR analysis. A complex of Fusarium species, including *F. graminearum*, *F. poae*, *F. avenaceum*, and *F. sporotrichioides* are found in these oat samples and *F. poae* is the most predominant, followed by *F. graminearum* and *F. sporotrichioides*. The level of mycotoxins in these samples are analyzed usingLC-MS/MS method. The correlation analysis between Fusarium DNA and mycotoxin level indicates that *F. poae*, *F. graminearum*, and *F. sporotrichioides* are the main contributors of mycotoxins in oat samples. The phylogenetic analysis of 160 *F. poae* isolates, using *ELF1-α, TRI1,* and *TRI8*, is currently in process.

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S198. 'New' pathotypes of *Plasmodiophora brassicae* in Canada are not new

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Clubroot, caused by *Plasmodiophora brassicae* Wor., is an important disease of brassica crops. Clubroot is generally managed using resistant cultivars, but new pathotypes are increasing rapidly on canola (*Brassica napus* L.) in Canada. Whole-genome DNA sequences of *P. brassicae* collections from across Canada were assessed to quantify genetic variation among populations. Many of the collections were also pathotyped (Williams' system + others) to assess the relatedness of new pathotypes to the previously predominant pathotypes on canola. In total, 43 single-spore and field collections of *P. brassicae* from Canada, the USA, and China were sequenced. The collections from Canada separated into four clades: two primarily from canola on the Prairies and two primarily from other regions of Canada, but 3 of 4 clades contained multiple pathotypes from various hosts. The 'new' pathotypes from the Prairies generally clustered together, separately from the previously predominant pathotypes on canola. At two sites in central Canada where a rapid breakdown in resistance had been documented, SNPs in about half of the genes differed between collections before and after the change. This indicated that the 'new' pathotypes were likely not the result of point mutation, but rather presented genotypes that had been maintained in the pathogen population at low frequency through balancing selection. These 'new' pathotypes became dominant at each site in response to selection from repeated exposure to resistant hosts.

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S199. Assessment of fruit and foliage resistance to bacterial spot (*Xanthomonas gardneri*) in commercial processing tomatoes (Solanum lycopersicum L)

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Bacterial spot (*Xanthomonas gardneri*) is a major production issue in Ontario field tomatoes. The traditional focus on breeding for host resistance is on foliar symptoms. To investigate anecdotal reports of differences in foliar and fruit resistance, nine commercial cultivars were inoculated at the Ridgetown Campus, University of Guelph at the vegetative (foliar experiment) or reproductive (fruit experiment) stage from 2016-2018. In the foliar experiments, symptoms appeared in 'CC337' four days later than 'TSH18', but no differences were observed in growth room trials. The standardized area under the disease progress curve for defoliation was 51 to 54% higher for 'TSH18' than 'H9706', 'Hypeel 696' and 'H3406', but equivalent to 'CC337'. Fruit incidence was 49 and 47% lower for 'CC337' than 'TSH18' and 'H9706', but equivalent to 'H3406' and 'Hypeel 696'. Fruit severity was 63 and 60% lower for 'CC337' than 'H9706' and 'H3406', respectively but equivalent to 'TSH18' and 'Hypeel 696'. In the fruit experiment, fruit incidence was equivalent among cultivars in randomly sampled fruit, while the disease severity index for 'H9706' (3.4) was higher than 'Hypeel 696' (0.7). The observation that 'H9706' was less susceptible to defoliation than 'TSH18' but had equivalent fruit incidence and severity to 'TSH18' suggests differences in resistance among plant organs. Mechanisms of fruit symptom development require further investigation and fruit susceptibility should be considered in breeding programs.

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S200. Management of crown and root rot, caused by *Fusarium oxysporum*, and powdery mildew, caused by *Golovinomyces cichoracearum* on *Cannabis sativa*

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Fusarium oxysporum, which causes crown rot, root rot and damping-off, and *Golovinomyces cichoracearum*, which causes powdery mildew, can affect cannabis plants at all stages of growth, reducing overall quality and yield. To investigate powdery mildew control, cuttings of a mildew-susceptible strain 'Copenhagen Kush' were potted in a 75% coir, 25% perlite mix. They were incubated for 14 days inside a humidity dome and then placed under two 54watt 6400K T5H0 lights with a 24 h photoperiod. Natural inoculum of *G. cichoracearum* caused mildew development. Treatments included Actinovate®, MilStop®, Neem oil, Regalia Maxx®, Rhapsody® ASO and ZeroTol®. Plants, in groups of four, received weekly sprays and disease assessments over five weeks. Assessments of disease severity (percentage of leaf area infected) were converted to AUDPC values. MilStop® and Regalia® provided significantly ($p<0.05$) lower AUDPC values compared to the control. Rhapsody® ASO, ZeroTol®, Neem, and Actinovate® were less effective but still had significantly lower AUDPC values than the control ($p<0.05$). A group of eight plants was exposed daily for 3-5 sec to UV-C light from a CleanLight Pro unit to test the effects on mildew development. Results showed a disease reduction of 45.2 %. For management of damping-off on cuttings caused by *F. oxysporum*, treatments including Rhapsody® ASO, Prestop®, RootShield® Plus WP, Regalia® and Karanja oil are being evaluated in a hydroponic system. Experiments are currently in progress

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S201. **Nutrients requirements of flax**

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Three replicated field experiments in RCBD were conducted at Thunder Bay to work out the N, P, K and S requirements of flax during 2016-'18. The treatments in experiment on N were: 0, 35, 70 and 105 kg N ha^{-1} from urea, 105 kg N ha^{-1} from urea + ESN (2:1 on N basis) and 105 kg N ha^{-1} from urea + Manipulator 620 spray @ 8 L ha^{-1} at 6" crop growth. Experiment on P and K included all combinations of P_2O_5 and K_2O each @ 0, 20 and 40 kg ha^{-1}. Experiment on S had four rates of S: 0, 10, 20 and 30 kg ha^{-1}. The results pooled over years indicated that (i) application of urea N increased the flax yield linearly from 1.67 Mg ha^{-1} in no N to 2.27 Mg ha^{-1} with 70 kg N ha^{-1} and levelled of thereafter (2.28 Mg ha^{-1} at 105 kg N ha^{-1}). Seed yield improvement by urea + ESN as compared to urea wasn't significant, (ii) Manipulator improved the seed yield significantly (0.25 Mg ha^{-1}) and (iii) there was no improvement in flax seed yield by application of P, K or S! The seed yield in P and K experiment ranged from 2.77 Mg ha^{-1} to 2.97 Mg ha^{-1} and that in the S experiment from 2.73 Mg ha^{-1} to 2.76 Mg ha^{-1}.

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S202. **Quantifying the effects of a carbonatite rock fertilizer on wheat (*Triticum aestivum* L.)**

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There is renewed interest in exploiting unprocessed rocks and minerals for agriculture to meet sustainability challenges. Carbonatites are of particular relevance as rock fertilizers because of their rapid weathering rates and nutrient-bearing accessory minerals. Here, we evaluated a Canadian carbonatite with the goal of determining potential beneficial effects on plants. Wheat was grown under greenhouse conditions in inorganic substrates amended with either carbonatite, calcitic lime (pH control), or silica sand (soil structure control). Plant growth, biomass, and yield were measured. The rhizospheric microbial respiration was also assessed, as it is known to be affected by substrate amendments. While plant biomass was not different with sand or lime, plants grown with the carbonatite displayed increased shoot growth within two weeks. After eight weeks, there was a nearly 200% increase in overall biomass of carbonatite-treated plants over plants in the other treatments, and the increased growth was accompanied by higher seed production. There was also significantly increased microbial respiration in the lime-treated substrate over the control and carbonatite-amended substrates. These results demonstrate that carbonatites used as rock fertilizers can positively affect plants as early as two weeks after planting, and that their effects on wheat are related to enhanced nutrient acquisition. However, further work is needed to characterize how carbonatites interact with different plant species, and how these benefits can be realized under field conditions.

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S203. The effects of nutrient enrichment on the community composition of arbuscular mycorrhizal fungi: a meta-analysis of fertilization studies

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Nutrient deposition from human sources has the potential to decouple nutrient-exchange mutualisms between plants and below-ground fungi. In the widespread mutualism between plants and arbuscular mycorrhizal (AM) fungi, plants decrease their interactions with AM fungi when resources are abundant because the cost of association exceeds the benefits. Thus, AM fungal biomass is consistently reduced by nutrient enrichment, but effects on community composition are less clear because results are variable across study systems. To address this, we used a meta-analysis to determine overall patterns across studies, while accounting for experimental factors that could introduce variability between experiments. We found that fertilization reduced the species richness of AM fungal communities but did not affect species diversity. Nitrogen (N) fertilization had the greatest negative effects on species richness, and these effects were more negative at higher dosages of fertilizer. Synthetic fertilizers had stronger negative effects on species richness than organic fertilizers. Phosphorus (P) addition or simultaneous fertilization with both N and P did not affect AM fungal species richness or diversity. Nutrient deposition increased the abundance of AM fungal genera with faster growth rates that specialize on disturbed environments but decreased the abundance of slow-growing AM fungal genera. This meta-analysis provides evidence that AM fungal communities are simplified by nutrient loading in favour of more ruderal species.

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S204. Endophytic bacteria: nitrogen-source for lodgepole pine trees on disturbed sites?

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Unreclaimed gravel mining pits located in the central interior of British Columbia have limited soil nitrogen-levels due to gravelly-textured soils, no organic forest floor and low atmospheric nitrogen-inputs through precipitation. However, lodgepole pine (*Pinus contorta*) trees have been growing well at these pits with tissue nitrogen-content and growth-rate unaffected by extremely low soil nitrogen-levels, indicating that pine trees can meet their nitrogen-requirements from an unknown source. We hypothesized that biological nitrogen fixation by endophytic bacteria could be a potential nitrogen-source for pine trees. Testing this hypothesis, we isolated 77 endophytic bacteria from needle, stem, and root tissues of pine trees. Of these, 14 bacteria that showed consistently positive results for nitrogenase enzyme activity were selected for a yearlong greenhouse study to quantify the amount of nitrogen-fixed and plant-growth-promoted by each bacterium *in planta*. After one year, bacteria-inoculated seedlings had significantly higher biomass (100-311%) and length (31-64%) than non-inoculated control seedlings and fulfilled 23-53% of their nitrogen-requirements through biological nitrogen fixation. Notably, *Pseudomonas migulae* AR1r and *Pseudomonas lini* SN1r inoculated seedlings accumulated 4-fold higher biomass than control seedlings and fixed about half of their nitrogen from the atmosphere. Thus, endophytic nitrogen-fixing bacteria naturally harboured by pine trees at these unreclaimed gravel pits are capable of providing fixed nitrogen to their host and could potentially be used for effective reclamation of such highly disturbed sites in a sustainable manner.

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S205. Cucurbit seeds: Reservoirs of functional and antagonistic microbiomes

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Seeds are potential vectors that transmit beneficial microbiomes across plant generations, to promote plant growth and antagonize phytopathogens. The *Cucurbitaceae* family is consumed by humans globally, however it is relatively overlooked in microbiome research. Here, we explored the cultivated and non-cultivated microbiomes associated with seeds of economically important cucurbits encompassing 21 varieties belonging to seven species. The cultivated bacterial library was subjected to *in vitro* functional and antagonistic tests along with *in planta* screening against cucumber powdery mildew. In parallel, seed DNA was sequenced using Illumina 16S miseq to characterize entire microbiomes. In total, 169 unique bacterial strains were cultured that almost entirely belonged to only two phyla (*Firmicutes*, *Proteobacteria*), with *Bacillus* constituting 50 % of the library and spanning all tested cucurbit species. Simultaneously, 16S reads from Illumina sequencing emphasized the dominance of *Firmicutes*, in particular spore-forming bacteria (e.g., *Clostridium*, *Bacillus* and *Paenibacillus*) followed by *Proteobacteria*. The endophytic library exhibited major beneficial functions such as indole-3-acetic acid (auxin) production and nitrogen fixation/N-scavenging required for nutrient acquisition and growth promotion. Surprisingly, the majority of the library (70%) exhibited antagonism to five soil-borne pathogens (*Rhizoctonia solani*, *Fusarium graminearum*, *Phytophthora capsici*, *Pythium aphanidermatum*) and a foliar pathogen, *Podosphaera fuliginea*. These findings highlight the importance of cucurbit seeds as natural reservoirs of biofertilizers and biocontrol agents and may help to explain the success of *Bacilli* as commercial inoculants.

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S206. Environmental factors and polyketide synthase gene expression in an usnic acid producing lichen-fungus

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Lichens are slow-growing and exposed to long-term, extreme micro-environmental conditions, which resulted in the evolution of unique secondary metabolites for adaptation to the environmental conditions. One of the most commonly produced secondary metabolites in lichens is usnic acid, thought to be produced by two genes. The objectives of the present study were to compare PKS gene expression and amount of usnic acid production in *Cladonia uncialis*, with two environmental factors (soil pH and moisture) as well as the presence of neighboring species. Lichen samples were collected within three locations in Newfoundland using a strip transect method (x5 transects x5 quadrats). Soil pH and moisture were measured in each quadrat. Usnic acid concentration was measured using HPLC and quantitative PCR was performed using two PKS genes (MPAO and MPAS) for each lichen thallus sample. The results showed that the percent ground cover of *Cladonia uncialis* was affected by soil pH level but not soil moisture; and it correlated with the percent cover of some other species. Usnic acid concentration was also affected by soil pH level but not soil moisture. MPAS and MPAO genes expression levels were not significantly affected by either soil pH level or soil moisture. These findings suggest that soil pH and neighbouring species may be important for the production of usnic acid by C. uncialis but the genes involved require further study.

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S207. Arabidopsis CTP:phosphocholine cytidylyltransferase is phosphorylated and inactivated by SnRK1

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De novo phosphatidylcholine (PC) biosynthesis via the Kennedy pathway involves highly endergonic biochemical reactions that must be fine-tuned with energy homeostasis. CTP:phosphocholine cytidylyltransferase (CCT) is an important regulatory enzyme in this pathway. In this study, an important mechanism regulating plant CCT1 activity was identified. Comparative analysis showed that *Arabidopsis thaliana* CCT1 (AtCCT1) exhibits homologous catalytic and membrane-binding domains to rat CCT1. Homology modelling indicated that AtCCT1 has similar Rossmann fold and localization of active site residues as rat CCT1. On the other hand, the C-terminal phosphorylation domain that is important for stringent regulation in rat CCT1 is apparently missing in plant CCT. Instead, AtCCT1 contains a putative consensus site (Ser187) of a sucrose-related non-fermenting kinase (SnRK1), a kinase involved in energy homeostasis. Phos-tag SDS-PAGE coupled with MS analysis showed that SnRK1 phosphorylates AtCCT1 primarily at this site. Phosphorylated AtCCT1 suffered a substantial reduction in enzyme activity. Protein truncation and liposome binding studies indicated that SnRK1 phosphorylation of AtCCT1 directly affects the catalytic domain instead of interfering with the phosphatidate-mediated activation of the enzyme. Overexpression of *AtCCT1* catalytic domain in *Nicotiana benthamiana* leaves resulted in higher PC content, but its co-expression with *SnRK1* reduced this effect. Taken together, our results suggest that SnRK1 mediates the phosphorylation and inactivation of AtCCT1, revealing a new mode of regulation for this key enzyme in plant PC biosynthesis.

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S208. Identifying sequences required to piggyback AtADT5 into the nucleus

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In *Arabidopsis thaliana* the last step of phenylalanine (Phe) biosynthesis is catalyzed by a family of AROGENATE DEHYDRATASES, and all six *At*ADT*s* localize to the chloroplast. *At*ADT5, however, is the only *At*ADT that also localizes to the nucleus despite the lack of a nuclear localization signal (NLS). We believe *At*ADT5 is a moonlighting protein, having a unique second function in the nucleus. Recently, a unique interaction partner of *At*ADT5 was identified, and only heterodimers of *At*ADT5 and this interactor localize to the nucleus. Compellingly, this interactor has two putative NLSs. We believe this interactor is piggybacking *At*ADT5 into the nucleus. To identify the amino acids required for this interaction, a series of domain-swapped constructs and targeted substitution constructs of *At*ADT4 and *At*ADT5 were made as *At*ADT4 and *At*ADT5 share 90% sequence identity on the protein level. In addition, deletion constructs were made removing the putative NLSs from the interactor to determine whether one or both NLSs are required for nuclear import of the heterodimer. Heterodimer formation and localization will be assessed using yeast-two-hybrid and bimolecular fluorescence complementation assays. We will present and discuss our initial results that indicate that although specific amino acids are involved, the story is more complex. This work will add to the growing body of research surrounding moonlighting proteins, and the effect subtle sequence changes can have on protein function.

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S209. **Evolutionary insights into the role of shikimate kinase-like 1 in chloroplast biogenesis**

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Chloroplast biology represents one of the most intensely studied topics within plant research that seeks to understand the complex processes related to photosynthesis. Shikimate kinase-like 1 (SKL1), a gene homolog of the well-studied shikimate kinase involved in the shikimate pathway, has been implicated in chloroplast biogenesis. *Arabidopsis thaliana* skl1 T-DNA insertional mutant (*skl1-8*) lacks developed chloroplasts and displays an albino phenotype. We are investigating the functional evolution of SKL1 through comparative mutational and biochemical analyses of a number plant species including *A. thaliana*, *Physcomitrella patens*, and *Marchantia polymorpha*, some of which include the earliest ancestral plants that contain an SKL1 homolog. Results from analyses thus far have shown that SKL1 has maintained its ancestral function by complementing *skl1-8* mutants with *P. patens* SKL1. The absence of SKL1 in organisms predating land plants, including green algae, make it an attractive candidate to study plant evolution. The major goal of this research seeks to expand our current knowledge on the topic of chloroplast biogenesis to understand how SKL1 participates in this complex process, and to provide knowledge on the evolution of SKL1 as a novel functional protein based on the divergence from shikimate kinase.

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S210. **Investigating quinate metabolism**

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Quinate is an abundant compound found in green plant tissue that is used in the biosynthesis of chlorogenic acids (CGAs). CGAs are antioxidants, UV light protectants and have antifungal properties. Recently, several genes were characterized as quinate dehydrogenases and proposed to be involved in quinate metabolism. We are conducting *in vivo* work to confirm the role of these genes in *Solanaceae* and *Brassicaceae* quinate metabolism. *S. lycopersicum* was found to have two genes involved in both anabolic and catabolic quinate metabolism. We are aiming to generate *S. lycopersicum* knockout mutants with CRISPR-Cas9 technology. Concurrently, we generated overexpression mutants in *A. thaliana*, a species which lacks quinate dehydrogenase genes. Once stable transgenic lines are generated we are hoping to conduct a series of metabolite analyses as well as to investigate the evolutionary advantages of quinate in biotic stress responses.

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S211. Autophosphorylation inhibits the Ca2+-dependent protein kinase RcCDPK1 from developing castor oil seeds

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Phosphoenolpyruvate carboxylase (PEPC) is a tightly-regulated enzyme that plays diverse roles in plant metabolism, particularly the anaplerotic replenishment of Krebs' cycle intermediates withdrawn for biosynthesis. An unusual PEPC isozyme known as 'bacterial-type PEPC' (BTPC) is highly expressed as a catalytic and regulatory subunit of a novel Class-2 PEPC heteromeric complex in developing castor oil seeds (COS). The 'allosterically-desensitized' Class-2 PEPC dynamically associates with mitochondria *in vivo*, and was hypothesized to mediate a large anaplerotic flux of PEP to oxaloacetate in support of COS storage oil and protein synthesis, while simultaneously recycling respired CO_2. During COS development BTPC is subject to *in vivo* inhibitory phosphorylation at Ser451, catalyzed by RcCDPK1, a soluble Ca^{2+}-dependent protein kinase. Although CDPK autophosphorylation has been well established, its functions remain elusive. Most CDPK transphosphorylation assays have employed non-physiologically relevant protein or synthetic peptide substrates, whereas the influence of autophosphorylation on CDPK activity may be substrate-dependent. Ca^{2+}-stimulated autokinase activity of recombinant RcCDPK1 was readily detected and multiple autophosphorylated Ser, Thr, and Tyr residues were mapped via nanoHPLC-MS/MS. Quantitative assays using [γ-^{32}P]ATP demonstrated that prior autophosphorylation markedly inhibits RcCDPK1's ability to transphosphorylate its BTPC substrate at Ser451. Ongoing research includes assessing the impact of autophosphorylation on RcCDPK1's Ca^{2+}-sensitivity, and Ca^{2+}-dependent interaction with BTPC. Results will provide insights into the link between plant C-metabolism, Ca^{2+}-dependent signaling, and the biological relevance of CDPK autophosphorylation.

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S212. Recent advances in plant ubiquinone (Coenzyme Q) biosynthesis and engineering

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Ubiquinone is a liposoluble and redox-active molecule that is made up of benzenoid and prenyl moieties. It serves as a vital electron carrier in the respiratory chain of mitochondria and some bacteria, and doubles as a potent lipid and protein antioxidant. Recent evidence from our laboratory indicates that land plants have evolved the unprecedented ability to derive the benzenoid ring of ubiquinone from the metabolism of phenylpropanoids (Plant Cell 26: 1938-1948). I will present data from gene network modeling combined with reverse genetics and isotopic tracer experiments in Arabidopsis and tomato that demonstrate that the cognate metabolic architecture is split into two branches, the first one originating from the β-oxidation of *p*-coumarate in peroxisomes, while the second one stems from the peroxidative cleavage of a flavonol, called kaempferol, in the cytosol (Plant Cell 30: 2910-2921). Having dissected the molecular determinants of such a cleavage, I will show that using a synthetic biology approach it is possible to capture this catabolic branch to re-route kaempferol towards the accumulation of ubiquinone in Arabidopsis leaves and tomato fruits. I will briefly discuss how this paradigm shift regarding the functional significance of flavonols in plant tissues offers new opportunities for increasing the nutritional value and stress resistance of crops.

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Listing of Abstracts for the Poster Program

TOPIC 1: Abiotic Stress (Posters P1-P24)

P1. **Photoperiodic injury in tomato involves opposing short-term and long-term acclimation of photosystem II operating efficiency and chlorophyll levels**

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University of Guelph

Photoperiodic injury (PI) is an abiotic stress observed in tomato when exposed to continuous or non-24hr artificial lighting photoperiods. After a week or more of treatment, chlorotic leaves and reduced biomass become evident. Little is known about the connection between short-term (<24hrs) and long-term (>5days) responses to PI. Light harvesting complex II (LHCII) has been implicated in tolerance to PI, and it is important for balancing excitation between photosystem I (PSI) and photosystem II (PSII). Chlorophyll (Chl) content and Chl a:b ratios were determined using *in-vitro* and *in-vivo* absorption-based assays. Chlorophyll fluorescence, to calculate PSII operating efficiency (YII), was measured every two hours over a two-week period using the automated PSP32 multi-probe plant stress monitor by Opti-Sciences. PSI/PSII fluorescence ratio was used for assessment of stress and fluorescence-based *in-vivo* Chl content. Under continuous light, both PI-tolerant and -intolerant cultivars showed similarity in short-term acclimation, where Y(II), Chl content, Chl a:b ratio, and PSI/PSII ratio all increased. Long-term acclimation decreased Chl a:b ratio; however, for the intolerant cultivar Chl content dropped, PSI/PSII ratio continued to increase, and Y(II) plateaued lower to eventually destabilize.

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P2. **Superoxide is diurnally rhythmic and dampens under continuous light in tomato**

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Once exposed to continuous light, tomato exhibits photoperiodic injury (PI) that is visualized as interveinal chlorosis and overall stunted growth. Radicals are one light-dependent chloroplastic metabolite that may be involved. It is hypothesised that radicals are a signal of redox poise, integrating metabolism between chloroplast and nucleus during light and dark cycles. Superoxide was assayed diurnally in both PI-tolerant and -intolerant tomato cultivars using nitroblue tetrazolium staining (NBT). The NBT protocol was modified to ensure homogenous infiltration of the substrate, providing a uniform intensity dependent visualisation of superoxide content. Staining was confirmed to be intracellular and light-dependent indicative of chloroplast localisation. Interestingly, plants grown under normal photoperiods have more superoxide than those under continuous light during the day. Furthermore, the difference in quantifiable superoxide content precedes visual chlorotic symptoms. Histological and image analysis reveals superoxide content is diurnally rhythmic under a normal photoperiod, and the rhythm is dampened under continuous light. A PI-tolerant cultivar shows more robust rhythms under continuous light for clock-regulated parameters, including nitrate assimilation, amino acid levels, stem extension and cotyledon movements. We propose that superoxide acts as an input to the circadian clock, which is essential for entrainment of arrhythmic clocks in PI-intolerant cultivars.

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P3. Effects of exogenous melatonin on improving the drought resistance of oat seedlings

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Drought is one of the severe constraints in oat production. The effects of exogenous melatonin on improving the drought resistance of oat seedlings were studied, which were subjected to water stress (-0.9MPa) induced by polyethylene glycol 6000. The roots of oat plants were pretreated with 0.1mmol melatonin for 7 days before water stress was implemented for 14 days in a growth chamber. The results showed that the exogenous melatonin effectively alleviated the damage effects from drought stress, as demonstrated by higher relative water content, chlorophyll content, soluble sugar content, free proline content, root vigor and antioxidant enzyme activities (superoxide dismutase, peroxidase, catalase, and ascorbate peroxidase), lower O_2^- generation rate, relative electronic conductivity, H_2O_2 and malondialdehyde content as compared to untreated plants. The accumulation of endogenous melatonin and abscisic acid were elevated, while the accumulation of indole-3-acetic acid (IAA) and gibberellin A_3 (GA_3) were decreased in oat seedlings under drought stress. The application of exogenous melatonin resulted in increased the endogenous melatonin and IAA contents, which also induced the synthesis of GA_3 and inhibit the synthesis of abscisic acid. These results suggest that ameliorating drought stress through exogenously applied melatonin may be associated with increased antioxidant protection capability and after a longer stress treatment with changed IAA and GA_3 accumulation level on account of improved endogenous melatonin content.

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P4. Wounding induces tomato Ve1 R-gene expression

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In tomato, Verticillium fungal resistance is determined by the *Ve*-gene locus, which encodes two leucine-rich repeat receptor-like proteins (Ve1, Ve2). The gene encoding Ve1 protein has two functional alleles; *Ve1*, encoding a resistance protein, and *ve1*, with a premature stop codon encoding a truncated product. In both resistant and susceptible plants, *Ve1* is induced differentially while *Ve2* is constitutively expressed throughout disease development. Contrary to their putative role in Verticillium resistance, these profiles have been observed even during compatible Verticillium interactions, colonization by some bacterial pathogens, and growth of transgenic tomato expressing the fungal Ave1 effector, suggesting broader roles in disease and/or stress. Here we have examined further *Ve*-gene expression in resistant and susceptible plants under abiotic stress, including drought, salinity and physical damage. Using qRT-PCR and label-free LC-MS methods, chnges have been evaluated at both the mRNA and protein levels. The results indicate that *Ve1*gene expression responds specifically to physical damage or plant wounding, resulting in a defense/stress cascade that resembles observations during Verticillium colonization. In addition, changes in Ve1 or Ve2 function also result in responses that occur with wilt pathogen and are consistent with an antagonistic relationship between the two genes. Mutational analyses also indicate the plant wounding hormone, systemin, is not required, while jasmonic acid appears to play a direct role in Ve1 induction.

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P5. High temperature and ovule failure in field pea (*Pisum sativum* L.)

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Heat stress during reproductive development is one of the main factors associated with yield reduction of field pea. Although sexual reproduction of the majority of angiosperms involves both male and female gametophytes, studies on the female gametophyte under heat stress are scarce. In this research, we aimed to investigate the effect of high temperature on ovule development following fertilization. Plants from 6 cultivars of field pea grown under 24°C day/18°C night were exposed to four days of heat stress (35°C day/18°C night) during flowering stage. The ovules at the plants' first four reproductive nodes were evaluated by employing clearing and light microscopy. The results indicated that heat stress caused a significant effect on ovule development mainly by accelerating flower ontogeny. Ovaries, ovules, and embryo sacs of these flowers had advanced stages; however, internal evaluation of the post-fertilization components of the embryo sacs revealed highly unequal development between ovules. Although fertilization of these ovules was not highly affected, many of the ovules displayed zygote, embryo, and endosperm at variable stages of development within the same ovary. Interestingly, heat stress increased aborted ovules with embryos sacs displaying signs of embryos at globular and heart stage on pods at maturity stage. Overall, heat stress seems to cause acceleration of reproductive development of the plants accompanied by an uneven development of the embryo sacs within nearby ovules.

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P6. Expression of the RING-type ubiquitin ligase, XBAT35, is regulated by ABA and abiotic stress

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The increasing concern of climate changes makes it increasingly important to understand the mechanisms plants use to tolerate stressful environments. One such mechanism involves the production of hormone abscisic acid (ABA) in response to abiotic stresses. One function of ABA signaling leads to the activation of multiple transcription factors, which control the expression of genes required to mitigate the stress response. ABA signalling is regulated by the ubiquitin proteasome system (UPS), which controls the abundance of signaling pathway components. The UPS uses three enzymes, E1, E2, and E3, to attach ubiquitin molecules to selected proteins, which are then degraded by the 26S proteasome. E3s or ubiquitin ligases are of particular importance as they confer substrate specificity. Our study focuses on characterizing the role of the RING-type E3, XB3 Ortholog 5 (XBAT35), in response to abiotic stress. *XBAT35* is alternatively spliced producing two isoforms; nuclear localized XBAT35.1 and Golgi-localized XBAT35.2 (1). During pathogen attack, XBAT35.2 is known to regulate the abundance of accelerated cell death 11 (ACD11), a cell death inhibitor (1). Here, we provide preliminary evidence for a potential role for XBAT35.1 and XBAT35.2 in the abiotic stress response. The expression of both isoforms of XBAT35 and ACD11 were found to be induced by ABA and salt. These results suggest that XBAT35 and ACD11 function to promote abiotic stress tolerance.

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P7. **Unravelling the aspects of PGPR-mediated modulation of antioxidative defense expression and secondary metabolic profiling in *Solanum lycopersicum* under Cd stress**

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Plant Growth Promoting Rhizobacteria (PGPR) colonize many plants and have been explored in rhizosphere for their ability to tolerate toxicities through strengthening antioxidative defense system of plants and stimulating the production of different secondary metabolites. Although, the role of *Pseudomonas aeruginosa* and *Burkholdera gladioli* in *Solanum lycopersicum* have not been investigated yet. Therefore, the present work was conducted to investigate the possible roles of *P. aeruginosa* and *B. gladioli* in mitigation of Cd-induced toxicity in *S. lycopersicum*. Cd exposure (0.4 mM) led to oxidative damage, alteration in the antioxidants (enzymatic and non-enzymatic) and secondary metabolites (phenolic compounds and organic acids). Cd stress resulted in accumulation of oxidative stress markers (superoxide anion,H_2O_2,MDA) that were further reduced in PGPR-inoculated seedlings, studied biochemically and through confocal microscopy. The antioxidants SOD (121%), POD (201%) were reduced while CAT(65%), GPOX(265%), APOX(126%), GR(95%), GST(124%), glutathione(75%), ascorbic acid(53%) and tocopherol(245%) were stimulated. However, PGPR exhibited plants further modulated these antioxidant levels. The secondary metabolites like phenols, flavonoids, anthocyanins, polyphenols and organic acids (citric, fumaric, succinic, malic) were also enhanced in Cd-treated plants and their levels were further improved by PGPR inoculation. Gene expression profiling of antioxidant enzymes (*SOD,POD,CAT,APOX,GPOX,GR,GST*) and secondary metabolites (*CS,FH,SUCLG1,SDH, MS*) was also studied and found to be modulated in PGPR-inoculated seedlings. As a novel aspect, present study highlighted the role of PGPR in Cd-stress tolerance in *S. lycopersicum*.

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P8. ***Brassica rapa*** **Serine/Arginine-rich protein-like 3 (BrSR-like 3) regulates drought tolerance via alternative splicing of target genes in a concentration-dependent pathway**

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Plants respond to signals including stresses via transcriptional reprogramming mainly through constitutive and alternative RNA splicing (AS) events. RNA splicing is a highly ordered and dynamic post-transcriptional modification catalyzed by numerous non-snRNP proteins including serine/arginine-rich (SR) proteins along with several other factors. In this study, we attempted to characterize the role of *BrSR45a* in drought stress response by comparing the phenotypes, chlorophyll a fluorescence and splicing pattern of drought-responsive genes of *BrSR45a* overexpressors, mutant (SALK_052345) along with control plant (Col-0) in Arabidopsis. No aberrant phenotype was observed in transgenic plants except that *SR45a* mutants results in relatively shorter leaf widths. Under drought conditions, the upregulation of *BrSR45a* positively correlates the photosynthesis efficiency, drought tolerance and recovery rate upon rewatering. Further analysis showed that the tolerance efficiency of BrSR45a overexpressors is concentration dependent. To gain insight into the mode of action of the SR45a proteins implicated in the drought tolerance mechanism, the AS pattern of 16 genes which includes known drought-responsive and *SR45a* interacting genes (U2AF, U4/U5.U6 tri snRNP associated protein (U4/U5.U6)) were investigated and compared among overexpressors, mutants and controls both under normal and drought conditions. The splicing pattern of DCP5, RD29A, GOLS1, AKR, U2AF and SDR were different between overexpressors and mutants under normal conditions. This study reveals that BrSR45a can regulate drought tolerance via alternative splicing of target genes in a concentration-dependent pathway.

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P9. Bioactive compounds in salt-stressed *Hypericum perforatum*: role of proline, salicylic acid and ascorbic acid pretreatments

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Hypericum perforatum is a medicinal plant vulnerable to environmental stresses. A field study was designed to test the effects of saline water (2, 6 and 10 dS/m) and foliar application of salicylic acid (0.25 mM), ascorbic acid (3 mM) and proline (1.75 mM) on the main active compounds (hyperforin, hypericin and pseudohypericin) of *Hypericum perforatum* flowers. Irrigation with saline water (6 and 10 dS/m) decreased hyperforin, hypericin and pseudohypericin yields. The effect of salicylic acid depended on the salinity stress intensity, a decrease in hyperforin yield was observed at moderate salt concentration (6 dS/m), whereas hypericin and psodohypericin yields were increased at 10 dS/m. At moderate and high level of salt, foliar application of ascorbic acid resulted in hyperforin, hypercin and pseudohypericin yields remaining at the same level than the control plants. There was an increase in the yield of hyperforin, hypericin and pseudohypericin at 10 dS/m and foliar application of proline while at 6 dS/m the response varied depending on the bioactive compound. Our results show that irrigation with saline water up to 10 dS/m would result in a 33% average loss in polyphenols yield in *H. perferatum*. Foliar application of salicylic acid, proline and to a lower extent ascorbic acid at high salinity level could alleviate, at least in part, the negative impact of salinity on the main active compounds.

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P10. Conditioning of nursery plants using irrigation scheduling and mycorrhizae for improving post-transplant success rates

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Global fresh water reserves are both limited and degraded. This is a significant concern for nursery operators that rely heavily on irrigation to maintain production. As the impacts of climate change continue to manifest, the pressure on these degraded water reserves will mount. Typical nursery practices are not sufficiently flexible, nor do they rely on timely and objective data to dictate irrigation events. The result being watering schedules that tend toward significant over-watering. Previous work quantified the relationship between cumulative plant water stress (cWS) and cumulative vapour pressure deficit (cVPD), identifying species-specific water stress thresholds in relation to cVPD. The objective of this study was to base irrigation on cVPD thresholds for the containerized ornamental plant *Spiraea japonica* 'Goldflame', such that water use would be reduced while maintaining market quality. A split-plot field trial with irrigation as the main-plot factor and mycorrhizae as the split-plot factor was employed. Three irrigation schedules were applied via overhead irrigation: (1) conventional practice, (2) moderate water stress, and (3) high water stress. Three mycorrhizae treatments were examined in combination; (1) inoculation at time of potting, (2) inoculation at time of potting and transplant, and (3) no inoculation. The growth and quality of the plants were recorded throughout a growing season. The results indicate that water use can be reduced by 64% compared to conventional practices while maintaining marketable quality.

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P11. Addition of sulfur decreases total cadmium uptake but increases cadmium translocation in soybean

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Cadmium (Cd) is a toxic metal that is increasing in concentration in agricultural soil due to anthropogenic activity (e.g., industrial waste, impure fertilizers). Contaminated crops could pose a potential health risk for consumers. Many studies have reported the positive effects of exogenous sulfur (S) in reducing Cd uptake and translocation in rice (*Oryza sativa*). However, the extent to which this phenomenon applies to other crop species is unknown. Soybean (*Glycine max*) seedlings were grown hydroponically in a full factorial design with 0 or 20 uM $CdCl_2$ and 0, 2.5, or 5 mM Na_2SO_3. The total amount of Cd taken up decreased from 72.5 ± 0.1 ug per plant (no S added) to 18.9 ± 0.04 ug per plant (5 mM S added) despite the S-induced 10-15% increase in bioavailable Cd in solution. Within S-treated root cross sections, more Cd was localized at the exodermis, less Cd was in the stele, and Casparian bands were visibly thicker. These patterns suggest reduced opportunity for Cd to enter the xylem and to be translocated aboveground. However, proportionately more of the internal Cd was translocated to the shoots (31% of total Cd with no S added; 88% of total Cd with 2.5 and 5 mM S added). Soybean is therefore an unsuitable crop for growth on Cd-contaminated soils treated with exogenous S.

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P12. Impacts of root-associated fungi on tree growth under elevated temperature and CO_2

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Growth of poplars, an economically important group of trees, has been declining due to elevated temperatures and droughts associated with climate change. Symbiotic microbes, such as root-associated fungi (RAF) may increase plant growth under climate change conditions, by altering tree metabolic profiles and increasing tree access to water and nutrients. To address this hypothesis, three RAF were isolated from poplar roots in the field. We then determined the effects of RAF inoculation on poplar growth under a range of future climate scenarios: ambient (400 ppm) or elevated CO_2 (750 ppm) with either ambient temperatures, or a +4 ˚C or +8˚C warming treatment. Colonization of poplar roots by RAF increased with elevated temperature and CO_2 with some RAF having up to a 336% increase. Inoculation with RAF did not increase plant height or total dry weight in plants grown at ambient CO_2. However, inoculated trees grown under +4 °C with elevated CO_2 were taller and had greater biomass than trees from ambient CO_2 treatments with either ambient or +4 °C temperatures. Non-inoculated trees also had a significant increase in biomass when grown at higher CO_2 and temperature conditions, although this CO_2 effect was reduced in the +8 °C treatment. Our results suggest that RAF increases tree growth under moderate warming (+4 °C) and may provide resilience to future climatic stresses.

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P13. Characterization of the role of SPL9 in drought stress tolerance in *Medicago sativa*

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Climate change has caused previously ideal agricultural lands to experience events of drought resulting in decreases to crop yield. Understanding the molecular mechanisms that underpin the response of plants to drought stress is crucial to maximizing the efficiency of our available agricultural land through the deployment of drought tolerant cultivars. The role of SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 9 (SPL9), a target of miR156, was studied in alfalfa's (*Medicago sativa*) response to drought. SPL9 was found to affect alfalfa's phenotype and abiotic stress response by regulating the biosynthesis of anthocyanins. Transgenic alfalfa plants with RNAi-silenced *SPL9* (SPL9-RNAi) have decreased height, increased branching and decreased average internode length. In response to 12 days of withholding water, SPL9-RNAi plants show increased drought tolerance and decreased leaf senescence compared to wild-type (WT) plants. When comparing well-watered control and drought conditions, SPL9-RNAi plants show no decreases in fresh weight of above-ground tissue that is otherwise observed in WT plants. SPL9-RNAi plants are also better able to continue normal growth under drought stress. Significant differences in plant growth between control and stress conditions are not seen in SPL9-RNAi plants but are observed in WT plants. This study identifies SPL9 as a candidate molecular tool for improving alfalfa's, and potentially other plants', tolerance to drought stress.

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P14. Exposure to low phosphate and salinity differentiate root systems for two ecotypes of the extremophyte crucifer *Eutrema salsugineum*

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Eutrema salsugineum is halophytic relative of *Arabidopsis thaliana* with a close phylogenic relationship to Brassicaceae crops. We compared seedlings of two *E. salsugineum* ecotypes originating from the Yukon, Canada and Shandong, China for their capacity to cope with low phosphate (Pi) and salt. Yukon soils are typically high in salt and low in Pi, and a high tolerance to both stresses has been reported for Yukon *E. salsugineum* but not for other ecotypes. In this study we compared root growth and architecture for Yukon and Shandong seedlings growing on a gel medium containing variable combinations of Pi and NaCl. Low Pi produced Yukon seedlings with longer main roots and lateral roots, higher root and shoot biomass, as well as longer root hairs and higher root hair density compared to Shandong seedlings. The addition of 100 mM NaCl to low Pi media did not alter the accession-specific features related to root architecture. Under the low Pi treatment, elevated reactive oxygen species were detected in Shandong but not Yukon *E. salsugineum* roots. Histochemical staining of roots for endogenous phosphatases showed less activity in roots and root hairs of Yukon relative to Shandong *E. salsugineum* seedlings. Thus Shandong and Yukon *E. salsugineum* plants are differentially tolerant to low Pi despite both ecotypes sharing a high tolerance to salt and an extremophyte designation.

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P15. Molecular and biochemical assessment of mechanisms driving abiotic stress tolerance in *Medicago sativa* subsp. falcata

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Alfalfa (*Medicago sativa* L.) is the most extensively grown perennial forage legume in Canada, with a cropping area of approximately 4M Ha. Unfortunately, alfalfa production is hindered by adverse environmental conditions such as drought and salinity, which are expected to worsen in coming years in terms of their severity and frequency. Since the demand for ruminant products such as meat and milk is anticipated to expand considerably in the foreseeable future as a result of our growing population and increasing affluence, the need for highly productive alfalfa cultivars with enhanced climate resiliency will be vital. The objective of this project is thus to identify novel sources of genetic variation for the downstream generation of alfalfa germplasm with improvements in abiotic stress tolerance through comparative analyses with *Medicago sativa* subsp. *falcata*, which is a close relative of cultivated alfalfa (*M. sativa* subsp. *sativa*) that is known for its high levels of resilience to environmental pressures. Responses to drought and salinity in terms of both performance and biochemical alterations are currently being assessed. The results of this study will contribute to our understanding of the mechanisms behind the superior ability of *M. sativa* subsp. *falcata* to withstand unfavourable conditions, which will facilitate the development of novel alfalfa cultivars in the future.

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P16. RNAi-mediated down-regulation of stress-response regulators in alfalfa for the improvement of abiotic stress tolerance

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The livestock industry is vitally dependent upon our capacity to grow forage crops in a highly productive manner. While alfalfa (*Medicago sativa* L.) is the most widely grown of the perennial leguminous forages, unfavourable environmental conditions frequently have a considerable negative impact on its production. It is anticipated that such climatic events will increase both in their severity and frequency in the future as a result of climate change, and as such, there is an imminent need to improve alfalfa productivity through the development of cultivars that are resilient to various types of abiotic stress. Although several studies have shown promise in this regard, the vast majority have involved the stable over-expression of transgenes. Despite their potential for economic benefit, public concern and regulatory constraints surrounding the use of such technology for trait improvement have proven challenging. Therefore, the aim of this project is to assess the effect of down-regulating a selection of gene homologs in alfalfa shown previously in other species to act as negative regulators of stress response. Six such homologs have been identified in alfalfa, and RNAi genotypes targeting each homolog have been generated and are currently under assessment. Such targets have the potential to be utilized downstream for the development of novel alfalfa cultivars with superior climate adaptability using either conventional breeding or genome editing platforms.

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P17. Investigating the relationship of HD2 family histone deacetylases in response to drought stress in Arabidopsis thaliana

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Despite the evidence that plant-specific histone deacetylase 2 (HD2) family plays significant role in the abiotic stress responses of plants, the relationship of histone deacetylases (HDACs) among HD2 family in response to environmental stresses remains largely unknown. Objective of this study is to investigate the relationship of four HD2-type HDACs in Arabidopsis in response to drought stress. In-vitro yeast two-hybrid assay showed interaction of HD2A, HD2C and HD2D proteins among each other. This indicates that HD2A, HD2C and HD2D proteins may be related to regulate the abiotic stress response. All HD2 genes demonstrated significant variation in their expression under drought stress. T-DNA insertion mutant lines of each HD2 gene were screened and expression of all HD2 genes was analysed in each single *hd2* mutant line. To further study the HD2 family relationships, overexpression (OE) lines of each HD2 gene were developed. Expression of all HD2 genes in each HD2-OE lines will be analysed. Moreover, effect of OE and knockout of HD2 genes on primary root length, no. of lateral roots, plant total biomass and plant survival under drought stress will be studied to investigate the relationships of HD2 family members. Knowledge generated from this research will be useful to improve our understanding about the interactional role of HD2-type HDACs in mediating the plant response toward drought stress.

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P18. Genetic variation for yield formation traits affecting drought tolerance in commercial soybean [*Glycine max* (L.) Merr.] varieties adapted to Ontario

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Drought stress significantly limits soybean yields in Ontario, Canada, with demonstrated losses ranging from 8-24%. In a greenhouse experiment, we compared fifteen Ontario-adapted soybean varieties for their drought tolerance. Plants were grown in field soil amended with sand in 1 m long, 10-cm diameter rooting columns. The soil water content was maintained at 100% field capacity by daily weighing and watering until the R1 developmental stage. From R1 until maturity, columns were maintained at either 100% (control) or 50% (drought stress) capacity. There were significant variety and treatment effects for seed yield and yield components (pod number, seeds per pod, seed size) and related traits (whole-plant biomass, water use, and water use efficiency). The drought stress significantly reduced seed yield, pod number, whole-plant biomass, and plant water use each by about 50%. There were significant variety x treatment interactions for seed yield, pod number, and water use. Based on their ratio of seed yield between drought stress and control conditions, we identified two drought-sensitive varieties (*Saska* and *OAC Drayton*) and three drought-tolerant varieties (*OAC Lakeview*, *OAC Champion*, and *PRO 2715R*). Principal component and correlation analyses revealed that high water use efficiency under stress was strongly associated with high seed yield ratio. Drought-tolerant varieties were also those that maintained high water use, shoot dry matter, and pod number under stress conditions relative to control conditions.

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P19. Temporal shifts in oxidative stress and fermentative metabolites are associated with physiological injuries in postharvest pear fruit

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The fresh market period for European pear (*Pyrus communis* L.) fruit can be extended by their storage at low temperature under controlled atmosphere (CA; which includes low O_2 and/or elevated CO_2 partial pressures). A complementary practice involves the application of the ethylene antagonist, 1-methylcyclopropene (1-MCP). Both practices limit ripening events, such as softening and peel yellowing, which are simultaneous with endogenous ethylene production. Unfortunately, 1-MCP and CA can promote the occurrence of physiological injuries (e.g., internal breakdown and cavities of the flesh) during storage. Herein, we investigated whether the occurrence of physiological injuries in stored pears is correlated with altered oxidative stress and fermentative metabolite profiles. 'AC Harrow Crisp' pears were treated with or without 1-MCP, and then held at 0 °C under refrigerated air or CA; disorder symptoms and metabolites were assessed in all stored fruit. Senescent scald and internal breakdown were most evident in non-1-MCP-treated fruit stored under refrigerated air, but limited by 1-MCP and CA. Internal breakdown and senescent scald were associated with the accumulation of citrate and fumarate, respectively. Internal cavities were evident in 1-MCP fruit held under CA, which coincided with the accumulation of 4-aminobutyrate and alanine. All disorders were linked to antioxidant depletion within the fruit. In summary, the temporal shifts in oxidative stress and fermentative metabolites are key indicators of postharvest stresses that promote the deterioration of pears.

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P20. A novel method for irrigating plants, tracking plant water use and imposing water deficits on plants grown in artificial environments

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Gravimetric methods for measuring single plant water use and simulating drought stress involve frequent weighing and watering of pots. This is labour intensive, requiring heavy lifting on a daily basis over the course of weeks. Here, we describe a novel, non-gravimetric system that address these shortcomings. Each plant is grown in a 110-cm tall, 10-cm diameter tube filled with a mixture of fine turface and granitic sand. The tube is divided into an upper rooting section and a lower wicking bed section by a nylon mesh barrier that prevents root incursion into the lower section, but maintains capillary connectivity. As the plant dries the soil in the rooting section, the water is rewetted passively from the lower section. A float valve fed by a reservoir ensures that the water table in the lower section is maintained at a set height, and so water depletion from the reservoir serves as a measure of cumulative plant water use. Drought stress can be induced by repositioning the float valve to drop the water table in the lower section. This soil mixture displays an unusually steep reduction in volumetric soil water content (VSWC) with a small change in gravimetric potential, so lowering the water table reduces VSWC of the rooting section enough to induce a significant stress, reducing soybean plant water use by 53%, and plant biomass by 50%.

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P21. **Screening for heat stress resistant genotypes and evaluating heat stress effect on yield in hard red spring wheat when exposed to heat stress during flowering**

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The reproductive phase of wheat (*Triticum aestivum* L.) is highly sensitive to high-temperature stress. Temperatures above the growth optimum (23 ^{0}C) interfere negatively with the reproductive development processes, resulting in poor seed set and weight in wheat. The growing season temperatures are predicted to rise in the future by at least 0.2 ^{o}C per decade, which will affect wheat crop growth and development. Therefore, we are screening a recombinant inbred (RI) population (173 RI lines) derived from the cross between parental lines 'Attila' and 'CDC Go' that vary in their high temperature sensitivity with respect to seed yield. High temperature treatment (35 ^{0}C for 6 hrs for 6 days) was imposed at an early reproductive growth stage (BBCH 41-45) to the RIL population in a growth chamber environment. Results from an analysis of variance (ANOVA) found that heat stress significantly reduced the grain number per spike (by 23%), grain weight per spike (by 20%), plant height (by 6%), and flag leaf width (by 2%) in the RIL population. A significant interaction between RIL lines and temperature treatment main effect means for grain number per spike indicates that the RIL population varies in this trait with respect to temperature at flowering. We will determine if specific gene markers within the RIL population are associated with heat stress sensitivity on grain yield.

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P22. **Expression and localization of the Arabidopsis thaliana HOTHEAD protein in response to stress.**

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Plants live in constantly changing, often unpredictable environments and have evolved diverse strategies to adapt to these changes. The first line of defense for land plants is the cuticle – a layer which covers the epidermis on above ground organs and serves to protect them from desiccation, irradiation, and pathogens. In addition to playing a key role in defense, the cuticle mediates organ separation and expansion. Many genes involved in regulating cuticle formation and function have been identified through forward genetic screens and one such gene is *HOTHEAD* (*HTH*). Plants harboring mutant *hth* alleles show ectopic organ fusion, a phenotype resulting from changes in cuticle permeability. Transgenic plants expressing HTH translationally fused to fluorescent reporter gene constructs fully restore *hth* mutants to wild type and show that the HTH protein is associated with the endoplasmic reticulum (ER). Our studies show that HTH is localized to a specific set of stress inducible ER-derived organelles known as "ER bodies" and can be isolated from cell fractions enriched for ER bodies. These findings suggest that HTH plays a role in both cuticle formation and stress responses. To further investigate the role of HTH in stress response pathways, HTH transcript and protein expression patterns were examined under stress conditions and were found to respond to both wounding and salt stress.

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P23. **Analysis of Abscisic acid (ABA) accumulation stressed and non stressed Brassicaceae plants**

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In order to respond to changing environmental conditions, the survival of crop plants depends on their ability to mount a whole plant response. Taking these conditions into consideration, our objective is to determine how abscisic acid (ABA) accumulates in a whole plant in response to water stress, such as osmotic stress and drought. We investigated the spatial patterns of ABA accumulation in stressed and non-stressed *Brassica napus*plants (NAM-0 cultivar). During vegetative growth, ABA levels were similar across different leaves of non-stressed plants, and osmotic stress induced ABA accumulation in the leaves whose ABA levels remained consistent across different leaves. During reproductive growth, ABA levels were highest in younger leaves of non-stressed plants and this pattern was consistent for stressed plants. The accumulation of ABA in young leaves was seen in both vegetative and reproductive growth stages showing that the plant prioritizes young leaves over older leaves. Using *B. rapa*,we also found that under osmotic stress conditions ABA accumulation increases significantly in whole plants when compared to non-stressed conditions. This result will allow a comparative study on spatial patterns of ABA accumulation under stressed and non-stressed conditions.

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P24. **The Drought Response Syndrome: A complex response mediated by water deficit severity and time**

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Drought is a critical factor constraining plant growth and development. Understanding the mechanisms by which forest trees respond to drought is of paramount importance. In this experiment on how hybrid poplar respond to different severity of water deficit, we find that poplar has different growth strategies in different water availability environment by different transcriptome activity. Moreover, samples collected at different time of day showed that transcription of internal circadian rhythm is predominant and has great interaction with transcriptome activities from water deficit.

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TOPIC 2: Agronomic Crop Production (Posters P25-P29)

P25. **Performances of early and late maturing oat varieties in cold regions, China**

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Oats are widely used in cold regions as forage and grain crop in China, with early maturing oat varieties having long planting history. However, the systematic evaluation on yield and quality of the oat varieties in these regions has not been conducted. Qinghai and Inner Mongolia are typically cold regions in China due to high elevation and high latitude respectively, and are representative areas for experimentation on growing oats in cold regions. In this study, we tested production and quality of early and late maturing oat varieties at five locations in Qinghai Province and one location in Inner Mongolia Autonomous Regions. The results showed that, in the regions of Qinghai Province with high altitude, forage yield and quality parameters of the early maturing varieties were not significantly different from those of the late maturing varieties. However, seed yield of the early maturing varieties (3702 kg/hm^2) was significantly higher than that of the late maturing varieties (2759 kg/hm^2). In the regions of Inner Mongolia with high latitude, the dried forage yield (3209 kg/hm^2) and seed yield (8110 kg/hm^2) of the early maturing varieties were significantly higher than those of the late maturing varieties. Therefore, early maturing oat varieties should be used as both cereal and forage in the cold regions.

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P26. **Yield stability of Canada Western Spring wheat under organically managed systems**

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Organically grown wheat normally needs to deal with multiple biotic and abiotic stresses to achieve high grain yield. There is an assumption that important traits to overcome such stresses have been lost as new wheat cultivars were bred under optimum growing conditions. Although the recognized advantages of old cultivars in organic systems, low yield potential in those cultivars need to be addressed. Moreover, yield stability under various stresses is not well explored between old and modern cultivars under organic systems. Therefore, in this study, fifteen spring wheat cultivars registered from 1910 to 2011 were grown in organically managed fields to evaluate whether old cultivars have more stable and higher grain yield compared to modern cultivars. Generally, modern wheat cultivars yielded well under tested organic fields. Modern wheat cultivars CDC Kernen and Superb showed high stability under tested environments, and their average grain yields were one of the highest among tested cultivars. CDC Stanley had the highest average grain yield but poor stability. According to AMMI biplots, CDC Stanley was high nitrogen responsiveness under adequate rainfall, while CDC Kernen and Superb yielded well even under dry conditions (e.g., 67 % of 30 years average precipitation). Our result indicated that high-yielding modern wheat cultivars can yield stable under organic systems. Further research is necessary to understand key traits in those modern cultivars that contribute to their yield stability.

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P27. What are the critical phenological periods in the annual development of intermediate wheatgrass for sustainable perennial grain production?

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Development of intermediate wheatgrass (*Thinopyrum intermedium*) as a perennial grain is well underway. The ability to manage grain production fields is necessary to provide producers with the needed confidence for production. Little has been published regarding the phenological development of intermediate wheatgrass. Experiments and trials have been ongoing at The University of Manitoba since 2011 and are now underway in France (2017 onwards). Data including key phenological events and the impact of temperature (growing degree days - gdd) and precipitation (ppt) have been collected. Based on data from Manitoba and France, a 13-hour day-length is hypothesized to be required for the induction of reproductive tiller elongation. Base temperature for gdd calculation appears to be 4°C. Critical growth periods are post-harvest through the fall where an interaction of gdd and ppt appears to be important. Once regrowth begins in the spring, (13-hour day-length) is needed for reproductive tiller elongation to begin (data and observations from France). Continued work is required to ascertain the impact of varying climatic impacts on grain productivity. Utilization of data collected in diverse global locations will aid in the determination of critical growth and development periods.

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P28. Effect of different colour rays on germination and mycoflora associated with maize caryopses

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In the present studies, seed treatment with different colour rays (red, blue, yellow, white and green) showed that green colour rays was effective for germination of seed as well as reduced the incidence of Aspergillus spp. Germination of maize seeds was significantly reduced due to the increase fungal infection and increase in storage time. Seed treatment with green colour rays was effective for the germination of maize seed followed by white and blue colour rays. Seed treatment with green colour rays significantly reduced the infection of Aspergillus spp. However incidence of A. fumigatus, A. niger and A. wentii was completely controlled in seed treated with blue, yellow, and green colour rays when stored for 30 days. Infection of Rhizopus species was highest in all rays treatments. Seed treatment with colour rays was not effective in the control of Rhizopus species. Decrease in infection of Aspergillus species and increase in germination was observed when seeds were treated with green colour rays followed by blue and transparent rays. Several works reported the effect of light rays in the control of fungal disease. They reported that green rays plays important role in the treatment of cancer disease. This ray should therefore, be effective to control the cancer producing fungi, like Aspergillus spp. A decrease in A. flavus infection up to 50% was found in seeds kept under green

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P29. **Phosphorus (P) and potassium (K) management in corn-soybean-winter wheat crop rotation in a long term experiment**

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Corn (*Zea mays* L.)-soybean (*Glycine max* L.) -winter wheat (*Triticum aestivum* L.) is a dominant crop rotation in Ontario. Increased production of these crops due to the adoption of higher yielding varieties and better management practices has led to a decrease in the soil P and K levels. Therefore, four long-term experiments established at Ridgetown (2013), Elora (2012), Lucan (2014), Bornholm (2012) were used to evaluate the grain yield response of corn, soybean, and winter wheat at four soil test P and K levels and five starter fertilizers. The four soil test levels were control (P <20ppm and K <120ppm), moderate P only (P >20ppm and K <120ppm), moderate K only (P <20ppm and K >120ppm), moderate P and K (P >20ppm and K >120ppm). Except control treatment, starter fertilizer treatments with different NPK grades were applied at crop-specific rates to attain the economic crop yields. At all the sites, grain yield of all three crops was significantly greater with moderate P and K treatment than control. In contrast, no significant difference in the grain yield was observed among the starter treatments under moderate soil P and K levels. Our results suggest the potential of achieving greater crop yield returns at moderate soil P and K levels and indicates less dependence of crop yield on the starter fertilizer application.

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TOPIC 3: Agronomic Cropping Systems & Soil Management (Posters P30-P40)

P30. **Lentil enhances the productivity and stability of oilseed-cereal cropping systems**

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Enhancing the stability of crop production is vital in agriculture under climate uncertainty. In this study, we assessed the effects of diversified rotation systems on the productivity and stability of oilseed-cereal cropping systems. A 3-year crop rotation system was tested for three cycles at three ecosites from 2013 to 2016. At each of the nine site-years, the phase-I of the rotation was summerfallow, lentil (*Lens culinaris*), and wheat (*Triticum aestivum*); followed by canola (*Brassica napus*), mustard (*Brassica juncea*), and camelina (*C. sativa*) in phase-II; and then by durum wheat (*Triticum durum*) in the phase-III. On average, lentil system increased system productivity, expressed by annualized durum wheat equivalent yield, by 24% and 78% compared with the spring wheat and fallow systems, respectively. Stability analysis revealed that the lentil – *B. juncea* – durum wheat and lentil – *B. napus* – durum wheat systems had the least variation across the environments and were well adapted to high-yielding sites. The integrated assessment of rotation cycles and fully-phased rotations revealed drought-related reductions in system productivity of 3-47% compared with normal weather. Quantitative assessments revealed that about 36% of the variation in system productivity were associated with crop rotation and additional 30% was weather-related factors. In conclusion, the inclusion of lentil in rotation enhances the productivity and stability of oilseed-cereal cropping systems in changing environments.

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P31. Pulse-cereal rotation affects soil carbon and the stability of system productivity

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Pulse-cereal rotations can increase short-term production, but little is known about if different types of pulses in rotations affect soil carbon, system productivity and stability in the long term. Chickpea-wheat (CW), lentil-wheat (LW), pea-wheat (PW) and continuous wheat (WW) were compared for four (4)-rotation cycles (in 8 years) at Swift Current, Saskatchewan, and Brooks, Alberta to determine how pulse type affects system performance in pulse-wheat rotation systems. Cumulative crop residue carbon during the 8-year-period was 33, 17 and 1% higher in the soil under PW system than those in CW, LW and WW, respectively. Cumulative residue soil N in the PW soil was 42, 17 and 57% higher than those in CW, LW and WW, respectively. At the 8-year end, soil carbon at 0-15 cm soil depth was similar among four rotations, while soil mineral N at 0-60 cm soil depth was 17, 4 and 14 kg N ha^{-1} greater in CW, LW and PW, respectively than in WW. Across the 4-rotation cycles, PW increased grain protein yields by 22-82%, 9-26% and 26-66% compared to CW, LW and WW, respectively. Stability analysis revealed that the PW system had lowest variation in yield and highest responsiveness to environments. In conclusion, pulse–wheat rotation provides an option to increase grain protein yield and enhance soil N sustainably.

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P32. Soil N gain from fall harvest to spring planting in soils under pulses, mustard and wheat

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Soil residual N is a critical factor to consider in establishing effective fertilizer programs in crop production. From fall harvest to planting time the next spring there is a 7-month between-crop fallow period on the northern Great Plains. Little is known about how much soil N gain (or loss) may occur during the period. Here, we quantified the amounts of N gained (lost) in the 0-30 and 0-60 cm soil under dry pea (Pisum sativum L.), lentil (Lens culinaris Medik.), chickpea (Cicer arietinum L.), mustard (Brassica juncea) and wheat (Triticum aestivum L.). Averaged across 21 site-years (Swift Current, Saskatchewan, and Brooks, Alberta, from 2010 to 2016), soils under lentil and pea gained an equivalent amount of N averaging 12.40 and 25.39 kg N ha-1 in the 0-30 and 0-60 cm layers, respectively, which was 149% and 62% greater than those under wheat. The soil under mustard had 76% lower N than that under lentil-pea but was 26% more than that under wheat. Soil N remained at crop fall harvest in the 0-60 cm layer ranged from 0.04 to 245 kg N ha-1, which influenced the soil N gain during the 7-month period, with the N-gain significantly ($P < 0.01$) greater in soils having a lower fall soil N. This information may be considered in developing fertilizer programs for cropping systems involving diverse crops in a rotation.

Yantai Gan (yantai.gan@canada.ca)

P33. Improving corn N fertilizer recommendations using rainfall effects on crop N demand

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Adequate Nitrogen (N) is critical in high yielding and profitable corn production systems. However, efficiency decreases when N fertilizer application exceeds crop N requirement resulting in significant environmental and economic costs. Data from a long-term N response trial at the Elora Research Station (Elora, Ontario) demonstrates large annual variation (140kg/ha to 260+kg/ha) in the Maximum Economic Rate of N (MERN) and suggests that precipitation is a significant source of variability in N response. We hypothesize that the existing Ontario corn N Decision Support System (DSS) can be improved by accounting for soil moisture effects on potential sink size and corn N demand. To test this hypothesis, we used over 120 N response curves and supporting data (weather, management, soil) generated from 1975-2017 on silt-loam soils at the Elora Research Station. Regressions between sums of rainfall during various growing periods over the season and MERN were conducted. Rainfall during June 15th to July 15th (the one month period before silking) was the most predictive of MERN while other time periods (i.e. early spring, grainfill) were non-predictive. Inclusion of a rainfall correction factor in the Ontario Corn N DSS significantly improved predictions of MERN. This rain-corrected DSS has significant potential to improve the economic and environmental sustainability of Ontario corn production.

Caleb Niemeyer (cniemeye@uoguelph.ca)

P34. Abiotic and biotic responses to cover crops and soil amendments in a vineyard

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Soil is the foundation of all agricultural systems and how it is managed can have implications on the structure and productivity of the entire agroecosystem. Agrominerals may have the potential to support soil systems in similar ways as synthetic fertilizers. In combination with cover crops, they may have synergistic benefits enhancing productivity. This study was conducted on an existing commercial vineyard in the Town of Lincoln, Ontario, to determine what effects a specific agromineral, Spanish River Carbonatite, and cover crops (either monoculture or mixture) would have on both biotic and abiotic variables such as soil nutrients, plant communities, and soil invertebrate community) over two growing seasons. While amendment type did not affect invertebrate community structure, cover crop combination mattered with monoculture of ryegrass resulting in higher plant species richness but mixtures having higher overall plant species diversity. Soil nutrients and plant and invertebrate diversities varied temporally, both seasonally and annually. Management techniques used by the grape grower most likely influenced amendment efficacy. To properly determine system effects of amendment and management technique, it is recommended that fields are monitored over a longer period considering the perennial nature of this agroecosystem and its complexity.

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P35. Using species and genetic diversity to address stand establishment issues in red clover (*Trifolium pratense*) as a Cover Crop

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Red clover (*Trifolium pratense*) frost seeded as a cover crop into winter wheat (*Triticum aestivum* L.) can experience poor stand establishment. Red clover enhances corn (*Zea mays* L.) yields by supplying nitrogen (N) to the subsequent corn crop and an additional rotational benefit. Despite red clover's positive ecosystem services, the variability in stand establishment has caused many producers to stop using red clover as a cover crop. This study addresses the stand establishment issue and examines the rotational benefit that red clover has on corn. The first objective is to examine if other clover species or blends of clover species result in more uniform clover stands. Three species of clovers [red, crimson (*Trifolium incarnatum*), and alsike (*Trifolium hybridum*)] will be used in pure-stands and in 2-way and 3-way blends. The experiment is a RCBD and consists of 3 location years, 6 replications, and 8 treatments. The second objective is to examine the rotation/clover effect on corn in the subsequent growing season. Half of each plot will be fertilized at a high rate of N to separate the N effect of clover from the rotation effect. In 2019, 4 additional treatments involving twin-row winter wheat were included in the clover trial, to compare conventional planting methods with wider row spacing intervals with regards to clover establishment. This research may allow for greater cover crop adoption in Ontario.

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P36. Common bean cultivar mixtures and crop productivity

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Common bean (*Phaseolus vulgaris* L.) is the most important legume crop used for direct human consumption. Canadian beans, especially large seeded cultivars of Andean origin, have relatively narrow genetic diversity. The objective of this study was to determine the effects of increasing in-field diversity, by using mixtures of bean cultivars instead of monocultures, on productivity. Seven diverse bean genotypes were evaluated at two Ontario locations as pure stands and binary mixtures in 2018. Conventional plot-based crop data were collected. Mixing efficiency was calculated from the yield data using a Relative Yield of the Mixture (RYM) index. Significant differences among seven bean genotypes and their mixtures were identified for all analyzed traits. A number of mixtures over-yielded component cultivars grown in pure stands. The results indicated multiple benefits of planting mixtures compared to monoculture, including higher RYMs. The research has the potential to provide a theoretical basis for the use of precision agriculture tools to plant fields with mixtures instead of monocultures. It could lead to greater in-field diversity in the crop and in the above and below ground ecosystems that might provide greater buffering capacity and resiliency to the cropping system as well as increased ecosystem services.

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P37. Exploring the potential of implementing pollinator friendly cover crop species in Southern Ontario.

Radcliffe, K.*; E. Lee; M. Raizada; B. Deen; N. Raine
University of Guelph

Pollinators provide ecological services crucial to the growth and development of many economically valuable crops. Research widely indicates a decline in both pollinator abundance and diversity across the agricultural landscape. In response the Ontario government developed a Pollinator Health Action Plan with the mandate of creating one million hectares of pollinator habitat. In Europe, strategies have been implemented to enhance pollinator habitat through the creation of semi-native habitats on marginal land. While margin plantings have been relatively successful, other research now suggests that the availability of mass flowering crops may have a greater impact on pollinator populations. What are some possible strategies for creating pollinator habitats within the agricultural landscape of SW Ontario, with particular attention to fall habitat? Is it possible to utilize cover crop species as a pollinator habitat, as they are abundant and relatively affordable? To address these questions, we are examining the potential of integrating these pollinator friendly species following winter wheat as a cover crop or as floral strips planted along field margins throughout the growing season. Preliminary results indicate that having a mix may be beneficial in attracting a larger diversity of pollinators and that the marginal land plantings may be more feasible in terms of coordinating fall flowering periods with crop rotations in Southern Ontario.

Kirsten Radcliffe (kradclif@uoguelph.ca)

P38. Stubble affects genetic potential for inorganic nitrogen cycling by root associated microbiomes of oilseed crops

Wang, L.[1]; Y. Gan[2]; L. Bainard[3]; C. Hamel[2]; M. St-Arnaud[4]; M. Hijri[1]
[1]*Université de Montréal and Jardin botanique de Montréal*
[2]*Agriculture and Agri-Food Canada*
[3]*Swift Current Research and Development Centre*
[4]*Université de Montréal and Jardin botanique de Montréal, Montréal*

Crop stubble may affect inorganic N-cycling pathways in soil as it influences microbial communities in plant roots and rhizosphere. Field experiments were conducted in the Canadian Prairies with five oilseed crops preceded by wheat, lentil or summerfallow in rotations. Seven microbial genes involved in N-cycling were quantified using RT-qPCR to determine gene expression for different pathways. The results showed a higher expression of archaeal *amo*A in rhizosphere microbiomes, while *nif* H, bacterial *amo*A, *nxr* A, *nir S* and *nos Z* had higher expression in roots. The highest overall expression of *nif* H and *nxr* A genes were found in oilseeds grown following lentil, which suggests more NH_4^+ and NO_3^- were derived with lentil. Bacterial *amo*A, *nir S* and *nir K* gene expression were highest in the *B. carinata* and lowest in the *C. sativa* microbiome, which suggests a higher potential for N_2O emissions with *B. carinata.* In root microbiomes, *nif H* gene expression had a positive correlation with oilseed yield and plant biomass, and negative correlation with bacterial *amo*A gene expression. In rhizosphere microbiomes, *nif H* and archaeal *amo*A gene expression were positively correlated, while bacterial *amo*A gene expression was positively correlated with *nxr* A and *nos Z* genes expression and plant biomass. This study showed that stubble from previous crops affects N-cycling pathways and the magnitude of the effect varies with oilseed crops.

Li Wang (li.wang.3@umontreal.ca)

P39. **Testing amendments and cover crops for improving soil health in vineyards**

Christie, R.[1]; R. Honor[1]; L. Vasseur[2]; Guinel, F.[1]
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[2]*Brock University*

With intensive agriculture, soils become impoverished because of nutrient depletion, structural changes, and reduction in microbial diversity. Vineyards are especially prone to soil degradation due to the heavy management required for effective yields. Using an operational vineyard in the Niagara Region, we tested whether amendments in combination with cover crops would be efficient at restoring soil health. Plots were exposed to one of the following treatments: an agromineral known as SRC, a synthetic fertilizer (N/P/K, 20/20/20), or water only (control) with either ryegrass or a mix of forbs and legumes. Soil properties, microbial abundance and respiration were measured. After two years, pH and microbial abundance decreased in all treatments. Date of soil collection impacted the base saturation of cations, especially that of Ca and K, which tended to decrease over the two-year period. The abundance of nitrogen-fixers was influenced by soil sampling date and cover crop, and that of phosphate-solubilizers was dependent on the soil sampling date + cover crop interaction. The microbial respiration varied significantly between cover crop and soil collection date, with ryegrass soil amended with SRC having the highest value at the end of the experiment. Although it is difficult to draw firm conclusions because of the complexity of the interactions, the results obtained so far suggest that cover crops play an important role in promoting vineyard soil health.

Frédérique Guinel (fguinel@wlu.ca)

P40. **Strike against Pseudomonas syringae: rye cover crop promotes a shift in squash phyllosphere bacterial abundance and plant gene expression**

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[1]*UQAM*
[2]*Agriculture and Agrifood Canada*
[3]*Université du Québec à Montréal (UQAM)*

Pseudomonas syringae, is considered one of the most important bacterial plant pathogens. Soil conservation practices, such as cover crops, are amongst tools that can contribute to reducing disease pressure caused by bacteria. We have recently demonstrated that leaf surface (phyllosphere) bacterial community structure changed when squash is grown with a rye cover crop treatment, followed by a decrease of *P.syringae* symptoms. In this work, our goal was to describe the differential bacterial abundance of the squash phyllosphere. We pursue the hypothesis that some abundant phyllosphere bacteria could explain the decrease in *P.syringae* population. Thus, we grew squash, within a two-year field, in four agricultural practices: bare soil, cover crops, chemically terminated cover crops and plastic cover. We sampled squash leaves at 3 different dates. From samples wash, total DNA was extracted and its 16S rDNA was sequenced and a bacterial bank was built with cultivable strains. With differential expression analysis (DeSeq2, LeFSe) we pinpoint abundant phyllosphere bacteria, issued from the cover crop treatment, belonging to *Sphingomonas* and *Methylobacterium* among others. Some of those bacteria were found in the bacterial bank and our current work involved in competition validation assays on petri dish against *P.syringae* population. We also measured gene expression from squash leaves. Plant expression profiles display strong correlation with treatments. The exploration of marker genes related to plant resistance is in progress.

Remi Maglione (remi.maglione@gmail.com)

TOPIC 4: Biochemistry, Metabolism, Photosynthesis (Posters P41-P68)

P41. **A central role for polyprenol reductase in plant dolichol biosynthesis**

Van Gelder, K.*; L. Virta; T. Akhtar
University of Guelph)

Dolichol is an essential polyisoprenoid within the endoplasmic reticulum of all eukaryotes. It serves as a membrane bound anchor onto which *N*-glycans are assembled prior to being transferred to nascent polypeptides that enter the secretory pathway. Historically, it has been posited that the 'rate-limiting' step in protein *N*-glycosylation, a process that affects the efficacy of approximately one fifth of the entire eukaryotic proteome, is determined by the extent to which dolichol accumulates. Therefore, this study aimed to enhance dolichol accumulation by manipulating the enzymes involved in its biosynthesis using an established *Nicotiana benthamiana* platform. Co-expression of a *Solanum lycopersicum* (tomato) *cis*-prenyltransferase and its cognate partner protein that catalyze the antepenultimate step in dolichol biosynthesis led to a 400-fold increase in the levels of long-chain polyprenols but resulted in only modest increases in dolichol accumulation. However, when combined with a newly characterized tomato polyprenol reductase, dolichol biosynthesis was enhanced by approximately 20-fold. We provide further evidence that in the aquatic macrophyte, *Lemna gibba*, dolichol is derived exclusively from the mevalonic acid (MVA) pathway with little participation from the evolutionary co-adopted non-MVA pathway. Taken together these results indicate that to effectively enhance the *in planta* accumulation of dolichol, coordinated synthesis and reduction of polyprenol to dolichol, is strictly required.

Kristen Van Gelder (kvangeld@uoguelph.ca)

P42. **Cytochrome P450 and O-methyltransferase catalyze the final steps in the biosynthesis of the anti-addictive alkaloid ibogaine from Tabernanthe iboga**

Farrow, S.; M. Kamileen; S. O'Connor
The John Innes Centre

Monoterpenoid indole alkaloids are a large and structurally diverse class of metabolites restricted to a limited number of plant families in the order Gentianales. Tabernanthe iboga is native to western equatorial Africa and has been used in traditional medicine for centuries. Howard Lotsof is credited with bringing iboga to the attention of modern medicine through his discovery that iboga can alleviate opioid withdrawal symptoms. Since this observation, iboga has been investigated for its use in general addiction management. We were interested in elucidating ibogaine biosynthesis to understand the unique reaction steps en route to ibogaine. Furthermore, because ibogaine is currently sourced from plant material, these will help improve the ibogaine supply chain through synthetic biology approaches. We used next-generation sequencing to generate the first iboga transcriptome and leveraged homology-guided gene discovery to identify the penultimate hydroxylase and final O-methyltransferase steps in ibogaine biosynthesis, herein named ibogamine 10-hydroxylase (I10H) and noribogaine-10-O-methyltransferase (N10OMT). Heterologous expression in S.cerevisiae (I10H) or E.coli (N10OMT) and incubation with putative precursors, along with HPLC–MS analysis, confirmed the predicted activities of both enzymes. Moreover, high expression levels of their transcripts were detected in ibogaine-accumulating plant tissues. These discoveries coupled with our publicly available iboga transcriptome will contribute to additional gene discovery efforts and could lead to the stabilization of the global ibogaine supply chain and its development as a treatment for addiction.

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P43. **Do r2r3-myb transcription factors directly regulate suberin biosynthesis?**

Garant, T.*; O. Rowland; J. Murmu
Carleton University

Suberin is a lipid heteropolymer that is deposited at plant-environment and tissue-tissue interfaces as a protective barrier. In the young roots of *Arabidopsis thaliana* suberin is found in the endodermis, where suberin prevents uncontrolled transcellular, and possibly apoplastic, movement of water and nutrients to and from the central vasculature. Controlling the movement of water and nutrients in the roots throughout development and in response to abiotic stress are vital to plant health. R2R3-MYB transcription factors (TFs) promote root suberin production constitutively and in response to abiotic stress, but it is unclear if they directly target suberin biosynthetic genes. The promoters of suberin biosynthetic genes can be sufficient for expression in the root endodermis. These promoters are rich in potential R2R3-MYB TF DNA binding motifs and contain many bHLH TF and WRKY TF DNA binding motifs. This suggests that each R2R3-MYB TF may form a complex with bHLH and WRKY TFs, when regulating suberin biosynthetic genes. Future work will use yeast-one-hybrid and promoter activation assays to confirm if R2R3-MYB TFs, and potential interacting partners (bHLH and WRKY TF), directly bind to and activate the transcription of suberin biosynthetic genes. Determining how suberin is regulated will improve our understanding of suberin production and how root suberin functions. This knowledge may lead to the development of hardier crops through improved root suberin content.

Timothy Garant (timgarant@cmail.carleton.ca)

P44. **Processing strategies to reduce the level of acrylamide formation in potato chips, and their influence on reducing sugar and asparagine concentrations**

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[2]*Alberta Agriculture and Forestry*
[3]*Agriculture and Agri-Food Canada*)

Potato chips contribute to the dietary intake of acrylamide, a probable carcinogen in heat-processed foods. The aim of this study was to determine the effects of frying conditions and additive treatments on the levels of reducing sugars, asparagine and acrylamide formation in fried potato chips. Three commercial potato cultivars (Atlantic, Snowden, and Vigor) were tested using different frying time (3, 5, and 7 min) and temperature (160, 170, 180, and 190°C) conditions. Acrylamide formation in potato chips increased with the frying time and temperature, and was accompanied by significant losses of reducing sugars and asparagine. The lowest acrylamide levels were detected in Snowden potato chips. Decreasing the frying temperature from 190 to 160°C for 7 min mitigated the acrylamide formation in processed potato chips of Atlantic, Snowden and Vigor by 84%, 67% and 78%, respectively. Acrylamide formation in potato chips was also examined after blanching potato slices in additive treatments before frying. The highest reduction (19-59%) was observed in potato samples that were blanched in distilled water. Among other blanching methods, the presence of 0.1 M glycine significantly reduced the acrylamide formation in potato chips from cultivars Atlantic and Vigor (by 49% and 27%, respectively), while 1% citric acid lowered acrylamide level in Atlantic (by 38%), and 1% acetic acid was effective at lowering acrylamide in Vigor potato chips (by 31%).

Dilumi Liyanage (kekulandala@uleth.ca)

P45. **Roadmap to potato suberin: an RNAseq approach**

Bernards, M.; K. Woolfson
The University of Western, Ontario

Suberin is a heteropolymer comprising a cell wall-bound poly(phenolic) domain (SPPD) covalently linked to a poly(aliphatic) domain (SPAD) that is deposited between the cell wall and plasma membrane. Potato tuber skin contains suberin to protect against water loss and microbial infection. Wounding triggers suberin biosynthesis in usually non-suberized tuber parenchyma, providing a model system to study suberin production. Spatial and temporal coordination of SPPD and SPAD-related metabolism are required for suberization, as the former is produced first after wounding, and the latter is synthesized later into wound-healing. Many steps involved in suberin biosynthesis remain uncharacterized, and the mechanism(s) that regulate and coordinate SPPD and SPAD production and assembly are not understood. Here, we took an RNA-seq approach to study broader transcriptional changes that occur during wound-healing. Our wound-healing transcriptome time-course illustrated that wounding leads to a substantial reconfiguration of transcription, followed by fine-tuning of responses dominated by suberization. Transcriptome analysis revealed that primary metabolic pathways demonstrate similar temporal expression patterns during wound-healing, but suberin-specific steps display distinct patterns at entire pathway and sub-branch levels. The observed transcriptional changes support a model in which wounding initially alters primary metabolism required to fuel SPPD, and subsequent SPAD, production. Overall, these findings offer further insight into the coordination and timing of metabolic and regulatory events involved in wound-healing and associated suberization.

Mark Bernards (bernards@uwo.ca)

P46. **Roadmap to potato suberin: an RNAseq approach**

Bernards, M.; K. Woolfson
The University of Western Ontario

Suberin is a heteropolymer comprising a cell wall-bound poly(phenolic) domain (SPPD) covalently linked to a poly(aliphatic) domain (SPAD) that is deposited between the cell wall and plasma membrane. Potato tuber skin contains suberin to protect against water loss and microbial infection. Wounding triggers suberin biosynthesis in usually non-suberized tuber parenchyma, providing a model system to study suberin production. Spatial and temporal coordination of SPPD and SPAD-related metabolism are required for suberization, as the former is produced first after wounding, and the latter is synthesized later into wound-healing. Many steps involved in suberin biosynthesis remain uncharacterized, and the mechanism(s) that regulate and coordinate SPPD and SPAD production and assembly are not understood. Here, we took an RNA-seq approach to study broader transcriptional changes that occur during wound-healing. Our wound-healing transcriptome time-course illustrated that wounding leads to a substantial reconfiguration of transcription, followed by fine-tuning of responses dominated by suberization. Transcriptome analysis revealed that primary metabolic pathways demonstrate similar temporal expression patterns during wound-healing, but suberin-specific steps display distinct patterns at entire pathway and sub-branch levels. The observed transcriptional changes support a model in which wounding initially alters primary metabolism required to fuel SPPD, and subsequent SPAD, production. Overall, these findings offer further insight into the coordination and timing of metabolic and regulatory events involved in wound-healing and associated suberization.

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Note: ***P45*** and ***P46*** are part of one large poster that requires two poster spots

P47. Post-translational modification in the regulation of starch branching enzyme 2.2 from *Arabidopsis thaliana*

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Starch, an insoluble carbon store comprised of glucose chains found in higher plants, is a major component of the human diet. Unlike storage starch which is produced for long term or cross-generational energy storage, transient starch is produced and degraded over the diurnal cycle. This temporary store of carbon in chloroplasts provides a source of energy and fixed carbon while plants are not photosynthesizing. Biosynthesis occurs through the coordinated activity of multiple classes of enzymes. Starch synthases polymerize ADP-glucose into linear α-glucan chains, while starch branching enzymes (SBE) introduce branch points to the growing glucan. SBEs form phosphorylation dependent complexes with other starch biosynthetic enzymes important for normal function. Two SBE isoforms exist in Arabidopsis (SBE2.1 and SBE2.2), of which SBE2.2 accounts for most of the measurable activity. Recombinant SBE2.2 was phosphorylated by chloroplast extracts on residues Ser^{290} and Ser^{301}. Site-directed mutagenesis was used to alter a conserved putative protein-protein interaction domain, phosphorylatable serines, and Cys residues 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 *sbe2.1/sbe2.2* knockout Arabidopsis line with wildtype and mutated SBE2.2 sequences. Effects on starch biosynthesis and granule structure will be determined. This research is significant for its applications to crop production and targeted manipulation of starch structure.

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P48. Natural variation in glucosinolate profiles in *Camelina sativa* and its wild relative

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Glucosinolates (GSs) are the major limiting factor for the use of *Camelina sativa* seed meal in animal feed. In addition to their bitter taste, GSs can be toxic at high levels. The goal of our work was to evaluate GS composition in *C. sativa* and its wild relatives to determine whether there is potential for introducing wild germplasm into breeding programs.

Three major glucosinolates were identified in our study using LC-MS/MS and were shown to have species-specific profiles. Principal component analysis revealed similar clustering at the metabolome level suggesting that GSs are chemotaxonomic markers for *Camelina* species.

Quantification by HPLC showed that *C. microcarpa* cytotypes 4x and 6x had the lowest total GS content. Interestingly, these same species had relatively higher amounts of GS nitrile (GSn) and GS isothiocyanate (GSi) degradation products indicating that there are species-specific differences in GS catabolism. *C. laxa* and the two *C. hispida* subspecies, which also had relatively low total GS content, had the lowest GS catabolite levels.

Based on differences in GS composition and metabolism, some wild relatives could be incorporated into breeding programs to reduce GS levels in *C. sativa*.

Lisa Amyot (Lisa.Amyot@canada.ca)

P49. Quality aspects of cooked early potatoes in relation to polyphenols/antioxidant content using a new LC-MS/MS technique (method development and application)

Varilla, C[1, 2]*, R.G. Pinhero[1], R.Y. Yada[3] and M. F. Marcone[1]
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[3]Faculty of Land and Food Systems, University of British Columbia

Potatoes are a valuable dietary food due to their diverse functional ingredients including protein, fiber, vitamins and phytochemicals. Genotype, maturity, color of the flesh and skin and processing conditions can affect the content of phytochemicals such as polyphenols. The objective of this study was to identify early potato varieties with higher phytochemical content by examining eight varieties with respect to their polyphenol contents using a new LC-MS-MS technique. Cooking methods included retrogradation (boiling followed by refrigeration at 4°C), retrogradation and reheating in the microwave, baking and microwaving. Phenolic acid (caffeic acid, chlorogenic acid, neochlorogenic acid and quinic acid) as high as 16 ppm were found in all eight varieties. Anthocyanidin- cyanidin as high as 40 ppm were found in Red Thumb and Purple fiesta varieties, while anthocyanidin-malvidin as high as 300 ppb was only found in Purple Fiesta.

Carolina Varilla (cvarilla@uoguelph.ca)

P50. Are sensory attributes of potatoes affected by the polyphenol contents?

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[2]AFL – Laboratory Services Division-University of Guelph
[3]Faculty of Land and Food Systems, University of British Columbia

Potatoes especially the colored varieties contain substantial levels of dietary polyphenols, and are the third leading source of dietary antioxidant in North America. These phytonutrients promote cardiovascular health, have chemo-preventative and anti-inflammatory properties. Genotype, maturity, color of the flesh and skin and processing conditions can affect the content of phytochemicals such as polyphenols. The objective of this study was to identify early potato varieties with higher phytochemical contents as well as the consumer preference by studying eight varieties with color ranging from white, yellow, red and purple. The highest total phenolic content was found in Red Thumb whereas the highest total flavonoid and anthocyanin contents were observed in Purple Fiesta. Highest antioxidant contents were observed in Purple Fiesta and Red Thumb. The flavor, texture and overall liking evaluated by a sensory panel identified French Fingerlings, Yellow Star and Smart as the most preferred varieties.

Carolina Varilla, cvarilla@uoguelph.ca

P51. Isoflavonoid metabolon and arogenate dehydratases in soybean (*Glycine max*): Identification and Functional Characterization

Sirjani, R.[*1]; K. Pannunzio[1]; S. Kohalmi[1]; S. Dhaubhadel[2]
[1]*The University of Western Ontario*
[2]*Agriculture and Agri-Food Canada*

Specialized metabolites in plants are imperative for a variety of stress response mechanisms. Understanding the processes by which these metabolites are synthesized may help to improve the genetic manipulation of crops. Previously we demonstrated the existence of an isoflavanoid metabolon in soybean. Among many phenylpropanoid enzymes, two arogenate dehydratases (ADTs), necessary for the synthesis of phenylalanine in plants, were shown to be part of the isoflavanoid metabolon. This was surprising as the isoflavanoid metabolon is anchored to the endoplasmic reticulum, but GmADTs mostly localize to the chloroplast. Phenylalanine is a precursor to many specialized metabolites, including isoflavanoids. In other plants, some ADTs have been shown to possess prephenate dehydratase (PDT) activity, which catalyzes an alternate route of phenylalanine synthesis. Soybean contains 9 putative GmADTs, some of which may possess PDT activity. Here, we aim to functionally characterize all GmADTs for their ADT/PDT activity. Six GmADTs were cloned into a yeast expression vector and transformed into *pha2*, a knockout yeast strain that lacks PDT activity rendering the strain unable to synthesize phenylalanine. PDT activity of GmADTs were determined by testing transformants for their ability to complement *pha2* on media without phenylalanine. Among the six GmADT isoforms, GmADTU4 and GmADT12B were able to grow on media lacking phenylalanine, demonstrating their ability to convert prephenate to phenylalanine. Characterization of other GmADTs for their PDT/ADT activities is ongoing.

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P52. Photoacclimation to high-light in *Chlamydomonas reinhardtii* during senescence relies on generating high-quenching centres at detached antenna

Meagher, E.; P. Rangsrikitphoti; B. Faridi; D. Durnford
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Microalgae can respond to increases in light intensity by altering the concentration of photosynthetic complexes. In exponential phase, the ability of *Chlamydomonas reinhardtii* to acclimate to excess light is, in part, dependent on cell division to reduce the concentration of photosynthetic complexes. But, when *Chlamydomonas reinhardtii* cells reach stationary phase, their ability to divide is limited. Our goal is to dissect excess-light responses as cells approach stationary phase and to determine how the kinetics and strategies of photoacclimation differ compared to cells in the exponential-growth phase. Cultures grown to late exponential enter a declining growth phase, where cells continued a slow rate of growth for the next seven days in both low (LL) and high-light (HL). Both cultures experience a conditional senescence-related decline in chlorophyll levels, that is accelerated in HL. In HL, however, there is a rapid decline in PSII reaction centers while the LHCII antenna remains stable. This was paralleled by a rapid and sustained increase in Fo under HL that is absent under LL and only present in cells approaching stationary phase. The antenna act as pH-dependent, quenching centres, presumably to protect the senescing chloroplast against HL. Ultimately, the photoacclimation mechanism in senescing cultures is distinct and shields the photosynthetic apparatus from excess light by long-term degradation of the PSII reaction centres, changes that coincide with the induction of autophagy.

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P53. Investigating high acetate as a regulator of senescence in *Chlamydomonas reinhardtii*

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While microalgae are typically immortal, cells approaching stationary phase when grown in batch culture initiate senescence that can lead to cell death. How microalgae proceed through senescence and their longevity in stationary phase depends on a number of factors. We tested the contribution of heterotrophic nutrition and light levels on longevity in stationary phase cultures of *Chlamydomonas reinhardtii*. We determined that cellular senescence is accelerated under high-acetate (30mM) compared to low-acetate (10mM) conditions. Interestingly, this high-acetate acceleration of senescence can be rescued by reducing light intensity, but so did increasing light intensity to moderate levels. Longevity of cells under different light intensities and acetate conditions was inversely related to starch accumulation. To explore this relationship, we examined stationary phase longevity in *Chlamydomonas* mutants with different capacities for starch accumulation. We found that decreased starch biosynthesis is correlated with a greater longevity of cultures in stationary phase. From these results, there is an unanticipated relationship between longevity and the use of starch reserves. Furthermore, the protective effects of low and high light illustrate the complexity of carbon metabolism in mixotrophic organisms. Our findings contribute to the understanding of how microalgal carbon reserves affect survival under growth-limiting conditions in response to carbon and light availability.

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P54. Establishing a link between flavonol catabolism and auxin-mediated stem growth

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Flavonols occur as glycosides in plants. In Arabidopsis, flavonol bisglycosides accumulate in response to high light intensity, nitrogen deficiency and low temperature. Moreover, the flavonol bisglycoside kaempferol 3-*O*-α-rhamnoside-7-*O*-α-rhamnoside restricts stem elongation by inhibiting the basipetal movement of endogenous auxin (i.e., indole-3-acetic acid). Our lab has demonstrated that the catabolism of flavonol 3-*O*-β-glucoside-7-*O*-α-rhamnosides in Arabidopsis shoots requires hydrolysis by the β-glucosidase BGLU15; all other flavonol bisglycosides (e.g., kaempferol 3-*O*-α-rhamnoside-7-*O*-α-rhamnoside) are not degraded in BGLU15 knockout mutants (*bglu15*). Here, we investigated whether indole-3-acetic acid levels and stem growth are altered in *bglu15* plants. Initiation of the primary inflorescence stem was delayed, stem length was decreased, and flavonol 3-*O*-β-glucoside-7-*O*-α-rhamnoside levels were up to 10% greater in the apical region of *bglu15* stems, compared to wild-type plants, but not in the middle and basal longitudinal regions of the stem. The levels of other flavonol bisglycosides were not altered by the *bglu15* mutation, regardless of the longitudinal stem region. Also, the levels of indole-3-acetic acid were as much as 28% greater in the apical region of *bglu15* stems relative to those of wild-type plants. These results suggest that flavonol 3-*O*-β-glucoside-7-*O*-α-rhamnoside accumulation in the stem apex modulates auxin distribution in the primary inflorescence stem. Future research will investigate whether polar auxin transport is reduced and whole plant morphology is altered in *bglu15* mutants.

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P55. Interactions between starch biosynthetic enzymes and 14-3-3 adaptor proteins in maize endosperm

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Storage starch deposited within the endosperm of cereal grains supports the majority of human caloric intake and serves several industrial applications. The process of synthesizing starch in storage tissues occurs within amyloplasts and is a highly regulated process involving the activities of various starch synthases (SSs), starch branching enzymes (SBEs) and starch debranching enzymes (DBEs). In *Zea mays*, amyloplasts display a phosphorylation-dependent trimeric protein complex formed between two starch synthases and a starch branching enzyme, SSI-SSIIa-SBEIIb. However, the precise nature of these interactions remains elusive. A class of regulatory proteins called 14-3-3 have been hypothesized to facilitate protein-protein interactions associated with a phosphorylation-dependent complex. Ubiquitous within all eukaryotes, 14-3-3 proteins are known to bind numerous client proteins at specified phosphorylated motifs. Such interactions can elicit altered enzyme activities, localization or provide scaffolding for protein interactions of client proteins. Large proteomic analyses from maize and barley whole cell extracts have shown 14-3-3 to interact *in vitro* with enzymes related to various biological processes including primary carbohydrate metabolism. To establish a regulatory role for 14-3-3 proteins in starch biosynthesis the subcellular localization of an amyloplast specific isoform was determined. Expression of a recombinant tagged 14-3-3 was used in combination with pull-down assays to identify *in vitro* putative interactors from amyloplast lysate.

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P56. Functional characterization of *Arabidopsis thaliana* HXXXD-motif (BAHD) acyltransferases involved in suberin metabolism

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Plants synthesize suberin, a lipophilic extracellular barrier that controls water and nutrient loss and protects plants against pathogen infection. In *Arabidopsis thaliana*, suberin is deposited in the cell walls of seed coats, endodermis, and periderm of roots. Suberin is a complex polymer formed by an aliphatic polyester and an aromatic polymer, co-deposited with soluble waxes. The aliphatic polyester is composed of ω-hydroxy fatty acids, α,ω-dicarboxylic acids, fatty alcohols, glycerol, and ferulate. Alkyl ferulates, alkyl coumarates and alkyl caffeates are major components of suberin-associated root waxes, which also contain alkanes, fatty acids and fatty alcohols. Two enzymes of the HXXXD-motif family of acyltransferases, ASFT (*AT5G41040*) and FACT (*AT5G63560*), function as feruloyl- and caffeoyl-CoA transferases, respectively. However, the enzyme responsible for transferring coumarate remains unknown. Individual mutants of these enzymes are not affected in either alkyl coumarates or suberin-bound coumarate, but *in vitro* both enzymes can transfer coumaroyl-CoA to fatty alcohols, suggesting that these enzymes may have partially redundant function in suberin and wax biosynthesis. To investigate redundant functionality *in vivo*, we generated double mutants (*asft x fact*). In addition, co-expression analysis with suberin-specific genes identified two BAHD candidate genes. We will report our progress in the characterization of *asft x fact* double mutants, and the new candidate genes.

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P57. Understanding the regulatory role of rbcL RNA S1-Binding domain (RLSB) protein in the single-cell C4 species *Bienertia sinuspersici*

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Compartmentalization of RuBisCO in C_4 plants prevents its premature interaction with atmospheric O_2 and allows for the C_4 pathway enzymes to concentrate CO_2 first, thereby reducing oxygenase activity. *rbc*L RNA S1-Binding domain protein (RLSB), encoded by the nuclear RLSB gene, has been previously implicated to play a role in the post-transcriptional regulation of the plastid encoded RuBisCO large subunit (*rbc*L) in C_3 and Kranz-type C_4 plants. RLSB, after import into chloroplasts, has been suggested to bind and stabilize *rbc*L transcripts in *Arabidopsis* (C_3) and *Zea mays* (Kranz - C_4), thus preventing degradation and promoting translation. RLSB has also been shown to post-transcriptionally regulate other plastid encoded genes via transcript stabilization and/or translational activation in the C_3 and Kranz-type C_4 systems. The following work aims to characterize the role of the RLSB homolog (BsRLSB) found in the model single-cell C_4 species *Bienertia sinuspersici*. Subcellular localization studies using RLSB-GFP fusions in protoplasts demonstrate chloroplast localization of the BsRLSB homolog and reveal that only the first 65 amino acids of BsRLSB are necessary and sufficient for the observed chloroplast import. Preliminary in-vitro binding assays reveal a BsRLSB interaction with the 5'UTR of the *rbc*L transcript derived from the *BIenertia sinuspersici rbc*L gene. This work will further our understanding of the mechanisms governing compartmentalization of RuBisCO and other plastid-encoded genes in single-cell C_4 species.

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P58. Biochemical evidence for flavonol α-rhamnosidase activity in plants

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Flavonols are plant antioxidants and photoprotectants that are bioactive in humans. In various plant species, including *Arabidopsis thaliana*, flavonols accumulate as rhamnoside conjugates, such as kaempferol 3-*O*-β-glucoside-7-*O*-α-rhamnoside, during abiotic stress. Recently, we determined that flavonol 3-*O*-β-glucoside-7-*O*-α-rhamnosides are catabolized to flavonol 7-*O*-α-rhamnosides in *Arabidopsis* leaves during the recovery from simultaneous nitrogen deficiency and low temperature stresses. The transient accumulation of flavonol 7-*O*-α-rhamnosides during the recovery from abiotic stress implies they are further catabolized *in planta*. We hypothesize that flavonol 7-*O*-α-rhamnoside degradation in plants is dependent upon α-rhamnosidase activity. High-performance liquid chromatography analysis revealed cell-free *Arabidopsis* leaf extracts contained α-rhamnosidase activity against various 7-*O*-α-rhamnosylated flavonols. This activity was highest in leaves of 5 week-old plants, and was inhibited in assays containing the monosaccharide rhamnose. Negligible activity was present in roots and stems. Preliminary analysis points to a similar flavonol 7-*O*-α-rhamnoside α-rhamnosidase activity in radish leaves. Consumption of flavonol-rich foods reduces the risk of chronic illnesses; thus the on-going biochemical and functional characterization of flavonol α-rhamnosidase activity in plants will facilitate biotechnological strategies aimed at boosting flavonol levels in genetically-related crucifer crops. Moreover, as flavonols are known to inhibit auxin-mediated plant development, this research will provide knowledge on the relationship between flavonol catabolism and renewed growth following transient abiotic stresses. This information is crucial for maximizing agricultural productivity in regions that are prone to climate change.

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P59. **Genomic, chemical and functional analysis of adult leaf cuticle development in maize**

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The cuticle is the outer physical barrier of plants and establishes a vital interaction interface with the environment. This hydrophobic layer consists of the lipid polymer cutin embedded with and covered by waxes, providing protection against environmental stresses including desiccation, UV radiation, and pathogen attack. Thickness, structure, and chemical composition of the cuticle vary widely among plant species, and even within a species, depend on organ identity, developmental stage, and growth conditions. The functional contributions of the maize cuticle and its components to abiotic and biotic stress responses have been rarely studied so far. Moreover, the cuticle biosynthesis and composition on the adult plant, agronomically the most important growth phase, are largely unknown. In this study, we utilized the expanding adult leaf as a model system to elucidate the timeline of maize cuticle development. We have characterized the cuticle maturation along the leaf developmental gradient functionally (by measuring cuticle permeability and resistance to water loss), biochemically (by performing a chemical analysis of cutin and waxes), and genetically (by conducting epidermal-specific transcriptomic analysis). Cross-referencing of the biochemical and transcriptomic data enabled the construction of gene regulatory and co-expression networks, revealing a previously undescribed function for PHYTOCHROME-mediated light signaling during cuticular wax deposition.

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P60. **The role of starch in the development, physiology, and reproduction of *Arabidopsis thaliana***

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Starch is an agronomically important polyglucan synthesized by plants as a means to store photoassimilates as an osmotically inactive carbon store for subsequent use in metabolism and growth. The synthesis of starch involves several enzymes working in concert, including starch branching enzyme (SBE), responsible for cleaving alpha-(1,4)-bonds on pre-existing glucan chains and reattaching them to the same or to neighbouring chains via alpha-(1,6)-linkages. SBE activity creates branch points and contributes to starch's semi-crystalline structure. Recently, SBEI and SBEIIb cloned from maize (*Zea mays*) endosperm were constitutively expressed in a starchless, null line of Arabidopsis, lacking endogenous SBEs. While both *Zm*SBEI and *Zm*SBEIIb were able to individually restore starch synthesis in the null line, transformants exhibited altered starch metabolism. Here, we have re-transformed the null line (*sbe2.1*$^{-}$*/sbe2.2*$^{-}$) as well as Columbia (Col-0) with *Zm*SBEI and *Zm*SBEIIb under the control of a CaMV 35S promotor, and are in the process of characterizing these lines. Functional complementation of Arabidopsis SBE null and Col-0 lines with maize SBEs represents a potential method to increase biomass and production in agronomically important oilseed crops such as canola, as well as to shape the physical characteristics of transient starch.

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P61. Characterizing a novel protein targeting mechanism to the outer envelope of chloroplasts

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The chloroplast contains roughly 3000 proteins, 95% of which are encoded by the nuclear genome and must be targeted to the chloroplast post-translationally. The majority of stroma targeted proteins possess a cleavable N-terminal transit peptide (TP) which is recognized by the translocon at the outer envelope membrane of chloroplasts (TOC complex). Recently, a TP-like sequence has been described at the C-terminus of a subset of chloroplast outer envelope proteins (OEPs), including one of the proteins in the TOC complex, Toc 159. This C-terminal TP-like sequence is hypothesized to represent a novel mechanism of OEP chloroplast targeting. This research project focusses on one of the proteins in the set of OEPs predicted to contain a C-terminal TP-like sequence, which has been named OEP15. Subcellular localization using transient expression assays have been performed in both onion epidermal cells and *Arabidopsis thaliana* protoplasts using an EGFP fusion construct to examine the subcellular localization of OEP15. The results of these localization assays are expected to aid in understanding of the new chloroplast outer membrane targeting pathway.

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P62. Exploring the role of the purple acid phosphatase AtPAP17 in Arabidopsis phosphate and ROS metabolism

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Purple acid phosphatases (PAPs) function in the recycling and acquisition of inorganic phosphate (Pi), a limiting macronutrient that is vital for plant growth. However, mammalian PAPs expressed in white blood cells participate in reactive oxygen species (ROS) metabolism and immunity/pathogen defense as they are 'moonlighting' enzymes that exhibit significant peroxidase in addition to phosphatase activities. Similarly, AtPAP17 (At3g17790), one of 29 predicted *Arabidopsis* PAP isozymes, is a 35-kDa PAP hypothesized to function in Pi and ROS metabolism owing to its marked induction during Pi starvation, leaf senescence, oxidative stress due to drought or excessive salinity, and fungal or bacterial pathogen-related biotic stress. No other *Arabidopsis* PAP shares this unique expression profile. We are integrating biochemical and genetic techniques to test AtPAP17's role in *Arabidopsis* Pi and ROS metabolism. A 35-kDa monomeric PAP exhibiting acid phosphatase and peroxidase activities was purified from the intracellular fraction and cell wall (CW) extracts of Pi-starved *Arabidopsis* and identified as AtPAP17. Transient expression of *AtPAP17-GFP* and imaging via epifluorescence microscopy confirmed AtPAP17 targeting to lytic vacuoles of Pi-deprived *Arabidopsis*. Loss of *AtPAP17* expression in an *atpap17* T-DNA mutant did not exert an obvious impact on ability of *Arabidopsis* to acclimate to nutritional Pi deprivation or to recycle Pi during leaf senescence. Work is in progress to assess oxidative stress and immune responses of the *atpap17* mutant.

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P63. Investigating post-translational regulation of UDP-Glucose pyrophosphorylase in maize endosperm

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Cereals are the most cultivated crops in the world, and the starch they produce represents a major component of caloric intake of the human diet. In cereal endosperms, starch synthesis requires the formation of precursors produced from the cleavage of sucrose in the cytoplasm which are imported into amyloplasts. Cytosolic UDP-glucose pyrophosphorylase (UGPase) plays an important role in producing and providing the precursor for starch biosynthesis. UGPase catalyzes a reversible reaction that contributes to sucrose and cell wall formation in the forward direction, and starch production in the reverse direction. In endosperm tissue UGPase uses UDP-Glc and inorganic pyrophosphate (PPi) to make Glc1P for starch biosynthesis, and Glc1P is in turn used by ADP-glucose pyrophosphorylase, the first dedicated step in starch formation. UGPase is ubiquitous and is known to be active as a monomer, showing reduced activity in an oligomeric form. While the role of UGPase in creating products used for starch synthesis is well understood, mechanisms that regulate this enzyme in relation to starch synthesis are unclear. A 14-3-3 binding motif at Ser-419, indicates the possible post-translational regulation of this enzyme *via* protein phosphorylation and protein-protein interactions during starch synthesis. The mechanisms of post-translational regulation for cereal endosperm UGPase in relation to starch biosynthesis are being studied and are suspected to involve a combination of redox modulation, protein phosphorylation, oligomer formation, and protein-protein interactions.

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P64. Investigating the functional evolution of plant shikimate kinase-like 1 (SKL1) in *Marchantia polymorpha*

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Chloroplasts house components of the photosynthetic machinery in addition to other critical metabolic processes and are thus essential for all living plants. The biogenesis of chloroplasts is a highly active area of study in plant biology. While there has been much progress in deciphering this complex process, many aspects are still not well understood. One example is shikimate kinase-like 1 (SKL1), an ancient gene duplicate of shikimate kinase that arose during the evolution of land plants between 400 and 500 million years ago. The *skl1-8* T-DNA insertional mutants of *Arabidopsis thaliana* exhibit an albino phenotype with vesiculated plastids. One of our objectives is to investigate the evolutionary history of SKL1 through studies of the bryophyte *Marchantia polymorpha*, the most ancient characterized species of land plant. Our investigation has shown that this species possesses two highly similar homologs of SK with distinct regions of dissimilarity. We have shown that one homolog is an active SK (MpSK), while the other lacks such activity and is hypothesized to be a putative SKL1 (MpSKL1). We are currently engineering SK activity into MpSKL1 through the reintroduction of specific functional domains in order to investigate the functional diversification of MpSK into MpSKL1. We are also developing a MpSKL1 mutant using CRISPR-Cas9 technology in order to confirm its function as an SKL1. Further work will provide functional insights associated with SKL1.

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P65. Distinct metabolic modes drive variation in cyclic and acyclic monoterpenoid biosynthesis in *Pelargonium graveolens* chemotypes

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Pelargonium (scented geraniums) is a genus of flowering plant in the Geraniaceae known for its pleasing aromas. Its essential oils are used for fragrance and flavoring but also possess arachnicidal and antimicrobial properties. Despite its widespread use in the cosmetics and cleaning industries, little is known about *Pelargonium* essential oil biosynthesis. Here we demonstrate the contribution of at least two distinct metabolic pathways responsible for the characteristic monoterpenoid volatile blend in *Pelargonium*. The first group consists of the cyclic *p*-menthane monoterpenes (-)-isomenthone and (+)-limonene which resemble high value monoterpenes found in peppermint but with inverted stereochemistry. The second group, referred to here as citronelloid monoterpenes, include acyclic monoterpene alcohols such as geraniol and (-)-citronellol, and their ester and aldehyde derivatives. Using untargeted volatile profiling of 22 seed-grown lines of wild-type *P. graveolens* we identified 3 distinct chemotypes which predominantly accumulate either (-)-isomenthone, geraniol, or (-)-citronellol with minor contributions from approximately 80 other volatile compounds. We exploited the metabolic differences of these chemotypes in whole plant $^{13}CO_2$ isotopic labelling assays to determine that (1) the *p*-menthane monoterpenoids are likely synthesized from (+)-limonene via (+)-piperitone , (2) these two groups of monoterpenes utilize a common pool of geranyl diphosphate (GDP) precursor supplied by the 2*C*-methyl-D-erythritol-4-phosphate pathway and (3) downstream of GDP, these two pathways are functionally independent and do not appear to share common intermediates.

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P66. Mapping metabolic carbon partitioning in Arabidopsis rosette tissue using $^{13}CO_2$ labeling and ammonia chemical ionization mass spectrometry

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Flux studies in Arabidopsis have been facilitated by $^{13}CO_2$ whole plant labeling techniques, but calculation of percent atom labeling across broad classes of metabolites remains a formidable task due to the fragmentation inherent in electron impact GCMS analysis. Here we present a soft chemical ionization (CI) approach to analyzing label incorporation into primary metabolites of Arabidopsis rosette tissue. Compared to other CI reagent gases, ammonia features the highest proton affinity, resulting in little to no fragmentation of analytes during ionization. We exploited this property to simplify the calculation of label incorporation by preserving the intact molecular ion cluster containing unlabeled (M+0) and labeled isotopologs (M+n) for any central metabolite detectable in a standard GCMS metabolomics strategy. We then subjected the same samples to isotope ratio mass spectrometry for an unbiased measure of total ^{13}C label assimilated by each plant during each labeling experiment. In this fashion, we were able to establish the absolute commitment of freshly fixed carbon to major pathways of central metabolism. For instance, we determined that while total carbon assimilation in plants increased with increasing light intensity, the fraction of the total fixed carbon pool committed to sucrose biosynthesis remained constant (~19%). Meanwhile, the methylerythritol-4-phosphate pathway received only about 1/3% of the plant's total carbon budget. This technique provides a quantitative basis for assessing metabolic engineering efforts to reprogram plant metabolism.

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P67. Enhancing yield and biomass in canola by modifying carbohydrate metabolism

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Carbohydrates such as starch provide the stored energy reserves of plants. We previously developed a novel technology which caused a remarkable boost in seed yield in Arabidopsis by modifying starch metabolism. When the Arabidopsis endogenous leaf starch branching enzymes (SBEs) were replaced with maize endosperm homologues ZmSBEI or ZmSBEIIb, the plants demonstrated significant increases in starch biosynthesis and a dramatic increase in seed production. Canola (*Brassica napus* L.) is genetically close to Arabidopsis with highly conserved gene functions between the two species. The homologous SBEs in canola are assembled on both A and C genomes with very high identities to those in Arabidopsis. This provided a feasible strategy to apply the above technology to canola. Canola is allotetraploid with a more complicated genetic background and, since no SBE knockout mutants are so far publicly available, generation of a *Bnsbe* null mutant becomes a critical step for replication of this effect in canola. Gene editing using the CRISPR/Cas9 system has been applied to edit the endogenous SBEs and transgenic plants obtained through Agrobacterium-mediated transformation of cotyledons. Mutant lines containing different copies of SBEs have been characterized and the advantage of gene editing in canola and other crops are discussed.

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P68. Recent advances in plant ubiquinone (Coenzyme Q) biosynthesis and engineering

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Ubiquinone is a liposoluble and redox-active molecule that is made up of benzenoid and prenyl moieties. It serves as a vital electron carrier in the respiratory chain of mitochondria and some bacteria, and doubles as a potent lipid and protein antioxidant. Recent evidence from our laboratory indicates that land plants have evolved the unprecedented ability to derive the benzenoid ring of ubiquinone from the metabolism of phenylpropanoids (Plant Cell 26: 1938-1948). I will present data from gene network modeling combined with reverse genetics and isotopic tracer experiments in Arabidopsis and tomato that demonstrate that the cognate metabolic architecture is split into two branches, the first one originating from the β-oxidation of *p*-coumarate in peroxisomes, while the second one stems from the peroxidative cleavage of a flavonol, called kaempferol, in the cytosol (Plant Cell 30: 2910-2921). Having dissected the molecular determinants of such a cleavage, I will show that using a synthetic biology approach it is possible to capture this catabolic branch to re-route kaempferol towards the accumulation of ubiquinone in Arabidopsis leaves and tomato fruits. I will briefly discuss how this paradigm shift regarding the functional significance of flavonols in plant tissues offers new opportunities for increasing the nutritional value and stress resistance of crops.

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TOPIC 5: Bioinformatics and Systems Biology (Posters P69-P73)

P69. **Custom selected reference genes outperform pre-defined reference genes in transcriptomic analysis**

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RNA sequencing allows the measuring of gene expression at a resolution unmet by expression arrays or RT-qPCR. It is however necessary to normalize sequencing data before comparing expression levels. The use of internal control genes or spike-ins is advocated in the literature for scaling read counts, but methods for choosing reference genes are mostly targeted at RT-qPCR studies and require a set of pre-selected candidate controls or pre-selected target genes. We report an R-based script to select internal control genes based solely on read counts and gene sizes. This novel method first normalizes the read counts and then excludes weakly expressed genes. It then selects as references the genes with lowest Transcripts per Million covariance. We picked custom reference genes for the differential expression analysis of three transcriptome sets from transgenic *Arabidopsis* plants expressing fungal effector proteins tagged with GFP (using GFP alone as the control). The custom reference genes showed lower covariance and fold change as well as a broader range of expression levels than commonly used reference genes. When analyzed with NormFinder and geNorm, the custom selected genes were more stable than the typical references. The proposed method is innovative, rapid and simple. Since it does not depend on genome annotation, it can be used with any organism, and does not require pre-selected reference candidates or target genes that are not always available.

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P70. **Redundancy removal in de novo transcriptomes of Piper nigrum (black pepper)**

Doering, M.*; J. Stout (*University of Manitoba*) The computationally complex problem of *de novo* transcriptome assembly, without a reference genome, has led to numerous algorithms to reliably and intelligently piece together short reads. Each method has its own strengths, and tuning with different *k*-mers can further improve the assembled transcriptome. Over-assembling, using multiple methods to take advantage of unique strengths, is gaining recognition. Redundancy musst then be removed from the combined assemblies. CD-HIT-EST is commonly used, as is the EvidentialGene (evigene) pipeline which incorporates CD-HIT-EST, to select the longest assembled isoforms but erroneous selection of long incorrectly assembled contigs is possible. The homology BLAST method (HBM) removes redundancy by comparison with known protein-coding sequences. Despite being proposed four years ago, its usage has been cited only three times (once in plants) and never in over-assembled RNA-Seq data. We extracted RNA from *Piper nigrum* roots and sequenced 125 bp paired end reads on the Illumina HiSeq 2500 platform. Quality-trimmed reads were assembled with SOAPdenovo-Trans, TransABySS, and BinPacker with multiple *k*-mers. Redundancy was removed with evigene and HBM. The same assembly and redundancy removal methods were applied to an *Arabidopsis* read set from the NCBI short read archive to allow for comparison to the Araport11 gene models. To our knowledge, this is the first application of over-assembling a transcriptome of the polyploid *P. nigrum*, and the first application of HBM in the over-assembly context.

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P71. Using interactome and ubiquitinome datasets to identify substrates for Arabidopsis RING-type ubiquitin ligases (E3s) and the ubiquitin system

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Ubiquitination involves the attachment of ubiquitin, a small ubiquitous protein, to a substrate leading to different outcomes. For example, attachment of one ubiquitin may influence localization, while a polyubiquitin chain may result in degradation by the proteasome. E3s facilitate ubiquitin conjugation, govern substrate protein selection, and are involved many processes including stress responses, growth and development. However, lack of substrate identity prevents a comprehensive understanding of E3 function. Utilizing interactome datasets we found 1484 interactions for 200 RING-type E3s representing 830 potential interactors. Survey of selected publications found 3768 ubiquitinated proteins, and 144 are among the identified interactors. Using in vivo degradation and interaction assays we demonstrate that interactors, such as CIPKs, are bona fide substrates. ESCRT III (not I and II) components and 10 of 24 TCP transcription factors are among the interactors. Other transcription factor families, e.g. MYB and NAC, were less represented among both datasets. MAPKs were mainly associated with SINAT E3s, many of which are ubiquitinated. 250 interactions were found for the ATL E3s including 14-3-3 proteins (14-3-3χ is an ATL31 interactor), which are amongst proteins found most frequently within ubiquitinome datasets. Many interactors are associated with multiple E3s and vice versa. The membrane-localized pathogen-responsive NHL3 is ubiquitinated and associates with over 20 membrane-localized (predicted) E3s. COP1 has the majority of potential interactors (>50). Although limited, the available data sheds light on potential substrates for the RING-type E3s and ubiquitin system.

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P72. Transcriptional control of bacterial cell division in a nitrogen fixing symbiosis

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The *Sinorhizobium meliloti* ExoR/ExoS/ChvI transcriptional regulatory system controls a large number of genes, several of which are directly or indirectly involved in symbiosis with alfalfa. Disruption or inactivation results in root nodules that do not fully develop, and nitrogen fixation does not occur. Other associated phenotypes include inability to grow on complex media, sensitivity to acidic pH and detergents, decreased production of PHB, and altered motility and carbon source utilization. Previous work identified a number of genes that are directly bound by ChvI transcriptional regulator, and resulted in the discovery of a binding site motif. To further investigate the regulatory circuitry, we performed transcriptome analysis using RNA-seq. This led to the prediction of an influence on the expression of cell cycle regulation genes, and a prominently localized effect proximal to the origin of replication of pSymA, the symbiotic megaplasmid. We propose that this transcriptional regulatory system, through control of the activity of the master cell cycle synchronization protein CtrA, is required for full transition of the invading bacterial cell to the nitrogen fixing symbiosis state.

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P73. **Expansion and diversification of the CCA1-LHY-RVE transcription factor family in monocots**

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The circadian clock is an endogenous timekeeping mechanism that coordinates plant growth and environmental responses with the fixed period of the Earth's rotation. Coordination of plant physiology with light-dark and warm-cool cycles of the terrestrial diel period confer on the plant improved growth and fitness. The circadian clock comprises multiple, interlocking feedback loops regulated by a diverse panel of transcription factors. The most extensive studies of the components and mechanisms of the circadian clock in plants have been performed in *Arabidopsis thaliana* and in other dicotyledonous species. Much less is known about the structure and function of the circadian clock in monocots. In this study, we characterize the expansion and diversification of the CCA1-LHY-RVE family of transcription factors in the genomes of 10 monocotyledonous species. This family was selected because members of the CCA1-LHY-RVE family in *A. thaliana* have demonstrated roles in the functioning of the clock. Here, we retrieved and curated a comprehensive set of monocot-genome-encoded CCA1-LHY-RVE proteins on which we performed a multiple sequence alignment and phylogenetic analysis. From these analyses, we identified high levels of sequence identity between proteins encoded by distantly related monocots. We also identified clear phylogenetic structures within this family that support a model of diverse transcription factor functions that have been conserved across evolution.

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TOPIC 6: Bioproduct Production in Plants (Posters P74-P80)

P74. **Seed yield and oil and protein contents of main oilseed crops on the Canadian prairie**

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Plant-based protein is preferable for human consumption, while vegetable oil is becoming increasingly popular for industrial uses. It is of importance to evaluate the oil and protein production potential of Brassicaceae oilseeds for use as feedstock. Here, we determined oil and protein contents and their relationship with seed yield in oriental mustard (*Brassica juncea* L.), canola (*Brassica napus* L.), camelina (*Camelina sativa* L.), Ethiopian mustard (*Brassica carinata* A. Braun), and yellow mustard (*Sinapis alba* L.) across diverse environments. Data across nine site-years (Lethbridge, Scott, and Swift Current, in 2014 to 2016) showed that seed oil and protein contents had an inverse relationship with a wide variation. On average, canola had highest oil (48%) but lowest protein (22%) contents, while *S. alba* had lowest oil (29%) but highest protein (34%) contents. Oil yield (concentration by seed mass) was highest in canola (1358 kg ha^{-1}). Protein yield was highest in canola and *S. alba* (617 and 597 kg ha^{-1}, respectively) and lowest in camelina (456 kg ha^{-1}). Oil yield was generally higher in site-years with higher precipitation coupled with lower temperature during grain filling, whereas protein yield did not have a consistent response to growing conditions. Considering oil and protein yields across site-years, *B. napus* is the most productive feedstock, while *B. juncea* and carinata could be an alternative source, on the Canadian prairies.

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P75. Plant-made virus-like particles for protection of piglets against porcine epidemic diarrhea virus

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Porcine epidemic diarrhea virus (PEDv) is a coronavirus that causes disease and mortality to piglets particularly new-born piglets worldwide. Most vaccines used to combat the disease have been ineffective live attenuated virus vaccines. The goal of this project is to produce a plant-made virus-like particle (VLP) displaying antigenic epitopes of the PEDv membrane protein, and to administer it orally to pregnant sows for inducing protective lactogenic immunity. To obtain sufficient protein and subsequent VLP assembly, we used an elastin-like polypeptide fusion with the membrane protein, and transient expression in *Nicotiana benthamiana.* M-ELP accumulated up to 0.8 mg/g of fresh leaf weight . Virus-like particles were both observed when the membrane protein was overexpressed, and when the membrane protein was co-expressed with the envelope protein. In the latter case, the VLPs were slightly larger in size. This represents the first time coronavirus-like particles have been made in plants. We scaled up production of the VLPs by vacuum infiltration of 15 kg of leaf tissue, and developed a simplified extraction, concentration and encapsulation process for the VLPs.

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P76. A rationally designed plant-produced IgA has improved yield and exhibits cross serotype protection against enterohemorrhagic Escherichia coli

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The seven most prevalent strains of *Enterohemorrhagic* Escherichia coli (EHEC) collectively comprise more than 95% of the disease burden globally, affecting an estimated 2.8 million people annually. Although a plant production system is well established as a useful platform for enabling the post-translational modifications necessary for IgA folding, yield continues to be the most significant hurdle preventing transitioning of these therapeutics to market. We identified a series of single domain antibodies that can enable cross-serotype protection against EHEC. Considering the modular nature of the IgA, we rationalized that we could engineer the Fc component for improved yield of Fc fusions with these single domain antibodies without impacting the folding of these binders. We have successfully engineered a more stable Fc, by supercharging and introducing *de novo* disulfide bonds, that shows higher yield *in planta* by three to four fold. Using immunofluorescent labelling, we also have demonstrated that the VHH is still able to exhibit cross-serotype binding and neutralization across four of the seven strains. Co-immunoprecipitation experiments indicate that the rationally designed mutations have also not impacted the Fc's ability to structurally assemble with other subunits into its secretory form. Overall, this study provides a proof of concept that stability engineering of plant-produced IgA biologics is a viable strategy for overcoming the yield hurdle of plant-produced antibodies and related therapeutics.

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P77. Expression of malaria antigens in the chloroplast of *Chlamydomonas reinhardtii*; the first step towards developing malaria algae-based oral vaccine candidates

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Among all recombinant platforms, microbes are the most common systems for the production of commercially valuable products. Over the past decades, transgenic plants have attracted much attention because of both cost and safety matters. To take the advantage of both microbes and plants, microalgae-based platforms have been developed as a cost-effective and easily scalable alternative, possessing the positive features of both plants and microorganisms.
Malaria is still a serious disease threatening the lives of millions of people annually. So, any effort to reduce the burden of malaria is of utmost significance. This project aims to exploit the potential of *Chlamydomonas reinhardtii* chloroplast in expressing malaria antigens as a first step towards developing malaria algae-based oral vaccine candidates. *C. reinhardtii* chloroplast is capable of folding complex proteins while lacking the ability to glycosylate proteins; a remarkable feature since the *Plasmodium* parasite has not *N*-linked glycosylation machinery.
Fusion constructs consisting of antigen and adjuvant were designed and analyzed computationally. Transplastomic *C. reinhardtii* expressing the verified construct were produced and transgene integration and homoplasmicity were confirmed. Recombinant products were assessed by western blotting and ELISA tests. Results obtained demonstrated that expressed recombinant proteins accumulate as a soluble and properly folded protein within algal chloroplasts. Future work includes animal immunization both through oral administration and by injection to assess immune responses to the designed vaccine candidate.

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P78. The effects of nutrient solution pH on protein expression and morphology of Agrobacterium-infiltrated Nicotiana benthamiana in hydroponic growth conditions

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The integration of vertical farming technology into plant based production of therapeutic proteins, monoclonal antibodies and vaccines has the potential to significantly improve plant productivity and target expression efficiency. Trastuzumab, an immunoglobulin G monoclonal antibody (IgG1), is used in the treatment of HER2-positive breast cancer and is successfully produced in *Nicotiana benthamiana* in greenhouse production using peat-based substrates. In order to better understand how to transition to vertical production using soilless hydroponic culture, this project focuses on composition and plant uptake of nutrient solution ions in hydroponic growth conditions. The pH of a solution directly affects nutrient availability for plants. By changing the pH of a solution, nutrients can become more readily available for plant uptake, and therefore may influence morphological growth and protein expression in plants. Results of a case study in which five groups of 12 *N. benthamiana* plants were grown using nutrient film technique (NFT) hydroponics at five different levels of pH: (1) 5.0, (2) 5.5, (3) 6.0, (4) 6.5 and (5) 7.0 is discussed. Genes encoding the heavy and light chains of trastuzumab were introduced into the plants at five weeks from the time of transplant using *Agrobacterium tumefaciens* through vacuum infiltration. Results from plant morphological measurements and protein expression found that a relatively wide pH range of 5 -6.5 yielded the best results for IgG1expression (mg/kg).

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P79. **Recombinant protein expression in plants: The key influence of basic growth conditions**
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Plants show practical advantages for the production of clinically valuable recombinant proteins, including low upstream production costs, convenient large-scale cultivation and low risks of pathogenic or toxin contamination. From a biotechnological standpoint, the yield of a plant-made protein depends on the amount of recombinant protein per biomass unit, and on the biomass per plant or plant culture area. Several strategies have been proposed to improve recombinant protein yield per plant biomass unit, mostly relying on molecular tools and procedures for increased transgene expression or protein stability *in planta*. By comparison, little attention has been paid to the influence of common cultural practices such as supplemental lighting, atmospheric CO_2 enrichment or ammonium nutrition in 'molecular pharming' contexts. For instance, extensive work has been done over the years to define optimal growth conditions for leafy crops like lettuce or tobacco but the best cultural conditions for these same plants used as bioreactors may differ, since the ultimate target is recombinant protein yield in leaf tissue, not maximal leaf biomass or increased endogenous protein content. We here show the importance of carefully defining cultural practices that are well suited to the particular constraints and goals pursued in recombinant protein production settings. We also show how certain cultural practices can be harnessed to generate recombinant protein yield gains on a whole-plant basis, notably via an impact on host plant architecture.

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P80. **Identification of candidate cinnamyl alcohol dehydrogenases in Tabernanthe iboga root**
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Vinblastine and vincristine are compounds used as chemotherapy drugs and as precursors to semi-synthetic alternatives. These compounds are produced in low quantities (0.002% dry weight) by *Catharanthus roseus* (rosy periwinkle). The low accumulation of these compounds contributes to their high cost and places a strain on the supply chain of these drugs. Catharanthine is a precursor to vinblastine and vincristine biosynthesis in rosy periwinkle.

Catharanthine is an intermediate in the biosynthesis of the iboga alkaloid ibogaine in *Tabernanthe iboga* (iboga). Iboga accumulates large quantities of iboga alkaloids (4% dry weight) in its root bark. It is hypothesized that a reductase belonging to the cinnamyl alcohol dehydrogenase (CAD) family is responsible for committing catharanthine to the ibogaine biosynthetic pathway in iboga.

To identify the enzyme involved in this committal step, we generated an iboga root transcriptome from plants confirmed to be producing ibogaine. A list of candidate reductase genes was generated by searching this transcriptome for sequences homologous to CAD proteins.

This search revealed seven candidate genes which will be cloned, expressed in a heterologous system, and purified. Purified protein will be used to determine *in vitro* function/substrate affinity of these candidate genes. Once the reductase is identified, RNAi will be used to knock down reductase expression in iboga hairy root cultures from which tissue will be harvested and analyzed for the accumulation of catharanthine.

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TOPIC 7: Breeding and Genetics (Posters P81-P98)

P81. **Peduncle Strength: a potential selection criterion to improve lodging tolerance in Oat**

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Breeding for tolerance to lodging (displacement of culms from an upright position) is a major objective in oat breeding programs. A widely adopted screening method to assess breeding lines for tolerance to lodging is based on visual scoring of plant standing power (1=erect; 9=flat). In hot and dry seasons, the stunted plant growth limits the screening for lodging using a visual approach. We propose a new approach to use traits associated with lodging to screen the tolerant lines regardless of the weather conditions. This approach provides objective selection of lines using quantitatively measurable traits rather than subjective scoring of the lodged plants. To identify the potential trait/s to be used as selection criteria for improvement of lodging tolerance, we tested six oat cultivars with varying levels of lodging tolerance at three site-year field experiments under three nitrogen rates. Our analysis suggested Peduncle Strength (PS) as a potential selection criterion to improve lodging tolerance. PS provided a good estimation of the whole plant culm strength and explained the varietal differences observed between cultivars in terms of lodging tolerance. PS can be easily integrated into the breeding programs because of the ease of peduncle sampling and quick measurements. A screening strategy integrating both plant height and straw strength, based on PS, would enhance the selection gain for lodging tolerance.

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P82. **Soybean protein content variation among genotypes grown in Morden, MB and Ottawa, ON**

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Soybean protein content varies among varieties and is also affected by environmental factors. Short growing seasons may reduce soybean protein content and coincidently increase the oil content. Low protein content in soybeans has become a major production concern in western Canada. In this project, soybean varieties and breeding lines have been evaluated for protein and oil content at two distant sites (Morden and Ottawa) for three years (2015-2017). The seed source and experimental designs were the same, but field maintenance was conducted following standard procedures for two separate sites. In 2015, the average protein content for Morden was 2.2% lower than the average grown at Ottawa, while the oil content was the same between two sites. In 2016, the average protein content was 41.6% when grown at Morden compared to 43.9% when grown at Ottawa, while the oil content was the same. In 2017, the average protein content for Morden was 5.8% lower than the average grown at Ottawa, while the oil content was not significantly different between two sites. Overall for three years, the average protein content of the soybean lines grown at Morden was 3.4% lower than Ottawa, while the average oil content was about the same. The experimental results will be presented at the conference.

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P83. Spring wheat breeding for eastern canada – challenges and opportunities

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The Spring Wheat breeding program for Eastern Canada is an Agriculture and Agri-Food Canada (AAFC) research program that is supported by a combination of grower funds and government research grants. The program produces spring wheat cultivars for growers across Eastern Canada, including Ontario, Quebec, and the Atlantic provinces. The program operates at two research centres in the AAFC system with staff located at Charlottetown, PE and Ottawa, ON. While the geographic area covered by the program is large, facing different regional requirements and priorities, the spring wheat acreages in Eastern Canada are relatively small. This creates a unique set of challenges for a small breeding program to address. The Eastern wheat program has traditionally produced tall, high yielding varieties with high levels of resistance to Fusarium head blight and powdery mildew, but with lower protein and milling quality than typical of Canadian export quality hard red spring bread wheat. The breeding program is currently focussed on increasing milling quality and resistance to rust and lodging while maintaining and building on the traditional strengths of the program.

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P84. Assessment of genetic structure of coleoptile length in spring wheat (Triticum aestivum L.) using a genome-wide association study

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In wheat growing regions which are subject to moisture deficits, deep planting is a common practice. In such environments, wheat varieties with longer coleoptiles are preferred, since short coleoptiles may affect the germination and overall crop yield. However, development of semi-dwarf varieties with *Rht-B1b* and *Rht-D1b*, the gibberellic acid (GA) insensitive dwarfing genes, has limited the development of dwarf/semi-dwarf wheat cultivars with longer coleoptiles. Therefore, the objective of my study was to assess the variability and genetic basis of coleoptile length in a diverse panel of spring wheat with 318 genotypes by performing a genome-wide association study. The panel was genotyped by using genotype by sequencing (GBS). A randomized complete blocked design (RCBD) with two factors (one with and the other without GA treatment) and three replications was used to phenotype the panel for the following traits: coleoptile length, root length and root-shoot dry biomass using a cigar-roll method. The plants were grown for seven days in a growth chamber at 20˚C after 48 hours of cold treatment. The results from the genome-wide association study (GWAS) will be presented.

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P85. Identification and mapping of an unknown resistant locus in *Brassica napus* against Leptosphaeria maculans

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Blackleg, caused by *Leptosphearia maculans* (*L. maculans*), is one of the most devastating diseases on canola (*Brassica napus*) and causes significant yield losses each year. Growing resistant varieties is believed to be the most durable, environmentally friendly and cost effective strategy for blackleg control. Through screening of Chinese *B. napus* lines using differential blackleg isolates, we discovered that one of the lines '8011' contains unknown *R* genes. To understand the inheritance model, F_1 and F_2 populations were developed from a cross of 'Westar' and '8011'. The parent lines, F_1 and F_2 populations were screened using the isolate umavr7 (*AvrLm6*), which caused resistant phenotype on '8011'. The results showed that F_1 was susceptible to umavr7, and separation of resistant and susceptible individuals were found in the F_2 population. Calculation of the segregation of resistant and susceptible individuals fitted an expected Mendelian inheritance ratio: 1:3 (X^2=0.005590, P=0.940402). Bulked Segregant RNA-Seq (BSR-seq) analysis was performed by RNA sequencing of segregated resistant pool and susceptible pool, and the unknown resistant locus was mapped onto A07 chromosome. Molecular markers will be developed from the information of BSR-seq to aid marker assisted selection as well as fine-mapping of this locus.

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P86. Validation and discovery of genetic markers associated with loose smut resistance genes in a durum wheat (*Triticum durum* L.) doubled haploid population DT676/DT802

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Identification and validation of genetic markers associated with loose smut *(Ustilago tritici*) resistance in wheat aids the deployment of genes into new cultivars. The objective of this study was to validate known SSR and KASP markers associated with loose smut resistance and find new SNP markers. A durum wheat doubled haploid population comprising 174 lines from DT676/DT802 was evaluated against major loose smut races T32 and T33, and a minor race T26. The population was genotyped by 2962 SNP markers across the genome, and 7 SSR and 4 KASP markers on chromosomes 3A, 5A, 5B, 6B, 7A and 7B. The population was inoculated in the field near Swift Current in 2014, 2015 and 2017 and evaluated in a greenhouse for disease incidence. Marker-trait associations were assessed by single point analysis and by MapQTL. The single point analysis revealed significant associations of the markers with loose smut resistance on 5A, 5BS, 7A and 7B derived from DT676. No association was discovered on 3A or 6B. The 5BS marker, *Xgwm443*, was associated with resistance to T32 and T33 over 3 years, and T26 in 1 year. The 5A, 7A and 7B markers were associated with resistance to T26 in a single year. The QTL mapping detected only the locus located on 5BS; the SNP markers were more tightly linked with the resistance than *Xgwm443*.

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P87. Leaf rust resistance genes in Canadian wheat cultivars Red Fife, Stettler, Vesper, Lillian, Carberry and AC Cadillac

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The wheat cultivars Stettler, Vesper, Lillian, Carberry and AC Cadillac are widely grown in Canada and have been frequently used as parents for the next generation of Canadian wheat cultivars. It is important to understand the genetic basis of leaf rust (*Puccinia triticina* Eriks.) resistance in these cultivars to improve this resistance in future cultivars. Five doubled haploid populations were analyzed for leaf rust resistance both in the field and using individual isolates indoors; Stettler/Red Fife, Vesper/Lillian, Vesper/Stettler, Carberry/Vesper, and Carberry/AC Cadillac. Preliminary gene determinations were made on these lines based on segregation of genes at the seedling stage, molecular markers, and QTLs determined by analysis of field data. Red Fife had two seedling resistance genes, that appear to be the temporarily named genes *LrMar* and *LrCen*. Stettler was thought to have *Lr2a* and *Lr16*, Vesper was hypothesized to have *Lr21* and *Lr17*. Lillian had a seedling resistance gene on chromosome 4A that could not be identified, *Lr34* and *LrCen*. Carberry had *Lr2a*, *Lr16* and *Lr34* and AC Cadillac had *Lr10* and *Lr34*.

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P88. Genetic analysis and molecular mapping of the oat crown rust seedling resistance gene Pc39

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Crown rust is a major disease of oat with race-specific seedling resistance genes being a primary means for control. *Pc39* is a seedling crown rust resistance gene that has been used in oat breeding programs. The objective of this study was to develop DNA markers linked to *Pc39* for marker-assisted selection. Two RIL populations developed from the crosses AC Assiniboia/MN841801 and AC Medallion/MN841801 were phenotyped at the seedling stage using oat crown rust race LMBG. *Pc39* was mapped to a linkage group consisting of 16 SNP markers, which placed the gene on Mrg11 LG of the oat consensus map. *Pc39* co-segregated with marker GMI_ES01_c12570_390, and was flanked by two markers avgbs_126086.1.41 and GMI_ES15_c276_702 with genetic distances of 1.7 cM and 0.3 cM in AsbMN. Similar results were obtained in MedMN with genetic distances of 0.4 cM and 0.4 cM. SNPs were converted to KASP markers. Two SNP loci defined a haplotype that predicted the presence of *Pc39* in a panel of oat germplasm. The newly developed markers could find applications in the identification of the *Pc39* gene in oat germplasm and the positional cloning of this gene.

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P89. **Genetic diversity of grain fatty acid composition in 295 accessions of Korean Rice Core Set**

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Fatty acid is an important phytonutrient as a component of lipids in rice grains. To understand genetic diversity in fatty acid compositions, 295 accessions of Korean Rice Core Set developed from 25,604 germplasm were cultivated in 3 separate locations in Korea, and the composition of fatty acids in harvested brown rice were evaluated according to one-step methylation/extraction method coupled with a GC-FID. Among 9 identified, linoleic, oleic, and palmitic acids were the 3 major fatty acids consisting 36.6%, 35.0%, and 23.4% of total fatty acids, respectively. Average compositions of other fatty acids such as stearic, linolenic, myristic, arachidic, eicosenoic, and behenic acids were 1.8%, 1.1%, 0.9%, 0.5%, 0.3%, and 0.3%, respectively. Throughout all tested accessions, oleic acid showed correlations negative with palmitic (r=-0.675) and linoleic (r=-0.657) acids, but positive with eicosenoic acid (r=0.639). Ecotype of rice also affected fatty acid compositions in that Aus-type rice accessions showed higher saturated fatty acids (31.8%), while japonica-type accessions exhibited higher unsaturated fatty acid compositions. All these results suggested wide genetic variations of fatty acid composition in tested Korean Rice Core Set accessions, which could be utilized in a breeding programs to develop a new rice variety of higher nutritional value.

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P90. **Regression data driven models on canopy hyperspectral reflectance for soybean yield prediction**

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Direct measurements of important agronomic traits, including morpho-physiological yield-related traits, are prone to human error, resource- and labour-intensive. Current advances in high-throughput phenotyping such as hyperspectral reflectance have provided breeders with new opportunities to measure these traits, indirectly, and screen large number of genotypes at early-generation. Although the interpretation of individual hyperspectral reflectance is challenging, it can be facilitated through the development of robust regression-data-driven models. Using 250 soybean lines grown in two environments in southwestern Ontario in 2018, we have collected data for yield and 188 discrete reflectance wavebands, ranged from 391 to 1010 nm, at three reproductive growth stages (R3, R4, and R5). These data were used to create 24 regression models based on ordinal least square regression (OLSR) and principal components with partial least square regression (PLSR). Furthermore, nine conventional vegetation indices (VIs) were constructed for predicting the soybean yield. The best model for yield prediction was the PLSR of 10 nm average binning wavelengths without normalization at R5 (PLSR-BWWN5) that explained up to 51% of the yield. In PLSR-BWWN5 model, 93% of the predicted yield was explained by only 25 binning wavebands with a heritability of 0.4. This information seems to be useful for soybean yield prediction at the early stage (i.e., R5), which in turn can facilitate the development of soybean cultivars with increased seed yield and the genetic gain.

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P91. **Major genomic regions underlying seed size, protein and sucrose in food-grade soybeans**

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The production of soy-based food products, such as tofu and soymilk, requires specific physical and chemical characteristics of the soybean seed. Identification of quantitative trait loci (QTL) associated with value-added traits, such as increased seed protein and sucrose concentrations as well as large seed size, could accelerate the development of competitive high-protein soybean cultivars for the Canadian food-grade market through marker-assisted selection (MAS). The objectives of this study were to identify and validate QTL associated with seed protein and sucrose concentrations, seed size, and yield in two high-protein recombinant inbred line (RIL) populations. The two RIL populations were derived from crosses between the high-protein cultivar AC X790P (49% protein, dry weight basis), and two high-yielding commercial cultivars, S18-R6 (41% protein) and S23-T5 (42% protein). The RIL populations were grown in five different environments in southwestern Ontario. In total, 14 large-effect QTL (R^2>10%) associated with seed protein concentration were identified with potential use in MAS. Six of these protein-related QTL were also co-localized with the QTL associated with seed sucrose concentration or size. Major protein-related QTL did not show significant impacts on seed yield QTL in these populations. The favorable alleles were sourced from both parental cultivars. The putative QTL identified in this study are desirable candidates for MAS programs, and could be utilized to develop new soybean cultivars for specific soy-based food products.

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P92. **Mapping cold hardiness in tetraploid garden roses (Rosa x hybrida)**

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Canadian roses such as the ‘Explorer’ series are known worldwide for their exceptional cold hardiness. While cold hardiness exists in wild roses, it is lacking in modern garden roses and limits their area of cultivation. Releasing cold hardy varieties is necessary to meet the demand for low maintenance roses but breeding for cold hardiness is difficult due to linkage drag and weather-dependant field assessments. Cold hardiness in roses is highly heritable and under the control of few major genes. High density SNP maps were available for both parents of a tetraploid population derived from an ‘Explorer’ rose. Progeny were planted in two locations in 2018 (Elora, ON, CA; Saskatoon, SK, CA) and evaluated for winter damage, spring regrowth and vigour in spring 2019. The same set of progeny were examined by artificial freezing where electrolyte leakage was measured on stem sections as an index of freezing resistance. Preliminary mapping analyses revealed a QTL for Elora winter damage on chromosome 2 and a QTL for artificial freezing resistance on chromosome 3. Winter damage data will be recorded again in 2020 and data from all four environments will be used to study the heritability of the cold-related traits and validate the QTLs in multiple environments. Candidate genes will be investigated. Resequencing data of the parental lines will be used to search for polymorphism in the candidate genes.

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P93. **Genome-wide analysis of thaumatin-like proteins in cereals**

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Beta-glucan is the major non-starch dietary fiber present in the barley grains. Barley with low beta-glucan is a desirable trait for the malting barley breeding and brewing industry. However, varieties with higher amounts of beta-glucan are tailored for feed and food purpose as higher levels of beta-glucan causes hindrance during malting. Recently, a barley Thaumatin-Like Protein (TLP), *HvTLP8* located on chromosome 4H has been reported for its interaction with beta-glucan. To further characterize *TLP*gene family in cereals, we identified 19, 37, 28 and 35 *TLP* genes from the barley, rice, *Brachypodium* and sorghum genomes using the TLP domain as a query. Two novel cysteine-rich genes on chromosome 3H, *HvTLP14* and*HvTLP17* were identified which possess carbohydrate-binding motif. We also observed the transcript abundance of *HvTLPs* in germinating grains at 16, 48 and 96 hrs of imbibition in barley malt and feed varieties. Expression of *HvTLP14* and *HvTLP17* was found to be higher in malting and lower in feed varieties. We are exploring the role of these carbohydrate binding proteins for their role during malting and developing a functional marker (genetic and ELISA-based biochemical) for the selection of superior malting varieties.

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P94. **Agronomic performance and nitrogen fixation of heirloom and conventional dry bean varieties under low-nitrogen field conditions**

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Dry bean (*Phaseolus vulgaris*) is a diverse species grown worldwide as an important source of protein and income. Beans engage in symbiotic nitrogen fixation (SNF) with rhizobia, but are poor nitrogen fixers among legumes. Whereas heirloom varieties developed under natural environmental conditions, conventional varieties are developed using modern practices including the use of SNF-suppressing N fertilizer potentially leading to the loss of SNF efficiency. Here we test the hypothesis that heirloom beans have a greater capacity for SNF than conventionally-bred bean varieties and examine whether they could be useful germplasm sources to improve this trait. We examined SNF capacity under low-N field conditions for a 42-genotype heirloom-conventional panel (HCP). The HCP was genotyped to investigate genetic relatedness and genepool membership. Three field trials were conducted in Ontario, Canada from 2014-15 and agronomic and seed composition traits were measured. Significant variation for SNF was found. Overall, heirloom genotypes did not fix significantly more nitrogen than conventional genotypes. However, five heirloom genotypes obtained > 60 % of their nitrogen through SNF. Grain yield was not significantly different between heirloom and conventional categories suggesting that using heirloom genotypes in a modern breeding program would not negatively impact yield. SNF was significantly higher among Middle American (MA) genotypes than among Andean (A) genotypes. Heirloom genotypes are a promising source of genetics to improve SNF in modern bean varieties.

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P95. Genetic transformation of oat to elucidate a gene associated with beta-glucan

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Oat is known to reduce blood pressure and cholesterol. This has been attributed to its high β-glucan content. β-glucan is a major non-starch component in oat, consisting of a double β-1,3 and β-1,4 linkages. Recently, a Thaumatin Like Protein, TLP8 has been identified in barley which interacts with β-glucan and regulates its content in the grain. Higher transcript abundance of *TLP8* in barley grains reflects a lower amount of β-glucan and vice-versa. In the current study, we hypothesized that the downregulation of *TLP8* could increase β-glucan content in oat. The TLP8 homolog in oat was retrieved and the RNAi construct has been created for oat transformation. The genetic transformation was conducted via bombardment gun method. Transformants were generated successfully in oat variety "Park", using *PAT* gene for selection, yielding a 17.2% transformation efficiency. Histochemical assay confirmed the expression of *PAT* gene and oat transgenic plants were found to be resistant to herbicide LIBERTY (0.2%) exposure. Currently, we are conducting a molecular characterization of transgenic lines in order to explain the association between TLP8 and β-glucan in oat.

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P96. Identification of five QTLs for clubroot resistance to three novel pathotypes of Plasmodiophora brassicae in *Brassica oleracea* through genotyping-by-sequencing

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Managing clubroot disease of canola in the Canadian prairies is a challenging problem due to the development of new pathotypes. Clubroot disease in canola widely managed with major genes, which is effective against single pathotypes, but multigenic resistance is effective against multiple pathotypes. *B. rapa* and *B. oleracea* are considered major sources of qualitative and quantitative resistance of clubroot disease, respectively. In this study, genotyping-by-sequencing (GBS) method was used to construct a high-density genetic map and to identify QTLs for clubroot resistance to three novel pathotypes 2B, 3A and 3D in backcross population derived from the cross between the resistant cabbage variety 'Badger Shipper'and the susceptible double haploid line TO10000DH3. A total of 42,923 SNPs were identified from 92 BC1 lines of which 10,289 SNPs found polymorphic. A total of 914 cM genetic map was constructed by 1,842 high quality polymorphic SNPs. Two QTLs, *CRQTL_2B_1* and *CRQTL_2B_2* were detected for resistance to pathotype 2B on chromosome C1 and C3 with phenotypic variation explained (PEV) of 15.9 and 15.5%. A single QTL, *CRQTL_3A_1* was detected for resistance to pathotype 3A on chromosome C3 with PEV of 19.3%. Two QTLs, *CRQTL_3D_1* and *CRQTL_3D_2* were detected for resistance to pathotype 3D on chromosome C3 and C4 with PEV of 11.6 and 13.5%. Associated SNP markers can be used for marker assisted breeding for clubroot resistance in canola

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P97. Evaluation of tissue culture and cloning propagation efficiencies of three industrial hemp varieties

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Tissue culture and vegetative cloning techniques are used by hemp producers to propagate and preserve plant genetics. We evaluated the efficiency of both techniques on three hemp varieties, Katani, Silesia and X59. For tissue culture propagation, five seed surface sterilization methods were compared. Sterile seeds were grown on ½ MS media for 8 days at 24 °C for 16 h in light and 22 °C for 8 h in dark. Hypocotyl, leaf segment and cotyledon were cut and plated on MS callus-induction media with 6.79 µM 2,4-Dichlorophenoxyacetic acid. Explants were monitored and transferred to fresh MS-shoot induction media then root elongation media based on their development. Rooted plants were transferred to pots with potting soil mix and grown to maturity. For cloning propagation, varieties were grown directly from seed in Promix potting soil. Terminal buds were removed from female plants at the 6-8 leaf stage. Lateral branches were excessed, treated with rooting hormone and planted in training pots for root establishment. Clones with established roots were transferred to a 7-inch pots and grown to maturity. The seed-born fungal contamination in hemp seed and the difficulty for shoots to develop roots in rooting media were the main obstacles for tissue culture propagation. Vegetative cloning was more efficient in producing numerous clones identical to the mother plant compared to tissue culture techniques.

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P98. Characterization of nested association mapping population in dry bean

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The common bean (*Phaseolus vulgaris* L.) is grown widely around the globe, providing an important staple food crop for subsistence farmers in the developing countries and a high-value commodity crop in the developed world. Understanding the genetic bases of different agronomic traits and quality traits are important for efforts to breed improved lines in common bean. The Nested Association Mapping (NAM) population of F4:5 recombinant inbred lines (RILs) was created with the cultivar Ex Rico 23, and 10 founder lines that span the genetic diversity of Ontario Mesoamerican germplasm. The NAM population was evaluated for different agronomic traits including yield, days to 50% flowering, and days to maturity in the field in four environments in 2016 and 2017 at the Elora Research Station (ERS) and Woodstock Research Station (WRS), and will be genotyped using Genotyping by Sequencing (GBS).

The distribution of all the traits, days to 50% flowering, days to maturity, and yield was continuous and showed some transgressive segregation compared to the parental lines for each environments. Statistical analysis of all four environments showed highly significant phenotypic effects for all the traits measured (P=0.05).

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TOPIC 8: Cell Biology (Posters P99-P109)

P99. **Characterization of the pokeweed antiviral protein (PAP) interactome by proximity-dependent biotin identification**

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Ribosome-inactivating proteins (RIPs) are produced primarily by plants, and are named for their enzymatic ability to remove a purine base from the sarcin-ricin loop of the large ribosomal RNA. However, little is known about the biological function of RIPs in the plant. *Phytolacca americana*, the American pokeweed, produces a RIP called pokeweed antiviral protein (PAP). We suspect that this protein is involved in defense against pathogens and adaptation to environmental stress. The objective of this work is to investigate the biological role of PAP by mapping out the PAP-protein interactome. Proximity dependent biotin ligase labelling (BioID) will be used to identify PAP interactors in both the apoplast, where PAP has been shown to primarily localize, and the cytoplasm, where the ribosomal target resides. PAP-biotin ligase fusions will be expressed transiently in Nicotiana tabacum, followed by affinity purification of biotinylated proteins and their identification using mass spectrometry. These protein interactors are important to understand how PAP functions in plant systemic responses while sequestered in the apoplast, as well as identify ribosomal proteins that mediate rRNA depurination by PAP in the cytoplasm. This work will represent the first protein interactome mapping for a RIP; identification of PAP interactors in living plant cells will help elucidate PAP's function and contribute to characterization of the biological role of RIPs in general.

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P100. **Understanding differential development and behaviour of plastids using the Arabidopsis immutans mutant**

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Plastids are characteristic organelles of plants. All plastids arise from pro-plastids and subsequent differentiation allows their categorization into three broad types; leucoplasts when they remain colourless, chloroplasts when they develop chlorophyll and chromoplasts when they predominantly have pigments other than chlorophyll. While the plastid types can interconvert, they are usually located in different regions and organs of a plant. Thus, chloroplasts are mainly found in leaves while leucoplasts occur primarily in roots. Their different locations make it difficult to study the cellular factors involved in plastid interconversions and the mechanisms whereby one particular type may predominate in a cell. An *Arabidopsis thaliana* mutant, *immutans* (*im*) develops leaves with randomly distributed green and white sectors corresponding to the presence of chloroplasts and leucoplasts, respectively. The introduction of a stroma targeted GFP revealed a range of plastid sizes and shapes in the mutant and as observed by transmission electron microscopy the different shapes correlated with differences in internal membrane architecture. Additional fluorescent protein probes targeted to the endoplasmic reticulum, peroxisomes, and mitochondria have been introduced in *im* to obtain more insights on the interactions of chloroplasts and leucoplasts with other organelles. The creation of transgenic *im* lines has resulted in a new set of fluorescent protein-based tools for studying the development and interconversion of plastids and understanding their differential responses to environmental stimuli.

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P101. Investigating the systematic regulation and function of cyclic nucleotide-gated channels in arabidopsis

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Despite the importance of Ca^{2+} signals, Ca^{2+} channels in plants are still not well understood. Cyclic nucleotide-gated channels (CNGCs), one of the largest cation channel families in plants, are involved in Ca^{2+} signaling and have been shown to be involved in a diverse array of physiological processes in plants through their Ca^{2+} channel activity. So far, genetic approaches have not been able to reveal the specific role of most individual CNGCs probably due to redundancies in their function. We have shown roles for several clade I CNGCs in pathogen resistance, senescence and programmed cell death. However, most single mutant phenotypes are very subtle. Therefore, we used a bioinformatics approach to investigate stimulus induced co-expression patterns of the 6 members of clade I to create higher order knockouts using a combination of T-DNA insertion lines and CRISPR/Cas9 technology. These mutants will be tested in conditions where they have been reported to be involved in, and where they show similar expression patterns. These conditions include pathogen resistance, salt and osmotic stress as well as hormone induced senescence.

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P102. Identification and characterization of new lipid droplet proteins in Arabidopsis thaliana

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Cytoplasmic lipid droplets (LDs) are evolutionarily-conserved organelles that function not only in neutral lipid storage, but also in several cellular processes, such as membrane remodeling, stress responses, and protein turnover. While LDs are known to form at the endoplasmic reticulum (ER), the molecular mechanisms underlying their biogenesis, maintenance, and breakdown are largely unknown, particularly in plants, where relatively few LD proteins have been studied. To help address the limited information, recent proteomics surveys of isolated LDs from *Arabidopsis thaliana* seedlings and protein-protein interactomes with known plant LD proteins serving as 'bait' were analyzed for new, putative LD proteins. Using cell biology and reverse genetics approaches, selected proteins were investigated further in terms of their localization to LDs or other intracellular compartments associated with LDs (e.g., ER). In addition, alterations in expression were generated to examine changes in LD phenotype(s) such as changes in LD size and/or number. Results from preliminary studies involving several candidate LD proteins will be presented, including those for a previously uncharacterized plant-specific protein that localizes to the surface of LDs and increases LD numbers when ectopically overexpressed in leaves. How these and other newly-identified LD proteins may function in LD biology will be discussed, as well as their potential as targets for bioengineering strategies directed at increasing storage oil content in seeds and vegetative tissues of food and bioenergy crops.

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P103. **Regulation of cell size in *A. thaliana* shoot apical meristem**

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The size and shape of individual cells can be remarkably constant for a given organ type, suggesting that cell geometry is an important biological factor. In growing organs, such as the shoot apical meristem, a delicate balance must be established between cell expansion and cell division to maintain cell size homeostasis. We used time-lapse confocal data to monitor division and expansion of individual cells in the shoot apical meristem. Next, we quantified cellular parameters and the expression of marker genes with the 3D image analysis software MorphoGraphX. With the help of Python scripts, we could compare cell dynamics between different regions of the meristem and across individuals. Preliminary results already reveal some of the complex relationships between cell size, cell expansion and cell division.

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P104. **A feedback loop modulates root apical meristem development**

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Modulating root growth in response to environmental signals enables plants to compete for nutrients or survive abiotic stress. Using cell, molecular and genetic strategies in Arabidopsis thaliana, we identified a negative feedback loop that modulates cell proliferation in the root apical meristem. This system involves brassinosteroid (BR) hormones suppressing expression of the microtubule-associated protein CLASP, which results in a dramatic reorganization of microtubule arrays and a shut down of cell division. CLASP, in turn, enhances brassinoteroid signalling by sustaining the BR receptor BRI1 at the plasma membrane by tethering BRI1 to microtubules via its direct interaction with the retromer component sorting nexin 1 (SNX1). To test our prediction that this feedback loop is important for modulating meristem cell proliferation, we mutated the promoter element of the CLASP gene to render it BR-insensitive (brinCLASP). Despite constitutively higher levels of CLASP and greater abundance of BRI1 receptors in these transgenic lines, cell cycle progression was delayed and cell proliferation and root lengths were reduced. The brinCLASP seedlings were also maladapted to drought and cold stress, indicating that CLASP is at the nexus of BR-mediated responses to environmental signals. Intriguingly, BLAST analysis of CLASP and SNX1 binding site sequences shows that CLASP-SNX1 interaction is plant-specific, and that it appears to have emerged in concert with organized root meristems in early land plants.

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P105. Investigating the role of e3 ubiquitin ligases in the Brassicaceae self-incompatible pollen response

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Following pollination, the dry stigmas in the Brassicaceae rapidly regulate pollen-stigma interactions, thereby leading to the acceptance of compatible pollen or the rejection of self-incompatible pollen. The self-incompatible pollen response inhibits pollen hydration and germination, ultimately deterring fertilization. The objective of this research is to investigate the role of the members of the Plant-U-Box (PUB) family of E3 Ubiquitin ligases in the self-incompatibility (SI) pathway in Brassicaceae. Previous studies showed that the ARM-Repeat Containing 1 (ARC1) gene, which is conserved in self-incompatible species, is required for SI as ARC1-knockdown constructs in transgenic *Brassica napus*and *Arabidopsis lyrata* confer a partial breakdown of SI. What remains unknown is how the SI response would be affected when ARC1 is completely knocked out and whether the closely-related PUB17 gene may play a redundant function. The two research goals to approach this question both utilize the CRISPR/Cas9 system to generate knockout deletion mutations. First, ARC1 deletion mutations will be generated in compatible *Capsella rubella*and then crossed into self-incompatible *Capsella grandiflora*. Second, a self-incompatible *Arabidopsis thaliana* C24 line carrying the *A. lyrataSCRb*and *SRKb*transgeneswill be used to investigate PUB17 as this line has a robust SI phenotype despite lacking a functional ARC1 protein. Currently, CRISPR/Cas9 constructs are being used to generate *ARC1* and *PUB17* knockouts and SI in the mutants will be observed through phenotypic assays. Overall, this research will further elucidate the role of E3 ubiquitin ligases in the rejection of self-incompatible pollen in the SI pathway.

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P106. Characterization of *Camelina sativa* germination: The effect of gibberellins on vacuolation

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Camelina sativa is an important oilseed crop, which has recently gained attention in biofuel production as more information emerges about its genomic characteristics and crop performance. The aim of this research is to compare germination of Camelina with that of Arabidopsis, as molecular mechanisms of germination are well studied in this species. Arabidopsis protein storage vacuoles (PSVs) increase in size and decrease in number as a consequence of germination progression. Through diphenyl boric acid aminoethyl ester (DPBA) staining of seed embryo and endosperm, Camelina showed similar results to Arabidopsis, however with distinct time points of vacuolation. The rate of this process increases by the addition of gibberellins (GA). Vacuolation was increased in seeds treated with exogenous GA and compared to seeds where endogenous GA was inhibited by paclobutrazol, a GA inhibitor. This result indicates that, similar to Arabidopsis, vacuolation is an indication of germination in Camelina and can be regulated by GA. It was also observed that micropylar regions of the endosperm had higher ratios of vacuolated cells, suggesting that these regions may have different roles in nutrient transfer and may be more sensitive to hormonal regulation during germination.

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P107. A novel method of producing the putative c-terminal transit peptide of attoc159 for characterization of its targeting to the chloroplast outer membrane

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Chloroplast preproteins that are destined for interior chloroplast compartments and that are encoded in the nucleus rely on N-terminal transit peptides (TPs) that are recognized and translocated by members of the Toc (translocon at the outer membrane of chloroplasts) complex, including Toc159. Proteins that reside in the chloroplast outer membrane (COM), instead, are typically directed to the chloroplast by intrinsic transmembrane domains. Recently two COM proteins, Toc159 and OEP18, have been shown to be targeted to the chloroplast outer membrane by a novel reverse TP-like C-terminal sequence. The objective of my research is to characterize this novel targeting mechanism in order to understand the molecular interactions involved and determine the role of membrane lipid composition in targeting specificity. Bioinformatic analysis revealed three highly conserved pseudo-domains within the putative C-terminal targeting sequence. One of these pseudo-domains is an amphipathic helix rich in hydrogen bonding partners with the potential to make preferential interactions with galactolipids that are unique to the chloroplast membrane. The Toc159 C-terminal peptide was overexpressed as a fusion protein in *E. coli* and purified from inclusion bodies using immobilized metal affinity chromatography. Biophysical techniques, including circular dichroism spectroscopy, will be used to investigate secondary structures and conformational changes under different conditions, and surface plasmon resonance will be used to investigate interactions with lipids and other proteins. Our most recent results will be presented.

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P108. Investigating protein localization to the outer membrane of chloroplasts

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The chloroplast evolved through an endosymbiotic event wherein a photosynthetic bacterium was engulfed by a heterotrophic eukaryote. Over time, genes have been transferred from the endosymbiotic bacterial genome to the host nuclear genome. Consequently, the proteins encoded by these genes gained chloroplast-targeting information; allowing them to be directed to the chloroplast post-translationally. For chloroplast stromal-localized proteins this targeting information is typically a peptide extension found on the N-terminus called a transit peptide (TP). With the exception of Toc75, the majority of chloroplast outer envelope proteins (OEPs) do not possess an N-terminal transit peptide and are targeted to the chloroplast by at least three different mechanisms. Recently, a novel chloroplast-targeting pathway was identified in the OEP, Toc159, of *Bienertia sinuspersici*. It was shown that Toc159 uses a transit peptide-like sorting signal in its C-terminus to target to the chloroplast outer membrane. The goal of my research is to investigate whether OEP16-2, one of eight OEPs predicted to have a TP-like targeting signal in the C-terminus, uses this novel targeting pathway. Transient expression assays of onion epidermal cells and *Arabidopsis* mesophyll protoplasts will be performed to examine the subcellular localization of OEP16-2. The findings from this study will enhance our knowledge of protein targeting to the chloroplast.

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P109. **Characterizing the role of *Striga hermonthica* gibberellic acid receptors**

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Hormones play a crucial role in the signal transduction of plant germination. In autotrophic plants, gibberellic acid (GA) is perceived by its receptor called GA-INSENSITIVE DWARF1 (GID1) and transduced by core signalling components to trigger germination. Conversely, a destructive parasitic plant to sub-Saharan Africa staple crops, *Striga hermonthica*, does not germinate in the presence of GA but rather, is dependent on strigolactones (SLs) emitted by nearby plant roots. In addition to the ability to synthesize GA, transcriptome analysis revealed that *S. hermonthica* has *Arabidopsis* homologs of GA core signalling components including GA receptors (GID1), downstream transcriptional repressors (DELLA) proteins and F-box proteins. To analyze the function of *S. hermonthica* GID1 genes, we expressed them in *Arabidopsis* loss-of-function *gid1* double mutants background. Furthermore, based on *in vivo* experiments, *S. hermonthica* GID1 receptors interact with DELLA proteins in a hormone dependent manner and is comparable to the protein interactions seen in *Arabidopsis.* Ultimately, identifying the role of GID1 genes in parasitic plant species germination will open up the field in understanding GA signalling in other plant species.

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TOPIC 9: Controlled-Environment Crop Production (Posters P110-P113)

P110. **Elongation and flowering promoted by blue light are independent of photoperiod: a comparison with red light in four bedding plant species**

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Our previous study on bedding plants indicates that under 24-h lighting, pure blue light, compared to red light, can promote elongation or flowering. The objective of this study was to investigate whether the blue light promotion effects are independent of photoperiod. The growth and morphology traits of petunia, calibrachoa, geranium, and marigold were compared under two light quality treatments: (1) R, “pure” red light (665 nm); and (2) B, “pure” blue light (440 nm) using continuous (24-h light/0-h dark) or periodic (16-h light/8-h dark) light-emitting diode lighting. A photosynthetic photon flux density of approximately 100 μmol m^{-2} s^{-1} and an air temperature of approximately 22°C was used for the above treatments. For either transplants or mature plants, regardless of photoperiod, B promoted elongation growth compared to R, as demonstrated by a greater daily stem elongation rate, main stem length, internode length, or petiole length, with varying sensitivity among species. Also, after transplanting, the plants under B light showed an earlier flowering time than those under R light, regardless of photoperiod. However, the magnitude of B light promotion was greater under 24-h than 16-h lighting in many cases. This suggests that the promoted elongation and flowering by blue light is not specifically from 24-h lighting, although the promotion degrees differ between photoperiods and among species.

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P111. Blue light can promote flowering of bedding plants when associated with low phytochrome activity

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To clarify the flowering response to blue light associated with varying phytochrome activity, the flowering traits of petunia, calibrachoa, geranium, and marigold were investigated under six light quality treatments: (1) R, “pure” red light; (2) B, “pure” blue light; and (3) BRF0, (4) BRF2, (5) BRF4, and (6) BRF6, “unpure” blue light created by mixing B with 6% R, and further adding far-red light of 0, 2, 4, and 6 μmol m^{-2} s^{-1}, respectively. B and BRF6 promoted flowering compared to R and BRF0, as demonstrated by an earlier flowering time for petunia and calibrachoa; and showed a greater flowering index, more visible flower buds, and more opened flowers for geranium and marigold. The promotion effect of “unpure” blue light on these traits increased following the order of BRF0, BRF2, BRF4 and BRF6, which varied in sensitivity among plant species. Also, a similar pattern of promotion by blue light was found in the flower size for calibrachoa, and in the canopy size for all the species. The calculated phytochrome photostationary state, an indication of phytochrome activity, was higher for R (0.89) than B (0.49), and decreased gradually for “unpure” blue light treatments: BRF0 (0.68), BRF2 (0.65), BRF4 (0.63), and BRF6 (0.60). This suggests that “blue” light associated with lower phytochrome activity can promote flowering, despite having a varying level of sensitivity among species.

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P112. NLOS-OG: A nitrogen simulation tool for managing organic greenhouses

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Because of the complexity of the nitrogen (N) cycle and the diversity of N molecules in the soil, N fertilization management is based on complex calculations and considerations. For organic farming, lack of data and management tools that predict N availability from organic fertilizers leads to overfertilization which results in both buildup of salinity and leaching of N. Better prediction of N availability following application of organic fertilizers is crucial in advancing sustainable organic horticulture. Our objective was to adapt a field-based N simulation tool to organic greenhouse production.

First, we adapted the NLOS model to organic greenhouse production by introducing N mineralization equations obtained from incubation experiments on common organic fertilizers (pelleted poultry manure and blood, feather, shrimp and alfalfa meals). Second, we monitored N flows in four organic greenhouse crops (two cucumber, one tomato and one pepper) to validate the model.

The current version of NLOS-OG accurately predicts N mineralization from several organic fertilizers. It also predicts N availability to greenhouse crops grown in native mineral soil. However, the model underestimates N availability to crops grown in containerized growing media. Further research will focus on the effect of water dynamics on N availability in containerized organic greenhouses. The web-based NLOS-OG, with a user-friendly interface, is available at https://exchange.iseesystems.com/public/pierrepauldion/nlos-og/ and can be used to assist growers to plan N fertilization in organic greenhouses.

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P113. **Minimizing unwanted callus during *in vitro* multiplication of daylilies**

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Daylilies (Hemerocallis spp.) are ornamental flowers renowned for their diversity, with over 80,000 registered cultivars varying in colour, shape and pattern. Traditionally propagated through division, multiplication ranges from 1-20 divisions per season depending on the cultivar. Unfortunately, this leads to a delay of up to 20 years for newly registered cultivars to reach marketable levels of plant material. Micropropagation offers an alternative approach that can dramatically increase multiplication rates and is used extensively for the species. However, protocols have only been developed for selected genotypes and many protocols go through a callus phase introducing concern related to genetic mutations due to somaclonal variation. Though direct regeneration has been documented, further research is needed to refine the protocol and apply it to multiple genotypes. Our objective was to identify and optimize the factors that encourage direct regeneration and evaluate their effect over multiple cultivars. From comparative studies analyzing liquid vs. semi-solid systems, to cytokinin compositions, we have significantly increased the leaf to callus ratio while maintaining a high rate of multiplication

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TOPIC 10: Crop Physiology (Poster P114)

P114. **Investigation of the critical growth period for yield component determination in quinoa**

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It has been shown that there is a critical growth period for different yield components in crops such as corn, soybean and sunflower. This experiment will investigate the critical growth stage of quinoa for seed number, 1000 seed weight and total seed yield. The experiment consists of 8 plots per rep with 4 reps. There were 3 treatments with 2 levels per treatment: Nitrogen (100 kg/ha and 21 kg/ha), seeding rate (9 kg/ha and 3 kg/ha) and irrigation (irrigated and rainfed). Treatments were designed to create variation in crop growth rates. Although nitrogen and irrigation treatments failed to cause statistical differences for the majority of harvests, plots still differed significantly from themselves. Eight biomass harvests were taken throughout the growing season and a final harvest was taken to measure yield components. These biomass measurements were fitted to a growth equation and crop growth rates were taken from the fitted curves. The correlation coefficient for crop growth rates at different times throughout the season and final yield components was calculated. Early results indicate that early growth is more critical to seed number and seed yield while later growth is more important for 1000 seed weight.

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TOPIC 11: Development and Reproduction (Posters P115-P119)

P115. **The effect of hermaphroditism versus cross-pollination on sex ratios and genetic variation in *Cannabis sativa* L.**

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Cannabis sativa L. is a dioecious plant in which genetically female plants are cultivated for their inflorescences (buds) which contain high levels of cannabinoids (THC, CBD). Male plants are undesired except during breeding, as seed formation in flower buds reduces cannabinoid levels and quality. Under certain environmental conditions, female flowers produce male anthers that form within the bud (hermaphrodites, HF) and release pollen, causing undesired seed formation (feminized seeds, FS). HF developing spontaneously during commercial production of three cannabis strains were studied. Anthers were collected and morphological features were found to be similar to those of anthers in genetically male flowers. The FS were viable and gave rise to 100% genetically female seedlings (compared to 50:50 female:male from cross-pollination) using a PCR-based gender identification test. In this test, a 540 bp size band was present in female plants and 540 bp + 390 bp bands (or only a 390 bp band) were seen in male plants. Features of LTR retrotransposons were found within these sequences. Anther tissues from HF displayed the female banding pattern. The extent of genetic variation within seedlings derived from FS was compared to that derived from cross-pollinated seeds using six ISSR primers. Percentage of polymorphic loci was 44% to 72 % and Nei's index of gene diversity and Shannon's Information index were comparable for both populations.

Janesse Holmes (janesseh@sfu.ca)

P116. **Characterizing and understanding the underlying molecular mechanism of the sugarcane anti-florigen ScFT2**

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Flowering time is a tightly regulated process that is essential for seed production and proliferation in higher plants. The vegetative to reproductive transition is controlled by diverse cues acting through distinct genetic pathways that converge at mobile floral integrators called florigens. These conserved phosphatidylethanolamine-binding proteins (PEBPs) are synthesized in leaves and migrate to the shoot apex to form a floral activation complex (FAC), which initiates reproductive growth by activating floral organ specificity. In sugarcane (*Saccharum* spp.), several florigen gene candidates have been identified, such as *ScFT2*. Interestingly, overexpression of this gene in *Arabidopsis* disrupts the floral transition and causes a dramatic change in shoot architecture. This research aims to characterize the mechanism behind this protein to determine how *ScFT2* overexpression causes an extreme vegetative phenotype. Localization experiments and interaction assays will be conducted to determine if ScFT2 interferes with FAC formation by outcompeting endogenous PEBPs, and to identify new entities involved in floral regulation. Mutants of well characterized floral genes will be complemented with *ScFT2* overexpression to prove clues as to the potential players involved in the anti-flowering phenotype. ScFT2 will also be transformed into other species to fine-tune flowering for agricultural applications.

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P117. Investigating the role of secretion in the *Arabidopsis thaliana* compatible pollen response pathway

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The acceptance of compatible pollen in the Brassicaceae is tightly regulated through interactions between the pollen and the pistil. Secretion in the stigmatic papillae is proposed to be key to this interaction to provide resources to the pollen for hydration and germination. The objective of this research is to investigate components of the *Arabidopsis thaliana* secretory pathway machinery for their requirement in the stigma for compatible pollen acceptance. Fluorescently-tagged markers that identify different compartments in the endomembrane system are being used to gain a fuller understanding of the secretory activity that occurs following compatible pollinations. In addition, the requirement of SNARE complex subunits, which are implicated in vesicle fusion and cargo release, is also being investigated through loss-of-function mutants. Our preliminary results have shown that combining SNARE knockout mutants leads to a reduction in compatible pollen hydration, supporting their role in the compatible pollen acceptance pathway. Higher order SNARE knockout mutants will be used in the future to further characterize the SNARE complex's role in compatible pollen acceptance. Together with fluorescently-tagged endomembrane marker lines, this research will provide a better understanding of the stigmatic papilla's secretory system, and how this system is employed in the acceptance of compatible pollen.

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P118. POPCORN modulates auxin flow and polarity to define adaxial-abaxial cell fate in Arabidopsis leaf development

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Co-ordinated developmental programs produce flat and symmetrical leaves to perform broad biological functions including efficient light capture, gas exchange and photosynthesis in plants. *Arabidopsis* leaves exhibit symmetry in three axes, across proximal-distal (base to tip), medial-lateral (mid-vein to edge), and adaxial-abaxial (upper to lower) planes. Among these, symmetry in the adaxial-abaxial plane is critical for precise cell and tissue specification and their organization within the leaf. The specification and maintenance of this important bilateral symmetry is regulated by a network of genes functioning within domains of the shoot apical meristem and the lateral organ primordia that produce leaves. Here, we demonstrate that *POPCORN* (*PCN*), a WD-40 protein required for shoot apical meristem functions, plays critical roles in coordinating regulatory networks of leaf development in Arabidopsis. Insights into these roles are based on our findings that loss of function *pcn* mutants exhibited abnormal leaf development with phenotypic defects that were further enhanced with mutations in adaxial- or abaxial-promoting genes, producing sterile, stunted plants with severe leaf defects including radialized leaves. The network of these genes and potential regulators downstream of *PCN* was examined through integrated analyses including RNA-seq, microRNAseq and pull-down assays along with developmental and cell biological focused analyses of vascular development, leaf venation, and auxin signaling. These studies revealed *PCN* as a key regulator of adaxial-abaxial polarity establishment and leaf development in Arabidopsis.

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P119. **Investigating the role of BKNs in pollen-stigma interactions**

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The Brassicaceae, are a family of plants that contain many scientifically as well as economically important plants. Brassicaceae have “dry stigma”, meaning that the papillae lack surface secretions and allows the plants to have greater control over the early post-pollination stages, with only compatible pollen grains receiving water from the stigma, this facilitates pollen germination and fertilization. The basal compatible response pathway in the stigma is initiated upon recognition of compatible pollen, followed by exocyst-mediated transduction of secretion from the stigma towards the pollen, and this pathway remains largely elusive. A previous attempt to identify candidate genes in the compatible pollen signal transduction pathway led to the discovery of pseudokinases, BRASSIKIN1 (BKN1) and BKN2. It was also discovered that BKN orthologous are found throughout the Brassicaceae family. The BKN loci between different *A. thaliana* ecotypes as well as different Brassicaceae species differ. *A. thaliana* ecotype Col-0 has a truncated *BKN1* caused by a premature stop codon, but *A. thaliana* ecotype Hh-0 as well as *A. lyrata* have fully intact *BKN1* and *2* genes. For this project, *BKN1* and *BKN2* mutants will be generated in Hh-0 and *A. lyrata* using the CRISPR-Cas9 system. As well, overexpression *BKN1* constructs will be transformed into Col-0. Pollen response characterization assays will be performed to further understand the potential importance of the *BKN* genes in the compatible pollen response pathway.

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TOPIC 12: Diagnostic Tools Applied to Crop Production (Poster P120)

P120. **Laboratory testing of qPCR assays designed in silico reveal promising results to rapidly identify phytopathogenic Tilletia species.**

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Tilletia species are grass fungal pathogens of concern, especially for grain-exporting countries like Canada, because some cause diseases on wheat. Among them, *Tilletia indica* (Karnal bunt) and *T. controversa* (dwarf bunt) are subject to quarantine regulations and therefore are highly unwanted in areas that are free of those species. Both pathogens are closely related to un-regulated species: *T. indica* to *T. walkeri* and *T. controversa* to *T. caries* or *T. laevis*. There is a need for more rapid and sensitive diagnostic tools compared to the morphological methods currently used by regulatory agencies. Recent *in silico* comparative genomics analyses identified sets of candidate qPCR primers and probes targeting single copy genes that are species-specific. These markers have been tested in the laboratory against DNA from pure culture isolates for nine species: *T. indica, T. walkeri, T. asperifolia, T. barclayana, T. fusca, T. rugispora, T. laevis, T. controversa,* and *T. caries*. Although some assays showed differing levels of cross-reactivity, one for *T. walkeri* and one for *T. indica* were highly specific with promising sensitivity values (30-200 fg). The next steps will be to increase sensitivity by optimizing the parameters and confirm efficacy by testing against *Tilletia*-infected field samples. The validated assays will help improve diagnostic throughput, speed and accuracy for these agriculturally important pathogens.

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TOPIC 13: Ecology and Ecophysiology (Posters P121-P133)

P121. **Short-term effects of partial and clearcuttings on woody debris and understory vegetation in mixed-wood stands**

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Ecosystem management provides a useful framework for understanding and mitigating impacts of forest industrial activities on biodiversity and ecosystem functions. When comparing the effects of partial cuttings on stand attributes, stand-scale silvicultural studies mostly focus on overstory attributes such as composition, growth and survival and functions such as habitat quality and regeneration impacts, whereas other ecosystem attributes such as deadwood and understory vegetation is often neglected. Current study intended to determine the influence of various levels of harvesting intensities on standing and downed dead wood, and on understory vegetation communities in northern mixed temperate forests. Twelve years following harvesting, we compared the effects of clearcutting and partial harvesting with variable-intensities, on the abundance of standing and downed deadwood, and on the composition of the understory plant communities. Our results show that standing dead wood stem density and diameter structure of the sites with moderate-intensity gap harvesting (62% basal area retention), were comparable to unharvested control sites. Additionally, gap harvesting did not change the levels of mid- (15cm diameter) and small-sized (<10cm diameter) downed dead wood. Moreover, the gap treatment preserved understory communities more similar to those of unharvested control stands than those in diameter-limit (% retention) and clearcutting treatments (% retention). These results illustrate the importance of tree retention levels for the maintenance of dead wood and understory species associated with closed-canopy or old-growth forests.

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P122. **Competition or facilitation: Examination of interactions between endangered *Sida hermaphrodita* and invasive *Phragmites australis***

Mulholland, S.[*]; M. Costea; K. Stevens
Wilfrid Laurier University

Virginia Mallow (*Sida hermaphrodita*) is a perennial herb native to riparian habitats in northeastern North America. Throughout most of its geographical distribution, however, it is considered threatened potentially due to the loss of habitat caused by exotic European Common reed (*Phragmites australis*) invasion. The biology and ecology of *S. hermaphrodita* are still poorly understood, and factors contributing to the species rarity are unknown. Allelopathic and phytotoxic alterations of soil environments have been mechanisms proposed to explain the invasion success of *P. australis.* Field vegetation surveys and a greenhouse study were conducted to quantify seedling growth and arbuscular mycorrhizal colonization of both species in soils that correspond to a gradient of vegetation ranging in proximity to either *S. hermaphrodita* or *P. australis* to determine the potential for *P. australis* to allelopathically alter soils making them inhospitable to native species. Results did not support previous allelopathic exclusion reports since field results suggested that proximity to *P. australis* has no significant effect on *S. hermaphrodita* seedling mortality. Additionally, greenhouse results indicated that species performance and AM colonization may be facilitated within competitor's soil. The soil nutrient analysis coupled with plant performance findings, suggest that nutrient enrichment may play an important role in *P. australis* invasion, and that aboveground competition for light, may be key to explaining *P. australis'* success in the competition with native species like *S. hermaphrodita*.

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P123. The interaction of marine phytoplankton cell size with capacities for reactive oxygen detoxification

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Production of reactive oxygen species (ROS) accompanies stress conditions in photosynthetic organisms including marine phytoplankton[1]. The ROS include hydrogen peroxide (H2O2), superoxide anion radical, hydroxyl radical and singlet oxygen, each with characteristic lifetimes and subject to different scavenging processes. We hypothesized that phytoplankton cell size interacts with light stress through influences on intra- and extracellular ROS accumulation. We, therefore, used fluorescent probes to examine cell size dependencies of detoxification capabilities and susceptibilities to externally supplied and internally generated ROS in five centric diatoms ranging from Minidiscus variabilis (3 µm diameter) to Coscinodiscus wailesii (300 µm diameter). Externally supplied 100 µM H2O2 provoked a 10-fold increase in intracellular H2O2, leading to significant decreases in PSII activity in larger, but not in smaller, diatom cultures. The resistance of the smaller diatoms is largely explicable through greater detoxification of H2O2 in dense cultures vs. lower density suspensions of the larger cells. Therefore, population or community level cooperative detoxification capacities are important to cellular level responses to ROS. We give an overview of results using fluorescence probes to track specific ROS accumulations in phytoplankton of different cell sizes.

1. Diaz, J. M. & Plummer, S. Production of extracellular reactive oxygen species by phytoplankton: past and future directions. Journal of Plankton Research (2018). doi:10.1093/plankt/fby039

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P124. Assessing threats and mitigation for Scarlet Ammannia (*Ammannia robusta*) in Southwestern Ontario

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Scarlet Ammannia (*Ammannia robusta)* is an annual emergent wetland plant of the Lythraceae family. Throughout most of its global distribution the species population is stable under present conditions. However, in Canada, *A. robusta* is considered endangered with only a few small populations documented in British Columbia and Ontario. In response, a recovery strategy was created for *A. robusta* outlining the lack of information on the species biology and ecology. Field vegetation surveys and seed bank assays were conducted to assess the current status of *A. robusta* in Southwestern Ontario (Pelee Island). Results show that although the species may not be present during field vegetation surveys in a certain area, it is present in the areas seed bank. Therefore, limiting factors will be examined to further understand why this pattern is occurring. Both field and greenhouse studies will be conducted with and without the presence of competitors to assess the effects of competitor removal on *A. robusta.* Additionally, *A. robusta* seeds will be used to conduct germination trials to fill in knowledge gaps pertaining to the influence of light duration, light intensity and temperature requirements. By examining these factors, I plan to verify what is limiting the distribution of *A. robusta* in Southwestern Ontario in order to establish conservation efforts that will improve the species distribution in Canada.

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P125. Assisted migration of whitebark pine to higher latitudes and elevations in the Canadian Cordillera

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Whitebark pine (*Pinus albicaulis*) is a western North America species highly susceptible to warming climate. An assisted migration trial, established at its northwest-northeast range limit in BC: (1) tested if lack of mycorrhizal fungal symbionts could inhibit seedling migration into alpine tundra beyond current range; (2) compared performance of 5 provenances (from western Washington to central BC) planted at elevations north and above native range. In 2008, seedlings were grown in a nursery trial in subalpine and alpine soils from the western and eastern Cordillera. Sub-sampled seedlings were out-planted at 3 elevations (Bulkley Ranges, western Cordillera, 2012), and two elevations (Rocky Mountain Ranges, eastern Cordillera, 2013). Ten years after germination, there was no evidence that lack of mycorrhizal fungi in alpine soils inhibited survival and growth. Nursery mycorrhizal colonization was excellent in alpine and subalpine soils. Out-planted seedlings grown in western and eastern alpine soils had larger diameters compared to subalpine soils (p = 0.001); seedlings retained this growth advantage 5-6 yr later (p = 0.05). All provenances survived at >80%. Significant differences in survival, height and diameter were not detected among provenances. Height and diameter appeared positively correlated to each provenance's seed collection elevation relative to treeline elevation. Apparently, all provenances are adapted to harsh, variable climates and can be translocated northward in latitude and into alpine zones at low risk for early establishment.

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P126. Below-ground facilitation between tree species in the re-vegetalization of a degraded site

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[2]*Université Paul Sabatier – CNRS*

Mycorrhizal symbiosis plays a key role in ecological processes like plant succession through the redistribution of resources among host plants with different needs. Mycorrhizal mycelia produce Common Mycorrhizal Networks (CMNs) by colonizing roots of neighboring trees, and these CMNs facilitate the uptake and transportation of nutrients among plants. In this study, we aim to determine how seedling growth and survival is affected by below-ground facilitation via mycorrhizal networks. Specifically, we will i) determine which intraspecific and interspecific interactions affect seedling growth at an early successional stage on a former mining site, ii) identify existing mycorrhizae species and types using molecular analysis and iii) if evidence of facilitation is found in i), determine whether this facilitation is due to mycorrhizal networks or due to other factors. *Betula papyrifera*, *Populus balsamifera*, *Picea glauca* and *Thuja occidentalis* will be used as focal species and the effect of neighbouring plants will be identified. Content (mg) and concentration (mg/g) of C, N, P, K, Ca, Mg and Mn in soil and leaf samples will be analyzed using CNS analyzer, colorimeter and atomic absorption methods. Communities of mycorrhizal fungi will be sequenced and analyzed to detect possible species sharing using genetic analysis. Structural equation models will be used to separate effects of tree age, soil nutrients and contaminants, CMNs and other possible factors on seedling growth.

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P127. **Is it possible to predict precipitation with readily available precipitation records?**

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Swift Current Research and Development Centre)

Drought is predicted to become more common in the future. A tool to provide a quick estimate of the probability of receiving the monthly normal (30-year mean) precipitation total during the months of the present growing season would be of value. Precipitation amounts that have occurred in previous years are readily available. However, this data does not provide any indication of the monthly precipitation totals that could occur during the remaining months of the growing season. The probability of receiving near normal precipitation would allow on-site decisions for forage production. Southwest Saskatchewan forage yields are largely determined by the amount of precipitation received from April to June. Precipitation records for Swift Current, Saskatchewan were used to calculate the possibility of receiving normal precipitation for April to June. The probability of receiving the 30-year monthly precipitation normals during this years growing season can be estimated from the 30-year normals combined with the previous months precipitation (Mosley 2019). The 30-year normal mean total precipitation for April, May, June is about 163 mm. This growing season (2019) April, May total precipitation is 21 mm. Knowing the precipitation for April and May, the probability of receiving precipitation during June 2019 so as to attain the 30-year median and mean (163 mm) precipitation totals for April to June was calculated as 10% for both.

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P128. **Exogenous ethylene increases methane emissions from canola**

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Methane is a potent greenhouse gas and its atmospheric concentration has been rising. Both natural and anthropogenic sources contribute to global methane budget. Methane is formed under both anaerobic and aerobic conditions. In plants, aerobically produced methane originates from different precursors, including pectin, lignin, wax and methionine. However, the mechanism of methane production remains unknown. We investigated the effects of exogenous ethylene on methane and other plant parameters in canola (*Brassica napus* L.). Plants were grown under a temperature regime of 22/18°C (16 h light/8 h dark) at a light intensity of 300 µmol m^{-2} s^{-1}, and were exposed to one of three ethylene treatments (36 µmol ml^{-1}): no exposure as control, one hour per day, and two hours per day. Plants were grown under the experimental conditions for 7, 14, or 21 days. Ethylene evolution increased with time and exogenous ethylene; it was highest from the 14- and 21-day-old plants with 2 h daily exposure and lowest from the control plants. Exogenous ethylene increased methane emission, which was highest from plants with 2 h daily exposure and lowest from the 21-day-old control plants. Plant growth, biomass, gas exchange, chlorophyll fluorescence, and photosynthetic pigments decreased by exogenous ethylene. Methane and ethylene were positively correlated, but they were negatively correlated with other parameters. Findings from this study should lead to the mechanistic understanding of plant-derived methane.

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P129. **An analysis of invasive species management in the Niagara region of Ontario, Canada: establishment of a database to improve knowledge sharing**

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The UN and Convention on Biological Diversity have declared invasive species a global initiative and requested increased data sharing on invasives. No database focuses on invasive species management for the Niagara Region, ON, Canada. This study used sustainability science and the Ecosystem Approach Principles to guide the design of an invasive species management database. The goal of the study was to document current aquatic and riparian invasive management activities in the Niagara Region and develop a database that would become a tool to facilitate collaboration at the regional level. The objectives were to (1) inventory current invasive detection and control activities in the Niagara Region and make comparisons to recommended techniques in the literature; (2) examine perceived efficacy of control techniques; and (3) develop a database integrated with a GIS mapping component. Seventy-one organizations involved in riparian/aquatic invasive management in the Niagara Region were contacted and 16 were interviewed in-depth. In 2017/2018 there were 35 separate control efforts reported, involving 10 riparian invasives and two aquatic invasives, with most concentrated along the Niagara River. Collaboration efforts were minimal, occurring for only six specific projects. Recommendations from this study include: develop a regional invasive species plan; increase control efforts along the Welland Canal and Lake Erie shoreline; consider a wider variety of control techniques; and increase collaboration, information-sharing and resource-sharing among organizations.

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P130. **Performance of Eastern white pine (*Pinus strobus* L.) at the limits of its distribution range in Western Newfoundland.**

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A dynamic population of Eastern white pine spans a 200 m elevation gradient in Western Newfoundland, growing in partially forested areas of flat or sloping fens, rocky boulder fields, and tuckamore-ericaceous shrublands. Seed cone production is notably lower at the upper level of the gradient. The introduced red squirrels remove the cones with a year-to-year effectiveness varying from zero to 100%, and similarly variable levels of seed predation by birds and small mammals occur on the ground. About a third of the remaining seeds germinate, and about a third of the first year juvenile seedlings survive the first winter. Further, established seedlings, either grown from seeds or transplanted from a greenhouse, show only occasional mortality, possibly assisted by unspecific damage by local fauna. Seed germination and juvenile seedling survival do not clearly correlate with elevation or location within the area. For established seedlings, as well as for mature trees, the temperature decrease up the gradient shortens the growth season by shifting the times of snowmelt and delaying bud break. Nevertheless**,** the rates of linear and radial seasonal growth in seedlings and mature trees do not directly follow the elevation, likely affected by the soil parameters and/or microclimates at their individual locations. Overall, suboptimal temperatures at the distribution range limit appear restrictive for Eastern white pine performance through impaired fecundity rather than through germination or survival.

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P131. Cold spring delays autumn senescence, elongates nutrient uptake period, but reduces nitrogen storage for winter in *Rhynchospora alba* (Cyperaceae)

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Factors underlying variation in timing of fall senescence are not well known. We investigated how a delay in the onset of the growth in spring affects senescence and N uptake in autumn, and the resulting storage of N for the winter in *Rhynchospora alba.* This species develops each year its sole organ for storage and overwintering, bulbils, anew. The plants were grown outdoors in a garden experiment with two treatments, identical except for three weeks difference in start of the growth in May. Above and below-ground growth and senescence, and N uptake were periodically recorded from August to November. By August, plants that started their growth later had caught up in total size and N content, but had smaller bulbils. Their higher delta^{13}C indicated a higher stomatal conductance during growth. Senescence of leaves and roots was delayed, resulting in an extended period of ^{15}N tracer uptake by four weeks. Nevertheless, after senescence, plants with an early start in the growing season had 55% more N in their overwintering bulbils, due to an earlier and more efficient remobilization. We conclude that timing of senescence in *R. alba* is a result of an interplay between the status of winter storage and cold temperatures, constrained by a trade-off between prolonged nutrient uptake and efficient remobilization of nutrients.

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P132. Effects of drought, plant hormones and arbuscular mycorrhizal fungi on photosynthesis, transpiration and plant growth in corn (*Zea mays*)

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Globally severe drought is projected to occur more frequently, which could negatively impact the growth and development of plants. Arbuscular mycorrhizal (AM) fungi colonization and plant hormones have been reported to enhance plant growth and development in some plant species. We investigated the effects of AM colonization, severe drought, and exogenous applications of abscisic acid (ABA) and benzylamino purine (BAP) on photosynthesis and transpiration rates, water potential, and fresh weight corn (*Zea mays* cv. Honey select). Three-week-old corn seedlings inoculated with or without AM, and with or without foliar hormone treatments were subjected to three weeks of drought stress. Our results showed that severe drought significantly lowered photosynthesis and transpiration rates, water potential and plant growth compared to well-watered treatments. However, AM and exogenous hormone treatments did not have a significant effect on photosynthesis and transpiration rates, and plant growth. In addition, AM and exogenous hormone treatments did not reverse the drought-induced decline in plant growth. The role of AM colonization, and plant hormones in photosynthesis and transpiration, and growth of corn plants grown under normal and drought-stress conditions will be discussed.

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P133. **Seasonal changes in photosynthesis, transpiration and chlorophyll levels in American Sweetgum (*Liquidambar styraciflua*) and Hungarian Oak (*Quercus frainetto*) and Japanese Katsura (*Cercidiphyllum japonicum*)**

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The environmental aspect of sustainability has become an increasingly important topic due to its impact on climate change and carbon sequestration processes. A diverse variety of tree species act as a living laboratory that can be used to investigate the effects of environmental factors on the growth, development, and physiology of plants. Therefore, it is important to analyze the effects of seasonal changes and environmental factors on the relative efficiency of various plant species in carbon sequestration, transpiration, and leaf chlorophyll levels. In this study, we analyzed the photosynthesis and transpiration rates, protein and chlorophyll levels in the leaves of American Sweetgum, Hungarian Oak and Japanese Katsura trees during 2018-2019. The results showed that the Hungarian Oak had the highest photosynthesis rate and that the stressed Japanese Katsura had the highest chlorophyll level while the American Sweetgum had the lowest chlorophyll level among the three species. The transpiration rates were relatively similar among the species. In addition, the soil compaction stress reduced the rates of photosynthesis in Japanese Oak trees. The relative effects of the developmental and environmental changes on photosynthesis and transpiration rates and leaf protein and chlorophyll levels in these species will be discussed.

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TOPIC 14: Entomology and Pest Management (Posters P134-P135)

P134. **Plastid transformation of Micro-tom tomato for RNAi interference in insects**

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[3]*Government of Canada*

RNA interference (RNAi) is used by eukaryotic organisms, including plants and arthropods, as a gene regulation and defense mechanism. It is also a promising tool for crop protection since it can be used to selectively silence insect genes essential for survival. One strategy to exploit the insect RNAi pathway for insect control is to develop plants that produce double-stranded RNA (dsRNA), the effector that activates the RNAi pathway, specific for insect genes. For optimum potency, dsRNA can be produced in plastids of plants since they lack intrinsic RNAi processing machinery, thus allowing maximum accumulation of intact dsRNA. Although plastid transformation of plants holds great promise for insect control, the feeding behavior of target insects also needs to be considered, as this affects insect uptake of plastids. In this study, we produced transplastomic Micro-Tom tomato plants expressing dsRNA for a highly conserved insect gene, v-*ATPaseA*. We then fed these plants to several insect species from different Orders that use either leaf-chewing, lacerate-and-flush, or sap-sucking mechanisms to feed. We show that conserved gene sequences can be used to silence genes in multiple insect species through plastid transformation. We also found that only insects feeding through leaf-chewing and lacerate-and-flush mechanisms were susceptible to RNAi when dsRNA is produced in plant plastids.

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P135. **Modulation of lipopeptides production by Bacillus subtilis PTB185 in response to different plant pathogens**

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Lipopeptides are essential compounds associated with the biocontrol activity of the *Bacillus* spp. In order to better understand the biological mechanisms involved in the production of lipopeptides by *Bacillus subtilis* strain PTB185, the bacterium was co-cultured on agar with one of the following plant pathogens: *Botrytis cinerea, Mucor* sp., *Pythium ultimum, Rhizoctonia solani, Sclerotinia sclerotiorum.* After 5-7 days of growth, lipopeptides (surfactin, iturin, and fengycin) produced by PTB185 were extracted and quantified using MALDI-TOF mass spectrometry. PTB185 was further cultivated in liquid media supplemented with cell wall powder (1 g L^{-1}) of each tested pathogen. After 3 days of growth, lipopeptides were quantified in the culture filtrates and bacterial suspensions were tested *in vitro* for their antagonistic activity against the plant pathogens. PTB185 inhibited on agar the growth of the pathogens that were shown to strongly enhance the production of surfactin, iturin, and fengycin. In addition, the incorporation of pathogen cell wall powders in the liquid medium was shown to stimulate the production of iturin and fengycin and to improve the antagonistic activity of PTB185. This study indicates that biological interactions stimulate the production of lipopeptides by *B. subtilis*. The results also suggest that *B. subtilis* biocontrol activity could be strengthened by the composition of the medium.

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TOPIC 15: Growth Regulators (Posters P136-P137)

P136. **Karrikins: important regulators of seed germination in wildfire-prone regions**

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Wildfires are having devastating and regenerative impacts on the ecosystems of the Pacific Northwest. We hypothesized that karrikins, a distinct class of plant growth regulators (PGRs) that are released from burning plants during wildfires, induce seed germination in two ecologically important species *Balsamorhiza sagittata* and *Balsamorhiza deltoidea. B. sagittata* grows in the dry ecosystems of the Okanagan and *B. deltoidea* grows along the rain-drenched coast.To investigate our hypothesis, we imbibed seeds in 0, 5 or 10 µM of gibberellic acid (GA), karrikin 1, 2 or 11 (KAR_1, KAR_2, KAR_{11}) alone and in combination. $KAR_2$was more effective than KAR_1or KAR_{11}increasing seed germination in *B. sagittata* by 3.35-fold (5 µM) and 5.4-fold (10 µM). 100% of viable *B. deltoidea* seeds germinated in response to 10 µM KAR_2.*B. sagittata* seedlings grown in axenic culture in a standard controlled environment growth room entered a dormant phase at temperatures > 15°C and were recovered by incubation in a refrigerated chamber at 3°C for 4-6 weeks. Thidiazuron (TDZ; 0 or 10 µM) induced *de novo* regeneration. *B. sagittata* seedlings produced between 3-12 *de novo* shoots in response to 10 µM TDZ. *B deltoidea* seedlings produced ≈66 (10 µM TDZ) regenerants resembling somatic embryos with globular, heart shaped, torpedo and cotyledonary structures. Following a heat-stress experiment, 5 putatively temperature resistant germplasm lines of *B. sagittata* were recovered. Together, these studies demonstrate that KAR_2induces seed germination and provide*in vitro*methods for conservation and mass-propagation of *Balsamorhiza* species.

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P137. **Indoleamine plant growth regulators perceive and initiate plant responses to specific light spectra in Scutellaria species**

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As sessile organisms, plants use light as an indicator of their environment as well as to mediate plant growth through signalling networks involving plant growth regulators (PGRs). We hypothesized that a novel class of PGRs, the indoleamines, are plant signaling molecules that perceive changes in light composition and initiate a cascade of metabolic responses. To examine this, we grew three *Scutellaria* species (skullcap): *S. lateriflora*, *S. galericulata* and *S. racemosa* in vitro. Axenic cultures were exposed to red, blue, green or white light spectra provided by light emitting diode (LED) lighting systems. The PGRs melatonin, serotonin, abscisic acid (ABA), auxin, and jasmonic acid (JA), were quantified by ultra performance liquid chromatography-tandem mass spectrometry. Serotonin was detected in plants grown under red and blue light. Melatonin was detected in plants grown under all of the different LED spectra and at highest levels in plants grown under blue and red light. Auxin was found at significant levels in plants grown under blue lights. In *S. galericulata* plants, the concentration of ABA was the highest under white light with decreasing amounts produced by plants grown under green, blue and red light. We propose that the indoleamines are an important signal which allow plants perceive and respond to changing light conditions and that *Scutellaria* is an excellent in vitro system for the investigation of these signaling events.

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TOPIC 16: Horticultural Field Production (Posters P138-P139)

P138. **Remote assessment of phenological and phenotypic variability in wild blueberry fields**

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Research and development activities using a PrecisionHawk Lancaster M4 and M5, and DJI Matrice 600 Pro unmanned aerial vehicles (UAV) equipped with 18.4 megapixel camera was conducted during the 2016 to 2018 field seasons to determine if the UAV system could accurately assess wild blueberry coverage, phenotypic population structure, and vegetative and floral bud growth stage. This was complimented with field level validation of blueberry coverage, vegetative and floral bud growth stage, and phenotypes identification. In addition, hyperspectral VIS/NIR scans of selected blueberry phenotypes were obtained using a radiometer equipped with a 10˚ foreoptic. Results indicated that it was possible to provide precise and accurate assessment of: (i) blueberry coverage and topographic features, (ii) the distribution of *Vaccinium angustifolium* Ait. and *V. myrtilloides* Michx. phenotypes, (iii) canopy growth and development stage, and (iv) several weed species including goldenrod, sheep sorrel and fescue grasses that were present within the fields. However, use of the high resolution digital camera did not consistently provide an accurate estimate of bloom intensity or yield potential. Therefore, results from the study have indicated that these technologies have the potential to significantly improve field assessment for blueberry plant coverage and pest related factors. This can be integrated with emerging agrochemical application technologies to significantly reduce agrochemical usage, decrease the cost of production and improve the overall sustainability of the production system.

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P139. **Evaluation of bottle and luffa gourds for commercial production in Canadian greenhouses**

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The bottle gourd (*Lagenaria siceraria)* and luffa gourd (*Luffa spp*) are not cultivated in Canada, but there is a demand from immigrants to Canada from warm regions of the World for these crops. We developed hydroponic production systems in rockwool slabs for both bottle and luffa gourd in a greenhouse at the University of Guelph. In addition, we screened 15 luffa and 5 bottle gourd varieties for their production of commercial quality fruit. Large variation was noted for flower initiation in bottle gourds (43 – 67 days) and luffa (45 – 50 days) after planting. In house pollination of luffa gourd by bees and of bottle gourd by tomato hornworm moths was demonstrated. The first fruit pick in luffa and bottle gourds varieties was 60 – 98 days and 57 – 92 days respectively. The fruit was ready to pick in 10 – 12 days in bottle gourd and 6 – 7 days in luffa after pollination. Average fresh fruit weight ranged from 118 – 257 grams in luffa and 760 – 1243 grams in bottle gourd varieties. The number of fruit per plant ranged from 0 – 11 in the luffa and 1-13 in the bottle gourd varieties over 2 months after planting. The initial results indicated that it would be feasible to establish commercial production of these crops in Ontario greenhouses.

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TOPIC 17: Mineral Nutrition (Posters P140-P142)

P140. **Towards low-input production of subirrigated chrysanthemums: Phosphorus acquisition and internal utilization efficiencies in two contrasting cultivars**

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Greenhouse floriculture operations pose significant environmental risk due to extensive inputs of fertilizer, especially N and P. Recent evidence shows that N and S use efficiencies are improved in subirrigated, potted, disbudded chrysanthemums by supplying a moderate level of the respective nutrient during vegetative growth, and removing the entire nutrient suite at the onset of reproductive growth, without adverse effects on plant quality. Here, a split-plot experiment was conducted with plants grown on four P regimens (2.6 mM P supplied during vegetative and reproductive stages, and 2.6, 1.95 or 1.3 mM P supplied during vegetative stage only) as the main plot and two cultivars (‘Olympia’ and ‘Covington’) as the sub-plot. Market quality plants with sufficient tissue-P were produced, even when P delivery was reduced by approximately 75% over the crop cycle, compared to industry standards. The primary mechanism for sustaining plant growth with decreasing P_i delivery was improved acquisition efficiency, although some changes in internal P utilization efficiency were evident, including the remobilization of both organic-P and inorganic-P during inflorescence development. Differences in biomass yields, tissue-P concentrations, content-based P use efficiency with constant P acquisition, and uptake- versus remobilization-based P supply for inflorescence growth established that ‘Olympia’ has a greater internal P utilization efficiency than ‘Covington’. This modified subirrigation practice could lay the foundation for low-input production of floricultural crops.

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P141. A single amino-acid substitution in the Lsi1 aquaporin of tobacco confers elevated Si transport and plasma-membrane localization

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Silicon (Si) is a non-essential yet beneficial substrate to many plants, conferring heightened resilience to environmental stress. A plant's ability to accumulate Si is primarily dependent on the presence of a Si-permeable Lsi1 (NIP2-1) aquaporin in its roots. Structure-function analyses of Lsi1s have thus far revealed two key molecular determinants of Si permeability: (1) the amino-acid motif GSGR in the aromatic/arginine selectivity filter, and (2) precisely 108 amino acids between two highly conserved NPA domains. Curiously, tobacco (*Nicotiana sylvestris*) stands as a rare exception as it possesses an Lsi1 (NsLsi1) with these molecular signatures but does not accumulate Si above background levels (0.1 % leaf dry weight), thus suggesting additional determinants of Si permeability exist. To this end, we first observed *NsLsi1* was expressed constitutively *in planta*. Next, Si influx was measured in NsLsi1-expressing *Xenopus* oocytes and found to be very low (<13% that of OsLsi1 from rice (*Oryza sativa*)), which likely explains why tobacco is a low Si accumulator. Interestingly, NsLsi1^{P125F} displayed a significant gain-of-function (3-fold increase in Si influx relative to NsLsi1^{WT}), which coincided with increased plasma-membrane localization *in planta*. These findings reveal a novel molecular determinant (Phe in position 125) contributing to Lsi1 cell localization and thus Si transport in plants, and inform breeding, biotechnological, and agricultural practices to effectively utilize this anomalous element.

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P142. Towards low-input production of sub-irrigated chrysanthemums: optimizing calcium and magnesium usage

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Excessive fertilizer use in greenhouse floricultural operations results in low nutrient use efficiency by plants, wastes nutrients, and poses significant environmental risk to water resources. Recently, we described a nutrient delivery strategy for subirrigated, potted, disbudded chrysanthemums, wherein a moderate level of N, S, K or P is provided during vegetative growth, in an otherwise complete nutrient solution, while eliminating the entire nutrient suite during reproductive growth, without adversely affecting plant yield and flower quality. Here, moderate levels of calcium (Ca) or magnesium (Mg) were provided during vegetative growth and then replaced with deionized water at the onset of reproductive growth. The experiments were conducted in a research greenhouse using pinched, potted plants in a split-plot design with Ca (6.76, 3.38, and 1.69 mM) or Mg (1.5, 0.75 and 0.38 mM) treatment as the main plot and cultivar ('Milton Dark Pink' and 'Williamsburg Purple') as the sub-plot. Market quality plants were produced with sufficient tissue-Ca or -Mg in a diagnostic leaf, even when delivery of the corresponding nutrient was reduced by approximately 87.5% over the crop cycle, compared to industry standards. Bloom development was unaffected by the treatments. This research contributes to the further development of a novel nutrient delivery strategy that reduces the rate of fertilizer application, and the concentration/ volume of nutrient-rich solution that must be managed in accordance with applicable environmental legislation.

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TOPIC 18: Molecular Host-Pathogen Interactions (Posters P143-P154)

P143. **Creation of pokeweed mosaic virus infectious clone to study host-pathogen interactions**

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Potyviridae is a prolific plant virus family whose members cause significant damage to agricultural crops. Potyviral genomes are ~10 kb ssRNA, and encode a polyprotein that is processed by viral proteases into at least 11 multifunctional proteins. P*hytolacca americana* (American Pokeweed) produces pokeweed antiviral protein (PAP) which has been shown to reduce replication of both plant and animal viruses by depurinating RNA of the viral genomes. Curiously, pokeweed is infected in the wild by a potyvirus known as Pokeweed mosaic virus (PkMV). To facilitate the identification of factors that overcome pokeweed antiviral defence, the first infectious clone of PkMV was constructed by assembling sections of the viral genome into a plant vector. Agroinfiltration of the clone into pokeweed leaves produced the typical chlorotic mottling and systemic movement through the plant, indicative of infection by PkMV. Viral particles isolated from plants inoculated with the infectious clone were morphologically identical to PkMV, and presence of viral RNA and proteins were verified by RT-PCR and immunoblot assay. As well, eGFP was cloned into the P1/HC-Pro junction to demonstrate the clone's ability to be modified while retaining infectious. The PkMV clone was engineered to contain PAP sequence which induced reduction in PAP levels. After knocking down PAP, the susceptibility of the pokeweed plant to other pathogens will be tested to expand our knowledge of PAP's role in pokeweed.

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P144. **Monaghan Lab: Plant immunology and immune homeostasis**

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Plants have evolved a multi-faceted immune system to fight against pathogen infection. While necessary for survival, pathogen perception and the activation of immune responses are energetically taxing for the host and have been linked to considerable fitness costs. Although defense signaling pathways must therefore be tightly regulated, very little is known about the biochemical mechanisms that tailor signaling to maintain cellular homeostasis. Our new research program at Queen's University focuses on understanding the basic mechanisms that allow plants to defend against a vast array of potential pathogens while maintaining normal growth and development. To this end, our work address the following biological questions using varied approaches: (1) What is the role of and interplay between different post-translational modifications on proteins involved in immune homeostasis? (2) What are the key regulators maintaining immune homeostasis and how do they function biochemically at the molecular level? (3) What developmental pathways are affected by immune signaling? Understanding the complexity of signaling events that underlie immune systems is integral to combating plant diseases that threaten food security world-wide.

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P145. Variation between Ilyonectria mors-panacis and I. robusta isolates causing root rot in Panax quinquefolius

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Ilyonectria mors-panacis is associated with ginseng replant disease causing disappearing root rot in replant soil versus only 2-5% rot in non-replant soils. *Ilyonectria mors-panacis* may be more common in ginseng roots because it is more virulent than other species, and isolates from roots in replant soil may be more virulent than from non-replant soil. One type of fungal virulence factor is small secreted proteins (SSPs) that can induce or suppress host triggered immunity. Measuring lesion size following inoculation of wounded ginseng roots with spores showed that virulence of three *I. mors-panacis* isolates from roots in replant soil was not significantly different from six isolates from roots in non-replant soil, and the average virulence of twelve *I. mors-panacis* isolates was not significantly different than that of four *I. robusta* isolates. Following genome sequencing, predicted homologs of SSPs were classified based on size, cysteine number and isoelectric point. PCA analyses of the SSPs showed that the twelve *I. mors-panacis* isolates clustered into two groups and the four *I. robusta* isolates clustered into two other groups with one isolate being more similar to *I. europaea*. There was no evidence that virulence of *I. mors-panacis* differed between isolates from replant and non-replant soils or that *I. mors-panacis* was more virulent than *I. robusta*, and clustering of isolates based on predicted SSPs was unrelated to virulence or replant/non-replant soil type.

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P146. Para-aminobenzoic acid (PABA) reducing *Botrytis cinerea* disease in leaves of Nicotiana benthamiana plants

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Para-aminobenzoic acid (PABA) is a folate precursor previously shown to induce resistance against *Xanthomonas axonopodis* pv. *vesicatoria* and cucumber mosaic virus in the field when pepper seedlings were dipped into 1 mM PABA. Induced resistance by PABA was demonstrated by up-regulation of the salicylic (SA) regulated genes, *CaPR4* and *CaPR9*, during the growing season. In this study, 18 mM PABA was applied 3 times weekly to soil around *Nicotiana benthamiana* seedlings. Seven days after the last application, leaves were inoculated with spores of the necrotroph, *Botrytis cinerea*. PABA-treated plants had 50% smaller lesions compared to water treated plants. No effects on plant growth were measured. Following treatment, up-regulation occurred only after inoculation for the SA regulated genes for acidic *NbPR-1a*, *Nb-ACC3* (1-aminocyclopropane-1-carboxylate oxidase3) and acidic *NbPR-2*, indicating priming. Up-regulation after treatment, but before inoculation, was observed for the SA regulated genes for acidic *NbPR-4B*, *NbSAR8.2a* (systemic acquired resistance protein 8.2a), and *Nb-CHn* (atypical basic endochitinase), indicating induction. Induction was also observed for *NbCP23* (cysteine protease 23) expression, which is not under ethephon (ET) or jasmonate (JA) regulation. Expression of the ET and JA-regulated genes for basic *NbPRb-1b*, basic *NbPR-2* were not affected by PABA, indicating that they were not involved in signaling resistance. This study showed that PABA can induce resistance against *B. cinerea*, which is due to both induction and priming of SA-regulated genes.

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P147. Development of a Grapevine rupestris stem pitting-associated virus strain Syrah clone and expression/VIGS vectors for *Vitis vinifera*

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Grapevines are an economically significant crop in Canada and there is increasing concern regarding the impact of pathogens on quality and health, particularly regarding viral pathogens. *Grapevine rupestris stem pitting associated virus* strain Syrah (GRSPaV-SY) is a single-stranded, positive-sense RNA virus of the genus *Foveavirus* in the family *Betaflexiviridae* that has been suggested to be a contributing factor to the Rugose Stem Pitting, Syrah Decline, and Grapevine Vein Necrosis diseases. Infection with multiple viruses makes it difficult to attribute symptoms and diseases to a specific virus, delaying development of treatment strategies for these diseases, as well as research on the fundamental biology of grapevine viruses. Full-length infectious clones (FLC) of viruses can be used to investigate disease associations and molecular biology by replicating singular infections and coinfections in grapevines. It is also difficult to study functional genomics and protein expression in woody plants like grapevines, which may be aided by more efficient virus-induced gene silencing (VIGS) and GFP expression vectors, respectively. The hypotheses are that GRSPaV-SY is one of the factors contributing to RWC, SD, and/or GVN and that a GRSPaV-SY-based viral vector can be used to develop GFP-tagged and/or VIGS vectors for *Nicotiana benthamiana* and *Vitis vinifera*.

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P148. Molecular characterization of plasmodesmata-located protein Osmotin34 from Arabidopsis and its association with Turnip Mosaic Virus Infection

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Plasmodesmata (PD) are plasmamembrane-lined pores that traverse the cell walls to establish cytoplasmic and endomembrane continuity between neighboring cells. As intercellular channels, PD controls the movement of protein complexes including plant viruses. Viral cell-to-cell movement via PD requires the coordinated action of virus-encoded proteins and host factors, especially PD-localized ones. To better understand the involvement of PD in viral infection, our lab conducted a quantitative proteomic study on the PD-enriched fraction from *Nicotiana benthamiana* leaves in response to turnip mosaic virus (TuMV) infection. Osmotin was identified to be significantly differentially accumulated in TuMV-infected leaves, when compared to its level in the corresponding healthy control. To characterize the possible role of osmotin in TuMV infection, we chose osmotin34 (OSM34), an ortholog from *Arabidopsis thaliana* (AtOSM34) for further study. Subcellular localization assay in *N. benthamiana* leaves reveals that AtOSM34 is indeed localized to PD. In Arabidopsis, *AtOSM34* expression is upregulated by TuMV infection, which is consistent with the previous quantitative proteomic data derived from *N. benthamiana*. Overexpression of AtOSM34 promotes TuMV replication and intercellular movement. Confocal microscopy revealed that AtOSM34 is recruited to the viral replication complex (VRC) of TuMV. Protein-protein interaction assay revealed that AtOSM34 interacts with the TuMV viral protein VPg, a key component of the VRC. These data suggest that AtOSM34 may play an important role in TuMV infection.

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P149. **Investigating the role of a family of receptor-like-cytoplasmic kinases in immune signaling**

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Plant disease resistance requires a tightly-coordinated signalling network to prevent the spread of infection. Cell surface-localized receptor protein kinases recognize danger signals such as microbial molecules and trigger phosphorylation-mediated signaling cascades resulting in cellular reprogramming and disease resistance. Several receptor-like cytoplasmic kinases (RLCKs) have demonstrated roles in immune phospho-relay across various plant species, making them a family of interest in the study of defense regulation. Here, we present our investigation of a family of RLCKs in *Arabidopsis thaliana* with hypothesized roles in immune signal transduction. Our ongoing work involves the functional analysis of mutant and overexpression lines, immune-induced activation, and protein-protein interactions with known regulators of immunity. This project seeks to characterize these interactions in order to place this family of RLCKs in immune signaling, which may be conserved in many agriculturally-significant crops.

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P150. **Identification of determinants in the turnip mosaic virus coat protein that are critical for viral cell-to-cell movement and virion assembly**

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Potyviruses represent the largest group of plant viruses including many agriculturally important pests such as Turnip mosaic virus (TuMV). TuMV coat proteins (CPs) form a protective shell for the viral genome, but many aspects of their role remain undefined. Here, we constructed a green fluorescent and mCherry fluorescent protein-tagged TuMV infectious clone and conducted a series of deletion and mutation analyses to determine the domains and specific residues of TuMV CP required for viral cell-to-cell movement and virion assembly. Our data indicate that the N-terminal amino acid residues 6 to 50 of TuMV CP are dispensable for replication, cell-to-cell movement and assembly, but the core domain residues 51 to 199, the C-terminal residues 200 to 288 or 265 to 274 are essential for cell-to-cell movement, albeit not for replication. Furthermore, mutation of the charged residues (R178 and D222) in the core domain of CP abolished cell-to-cell movement and prevented formation of virions in protoplasts. An alanine scanning mutagenesis study of the C-terminal region of CP suggests that the point mutant R269A exhibits a slow cell-to-cell movement phenotype with a delayed onset of systemic infection, independent of virion assembly. Moreover, these mutated CPs seem unstable, likely due to rapid proteasomal degradation. These data advance our understanding about the essential role of specific residues and domains of CP in TuMV cell-to-cell movement which are potential targets for the control of potyviruses.

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P151. **The Ve-resistance locus in tomato, a plant signalling intercept**

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The Ve-resistance locus in tomato, a plant signalling intercept Robb, J.*1, H.O. Shittu1, C.D.M. Castroverde1, X.Xu1, A. Kurosky2, R.N. Nazar1 Department of Molecular and Cellular Biology, University of Guelph, Guelph. ON, N1G 2W11 and Department of Biochemistry and Molecular Biology, University of Texas Medical Branch, Galveston, TX, 775552 Signalling crosstalk in plants has been recognized for several decades but the manner in which these interactions occur continues to pose many questions. Examples of crosstalk between plant defense responses and growth have been recognized but little is known about receptors that may be shared in this crosstalk. In tomato, resistance to Verticillium dahliae and V. albo-atrum, race 1 has been attributed to the Ve-resistance locus, comprising two closely related back-to-back genes, Ve1 and Ve2. Both appear to encode plasma membrane receptor proteins. Ve1 gene expression is induced and Ve2 is constitutive. Recent studies in our laboratories have shown that Ve2 controls the expression of the defense cascade, which appears to contribute to symptom development, while induction of Ve1 promotes root growth, which permits the plant to lower the concentration of Verticillium by outgrowing the fungus. Furthermore, proteomic analyses indicate that the two receptor proteins act antagonistically, the induction of Ve1 also causing a down regulation of Ve2 gene expression and a subsequent reduction in defense protein levels. These observations suggest strongly that the Ve-locus is a

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P152. **Subcellular localization of prune dwarf virus coat and movement proteins**

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Prune Dwarf Virus (PDV) is an important viral pathogen infecting many fruit trees in the *Prunus* genus such as sweet cherry, peach and plum. Phylogenetic relationships of the coat and movement proteins (CP and MP) of PDV have been major foci of research. Until recently, little research was conducted regarding intercellular movement of this virus. The aim of this work was to investigate the sub-cellular localization of these two proteins and findings indicate that CP and MP localize to the tonoplast and plasmodesmata respectively. After these initial results further studies were performed to identify regions of the viral protein which produce organelle targeting signals. Truncated versions of each protein show that deletions of the C terminal regions had minimal impact on organelle targeting, however deletion of the N terminal region negatively affected the formation of punctate structures of the fluorescent tagged viral proteins at their putative host protein targets. Future work includes the further identification of organelle targeting signals encoded by each viral protein, and the impact of mutations of these targeting signals in the PDV infection movement and infection cycle via the use of a PDV infectious clone on herbaceous indicator hosts.

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P153. Control of Fusarium head blight using the Next-generation of fungicides

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Fusarium head blight (FHB) is the most devastating disease of cereals which is caused by *Fusarium graminearum* (*Fg*). Infection of the heads of cereals with FHB negatively impacts the yield. Additionally, accumulation of the mycotoxin Deoxynivalenol (DON) during the progression of the disease on infected kernels imposes strict limits to its consumption in the food or the feed. Management of FHB disease in wheat is largely based on basal resistance of cereal plants and chemical control. The completion of the genomes of wheat and *Fg* help scientists to develop new tools/more targeted strategies to control FHB. We examined alterations in the transcriptome of a range of wheat varieties expressing different levels of kernel resistance to *Fg*. These results uncovered the *Fg* genes that are likely to play a role in early FHB infection of wheat kernels. A subset of early expressed genes involved in FHB infection were selected for silencing to reduce pathogen growth using Spray-Induced Gene Silencing (SIGS). SIGS is a non-GMO based technology that uses sequence specificity in dsRNA molecules to transcriptionally silence target genes. The use of dsRNA molecules to silence genes that support pathogen growth and mycotoxin production might offer a viable strategy to control future FHB epidemics. Here we report our progress of identifying novel *Fg* gene targets that can be used as future next-generation fungicides.

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P154. Comparative transcriptomics of root responses to pathogenic (*Fusarium oxysporum* f. sp. lini) and non-pathogenic (*Rhizoglomus irregulare*) fungi

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Fusarium oxysporum f. sp. *lini* is a hemibiotrophic pathogen, and the cause of wilt in flax (*Linum usitatissimum*). In contrast, *Rhizoglomus irregulare* is an arbuscular mycorrhizal fungus that generally forms mutualisms with flax. Both *F. oxysporum* and *R. irregulare* colonize roots at the beginning of their symbioses. We were therefore interested to compare how gene expression patterns in roots of flax inoculated with *F. oxysporum* differed from roots inoculated with *R. irregulare*. We sowed flax (linseed) seeds on autoclaved medium (vermiculite with mineral nutrients) that had been inoculated with one of four treatments: a mock control; *F. oxysporum*; *R. irregulare*; or both fungi simultaneously. We measured plant growth at three time points (9 d, 14 d, 22 d), and found that by 14 d, *F. oxysporum*-inoculated plants had significantly lower biomass and shoot length than any of the other treatments. We extracted RNA from plants at 9 d and 14 d, and used RNA-Seq to compare transcript expression patterns between the four treatments in three replicates. The number of differentially expressed genes was highest in the *F. oxysporum*-inoculated sample with 920 genes increased and 1,061 genes decreased in transcript abundance (FDR <0.05, FC 2) after 14 d. Only 8 genes had increased transcript abundance, and 69 had decreased abundance in the R. irregulare sample after 14 d. Here we describe the expression patterns observed.

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TOPIC 19: Molecular Plant Improvement and Genome Editing (Posters P155-P158)

P155. **Characterization of *Arabidopsis thaliana* MYB transcription factor complexes and their roles in the regulation of suberin biosynthetic genes**

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Terrestrial plants deposit cell wall-associated, lipid-based polymeric barriers in specific tissue layers to help protect themselves from various environmental stresses (e.g. drought, salinity, insects, and pathogens). One of these barriers, suberin, is found in various underground and aerial tissues, including root endodermis, tuber periderms, and bark (cork). Suberin mediates water uptake, ion transport, and gas exchange within roots. The degree of root suberization influences water relations and stress tolerance. Some of the Myeloblastosis (MYB)-type transcription factors (TFs) have been identified in regulating suberin biosynthetic genes. The transcriptional activities of MYBs are known to be influenced by specific protein-protein interactions forming larger regulatory complexes. Therefore, the focus of this study is to characterize the protein-protein interaction network of MYBs that up-regulate suberin biosynthesis. Here, we used yeast two-hybrid screening of bioinformatics-guided gene candidates and an *Arabidopsis thaliana* cDNA library to identify the potential protein interactors of suberin-associated MYB TFs. These binding partners are being further investigated by a combination of reverse genetic, biochemical, and bioinformatics approaches. This study will be important for the future generation of sustainable metabolically engineered crops that are more stress resistant, via enhancement of suberin deposition along their cell walls. Environmental stress can cause major yield loss of harvested crops, and improvement of stress tolerance can mitigate, and potentially eliminate these problems.

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P156. **Targeted mutagenesis in soybean using CRISPR-Cas9 system**

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Genome editing using CRISPR/Cas9 (clustered regularly interspaced short palindromic repeats/CRISPR-associated 9) has become a popular approach to induce targeted mutations for crop trait improvement. Soybean (*Glycine max*) is an economically important crop worldwide. As the first step to develop CRISPR technology to modify soybean genes for soybean cyst nematode resistance, phytoene desaturase (PDS) genes were selected as targets. Two PDS genes are present in soybean: Glyma.18G003900 (GmPDS18g) and Glyma.11G253000 (GmPDS11g). Constructs specifically targeting each gene, as well as simultaneously targeting both in the conserved regions were created. Each construct contains 35S promoter driving the expression of Cas9 translationally fused to green fluorescent protein (eGFP), and Arabidopsis AtU6 promoter driving the expression of single-guide RNA (sgRNA) containing a 20-nucleotide guide sequence. Agrobacterium-mediated genetic transformation of soybean cultivar Williams 82 were carried out using 2 constructs targeting different sites in GmPDS18g. Plantlets were recovered from tissue culture. Polymerase chain reaction (PCR) using vector-specific primers verified transformation in 33% and 100% of regenerated plantlets introduced with each construct. Among the positive transformants, insertion and deletion mutations at desired sites were detected from leaf tissues, validating genome editing in soybean using CRISPR/Cas9 system. Genetic transformation with additional constructs targeting PDS genes is underway. This technology will be subsequently employed to modify genes involved in soybean cyst nematode infection, towards potential disease resistance.

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P157. Characterization of the EPF family of signalling peptides controlling stomatal development in Monocots

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Stomata, which control water and gaseous exchange between plants and the atmosphere, are pores found on the plant epidermis. Proper stomatal density and distribution are critical for plant growth and survival. In *Arabidopsis thaliana*, several Epidermal Patterning Factor (EPF) family of cysteine-rich peptides are critical for controlling stomatal patterning and differentiation. EPF1 and EPF2, emitted from stomatal precursor cells, enforce stomatal spacing divisions and inhibit initiation of stomatal cell lineage, respectively. STOMAGEN/EPFL9, however, is expressed in underlying mesophyll tissues, promoting stomatal differentiation in epidermis. Here, we searched for stomatal EPF homologs in other agriculturally important cereal crops using a combination of bioinformatics and transcriptomics followed by functional genomics studies. We discovered orthologs of stomatal EPF peptides which are present in cereals despite distinct stomatal morphologies between dicots and monocots. Grass EPFs can complement stomatal developmental defects of *Arabidopsis epf* mutants and their elevated expression produces *Arabidopsis* plants with abnormal stomatal phenotypes. Additionally, application of each bioactive grass EPF triggered unique response in monocot stomatal development. Our data suggests that STOMAGEN function is conserved between dicots and monocots, but the roles of EPF1 and EPF2 in grasses are somewhat different than their functions in *Arabidopsis*. Collectively, our studies will enrich our knowledge on peptide signaling networks, enforcing proper development in plants. Anticipated results will provide fundamental knowledge that can help increase crop productivity and water-use efficiency.

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P158. The Global Industry Coalition (GIC) contributions to the work of Implementing the Cartagena Protocol on Biosafety

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Since the inception of the BSP, the plant science industry has recognized the need to engage in these negotiations in a committed, sustained and coordinated manner. To that end, the Global Industry Coalition (GIC) – a coalition of trade associations and companies involved in plant science, seeds, agricultural biotechnology, food production, animal agriculture, human and animal health care, and the environment – was established as a source for concrete and accurate information for countries involved in the global trade of LMOs. GIC members participate in every Meeting of the Parties to the Convention (COP) and to the Cartagena Protocol on Biosafety (COP-MOP) and are active contributors to the work under BSP on risk assessment and risk management of LMOs and, more recently, synthetic biology. While the GIC is officially recognized as “Industry,” its input is drawn from collaboration with experts in academia, government and the private sector with real-world experiences in order to share best practices and state-of-the-art, science-based information on risk assessment and risk management of LMOs and synthetic biology.

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TOPIC 20: Mycology (Posters P159-P161)

P159. **Genetic diversity of *Fusarium poae* field populations affecting small grain cereals in western Canada.**

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Fusarium head blight (FHB) is a serious threat to the production of small grain cereals, reducing both the yield and quality of crops. FHB is caused by multiple species within the genus Fusarium. On oat, *F. poae*, *F. graminearum*, and *F. sporotrichioides* are the most common species associated with FHB. In recent years. *F. poae* has become the predominant Fusarium species isolated from commercial oat fields in western Canada. Currently, the impact of this Fusarium species on the production of oat and the dynamics of *F. poae* populations in western Canada are largely unknown. In this study, we are applying a high throughput genotyping by sequencing (GBS) method to study the diversity of *F. poae* populations. The GBS libraries were prepared from 96 *F. poae* strains using a PstI/MspI protocol. Approximately 323 million 150bp pair-end reads were generated by Illumina HiSeq2500. The sequence reads were mapped to the reference genome of *F. poae* strain 2516. A total of 41,127 quality filtered variants were discovered with 4,819 sites existing in all 96 *F. poae* stains. Of these variants, 30,516 are single nucleotide variants (SNV) and 5,609 inserts and deletions (INDELs). Currently, we are utilizing these variants to study the structure of *F. poae* populations in western Canada, to determine the extent of linkage disequilibrium and identify regions of higher recombination frequency in the *F. poae* genome.

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P160. **Over-expression of a constitutively active MAP kinase kinase, MKK2, in *Fusarium graminearum* reduces its vegetative growth and disease progression in wheat**

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Kinases are enzymes that transfer phosphate groups to target proteins, regulating their activity or cellular localization. The mitogen-activated protein (MAP) kinases are involved in cellular communication, influencing various aspects of growth and development. These enzymes function in cascades, where a MAP kinase kinase kinase phosphorylates and activates a MAP kinase kinase, which in turn phosphorylates a MAP kinase. In *Fusarium graminearum*, one of the causal agents of the Fusarium head blight disease of cereal crops, the MAP kinase Mgv1 is known to play key roles in sexual reproduction, mycotoxin production and virulence. To further characterize the *MGV1* pathway and to identify downstream elements of this kinase, we over-expressed a phosphomimic of *MKK2*, the MAP kinase kinase that functions upstream of *MGV1*. The MKK2 phosphomimic is constitutively active, and it's over-expression will enable continuous phosphorylation of MGV1. Four colonies of the transformation were obtained. Interestingly, constitutive activation of the MGV1 pathway resulted in reduced vegetative growth on potato dextrose agar, similar to what has been reported for *MGV1* gene disruption. Reduced disease symptoms were also observed in the inoculated wheat spikes. Further characterization of these strains are underway towards identification of MGV1 phosphorylation targets.

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P161. **The Canadian Collection of Fungal Cultures: What we have for you and what you have for us.**
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Preserving representatives of fungi can help farmers devise effective anti-fungal treatments for agriculture, add to the growing body of knowledge of mycotoxins, identify invasive organisms or beneficial fungi that could enhance agricultural or economic productivity. The Canadian Collection of Fungal Cultures (DAOMC), in Ottawa, ON, is an internationally recognized culture collection maintaining ~20,000 living cultures, representing more than 4,000 species of fungi. This poster will present a synopsis of the diversity of the accessioned lineages within the collection. Partner institutions submit and requested fungal isolates in support of research in a variety of research fields. These include: zoosporic fungi, mycotoxigenic fungi, *Aspergillius* sp., *Penicillium* sp., *Fusarium* sp., Basidiomycota obtained from Canadian agricultural environments, and members of the families Clavicipitaceae , Erysiphales and Dothideomycetes. We house a variety of known plant pathogenic fungi including: *Claviceps purpurea* Ergot on rye, *Pythium* sp. and *Phytophthora* sp. the causal agent of damping off and root rot, *Fusarium* head blight in wheat, barley and other grains *caused by Fusarium sp.*, and *Tilletia sp*., the causal agent of bunts and smuts in cereals.

It is the hope and mandate of the Canadian Collection of Fungal Cultures to receive, store, preserve and share fungal organisms in collaboration with the scientific community. Researchers are invited to contact the CCFC to acquire or deposit fungal cultures.

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TOPIC 21: Pathology, Epidemiology and Disease Management (Posters P162-P196)

P162. **Buckwheat rhizosphere as a host for unique bacterial species**
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Wireworm has become a major problem causing extensive crop loss in many potato production areas in Canada. Control measures include the use of chemical pesticides. However, pesticides can affect human health and the environment, and their use has consequently been limited in many countries. Alternative control measures rely on integrated pest management including crop rotation. Hence, buckwheat is used as a rotation crop to mitigate wireworm damage in potatoes. However, less is known about how buckwheat contributes to mitigating the pest incidence. A 16S rRNA metagenomic study was conducted to determine the microbiome associated with buckwheat in comparison with barley grown in two locations with contrasting wireworm densities. The study identified 27 phyla associated with the rhizosphere of the two crops and *Proteobacteira, Bacteroidetes, Actinobacteria* were found to be the most abundant. Three non-pathogenic endophytic species, *Methylophilus flavus, Saccharopolyspora tripterygii* and *Deinococcus yunweiensis* belonging to the *Proteobacteira, Actinobacteria* and *Deinococcus-Thermus* phyla were found to be unique to the buckwheat rhizosphere soil from the two locations. The data will be presented and discussed in the context of sustainable agriculture and rhizosphere microbiome reformatting by rotation crops.

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P163. **A mycovirus cause hypovirulence in rice pathogen *Microdochium albescens***

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Mycoviruses are widely distributed in the major taxonomic groups of filamentous fungi. The association established between mycovirus and their hosts may occur in a latent form or can change the phenotype of the host causing hypervirulence or hypovirulence. In this study we describe a mycovirus infecting *Microdochium albescens,* etiological agent of leaf scald in rice, and evaluated phenotype effects of virus infection on the host. The mycovirus genome consists of four dsRNA segments with sizes of ≈2.5, 3.4, 3.5 and 3.8 kb. Viral particles with ≈40 nm were purified and the genomic segments were partially sequenced. Together these results suggest that the virus isolated is a member of Chrysoviridae family. We obtained a virus-free isogenic lineage and we found that the virus infected isolate produces 70% fewer spores than virus free and presented 30% decrease in ground index. The isolated virus infected was less aggressive than virus free isolate, with average in lesion length of 4.52 mm and 47.9 mm respectively. Our results show that this mycovirus infection has a strong effect on *M. albescens* fitness and phenotype, suggesting that the mycovirus isolated modulates important characteristics of the host that contributes to pathogenicity. Together, the findings potentiate the use of this mycovirus as tools for studies on the mechanisms of fungal pathogenicity as well as the use of these virus as biocontrol agents.

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P164. **Development of a novel, eco-friendly plant defense activator against Botrytis blight**

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Conventional fungicides against gray mold disease are available, but they often do not offer complete control, and negative health and environmental consequences have been ascribed to many of them. Therefore, the development of novel resistance-enhancing and eco-friendly controls for such an important disease is important for the production of field and horticultural crops, as well as for organic production in particular. In this study, we report that exogenous application of the polyamine spermine (Spm) is specifically effective in the induction of resistance against infection by the causal fungal agent, *Botrytis cinerea*,on *Arabidopsis*, tomato and bean plants. RNA-Seq-based transcriptomic and microscopic analyses revealed a priming role for Spm, leading to systemic-acquired resistance. Moreover, co-application of Spm and salicylic acid (SA) resulted in a synergistic effect against the pathogen, leading to higher levels of resistance than those induced by their separate applications. The Spm plus SA treatment also reduced infection in systemic, non-treated leaves of tomato plants. Our findings suggest that the Spm/SA mixture is a potent plant defense activator that leads to effective local and systemic resistance against *B. cinerea* and possibly other necrotrophic pathogens.

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P165. A potential QTL on Chromosome 3BS with major effect on adult plant resistance to stripe rust in a Canadian winter wheat diversity panel

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Stripe rust caused by *Puccinia striiformis* has been spreading to new areas in North America with highest severity on Ontario winter wheat in 2016 due to pathogen and climate changes. The objective of this research was to identify stripe rust resistance genes in winter wheat by examining seedling and adult plant responses of a Canadian Winter Wheat Diversity Panel (CWWDP; n = 430). Seedling and field infection analyses indicated that about 5% and 56% of the panel carry effective seedling and adult plant resistance, respectively, against the Ontario *P. striiformis* isolate UOGWYR16001. This population was genotyped using Illumina iSelect wheat 90K SNP beadchip, which provided 20K SNPs for a Genome-Wide Association Study (GWAS) of stripe rust resistance components. GWAS revealed a significant marker-trait association for adult plant resistance on the short arm of chromosome 3B. The associated region to the SNP marker RAC875_c3956_659 decreased stripe rust severity by 30% in the field. Further analysis of the chromosomal region linked to this marker detected 44 genes. *TraesCS3B01G063100*, the closest gene to the marker, is located in the 35.3 Mbp region distal to the tip of the chromosome 3BS and encodes a protease inhibitor/seed storage/lipid transfer protein (LTP). LTP is a member of the pathogenesis-related proteins family. *TraesCS3B01G063100* represents an interesting candidate gene for adult plant stripe rust resistance in winter wheat.

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P166. Several grass crops reduce resting spores of *Plasmodiophora brassicae* in soil

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Plasmodiophora brassicae Woronin causes clubroot on brassica plants. It also infects non-brassica species such as perennial ryegrass but cannot complete its life cycle in these plants. Our objective was to determine if sod-forming grasses reduce the concentration of resting spores in soil, by stimulating spore germination. The grasses assessed were: smooth bromegrass (*Bromus inermis* L.) cvs. Radisson, Signal and a common seedlot, meadow bromegrass (*B. riparius* R.) cv. Fleet, and perennial ryegrass (*Lolium perenne* L.) cvs. Norlea, Fiesta, and All Star. Plants were grown for 6 weeks in pots of field soil inoculated with 5 x 10^5 resting spores of *P. brassicae* g^{-1} soil under controlled conditions in three similar studies. There was a negative control (bare soil) and a positive control (pak choi, *Brassica rapa* cv. Mei Qing Choi, susceptible). Clubroot developed on the positive control. The spore concentration in soil was quantified using qPCR conducted with and without propidium monoazide (PMA), which suppresses amplification of non-viable spores. Pretreatment with PMA did not affect spore counts. Resting spore concentration was reduced by one or more cultivars of all three grass species (Fleet, Fiesta, Radisson, and common smooth bromegrass) compared to the bare soil, but Norlea, All Star and Signal had no effect. This indicated that many cover crops can reduce spore numbers in patches of clubroot, as well as reducing spore movement from the patches.

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P167. Development of an Immuno-PCR for the detection of pea root rot causal agent, Aphanomyces euteiches

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Pea root rot, caused by the oomycete *Aphanomyces euteiches*, is one of the most destructive diseases of pea. Effective measures to control this disease are lacking. An indirect ELISA and a real time immuno-PCR (RT-iPCR) assay for the timely and sensitive detection of *A. euteiches* were developed using antiserum specific to oospores of *A. euteiches* field isolates. The indirect ELISA exhibited a linear working range of 62 to 500 oospores, while the RT-iPCR could detect as low as 1 oospore for all isolates examined. To assess the performance of the RT-iPCR assay with soil samples, non-infested soils representing a range of soil textures were collected from different locations in Alberta. An extraction protocol was developed by spiking the treated soils with *A. euteiches* oospores and the RT-iPCR assay was used to quantify oospores in the soil extracts. Detection levels in soil extracts were as low as 10 oospores per g of soil. Infested soils collected from different locations across Western Canada are being tested by RT-iPCR for the presence of *A. euteiches*. To validate results obtained by the RT-iPCR assay, a greenhouse bioassay was also performed and showed good agreement with RT-iPCR results. The current RT-iPCR assay is more sensitive than quantitative PCR (qPCR) to detect low levels of oospores, and may be an invaluable tool for field diagnostics.

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P168. Fusarium head blight of wheat in Alberta: species complex and related trichothecene genotypes.

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Fusarium head blight (FHB) is the most damaging fungal disease of wheat in Canada and *Fusarium graminearum* is the primary causal organism of it. In this study infected wheat stem and grain samples were collected from three field experiments in Alberta (Lethbridge, Lacombe and Beaverlodge) to characterize the major *Fusarium* species associated with FHB. A *Fusarium*-selective medium was used to isolate *Fusarium* species and the elongation factor 1 alpha (EF1α) gene was used for molecular identification of the isolates. The results showed that, *F. graminearum* was recovered at very low rates from Lethbridge and was not detected in Lacombe or Beaverlodge. *F. avenaceum* was the most dominant species in Lethbridge (46%) as well as in Lacombe (59%), while *F. culmorum* was the most frequently isolated species in Beaverlodge (51%). Trichothecene genotyping using two multiplex PCR assays based on the *Tri*3 and *Tri*12 genes respectively, showed that the 3ADON was the most dominant genotype in all type B trichothecene producing *Fusarium* species tested from these three experimental sites (*F. culmorum*, *F. pseudograminearum*, *F. acuminatum*). In contrast, the 15ADON was the only genotype recorded for all *F. graminearum* isolates. In conclusion, *F. graminearum* was not the main causal agent associated with stem and grain samples from the three experiments, and more concern should be given to the other *Fusarium* species involved in FHB complex.

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P169. A Brevibacillus fortis isolate produces extracellular antibiotics that inhibit the growth of the onion pathogen Fusarium oxysporum f. sp. cepae and other Fusarium species

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Tan spot is an important foliar disease of wheat caused by the fungus *Pyrenophora tritici-rentis* (*Ptr*), which produces at least three necrotrophic effectors. In North America, Ptr ToxA-producing isolates are predominant (races 1 and 2), while race 3 isolates (Ptr ToxC-producers) are less frequent. Race 4, which is non-pathogenic and lacks the ability to produce any effectors, is rare. This study aimed to investigate virulence and effector genotypes in *Ptr* isolates obtained from different host types. The virulence of 130 isolates collected from durum and winter wheat, as well as from native grasses, was evaluated by inoculating four differential wheat genotypes. This was followed by PCR analysis with *ToxA* and *ToxB*-specific primers. The results showed that races 1 and 2 are the most common on wheat, but interestingly, the non-pathogenic race 4 is dominant on native grasses, and race 3 occurs more frequently when durum wheat is surveyed. Atypical virulence was reported when isolates were obtained from winter wheat, with isolates recovered that induced necrosis but did not produce Ptr ToxA, the only known necrotrophic effector. In conclusion, *Ptr* races and effector genotypes vary depending on the host, and this was the first study to investigate the virulence of *Ptr* collected from native grasses in Canada. Moreover, additional necrotrophic effector(s) that await further characterization may play an important role in *Ptr* pathogenicity.

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P170. Post-harvest root decay of American ginseng (*Panax quinquefolious*) and the relationship with ginseng replant disease

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Ilyonectria mors-panacis causes low levels of root rot of American ginseng in soil not previously planted to ginseng but high levels of root rot when grown again in soil used for ginseng, which results in replant disease. One explanation for this could be changes due to relatively large amounts of root debris left in the soil after harvesting, whose decay could increase levels of *I. mors-panacis* and soil ginsenosides. After harvest, approximately 10% by fresh weight of roots remained in the field. By 41 days post-harvest (dph), fibrous root pieces had completely decayed and 80% of the total root debris by fresh weight remained. By 198 dph, only 5.8% by fresh weight remained. Root decay typically started near the bud of intact roots. Among ginseng root grades, pencil grade was the least susceptible to decay. By 73 dph, 15% of the roots had visible lesions, and *I. mors-panacis* could be detected in 36% of those lesions. These results indicate that there are relatively large amounts of root debris left after harvesting, and decay of the roots occurs rapidly increasing *I. mors-panacis* soil populations. As ginsenosides comprise 3-5% dry weight of ginseng roots, this decay likely also releases significant amounts of ginsenosides into the soil. These changes in soil biology and chemistry may be important elements in creating ginseng replant disease.

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P171. Validation of antagonistic activity against fungal pathogens and the presence of antifungal genes in Pseudomonas chlororaphis strain S1Bt23

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Fungal pathogens cause significant yield losses annually to agricultural crops. The use of chemical pesticides is faced with fungal resistance as well as reported risks to the environment and public health. Bacterial pesticides are emerging as reliable alternatives. Strains of Pseudomonas chlororaphis are reported to be excellent candidates due to their ability to produce antifungal compounds. In 2015, a new strain, S1Bt23, was isolated and classified as Pseudomonas chlororaphis by multilocus sequence analysis (16S rRNA, recA, gyrB, rpoB and rpoD). The objectives of this project were (1) to confirm the antagonistic activity of strain S1Bt23; (2) to detect, by PCR, the presence of phenazine and pyrrolnitrin antifungal gene clusters; and (3) to visualize the antifungal metabolites using thin layer chromatography (TLC). In in vitro dual-cultures, strain S1Bt23 significantly inhibited the mycelial growth of the six fungi Rhizoctonia solani, Fusarium graminearum, Alternaria solani, Pythium ultimum, Pythium arrhenomanes and Sclerotinia sclerotinium. Pyrrolnitrin (4 genes, prnA-D; 5.8 kb) and phenazine (7 genes, phzA-G; 10.2 kb) operons were PCR amplified from the genomic DNA of strain S1Bt23, confirming the presence of complete clusters. TLC analysis validated the hypothesis that S1Bt23 secretes phenazine-1-carboxylic acid (PCA) and the extracts inhibited the growth of Pythium arrhenomanes. TLC results were confirmed by high pressure liquid chromatography. In conclusion, strain S1Bt23 embodies the desired characteristics for greenhouse and field studies as a potent biopesticide.

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P172. Growth inhibition of the plant pathogen, Streptomyces scabies, using plant tinctures

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Streptomyces scabies is a species of pathogenic bacteria that infects tuber crops through a specific pathway, causing the common scab disease. When this bacterium is in a germinating spore state, it infects tubers in various crops through natural openings and lesions. *S. scabies* uses a virulence factor called thaxtomin A in its infectious pathway once the crop has been contaminated. This poster outlines multiple methods used to measure *S. scabies* growth and for discovery of plant tinctures as natural antimicrobials towards this pathogen. It was determined that the Methylene Blue Assay (MBA) is an effective method for monitoring bacterial growth. A growth curve for *S. scabies* constructed using the MBA gave a doubling time of 6 hours. The MBA, in tandem with agar diffusion, was used to test a library of plant tinctures as *S. scabies* growth inhibitors. These experiments demonstrate the potential role of plant tinctures as antimicrobials and their utility for bacterial disease management.

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P173. Reactions of Eastern Canada oat genotypes to crown rust

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Crown rust, caused by *Puccinia coronate* f. sp. *avenae* (*Pca*), is the most important disease and yield limiting factor of oat production in Eastern Canada. In this study 101 oat genotypes composed of 51 cultivars and 50 breeding lines from eight oat breeding programs across Canada were evaluated for seedling reactions to six common *Pca* races and a bulk inoculum of *Pca* in greenhouse trials and for adult plant resistance (APR) to natural populations of *Pca* in field trials in 2014 and 2015. Sixty six genotypes showed resistant reactions to at least one of the six races; of which, 22 were resistant to all six races. These 22 genotypes also showed resistance to the bulk inoculum at the seeding stage and to the natural populations of *Pca* at the adult plant stage, suggesting that these current and future oat varieties have effective resistance against the common races and *Pca* populations in the region. Eleven genotypes, including 12ANS03, AAC Bullet, CFA1213, CFA1306, Idaho, OA1301-1w-3, OA1369-5, OA1370-2, OA1371-2, OA1383-2, and Oscar, were susceptible as seedlings but resistant as adult plants. APR is proven to be long lasting and provide broad-spectrum resistance to *Pca* populations and the 11 oat genotypes identified with APR in the present study are more desirable as sources of resistance for breeding programs aiming to develop durable crown rust resistant cultivars for Eastern Canada.

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P174. Diversity in virulence frequencies and race structure of extensively and intensively sampled populations of *Puccinia coronata* Corda var avenae f.sp. avenae.

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Virulence frequencies and race structure of populations of *Puccinia coronata* Corda var *avenae* f.sp. *avenae* (*Pca*) in Manitoba and Eastern Saskatchewan are monitored annually. Samples are collected each year using an extensive sampling procedure which involves collecting one *Pca* isolate per field from many fields. Another approach would be to use an intensive sampling procedure involving collecting many *Pca* isolates per field from a few fields. The objective of this study was to compare the virulence frequencies and race structure of two *Pca* populations; one collected using an extensive sampling procedure and the second collected using an intensive sampling procedure. A single pustule isolate (spi) was collected from each of 13 fields of cultivated oat, and 69 fields infested with wild oat for the extensive sampling procedure, and 49 spi were collected from two fields of cultivated oat and 59 spi from two fields infested with wild oat for the intensive sampling procedure in the target areas in 2018. The individual spi were used to determine virulence frequencies and races on 24 differential lines. Virulence frequencies were similar among the two collections, but the race structure was more diverse in the extensive sampling population compared to the intensive sampling population.

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P175. **Effect of host type on the virulence of Pyrenophora tritici-repentis (Ptr) in Canada**

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Onions are susceptible to Fusarium basal rot caused by the soilborne fungus *Fusarium oxysporum* f. sp. *cepae* (FOC). Control of this pathogen is difficult with limited genetic resistance in onion. It is therefore worthwhile to identify compounds that inhibit this fungus. We identified a strain of *Brevibacillus fortis* that secreted antifungal compounds into the growth media. The spent media, diluted 1:1, inhibited growth of FOC conidia after seven hours and killed 90% of conidia after 11 hours. The secreted antifungal compounds retained much of their inhibitory activity after a one hour incubation at 75° C. The spent media also inhibited growth of conidia from *F. graminearum*, *F. proliferatum*, *F. verticillioides* and *Galactomyces citri-aurantii*. Analysis of the genome sequence indicated a number of antibiotics could be produced by this bacteria isolate. Fractionation of spent media followed by reverse phase LC-MS determined that fractions with antifungal activity contained a mixture of edeines A, B and F and no other known antibiotics. These data indicate that this isolate could be utilized as a biological control organism for onions. Alternatively, development of edeine as a *Fusarium* control product should be investigated with more experiments.

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P176. **Emerging diseases of new hazelnut varieties grown in the Fraser Valley, British Columbia.**

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Four to ten year-old orchards, planted with new hazelnut (*Corylus avellana L.*) varieties, were surveyed in 2017 and 2018 for overall plant-health and diseases caused by plant pathogens. The most common symptoms were brown to dark-brown enlarging cankers with yellow-brown margins or sunken cankers with splitting margins and 'V-shaped' internal discoloured tissues on branches of hazelnut varieties 'Jefferson', 'Yamhill', 'Sacajawea', 'Theta', 'Eta', and 'Gamm', resulted in 'flagging' and dieback of the infected branches. Dark coloured pycnidia with pycniospores on the cankers and the pathogen isolated from the tissues were confirmed as *Phomopsis* sp. by DNA analysis. On some tree-trunks, dark-brown to black bleeding lesions and dark-brown discolouration of tissues beneath the lesions were observed. Although the symptoms were suspected of *Phytophthora* spp. or *Pseudomonas avellanae* (Psallidas), which causes bacterial canker, no pathogen was isolated from the symptomatic trunk tissues. In poorly drained soils, root rot was commonly observed on 4 to 10 year-old trees. Affected trees displayed weakened foliage, chlorosis and tree-decline. *Phytophthora* sp. "*hungarica*" was isolated from the symptomatic roots and confirmed by DNA analysis. Besides *Phytophthora*, *Cylindrocarpon* and *Fusarium* species were also isolated. Studies have been undertaken to identify the pathogens responsible for the diseases, and to determine their pathogenicity and epidemiology for developing management strategies to protect young hazelnut orchards in British Columbia.

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P177. In the footsteps of Dr. Margaret Newton: women plant pathologists leading the Canadian Phytopathological Society

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On this 90th anniversary of the Canadian Phytopathological Society (CPS), we celebrate the contribution of women scientists in plant pathology. We first highlight the remarkable accomplishments of a few trailblazer women who earned recognition for their pioneering plant pathology work in the early days of the Society at a time when it was difficult to break into the prevailing male-dominated scientific community. With their dedication and audacity, they succeeded in tackling some challenging diseases of economic importance for Canadian agriculture and forestry. Undoubtedly, these women became great role models for future generations. Since the era of Dr. Margaret Newton, the first Canadian woman to obtain a Ph.D. in agriculture in 1922, and others such as Drs. Irene Mounce, Mildred Nobles, Ruth Macrae and Clara Fritz, many women scientists have pursued their careers in plant pathology research and have contributed significant achievements to the science of crop protection in Canada. However, only within the last 30 years have women scientists started to serve beyond their lab and field research or teaching in classrooms, to provide a valuable contribution to advancing the cause of plant pathology as Presidents of the Society. The election of Dr. Verna Higgins in 1989 marked the turning point. Here we feature the distinguished women leaders in plant pathology who have served as CPS Presidents since the Society was founded in 1929.

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P178. Integrated management of Cucumber Downey Mildew: a strategic approach

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Cucumber downy mildew (CDM), caused by *Pseudoperonospora cubensis* is the most important yield reducing disease of cucumbers leading to significant economic losses. The disease is typically managed by the application of fungicides following a 7-day calendar spray schedule. However, the regulatory use pattern for some of these fungicides has recently changed, other fungicides are under regulatory re-evaluation and some have shown decreased efficacy due to resistance development in the pathogen population. To address the needs of producers for more efficient control solutions to diversify their CDM toolbox and enable integrated CDM management, AAFC's Pest Management Centre (PMC) established the CDM strategy in 2012. As part of this strategy, funding support was provided for several projects. First, a literature review documented existing gaps and recommended key areas in need of further research regarding CDM epidemiology and best management practices. Then, three projects addressing review recommendations studied: 1) CDM infection pathways and transmission sources to elucidate pathogen lifecycle and disease epidemiology in Ontario; 2) the possibility of reducing the number of fungicide applications to control CDM in partially resistant cucumber hybrids; and 3) the extent of pathogen resistance to single-site fungicides through surveying infected greenhouse and field cucumbers in Quebec and Ontario. In addition, new control products are currently being investigated by the PMC's Minor Use Pesticide Team. Outcomes from the above studies will be discussed.

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P179. **Effect of Miravis Neo on Gibberella ear rot and related mycotoxins in corn grain**

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Fusarium graminearum Schwabe causes Gibberella ear rot in corn, resulting in yield loss, and poor grain quality due its ability to produce mycotoxins, mainly deoxynivalenol (DON). Fungicides are important for managing *Fusarium* spp. A proper fungicide resistance management plan has not been possible, because all the recommended fungicides are from the same triazole class of chemistry. A new fungicide Miravis Neo has been developed by Syngenta. It contains adepidyn® belonging to the novel class of carboxamides, making it possible to rotate classes of fungicides with different modes of action. The objective of this study was to compare the effectiveness of Miravis Neo to standard fungicides for control of Gibberella ear rot and reduction of mycotoxins in corn. Field experiments were conducted in misted and inoculated plots in 2017 and 2018. Severity of GER was assessed visually and mycotoxins were analyzed using HPLC-MS-MS. Under high disease pressure, Gibberella ear rot severity was reduced by up to 60% compared to control. Fungicide treatments reduced DON concentration by 33 to 41%. Zearalenone and total fumonisins were reduced by up to 90% and 67% respectively. Miravis Neo showed similar levels of control to the standard fungicides, Proline and Caramba to reduce Gibberella ear rot and mycotoxins, making it a good candidate to help manage resistance to fungicides by class rotation.

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P180. **A rapid molecular assay to identify *Plasmodiophora brassicae* pathotypes from plant, soil and water samples**

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Clubroot of canola (*Brassica napus*), caused by the pathogen *Plasmodiophora brassicae* Wor., constitutes a significant threat to the Canadian agricultural industry. The deployment of clubroot-resistant cultivars is an effective management strategy; however, their widespread use has resulted in the emergence of new pathotypes capable of overcoming resistance. Several host differential sets have been reported for pathotype identification, including the differentials of Williams and the Canadian Clubroot Differential (CCD) set. The current identification method is time-consuming, labour-intensive, and requires biosecure facilities. The development of a rapid assay would facilitate pathotype identification and enable testing of a much larger number of samples. We are focusing on single nucleotide polymorphisms found among genomes of different pathotypes to generate highly specific ribonuclease H-dependent PCR (rhPCR) assays. rhPCR amplification requires perfect binding of primers to the target, allowing for pathotype differentiation with a single nucleotide difference. The blocked primers, containing a single ribonucleotide residue, are activated via cleavage of the RNA base by the RNase H2 enzyme. To design rhPCR primers, we obtained variant genome information for 45 full genome *P. brassicae* isolates, by aligning them to the reference e3 *P. brassicae* genome. Analysis revealed that most polymorphisms cluster CCD variants of pathotypes 5 and 6, grouping them separately from pathotypes 2 and 3. Preliminary results suggest that rhPCR is promising as a rapid and efficient tool for pathotype detection.

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P181. Potential use of *Acer saccharum* leaf extract for the control of lettuce bacterial leaf spot and varnish spot

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Extracts prepared from wastes of different forest species (*Abies balsamea*, *Acer rubrum*, *Acer saccharum*, *Alnus incana* subsp. *rugosa*, *Larix laricina*, *Picea glauca*, *Picea mariana*, *Pinus banksiana*, *Pinus strobus*, *Populus tremuloides*, *Prunus avium*, *Quercus rubra*) were tested for their antibacterial activity against *Pseudomonas cichorii* (Swingle) Stapp (the causal agent of lettuce varnish spot) and *Xanthomonas campestris* pv. *vitians* (Brown) Dye (the causal agent of lettuce bacterial leaf spot). Extracts were first screened for their antibacterial activities using the *in vitro* disk diffusion assay. According to the inhibition zone, *A. saccharum* leaf extract and, to a lesser extent, *Q. rubra* and *A. incana* subsp. *rugosa* bark extracts showed antibacterial activities. *Acer saccharum* leaf extract (0.8 g L^{-1}, 1.6 g L^{-1}, 3.2 g L^{-1}) was further tested for its effect on the development of varnish spot and bacterial leaf spot on lettuce plants grown in greenhouse. Foliar sprays of *A. saccharum* leaf extract at a concentration of 3.2 g L^{-1} reduced significantly ($P \leq 0.05$) bacterial leaf spot severity and, in one experiment out of two, varnish spot severity. This study points out for the first time the possibility of exploiting *A. saccharum* leaf extract for the control of lettuce bacterial leaf spot and varnish spot.

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P182. Genetic mapping of adult plant leaf rust resistance in spring wheat line BW278

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Leaf rust caused by fungal pathogen *Puccinia triticina* is a widespread disease of wheat that affects both yield and quality. The preferred method of leaf rust control is through genetic host resistance as it provides protection throughout the growing season without additional costs to the producer and environment. To date there are over 80 characterized leaf rust resistance genes, the majority of which are race-specific and condition resistance to a subset of *P. triticina* races. *Lr46*, a non-race specific adult plant resistance (APR) gene located on the long arm of chromosome 1B, is thought to be present in spring wheat line BW278. A doubled haploid (DH) population (Superb/BW278) and a recombinant inbred line (RIL) population (BW278/AC Foremost) were inoculated under field conditions with an epidemic mix of *P. triticina* races, as well as indoors with *P. triticina* race MBDS. Initial results suggest that a single leaf rust (Lr) APR gene is segregating at the adult plant stage in both populations. The objectives of the current study include: (i) confirm the presence of *Lr46* in BW278, (ii) genetically map the resistance and identify closely linked genetic markers for future use in breeding programs and (iii) screen a panel of Canadian wheat cultivars to determine the distribution of *Lr46.*

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P183. **Resting spores of *Plasmodiophora brassicae* continue to develop after death of their host.**
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Plasmodiophora brassicae Woronin causes clubroot on canola (*Brassica napus* L.) and other brassica crops. The pathogen infects host roots, where it stimulates hypertrophy and hyperplasia. Following infection, young plasmodia develop into vegetative plasmodia, then immature resting spores, and finally mature resting spores are released into the soil as the clubbed root deteriorates at plant maturity. Field trials were conducted with clubroot susceptible canola, followed by bioassays, to determine if a living host was required for spore maturation. Plants were treated 5 wk after seeding. Glyphosate was sprayed to kill the roots, or clubs were harvested and kept at 5, 10 or 22 ºC or frozen for 3 days and then stored at these temperatures. Control plants were left to grow for 9 wk. Resting spores from 9-wk-old clubs were used as inoculum on canola in bioassays in a controlled environment. Clubroot symptoms were assessed after 6 weeks. Spore maturation continued in all treatments except when young clubs were continuously frozen or stored at 5 ºC. Freezing clubs before storing them at 5 or 10 ºC resulted in more clubroot in bioassays, compared to clubs that were harvested (not frozen) and stored. This demonstrated that a living host was not required for spore maturation. Indeed, host death may speed spore maturation. Clubroot infected plants must be controlled early to avoid adding inoculum to the soil.

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P184. **Identifying clubroot resistance in canola and Brassica vegetable cultivars for Ontario, 2018**
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Clubroot, caused by the obligate parasite *Plasmodiophora brassicae* Woronin, has been present for many years on Brassica vegetables in Ontario, but was only recently identified on canola (*Brassica napus* L.). Once *P. brassicae* is present in a field, eradication is difficult, but resistant cultivars can provide effective management. Two field trials to assess clubroot reaction were conducted at the Muck Crops Research Station, King, Ontario. Pathotype 2 is now predominant at this site, having replaced pathotype 6 that mainly attacks Brassica vegetables. Trial 1 consisted of 3 putative clubroot-resistant canola cultivars, 2 cultivars expected to be susceptible and 3 susceptible control cultivars. Trial 2 assessed cultivars of cabbage, cauliflower, broccoli, napa cabbage, rutabaga, and a susceptible Shanghai pak choi control. The canola cultivars expected to be resistant were highly resistant (disease severity index, DSI = 1%) and the cultivars not marketed as resistant were susceptible (DSI = 98%). The broccoli cultivars were all susceptible, the rutabaga cultivars showed intermediate resistance, and there were both resistant and susceptible cultivars of cabbage and cauliflower. Clubroot reduced fresh shoot weight in susceptible canola by 57% and in susceptible vegetables by 42–65% relative to resistant cultivars. Inoculation studies of canola under controlled conditions showed a similar pattern of response. This research will help Ontario growers to select cultivars if *P. brassicae* pathotype 2 is present in their fields.

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P185. Chitosan inhibits growth and development of *Phytophthora nicotianae* and induces tomato resistance against this pathogen

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Chitosan is a glucosamine polymer with activity as an antimicrobial compound and also as an elicitor of defense responses in plants. The effect of chitosan on different life cycle stages of *Phytophthora nicotianae*, an Oomycete that causes severe damage in tobacco and tomato crops, was evaluated in the present study. Addition of this compound, from 0.5 to 2.5 $g.L^{-1}$, to culture media decreased the isolates mycelial growth. The colony pattern and the hyphae diameter were not affected by the polymer; however, a reduction in the number of the sexual reproduction structures (oospores) was observed at the lowest concentration (0.5 $g.L^{-1}$) tested. Low chitosan concentration stimulated sporangia production, while high concentrations reduced this number. The sporangia length/width ratio was not affected by the polymer. Indirect germination of sporangia was completely abolished with 1.5 $g.L^{-1}$ of chitosan. Zoospores incubated with different polymer concentrations did not germinate and they were not able to infect tomato plants roots at the lowest concentration tested (0.5 $g.L^{-1}$). Moreover, chitosan activated tomato plantlet protection against *P. nicotianae* infection when applied as a foliar application (0.1 and 1 $g.L^{-1}$) prior to inoculation. The induced resistance was concurrent with increased activity of phenyl-propanoid pathway markers. Taken together these results show that it is possible to control the spread of this pathogen in solanaceous crops with the application of this compound.

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P186. Rotation with Aphanomyces-resistant pulse crops or intercropping with Brassicas to reduce impact of Aphanomyces root rot on field pea

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The oomycete pathogen *Aphanomyces euteiches* is a threat to field pea production on the Canadian prairies. The only management strategy for Aphanomyces root rot is rotation away from susceptible hosts (pea and lentil) for at least six – eight years. Field trials to evaluate the effect of rotation with resistant pulse crops (soybean, faba bean, or chickpea) or intercropping with Brassica crops on disease severity and inoculum potential were initiated in 2018. Trials were located in producer's fields naturally infested with *A. euteiches*. Rotation trials were conducted at six locations, and intercropping trials at two locations. Disease severity, and levels of *A. euteiches* and select *Fusarium* spp. on the roots were assessed at two time points. Depending on location, 5 – 325 oospores were produced per gram of pea root tissue. Faba bean and soybean did not support *A. euteiches*, but low levels of oospores were produced on chickpea roots at one location. Root rot occurred on faba bean, soybean and chickpea, but it was caused by *Fusarium* spp., not *A. euteiches*. Intercropping with mustard or canola did not reduce disease levels on pea nor the number of oospores in pea roots. However, land equivalence ratios for intercrops were generally higher than monocrops. These field trials, that will also evaluate the effect of frequency of pea on soil inoculum potential, will continue for four years.

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P187. Enniatin production does not influence *Fusarium avenaceum* pathogenicity on durum wheat or peas

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Fusarium avenaceum is a generalist pathogen affecting multiple Canadian crop species. The fungus produces a series of mycotoxins including the cyclohexadepsipeptide class of toxins called enniatins. Mycotoxins have been identified as pathogenicity factors in various plant-pathogen interactions, and enniatins have been shown to influence pathogenicity on potato tubers. To determine the role of these mycotoxins in other *F. avenaceum*-host interactions we generated enniatin synthase (ESYN) disruption mutants in two Canadian isolates, *Fa*LH03 and *Fa*LH27, and studied their ability to affect wheat and peas. Metabolic profiling confirmed that the disruption mutants are unable to produce enniatins. Additionally, an ESYN over-expression strain of *Fa*LH27 was able to produce more enniatins compared with its wild-type progenitor isolate. As a preliminary study, we screened the disruption and over-expression mutants on potato tubers, and as previously reported, disruption of ESYN leads to reduced necrosis. We also found that ESYN over-expression resulted in increased necrotic lesion size on the tubers. By contrast, when the same mutants were assessed in Fusarium root rot assays of pea, or Fusarium head blight of durum wheat, no changes in disease symptoms or virulence were observed. While it is known that, at least in the case of wheat, exogenously applied enniatins can cause tissue necrosis, this group of mycotoxins does not appear to be a key factor in disease development on peas or durum wheat.

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P188. SaltroTM: a SDHI seed applied fungicide for early control of blackleg in canola

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Blackleg disease caused by *Leptosphaeria maculans* is one of the most destructive diseases of canola and using fungicides is one of the control measures of the disease. However, there is no well established effective fungicide to control this devastating disease. Saltro™ is a newly developed broad-spectrum seed-applied fungicide, developed by Syngenta. It is a carboxamide fungicide which shows succinate dehydrogenase inhibitory mode of action. Early season control of blackleg disease occurrence was evaluated. The study was conducted under greenhouse conditions compared to the current fungicide, Vibrance Flexi. The effect of Saltro™ and Vibrance Flexi was tested by applying them separately and as a combination with a no-fungicide control. Green fluorescent protein tagged *L. maculans* inoculated seedling showed clear lesion development and mycelial growth in the apoplast of the cotyledons in control and Vibrance Flexi alone treated seedlings. However, Saltro™ treated seedlings did not show lesion development or mycelial growth after 14 days post inoculation. The disease severity was significantly reduced with Saltro™ compared to the control and Vibrance Flexi alone treated seedlings/cotyledons. The results reveal seed-applied Saltro™ is an effective treatment in controlling canola blackleg disease.

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P189. A novel approach to blackleg management in canola: Combining a new fungicide seed treatment with improved flea beetle control

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Blackleg or stem canker, caused by the fungal pathogen *Leptosphaeria maculans* Ces. & de Not, is a serous disease on canola (*Brassica napus* L.). The disease is managed primarily with resistant cultivars carrying major and/or minor resistance genes. However, the genetic resistance, especially that relying only on specific R genes, can often be eroded due to race shits in the fungal populations. Prior work has shown that cotyledon is the key pathway to stem infection, but wounds are possibly required for successful infection of cotyledons by *L. maculans* in western Canada due to generally dry conditions after seeding. Flea beetles often wound cotyledons, especially under warm and dry conditions, potentially favoring blackleg infection. Here, we initiated a study to explore a novel approach combining new fungicide seed treatment based on a succinate dehydrogenase inhibitor (SDHI) with improved flea beetle control to minimize the early infection that can lead to blackleg of canola. To test this hypothesis, the susceptible canola cultivar Westar was treated with (1) one of the current industry-standard seed treatments Prosper EverGol (PEG), (2) PEG plus SDHI and (3) PEG plus foliar insecticide applications targeting flea beetles up to the 4-leaf stage of canola. 74-44 BL, a Canadian canola cultivar with blackleg resistance, will be treated similarly to assess the benefit of the treatments on a representative resistant cultivar in western Canada.

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P190. Sensitivity of *Pseudoperonospora humuli* to the systemic fungicides, metalaxyl and fosetyl-Al.

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Pseudoperonospora humuli causes systemic downy mildew in hops (*Humulus lupulus*). Currently, the only systemic fungicide registered for hops in Canada is metalaxyl (Ridomil). Another systemic fungicide with potential for registration is Aliette (fosetyl-Al). However, sensitivity of *P. humuli* to both metalaxyl and fosetyl-Al is unknown in Ontario. This study was designed to determine the sensitivity of Ontario isolates to these systemic fungicides. From 2017-2019, the entire population on each of 61 basal spikes, collected from 1 research and 8 commercial hop yards were tested using a leaf disk assay for metalaxyl. The population from spikes having less than 50% growth on the control plate or showing irregular response by growing only onto higher concentrations of metalaxyl was excluded from the data. Based on these two criteria, the population from 25 spikes were included in the data analysis. The population from ten spikes was found resistant to metalaxyl at 50 and 100 ug/ml. Twenty spikes from a total of 46, collected from 8 hop yards from 2018-2019, showed 50% or more sporulation in leaf disk assay for fosetyl-Al. The population from six spikes showed resistance to fosetyl-Al at either 100 ppm, or 100-200 ppm or 100-400 ppm. The results of the current study indicate the presence of resistant isolates of *P. humuli* in Ontario to both fungicides and requires further investigation to improve management practices.

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P191. Effect of biochar, vermicompost, micronutrient, and biofungicides for suppression of Sclerotinia rot of cabbage

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Sclerotinia rot is a major disease of Brassica vegetables in the Fraser Valley of British Columbia and other vegetable growing regions in Canada. Sustainable management of Sclerotinia rot in vegetable crops is challenging as there are few pest control products of any kind, either chemical or biological. The objective of this research was to assess eco-friendly products such as biochar, vermicompost, micronutrient, and biofungicides in reducing Sclerotinia rot of cabbage. These products were evaluated in the laboratory to assess their antimicrobial effects on several strains of *Sclerotinia sclerotiorum* isolated from cabbage fields of the Fraser Valley. In laboratory assays, growth of *S. sclerotiorum* strains was inhibited by the biofungicide Serenade® Opti™ (*Bacillus subtilis*), however, the biofungicide Prestop® (*Gliocladium catenulatum*) was not effective in inhibiting the growth of *S. sclerotiorum* strains. In greenhouse assays, single and combined treatments of Serenade® Opti™, biochar, vermicompost, and Active Flower™ (boron) were evaluated for the suppression of Sclerotinia rot in cabbage. These treatments were compared with the standard chemical fungicide, Luna Sensation (a.i. Fluopyram + Trifloxystrobin). Among these products, Serenade® Opti™ and Active Flower™ were effective in reducing the Sclerotinia rot of cabbage, whereas biochar and vermicompost were not very effective.

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P192. Effects of temperature, light quality and nutrients on spore germination and growth rate of *Colletotrichum acutatum*

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Colletotrichum acutatum is one of the most successful plant pathogenic fungi responsible for a wide range of pre and postharvest anthracnose diseases. This pathogen threatens strawberry production in Canada. Similar to other phytopathogens, spore germination is the first step in the pathogenicity process and plays an important role in disease development for *C. acutatum*. Environmental conditions such as temperature, light quality, and plant nutrient levels are expected to affect spore germination percentage. In this study, in order to contribute to the management of strawberry anthracnose, the impacts of these three different environmental factors, on spore germination were investigated. First, in an in-vitro assay on potato dextrose agar, spore germination percentage and mycelia growth were measured at 5°C, 25°C, and 30°C. The highest spore germination and mycelial growth rates were observed at 25°C and the lowest rates were observed at 5°C. Also, the same factors were measured under four light qualities (5:1, 1:5, 1:1 red:blue ratios and darkness) which are known to affect flower bud induction in strawberry plants. The germination percentage and mycelial growth rates were minimal when treated with the ratio of 1:5 red:blue. Finally, spore germination was assessed on detached leaves obtained from strawberry plants grown under different levels of nutrients (N, P, K, and Ca) to determine the potential effects of the fertilizer on the spore germination.

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P193. **Screening disinfectants for those effective against *Plasmodiophora brassicae* resting spores**

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Clubroot is an important disease of canola caused by the protist *Plasmodiophora brassicae*. The pathogen produces large amounts of small resting spores that can survive dormant in soil for many years. The longevity of the resting spores makes management and containment of the disease very challenging. For example, soil infested with resting spores is easily spread by farm and construction machinery. As a result, equipment sanitization is an important method for preventing the spread of clubroot to new fields. In order to understand which disinfectants could inactivate clubroot spores we evaluated disinfectant efficacy using the Evans blue vital stain procedure. Of the 24 disinfectants tested, seven were able to inactivate more than 95% of spores within 20 minutes of contact. The top two disinfectants were 2% sodium hypochlorite and Spray Nine®. Other effective products were Adhere NC, Premise Degreaser and AES 2500. Finally, ethanol and SaniDate® were also effective, but only at concentrations above 75% and 90% respectively.

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P194. **Apple and apricot decline in Ontario**

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In Ontario, commercial fruit producers grow more than 450000 tonnes of fruit annually, with a total farm gate of over $225 million. As recently as 2014, an emerging and complex disease has been described that results in the rapid and sudden decline of apple trees (RAD). First reported in the United States, RAD has since been reported in Ontario and BC. The disease affects young (2-8yrs) trees, and is described by trees rapidly and unexpectedly declining over a period of two weeks resulting in death of the tree. Other symptoms can include dead tissue at the graft union that then proceeds up the trunk of the tree, and rapid reddening of the leaves over the two week period. Trees can collapse with a full load of fruit. A similar disease has recently been reported in other fruit trees including apricots, plums, and peaches. This second disease, which we are calling Tree Fruit Decline (TFD) occurs more slowly, over the course of two years, but also affects young trees. Up to 50% of newly planted trees can be affected by these diseases, and up to 10% of an orchard can be lost each year. The cause of these diseases is unknown. Here we report an update on the extent and symptoms of these diseases, as well as recent progress in identifying the cause of these diseases.

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P195. Exobasidium diseases of *Vaccinium* spp. in Newfoundland

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Members of the genus Exobasidium are responsible for diseases that result in swellings, such as blisters and galls, and discoloration in a range of plants, including many members of the order Ericales. Most Exobasidium spp. are host-specific hemibiotrophs. Commercially important diseases caused by Exobasidium spp. include blister blight of tea (Camellia sinensis; caused by E. vexans) and Exobasidium fruit and leaf spot of blueberries (Vaccinium spp.; caused by E. maculosum). Athough many Vaccinium spp. are culturally and commercially important in the province of Newfoundland and Labrador, Canada, little information is available on the prevalence and importance of Exobasidium diseases in this province. A survey was thus conducted of managed highbush blueberry (V. corymbosum); managed and unmanaged lowbush blueberry (V. angustifolium); and unmanaged stands of partridgeberry (V. vitis-idaea; known by many common names including red berry and lingonberry) and cranberry (V. oxycoccos). Red leaf diseases were observed on partridgeberry, cranberry, and both highbush and lowbush blueberries. Exobasidium fruit and leaf spot diseases were observed on both high and lowbush blueberry. In addition, a disease with symptoms similar to Exobasidium leaf spot but with a singular, large “blister" rather than multiple spots, was frequently observed on lowbush blueberry. Molecular characterization of the causal pathogens is underway.

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P196. Revysol ® a new fungicide for horticulture crops and turf

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Revysol ® fungicide is an innovative active ingredient for crop protection that was discovered and developed by BASF. Revysol provides outstanding curative and long-lasting preventative control of a broad range of diseases in numerous key crops worldwide including cereals, corn, soybean, legumes, potato, horticulture, and turf. Revysol belongs to the group of the sterol biosynthesis inhibitors (SBI); within the SBIs, it belongs to the sub-group of demethylation inhibitors (DMI) and the chemical group of triazoles. Revysol is a unique fungicide amongst the triazole group and is the first Isopropanol-Azole. Its chemical characteristics allow for rapid uptake and steady translocation through the plant. The molecular shape binds strongly to the target enzyme for effective disease control. Revysol is highly effective against key fungal diseases in specialty crops including apple, grape, and turf. In research trials conducted across North America, Revysol was highly effective against apple scab in pome fruit, powdery mildew in grape, and a variety of diseases in turf. In research trials, disease reduction by Revysol exceeded commercial standards and improved both yield and quality. Revysol applied to horticulture crops and turf can be an effective tool to protect crops, manage resistance and increase yield in a sustainable way. Revysol is not registered by the PMRA but is currently being assessed for registration under the *Pest Control Products Act*.

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P197. **Efficacy of registered fungicides to control cucurbit downy mildew isolates collected in 2017 and 2018 from Québec and Ontario**

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Cucurbit downy mildew (CDM), caused by the oomycete pathogen *Pseudoperonospora cubensis*, is a threat to the production of field and greenhouse cucumbers in Canada, particularly for pickling cucumbers as even low amounts of the pathogen interfere with the fermentation process. Host resistance has largely been overcome by the pathogen, forcing growers to rely on fixed interval spray programs for management of this disease. Resistance of *P. cubensis* to some currently registered fungicides (strobilurins, fluopicolide) has previously been reported. A two year project was initiated in 2017 to evaluate the efficacy of registered fungicides against this pathogen under controlled conditions. Isolates were collected from field and greenhouse sites in Québec and Ontario in 2017 and 2018, and their susceptibility to nine single site fungicide currently registered in Canada for CDM control was tested in growth chambers, greenhouses, and fields at the St-Jean-sur-Richelieu (QC) and Harrow (ON) Research and Development Centres between 2017 and 2019. Over the two years of testing at both sites, efficacy was consistently low for strobilurin active ingredients (pyraclostrobin, fenamidone), while propamocarb, cyazofamid, and oxathiapiprolin reliably provided the expected level of control. Results with fluopicolide, dimethomorph, and mandipropamid were more variable, although the co-formulation of dimethomorph and ametoctradin (Zampro) consistently provided control. Continued monitoring of fungicide efficacy is important, particularly in the context of the re-evaluation of some protectant fungicides.

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TOPIC 22: Plant Physiology (Posters P198-P204)

P198. **Characterization of a novel Arabidopsis protein kinase involved in flowering**

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Flowering transition is an important event that determines both the reproductive and vegetative development of plants. Although many of the transcriptional elements involved in the flowering pathway have been resolved, post-translational regulators of flowering transition remain largely unknown. So far, protein kinases (e.g. SUCROSE NON-FERMENTING KINASE 1; SnRK1) and MAPK phosphatases (e.g. PROPYZAMIDE HYPERSENSITIVE 1; PHS1) have been shown to have a role. SnRK1, for example, functions as a central regulator of sugar and ABA signalling pathway, while being simultaneously suggested to intersect with the flowering pathway through AKIN10-mediated phosphorylation. With protein phosphorylation representing the most prolific regulatory post-translational modification across all eukaryotes, characterization of proteins such as protein kinases and their involvement in flowering can provide a deeper insight into the flowering transition network. Here we present a new candidate, flowering kinase 1 (FK1), which is a suspected protein kinase involved in the negative regulation of flowering. By using a combination of phenotypic, transcriptomic, proteomic, and biochemical experimentation, our results outline a role for FK1 in the negative phosphorylation-mediated regulation of flowering activities.

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P199. Pathogens and molds affecting quality of medical cannabis (*Cannabis sativa* L.) inflorescences.

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Cannabis (*Cannabis sativa* L.) is cultivated by licensed producers in Canada under greenhouse and indoor environments. With the increasingly large-scale production of cannabis, a number of pathogens and molds that reduce yield and quality have been identified within several facilities and are described here. Isolations were performed and colonies identified using PCR of the ITS1-5.8S-ITS2 region. Botrytis bud rot (*Botrytis cinerea*) affects inflorescences at the flowering stage and causes post-harvest disease. Powdery mildew (*Golovinomyces chicoracearum*) infects the foliage and inflorescences. A range of fungi isolated from freshly harvested inflorescences included *Fusarium oxysporum, Alternaria alternata, A. tenuissima,* A. *chlamydosporigena* and *Cladosporium westeerdijkieae*. Post-harvest inflorescences yielded a range of *Penicillium* species, including *P. olsonii, P. copticola, P. citrinum, P. corylophilum, P. griseofulvum, P. simplicissimum, P. spathulatum,* and *P. sclerotiorum*. *Rhizopus stolonifer, Aspergillus niger* and *A. flavus* were also recovered. Cannabis products which fail Health Canada's limits for number of colony forming units (cfu) of mold per gram likely contain a combination of these fungi. Sources of spores include diseased and decomposing plant materials, internal and external airborne contaminants, and growing substrates (soil, cocofibre). The presence of previously unreported and potentially mycotoxigenic mold species on cannabis inflorescences points to the need for specific identification in addition to obtaining total cfu counts, as well as comparisons of mold populations that occur in different growing environments and regions of Canada.

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P200. Role of aquaporins in root water transport of canola (*Brassica napus*) plants following waterlogging

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We investigated the effects of waterlogging on water transport properties in roots of canola (*Brassica napus*) plants at the seedling, flowering, and podding stages of growth. We also examined the anatomy of roots, root aquaporin expression and the relative contributions of cell-to-cell and apoplastic root water transport pathways under waterlogged and control conditions. The results showed significant decreases in plant dry weights, net photosynthesis, and root hydraulic conductivity as a result of waterlogging. The root hydraulic conductivity peaked at the seedling stage in control plants, but markedly declined within two days following waterlogging. Root suberization and lignification increased with increasing exposure to waterlogging resulting in an increased contribution of aquaporins to the overall root water transport. The relative aquaporin expression level indicate consistency with those results. The findings suggest that maintaining the functionality of aquaporins in waterlogged canola plants is highly important in canola during flooding stress.

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P201. Identification and characterization of a photosynthesis-related phosphatidylinositide transfer protein in Arabidopsis

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We identified a phosphatidylinositide transfer protein, PITP1, localized to chloroplast in Arabidopsis. PITP1 is crucial to plant development under both optimal and stress conditions. Three T-DNA mutants for PITP1 were characterized: a complete knockout, pitp1-1 plant, a partial knockdown, pitp1-2 plant, and an indistinguishable mutation from wild type, pitp1-3 plant. pitp1-1 was seedling-lethal, and pitp1-2 plant showed smaller and pale greener than WT while pitp1-3 were not different. Essential role of pitp1 for viability was confirmed by the complementation of pitp1-1 plant by 35S:PITP1 over expression. In addition, phenotypes of XVE:PITP1 transgenic plant were recovered in the presence of β-estradiol. Plants containing defective PITP1 accumulated significantly less plastoquinone-9 and its cyclized product, plastochromanol-8, but the levels of tocopherols were not affected. pitp1-2 plant exhibited lower photosynthetic performance under high light stress and cold stress. Accumulation of QA- was shown by the induction of OJIP fluorescence, indicating the slow electron transfer from QA- to QB even without DCMU. PITP1 bound to phosphatidylinositol monophosphates, phosphatidylinositol bisphosphates, cardiolipin, and sulfatide on lipid-spotted membrane. PITP1E162K and PITP1H125Q mutation affected the binding capacity to these lipids strongly and moderately, respectively in vitro. Expression of PITP1E162K and PITP1H125Q in pitp1-3 plant did not fully complemented PITP1 functions. These findings suggest that PITP1 plays important roles by binding with phosphatidylinositides in chloroplasts for photosynthetic function, plant development, and stress responses in Arabidopsis.

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P202. What would you do if you had more days before shedding your leaves? Not much, said the sink-limited plant *E. americanum*

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Growth in spring ephemerals such as *Erythronium americanum* is modulated by sink strength rather than source strength. Higher photosynthetic rates do not translate into higher growth rate nor higher final bulb biomass. The excess C produced by leaves, for example under elevated CO_2, is instead respired in the bulb via the alternative respiratory pathway. However, plants growing at lower temperature appear to maintain a better equilibrium between source and sink activity, leading to a prolonged leaf life span and a larger bulb at the end of the growing season. We artificially prolonged leaf life span by applying Promalin (mixture of cytokinins and gibberellins) on the leaves and examine its impact on final bulb biomass, photosynthetic activity (gas exchange and chlorophyll a fluorescence) and respiratory rates. Photosynthetic rates decreased through time but at a slightly slower rate in the Promalin treated plants compared to the control. Quenching of chlorophyll fluorescence confirmed that the reduction in photosynthetic rates was due to feed back inhibition. The prolonged leaf life of plants treated with Promalin thus added a negligible amount of C to the bulb, as most of the C is assimilated before the initiation of leaf senescence. These results suggest that bulb C accumulation capacity is defined during the sink initiation phase and cannot be easily modified by prolonging leaf life span.

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P203. Nitrogen isotope composition and content varied along xylem transport pathway of black cottonwood (Populus trichocarpa) under near steady-state hydroponics

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Xylem is essential for water and nutrient transport in plants. To investigate nitrate uptake, assimilation and translocation in trees, 60 black cottonwoods from three randomly selected genotypes were grown hydroponically under glasshouse conditions. A large and regularly replaced volume (2000 L) of 1/10th Johnson's solution was used to ensure a realistic rate of nutrient supply with little change in isotopic ($d^{15}N$) composition or concentration (<10%). After 90 days of growth, xylem sap was collected by pressure bombing at different position (root, lower shoot and upper shoot) at 0-1MPa and 1-1.5MPa, sequentially. An elemental analyzer–isotope ratio mass spectrometer (EA-IRMS) was used to analyze the N content and isotopic composition of bulk N in xylem sap. A denitrifying method followed by gas chromatography–IRMS was used to analyze the N content and isotopic composition of nitrate in xylem sap. Our results showed the overall average nitrate concentration in the xylem sap is ~1.18 mM, while the bulk N in xylem sap is ~5.28 mM. The average nitrate discrimination against the hydroponic source is ~19.35‰. There were changes in $d^{15}N$ of xylem nitrate and bulk N at the different bomb pressures, with lower nitrate concentrations and higher $d^{15}N$ at the higher pressure, suggesting that nitrate assimilation occurs progressively along the xylem transport pathway.

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P204. Development of an efficient temporary immersion system for the micropropagation of American chestnut (*Castanea dentata* (Marsh.) Borkh.)

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American chestnut (*Castanea dentata*), a native species of eastern North America, is an economically important deciduous hardwood tree that has been designated as endangered in Canada. The population of American chestnut trees has dwindled significantly across Southern Ontario due to chestnut blight disease and many of the surviving trees continue to show blight disease symptoms. Micropropagation is a highly effective tool to rapidly clone disease-free germplasms from limited material to large-scale production under controlled environmental conditions. Facilitating long-term plant conservation and reintroduction, the objective of this study was to develop an efficient micropropagation protocol for in vitro multiplication of American chestnut in a temporary immersion system (TIS). The highest rate of shoot multiplication was observed in cultures grown in DKW (Driver and Kuniyuki 1984) basal medium supplemented with 2.2 µmol L-1 6-benzylaminopurine and 1.0 µmol L-1 gibberellic acid. More than 95% of microshoots 30-40 mm in size developed roots after 30 days in vitro within bioreactor vessels containing DKW basal medium supplemented with 15 µmolL-1 3-Indolebutyric acid. Rooted plantlets transplanted to the greenhouse expressed a survival rate of 52% after one month in ex vitro conditions. This study confirms the potential of TIS for micropropagation in ex-situ conservation and reintroduction of endangered American chestnuts in their natural habitat.

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TOPIC 23: Plant-Biotic Interactions (Posters P205-P211)

P205. **Foliar selenium application for controlling fungal diseases in greenhouse**

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Potato is the third most important food crop consumed globally. However, potato yield and production are compromised by diseases including late blight, the most devastating potato disease. Despite the availability of effective fungicides for controlling late blight in conventional production systems, fungicide resistance has become common and not many options are available for organic production systems. Selenium as a mineral micronutrient is essential to human and animal health in trace amounts, is widely used for crop and livestock biofortification and its roles for protection against fungal infection and aphid feeding has been purported. In this study, the effect of selenium on late blight was assessed in potato and tomato plants and its mode of action determined *in vitro*. Our results showed that foliar selenium applications increase the production of secondary metabolites in potato leaves and tubers and reduce the late blight severity and incidence in potatoes and tomatoes. Selenium's disease control effect was attributed to its direct toxicity to a wide range of pathogenic fungi at level as low as 2 ppm. The data will be presented and discussed in relation with the potential use of selenium as disease control agent in greenhouse horticultural crops while contributing to bio fortify crops.

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P206. **Diversity of rhizosphere microbiomes in pea plant with and without root rot**

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Root and rhizosphere microbiomes are affected by crop growth environment and are closely associated with plant health. Here we studied the impact of root rot on pea (*Pisum sativum* L.) root and rhizosphere microbiomes using amplicon metagenomic sequencing. At early flowering, diseased and healthy samples were collected from nine fields in Saskatchewan, Canada. Bacterial and oomycete alpha-diversity (i.e., richness, Shannon index) was higher in diseased root and rhizosphere samples than their healthy counterparts, while fungal diversity was unaffected. The community structure of the root and rhizosphere microbiomes were also significantly affected by the health status of the plants, with bacterial communities exhibiting the strongest differences between healthy and diseased samples. Overall, the microbiome structure of diseased samples were more predictable than healthy samples (i.e., higher number of indicator species: 42 diseased vs. 11 healthy). In addition, the diseased core microbiome included a greater number of taxa compared to the healthy core microbiome. Our results show key differences between the microbiomes of healthy and diseased pea. Further research into determining whether differences in the microbiome influence pea susceptibility to root rot, as opposed to root rot inducing changes in the microbiome, are merited. Combined with the current results, such information could help assess root rot risks and/or develop management strategies to improve the potential of agricultural soils to suppress disease.

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P207. Cucurbit seed biogels antagonize major plant pathogens

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The amniotic fluid that surrounds the human embryo possesses compounds with antimicrobial activity needed to maintain healthy pregnancy and prevent premature delivery. Here we hypothesized that the mucilaginous tissue (biogel) that naturally coats cucurbit seeds may exhibit antimicrobial protection by hosting beneficial microbes with antagonistic activity against pathogens. We isolated 34 unique strains from the wash of aseptically isolated fresh seeds, including the mucilage, belonging to 3 domesticated cucurbit species (*Cucumis sativus*, *Cucumis melo*, *Cucurbita pepo*) and a wild non-edible cucumber species (*Echinocystis lobata*) native to North America.16S rRNA sequences of biogel microbes (endophytes) assigned them to 12 bacterial genera within three phyla (*Firmicutes*, *Proteobacteria* and *Actinobacteria*). *Bacillus* was the most dominant bacterial genus constituting 32% of the identified endophytes. Interestingly, 62% of the biogel endophytic library showed *in vitro* antagonism against 4 major soil-borne phytopathogens (*Fusarium graminearum*, *Rhizoctonia solani*, *Phytophthora capsici*, *Pythium aphanidermatum*). We conclude that cucurbit seed biogels host potential disease-suppressive microbiota dominated by Bacilli. We speculate that the biogel microbiomes protect germinating seeds and seedlings against soil borne pathogens.

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P208. Evaluating the ability of endophytic bacteria to support boreal forest tree growth

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In natural ecosystems like boreal forests, nitrogen-fixing bacteria could be a potent nitrogen source for trees growing on nutrient-poor soils. West Chilcotin region in British Columbia is located in the Sub-Boreal zone where cold climate and low annual precipitation have resulted in dry and weakly-developed soils lacking essential plant nutrients, particularly nitrogen. Lodgepole pine is the most common tree species growing in this region. The ability of pine to grow on such nitrogen-limited soils raises a crucial question regarding its nitrogen sources. We found that pine trees growing in this region harbour several nitrogen-fixing bacteria in their internal tissues. But, can these bacteria sustain tree growth on nitrogen-limited soils of this region? To answer this question, we selected six of these bacteria based on their *in vitro* nitrogen-fixing ability and tested them in a yearlong greenhouse study with their original host (lodgepole pine) and another host native to this region (hybrid white spruce). Each bacterium fixed significant amounts of nitrogen from the atmosphere and considerably enhanced pine and spruce seedling length and biomass. Particularly, two bacterial strains, *Caballeronia sordidicola* HP-S1r and *Caballeronia udeis* LP-R2r, fulfilled about 50% of nitrogen-requirements of pine and spruce, and enhanced seedling length and biomass by nearly 1.5-fold and 4-fold, respectively. Therefore, such bacteria could potentially be used as biofertilizers for trees native to this region, since they represent a low-cost, environment-friendly alternative to chemical fertilizers.

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P209. Investigating the Role of *Brachypodium distachyon* Cellulose Synthase 8 in *Gluconacetobacter diazotrophicus* Colonization

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Alternatives to synthetic nitrogen fertilizer are needed to reduce the costs of crop production and offset environmental damage. Nitrogen fixing bacterium *Gluconacetobacter diazotrophicus* has been proposed as a possible biofertilizer for monocot crop production. However, the colonization of *G. diazotrophicus* in most monocot crops is limited and deep understanding of the response of host plants to *G. diazotrophicus* colonization is still lacking. In this research, experiments were conducted to study the role of host plant in the *G. diazotrophicus* colonization establishment using a new monocot model plant, *Brachypodium distachyon*. The gene expression profile of *G. diazotrophicus* colonized *B. distachyon* root tissues was generated via next generation RNA sequencing and then investigated through gene ontology and metabolic pathway analysis. The RNA sequencing results indicated that *Brachypodium* may be actively involved in the establishment of *G. diazotrophicus* colonization via cell wall synthesis, and jasmonic acid, ethylene, and giberrelin biosynthesis. Therefore, the genes in these biosynthesis pathways potentially play important roles in the beneficial association between the plant and *G. diazotrophicus*. The loss of function muta ***P2.*** nt for *Brachypodium* cellulose synthase 8 (*BdCESA8*) showed decreased cellulose content in xylem and increased resistance to *G. diazotrophicus* colonization. This result suggested that the cellulose synthesis of the secondary cell wall is involved in *G. diazotrophicus* colonization.

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P210. Interaction of Arabidopsis calmodulin-like proteins with the protein 2b, an RNA silencing suppressor of cucumber mosaic virus

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RNA silencing is one of major antiviral systems in plants and most plant viruses encode RNA silencing suppressors (RSS) to facilitate their infection of plants by inhibiting the plant's endogenous antiviral RNA silencing machinery. Previously, a tobacco calmodulin-like protein (CML) has been reported to interact with HC-Pro and 2b, which are RSSs encoded by members of the genus *Potyvirus* and *Cucumovirus*, respectively. We have shown that the tobacco CML, which was named rgs-CaM, counteractively functions as an antiviral defense factor to direct degradation of its interacting RSS proteins via autophagy. Plants encode dozens of CMLs (50 and 32 CMLs in *Arabidopsis*and rice, respectively). Several CMLs of tobacco and other plants are similar to rgs-CaM in their amino acid sequences, suggesting possible binding to viral RSSs. Here, we examined whether 5 closely-related CMLs from *Arabidopsis*(CML37, CML38, CML39, CML40 and CML41) which are similar to rgs-CaM bind to 2b of cucumber mosaic virus (CMV) within a yeast two-hybrid system. The results suggest that all these 5 CMLs bind to 2b whereas unrelated CMLs do not.
When *Arabidopsis*mutants lacking CML37, CML38 and CML39, singly or doubly, were inoculated with CMV, viral genomic RNAs accumulated more in these mutants, especially in double mutants, suggesting that these *Arabidopsis* CMLs collaboratively function to control CMV infection by interacting with 2b.

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P211. **Context is everything: benefits of carbonatite rock fertilizers depend strongly on growing conditions and plant type**

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With growing concerns about agricultural sustainability and food security, the use of rock fertilizers and agrominerals is receiving renewed interest. A wide variety of geological resources have been proposed as crop nutrient sources, with silicate rocks the predominant focus. Carbonatite rocks are known to weather more readily than silicate rocks; yet, they have received relatively little attention as it is thought their high Ca and Mg contents hinder effective nutrient release. However, there is strong evidence that the nutrients within carbonatite rocks are easily accessible to plants, and that these rocks have appreciable effects on crop plant growth. Here we propose a framework to understand the mode of action of carbonatites on soil fertility and plant nutrition by integrating research at multiple scales, i.e., from individual plants to the ecosystem, including soil microorganisms. The model stems from greenhouse experiments on two crops, pea and wheat, and an extensive survey of the carbonatite deposit. It is emphasized that a systems-approach must be taken when examining carbonatites as their effects are strongly context-dependant, and there is evidence that a three-way interaction between plant-carbonatite-microorganisms is responsible for some of the observed effects on plants. The framework presented is intended not only to synthesize the currently knowledge on carbonatites as rock fertilizers but also to guide future research on this and other similar geological resources.

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TOPIC 24: Post-Harvest Physiology and Management (Posters P212-P213)

P212. **Effect of pre-harvest hexanal spray on the quality of 'Honeycrisp' apples during post-harvest storage**

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'Honeycrisp' is most popular apple variety among consumers due to its desirable flavor and texture characteristics. However, its quality can decline over time in storage, that challenges the growers to fetch the price in market. Hexanal is a natural product which has proven to enhance the post-harvest shelf life of many fruits by inhibiting phospholipase-D enzyme (PLD), the key enzyme that triggers the membrane breakdown. Ethylene is one of the prime stimuli that triggers the PLD enzyme to initiate the membrane deterioration cascade. Eventually, this process accelerates softening and reduces the quality characteristics. 'Honeycrisp' apples from trees that were sprayed with hexanal (as a formulation) were harvested and compared against control during post-harvest storage. Internal Ethylene Concentration (IEC), PLD enzyme and quality parameters such as color, firmness, total soluble solids and physiological loss of weight were assessed throughout the storage. IEC was significantly lower on the 60th day of storage on treated fruits and subsequently progressed at lower level (45 % - 15 %) throughout remaining storage compared to other treatments. PLD enzyme activity was increased throughout the storage, however hexanal treated fruits showed 5 - 7 % reduction. No significant differences were observed in quality characteristics among the treatments. By assessing these parameters, we show that hexanal could enhance the storability and marketability of 'honeycrisp' apples.
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P213. **Smart delivery of hexanal from nanomatrix for extending the shelf life of fruits**
Ranjan, S.*; L. Lim; A. Sullivan; G. Paliyath; J. Subramanian
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Innovations in the post-harvest technology is an important aspect to reduce the fruits and vegetable loss. In recent years, several novel postharvest technologies have been developed and used to minimize these losses, and, increase the shelf life of fruits and vegetables. Hexanal is one of those technologies used to enhance the shelf life of fruits through inhibition of Phospholipase D (PLD) enzyme during ripening. Postharvest application of hexanal on fruits especially in fruit packaging is limited due to its high volatile nature. Nanotechnology-based approach was used to develop fiber that can hold hexanal and sustain its release through external stimuli. The substrate triggers the release of hexanal from the fiber due to the increase in relative humidity developed during the respiration of fruits in the confined environment. The developed fibers were characterized using electron microscopy and release of hexanal from the matrix was studied using Gas Chromatography technique. The developed fibers were tested on plums and nectarines and shelf life parameters were analyzed. Result showed that the shelf life of plums can be extended up to 5 days and pears by 7 days. Thus, nanofiber impregnated with hexanal, when exposed on fruits in packaging, can extend the shelf life of perishables for extended periods of time during export.

Syndhiya Ranjan (sranjan@uoguelph.ca)

TOPIC 25: Teaching in the Plant Sciences (Posters P214-P215)

P214. **Environmental issues, concerns and education in rural districts**
Elawana Mudiyanselage, N.
Central Environmental Authority in Sri Lanka

Abstract to be submitted

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P215. **The power of pi: using raspberry pis to photograph actively growing plants**
Meyer, C.; K. Raymond
University of Guelph

Raspberry Pis are inexpensive, modular computers that are powerful enough to be used in various innovative ways as a part of scientific research and teaching. For instance, Pis can be used to help conduct high-throughput plant phenotyping. Using this technology in undergraduate coursework can help students assess plant growth and development in more comprehensive and dynamic ways, and provide students with a meaningful introduction to computational plant biology. Raspberry Pis with cameras were configured to perform time-lapse and infrared photography of Arabidopsis plants in growth chambers. During the semester, students could remotely access the Pis as well as download and process images. Students had access to thousands of images taken over seven weeks, allowing them to prepare time-lapsed videos of Arabidopsis growth and to thoroughly characterize development through the life cycle. Furthermore, they processed infrared photos with the Normalized Difference Vegetation Index (NDVI) to semi-quantify chlorophyll concentrations in rosette leaves. Students appreciated the value of Raspberry Pi and computer vision technology for their projects, and were fascinated by its broad applicability for biological science. Future work will involve imaging seedlings on hormone-amended media and testing semi-automated phenotyping software with a graphical user interface that leverages machine-learning principles. Videos and additional details are available at: https://qrgo.page.link/n5fg

Chris Meyer (cmeyer02@uoguelph.ca)

Late Submissions

P216. **Creating broad-range disease resistance in greenhouse vegetables**

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The level of plant innate immunity that results from perception of microbe-associated molecular patterns (MAMPs) such as 'flagellin22' (flg22) by receptors is commonly termed pattern-triggered immunity (PTI). Traditional plant breeding has focused on introducing R-genes into susceptible cultivars as this can result in excellent protection of the new variety; however, this protection is often race-specific or pathogen-specific. Targeting PTI for crop protection is attractive because it promises a more durable and broad-spectrum protection. A previously uncharacterized family of 6 genes encoding immune receptors in Arabidopsis was discovered in a screen of insertional knockouts in 169 candidate immune receptors. Knock-out mutants in four of these genes show improved disease resistance against bacteria and oomycetes and are thus termed broad-range resistance (BRR) genes. Translation of this discovery into tomato, pepper and cucumber was initiated by identifying BRR gene knock-outs in EMS mutant populations of these species. A diagnostic, in vitro test for PTI was adopted that measures the peroxidase enzyme activity from leaf discs that are challenged with MAMPs. Tomato homozygous mutants in two genes showed increased activity when challenged with flg22 relative to homozygous wild type segregants. Further, these same mutant plants were challenged with Pseudomonas syringae DC3000 to test for pathogen resistance. Homozygous mutants in BRR5 and BRR6 showed 2-fold and 3-fold reduction in bacterial colonization 3 days post inoculation respectively.

Jessica Pinder (jessica.pinder@vinelandresearch.com) Topic: Biochemistry, Metabolism, Photosynthesis

P217. **Linking potato cold-sweetening to the regulation of VACULOLAR INVERTASE: Sequence diversity and in silico structure prediction**

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During long term cold storage of potatoes, cold-induced sweetening can occur where starch is converted into reducing sugars via VACUOLAR INVERTASE. These high sugar potato tubers reduce the processing quality of fried potato products. The levels of VACUOLAR INVERTASE is controlled by VACUOLAR INVERTASE INHIBITOR at the post-translational level. The variations in the sugar content and sequence diversity of the vacuolar invertase inhibitor gene from Indian non-processing (Kufri Jyoti, Kufri Pukhraj and PU1) and exotic processing (Atlantic and Frito Lay-1533) potato cultivars were examined. Cold storage (4°C) resulted in significantly different reducing sugar and total sugar content in all cultivars with processing cultivars having lower reducing sugars compared to the non-processing cultivars upon cold storage. Sequencing of the vacuolar invertase inhibitor gene identified four alleles of which three identified as novel alleles based on the single nucleotide polymorphisms. A total of twelve single nucleotide polymorphisms resulted in silent mutations, and five would cause amino acid substitutions. The 3D predicted structures generated for all the alleles revealed slight variations in the orientation of the helices (α1-3) in N-terminal region. Sequence polymorphism observed in vacuolar invertase inhibitor alleles in processing and non-processing potato cultivars can be correlated with the observed variations in the sugar content suggesting a possible role in cold-induced sweetening.

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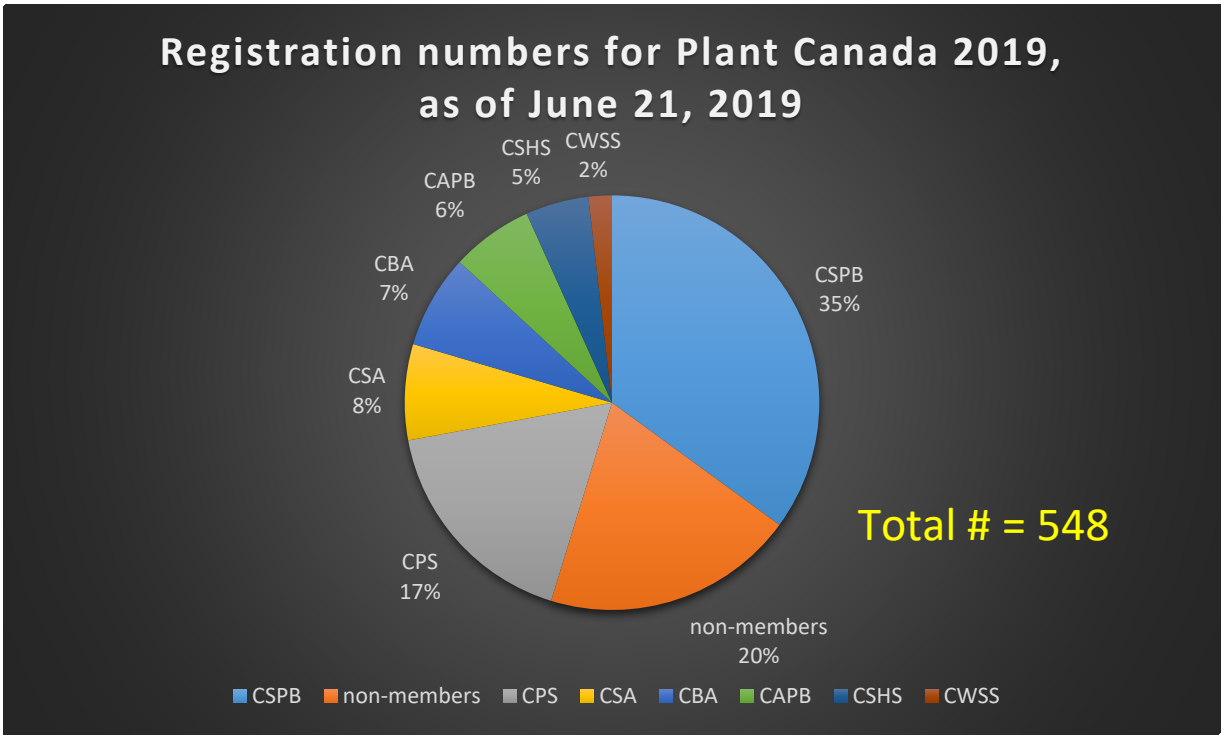

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The fun and entertaining band STARPOWER www.starpowerband.ca .