PLANTS: Adapting to a Changing World

July 7–10, 2024
Winnipeg, MB

PLANT CANADA

PROCEEDINGS

Welcome to the 2024 Meeting

Federation of Canadian Plant Science Societies

Canadian Botanical Association (CBA)

Canadian Society of Plant Biologists (CSPB)

Canadian Phytopathological Society (CPS)

Canadian Weed Science Society (CWSS)

Canadian Society of Agronomy (CSA)

Canadian Society for Horticultural Science (CSHS)

Canadian Association of Plant Biotechnology (CAPB)

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

Plant Canada President's Message

Plants: Adapting to a Changing World is the eighth meeting of the Plant Canada-affiliated Societies and Associations since our first gathering in London Ontario in 2000. The idea behind Plant Canada, to periodically bring together the specialized disciplines represented by its current seven Canadian member organizations, remains as relevant as it was back then.

This is an important and rewarding time to be a plant scientist. There is no question that our knowledge and expertise will increasingly contribute to tackling current global challenges associated with climate change and overpopulation, which extend to social injustice and political instability. We have the capacity, for example, to harness and enhance the carbon capturing capabilities of plants, mitigate losses from abiotic and biotic stress, and generate new crops and cultivars that will produce more nutritious food, bio-products and medicines.

As scientists, we also need to adapt to a stunning array of technological advances that are changing the way we conduct research, enabling us to uncover at unprecedented rates the intricate mechanisms plants employ to optimize their success. At our disposal are continually evolving genomic, transcriptomic, proteomic and metabolomic tools and databases. Who would have thought the relative ease at which it is currently possible to edit genomes, visualize dynamic processes in living plant cells, or to model protein structures with generative AI?

And yet, despite the obvious and urgent need for plant science to move to the forefront of human endeavours, there are barriers. Increasingly, evidence-based scientific information is taking a back seat to agendas of opinion, misinformation and conspiracy theories, resulting in lackluster and often disturbing political outcomes. Climate change denial, anti-vaccination debates and anti-GMO campaigns are obvious examples of the loss of trust in science by large swathes of society. In Canada, plant scientists continue to receive only a tiny fraction of the overall research budget, and there is little political motivation for this to shift. How can we change this?

As individuals, we have little clout. The collective voice of scientific societies, presenting the informed opinion of many, is the way forward to engaging with policy makers, and informing public opinion. Working together to champion our collective success and foster a supportive network in which researchers can thrive throughout their careers is another objective. Plant Canada was founded for these purposes.

Plant Canada is a founding member of the Global Plant Council, which since 2009, has been "a single, strong voice in the policy and decision-making arena, promoting plant science research and teaching around the world". Our Past President, Deena Errampalli, has been the Treasurer of GPC since 2017, and for the past year, I have had observer status on the Board of Directors.

This year's meeting at the RBC Convention Centre in Winnipeg has been organized by the Canadian Phytopathological Society (CPS), and there are many people to thank for their hard efforts and ideas that have brought the meeting to fruition. I am especially grateful to the meeting **co-chairs Dilantha Fernando (CPS)** and **Tom Fetch (CPS)**, and meeting coordinator **Brenda Trask** (SeCan) for overseeing the development of this conference. Special thanks also go to **Gary Peng** (CPS) for kick starting this meeting and the early stages of its planning. I would also of course acknowledge the hard work and involvement of the Scientific Organizing, Fund-Raising, and Local Arrangements Committees, and Board Members of Plant Canada who have contributed to making this event happen, whose names and affiliations are listed below. Importantly, the meeting would not happen without the generous support and involvement of our sponsors.

Science Committee
Lord Abbey (CSHS); Guillaume Bilodeau (CPS); Bourlaye Fofana (CSHS); John Markham (CBA); Andrew McKenzie-Gopsill (CWSS); Harpinder Randhawa (CSA); Marcus Samuel (CSPB); Barry Saville (CPS); Stacy Singer (CAPB); Stephen Strelkov (CPS)

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Local Arrangements Committee
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Plant Canada Board of Directors and Executive (prior to 2023):
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I will take this opportunity to thank members of the Plant Canada Executive who have been a delight to work with during my time as President. They are Vice President Valérie Gravel (McGill), Secretary Rima Menassa, Treasurers Gayle Jesperson (2015-2023) and Teagen Quilichini (since 2023), and Immediate Past-President Deena Errampalli. Special thanks to Past-President Shahrokh Khanizadeh for continuing to serve as Plant Canada Webmaster.

Finally, after five long and challenging years since our 2019 Plant Canada meeting in Guelph, it is a pleasure to welcome you to our 2024 Plant Canada meeting. Whether you are returning or attending your first Plant Canada meeting, presenting your latest research findings, or here to be inspired by Canada's best plant research, I hope that the experience will be rewarding.

Geoffrey Wasteneys
President, Plant Canada

For further information about Plant Canada:
Website: http://www.plantcanada.ca/
Facebook: https://www.facebook.com/PlantCanada/
Twitter: https://twitter.com/plantcanada


Lord Abbey (CSHS)


Mark Belmonte (CSPB)


Dilshan Benaagama (CWSS)


Pankaj Bhowmik (CAPB)


Guillaume Bilodeau (CPS)


Vikram Bisht (CPS)


Dilantha Fernando (CPS)


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Mindy Liu (CPS)


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Stephen Strelkov (CPS)


Albert Tenuta (CSA)


Mario Tenuta (CSA)


Brenda Trask (SeCan)


Champa Wijikoon (CSHS)


Hugo Zheng (CSPB)

Welcome from Conference Co-Chairs

With great pleasure, we welcome you to Winnipeg and to the Plant Canada conference.

We have been working to bring you the best in science, food, and attractions so you will remember this Plant Canada conference for a long time.

Plant Canada is the largest Canadian Agriculture Network, comprising seven scientific societies: Canadian Phytopathological Society, Canadian Society of Horticultural Science, Canadian Society of Plant Biologists, Canadian Society of Agronomy, Canadian Botanical Association, Canadian Association of Plant Biologists, and Canadian Weed Science Society. This scientific conference is held every five years and provides distinguished lecturers, networking opportunities, and innovative scientific discoveries to be reported in oral and poster sessions, technical workshops, and tours. This conference allows students and professionals working in plant sciences to hear about the latest research, meet and learn from their peers, expand their knowledge base, and use networking opportunities to enhance their careers.

The theme of our meeting, 'Plants: Adapting to a Changing World ', is not just a topic, but a crucial aspect of our current global scenario. The meeting will be held at the Winnipeg RBC Convention Centre in downtown Winnipeg, a perfect setting for such a significant event.

We hope you have a great time in Winnipeg, a vibrant multicultural city of 849,000 people, also known as the Gateway to the West.

For more information about the conference, visit the CPS website: https://phytopath.ca/meetings/plant-canada-2024/. If you have any questions, don't hesitate to contact us.

We eagerly await your arrival in Winnipeg, ready to provide you with a memorable and enriching experience at the Plant Canada conference.

Dilantha Fernando, PhD
Co-Chair Plant Canada
University of Manitoba

Tom Fetch, PhD
Co-Chair Plant Canada
AAFC (Retired)

Welcome from Conference Scientific Committee

On behalf of the Scientific Program Organizing Committee, I am honored and delighted to welcome you to this Plant Canada 2024 Conference. With all seven Plant Canada Societies and Associations members we have prepared this event and happy to see you on July 7th to 11th 2024 in Winnipeg, MB. This meeting will bring together researchers in plant science research reflecting our diverse interests with a thematic on “Plants: Adapting to a Changing World”.

There will be scientific workshops, tours, special sessions, keynote and plenary sessions organized by our different societies. Moreover, multiple concurrent sessions, posters, networking and social events activities that will offer opportunities for professionals working in plant sciences to discuss the latest research, learn from peers, and expand their knowledge and students to develop their career. Our program features talks from our Keynote speaker Dr. Sylvain Charlebois known as the “Food Professor” followed by four Plenary sessions responding to our conference theme: 1) Plant Biotechnology for a Changing World; 2) Emerging Technologies to Enhance Production in a Changing Environment; 3) Emerging Technologies in Plant Health; 4) Emerging Concepts in Plant Biology.

A huge team effort has gone into organizing the scientific program and coordinating the events of this meeting, thanks to the committee for the seven organizations. The event would be impossible without huge efforts from the Local Arrangements Committee (LAC) led by Tom Fetch, Dilantha Fernando, Brenda Trask and the CPS, and the financial support of our many sponsors helping to support our event – the efforts of the fundraising committee is much appreciated.

To the participants, we could not have a successful conference without you. Thanks so much for your participation in this meeting. We received over 350 abstracts and have a program we hope you will love, with the opportunity to everyone to present with talks and posters. Your participation makes this event a success, thank you! I wish you a great week in this 2024 Plant Canada meeting in Winnipeg. Very happy to see you in person. Have a good meeting!

Dr. Guillaume J. Bilodeau
Chair, Scientific Program Organizing Committee for Plant Canada

THANK YOU to our **INDUSTRY SPONSORS** for making Plant Canada 2024 possible!

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- Elementar, Booth #1
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- Manitoba Association of Plant Biologists Booth #2
- Manitoba Hydro
- New England BioLabs, Booth #3
- Performance Plants
- PhytoAB, Booth #4
- Qubit Systems
- The Royal Society Publishing Booth #5


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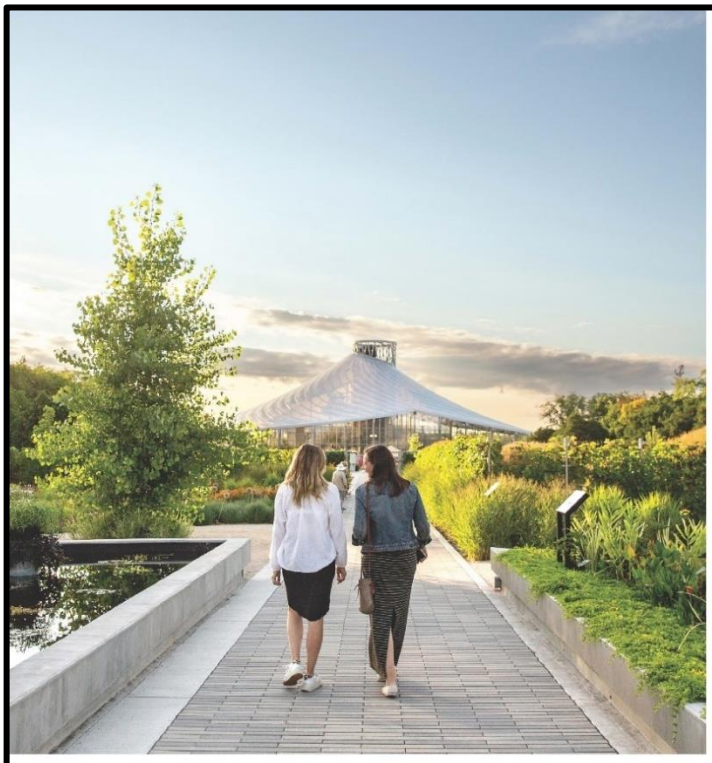

WELCOME TO WINNIPEG!

Winnipeg extends a warm welcome to **Plant Canada 2024!**

Now that you are here, you'll see why Vogue magazine calls Winnipeg "an absolute must-visit destination."

During your spare time experience the joy of polar bears swimming and playing over your head at Assiniboine Park Zoo's Journey to Churchill, then and take an interactive journey through humanity's struggles and triumphs at the Canadian Museum for Human Rights. The Exchange District beckons with its handsome architecture, hip restaurants, and fashionable shops, while The Forks has it all—from Canada's most unique public market, to scenic trips along the city's rivers.

Visit **tourismwinnipeg.com** to immerse yourself in all things Winnipeg.

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THE ROYAL SOCIETY PUBLISHING

Individual Reports
from the Member Societies of Plant Canada

Plant Canada 2024 is a joint meeting of the following seven scientific societies from Canada:

Canadian Botanical Association (CBA)

Canadian Society of Plant Biologists (CSPB)

Canadian Phytopathological Society (CPS)

Canadian Weed Science Society (CWSS)

Canadian Society of Agronomy (CSA)

Canadian Society for Horticultural Science (CSHS)

Canadian Association of Plant Biotechnology (CAPB)

Canadian Association for Plant Biotechnology

The Canadian Association for Plant Biotechnology (CAPB) was founded in 1970-1971 as the International Association for Plant Biotechnology Canada (IAPB Canada). The association has undergone several name changes, in 1998 and 2006, before adopting its current name in 2015. 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 for communication among its members to further the development of Plant Biotechnology in Canada. It also offers excellent opportunities for new collaborations among industry leaders and researchers, helping to connect people involved in plant biotechnology research. The association holds biennial meetings in Canada. More information about the association can be found at www.canadianplantbiotech.ca.

CAPB Executives (2022-2024)

- President, National Correspondent and Gov't Liaison • Dr. Dominique Michaud, Université Laval
- Vice-President, Deputy National Correspondent • Dr. Pankaj Kumar Bhowmik, NRC–Saskatoon
- Immediate Past President as Observer • Dr. Rima Menassa, AAFC–London
- Secretary • Dr. Stacy Singer, AAFC–Lethbridge
- Treasurer • Dr. Sangeeta Dhaubhadel, AAFC–London
- Director of Communication • Dr. Dinesh Adhikari, University of Alberta
- Membership Director • Dr. Susanne Kohalmi, Western Ontario
- Seminar Coordinator • Dr. Allyson MacLean, University of Ottawa
- Industry Liaison • Dr. Pooja Saxena, BlueRock Therapeutics
- Regulatory Affairs • Jennifer Hubert, CropLife Canada
- Postdoc and Student Affairs • Justin Boissinot, Université Laval
- Webmasters • Jordan VanderBurgt and Carly Charron, Western University

More information on Executive Committee can be found at

https://www.canadianplantbiotech.ca/iapb-canada-executive-committe/

CAPB at Plant Canada 2024
Winnipeg, MB

PLENARY 1 • PLANT BIOTECHNOLOGY FOR A CHANGING WORLD

Monday July 8, Hall C East, 8:30–11:00

- **Dr. Louis-Philippe Hamel, Medicago inc.**

Understanding plant molecular responses to the production of enveloped VLPs leads to the improvement of a molecular farming expression platform

- **Dr. Dan Voytas, University of Minnesota**

Overcoming Bottlenecks in Plant Gene Editing

- **Dr. Nicola Patron, University of Cambridge**

Synthetic biology for metabolic pathway engineering in photosynthetic organisms

WORKSHOP – A BRIEF OVERVIEW OF THE GENE EDITING LANDSCAPE IN CANADA

Tuesday July 9, 11:15–13:00, Presentation Theatre

- Moderator: Dominique Michaud (Université Laval)
- Panelists: Stacy Singer (AAFC), Hannah Clouthier (CFIA), Jennifer Hubert (CropLife Canada), Steve Webb (GIFS), Pankaj Bhowmik (NRC)

CAPB / PLANT CANADA BUSINESS MEETINGS

- CAPB Executive Outgoing Board meeting – Sunday July 7, 15:30–17:00, President's Boardroom
- CAPB Annual General Meeting – Monday July 8, 11:15–13:00, Room 2G
- CAPB Award Deliberations – Wednesday July 10, 11:30–12:30, York 2-3
- CAPB Student Presentation Awards – Wednesday July 10, 12:30–13-30, York 2-3
- Plant Canada Outgoing Board, Sunday July 7, 13:00–15:00, Meeting Room 16
- Plant Canada Incoming Board, Wednesday July 10, 17:30–18:30, President's Boardroom

Canadian Botanical Association
L'Association Botanique

Canadian Botanical Association
L'Association Botanique du Canada

Canadian Botanical Association/ L' Association Botanique du Canada was founded in 1964, became a corporation in 1979, and in 2014, in its 50th anniversary year, was continued as a not-for-profit corporation under the Canada Not for Profit Corporations Act, and adopted the Institut de recherche en biologie végétale (IRBV) in Montréal as its permanent address. The Canadian Botanical Association (CBA/ABC) serves as the national organization for botanists in Canada, including professional botanists at universities, colleges, schools, government and industry as well as students, technicians and amateurs. The Association represents Canadian Botany and botanists in matters of local, national and international importance. The preservation of botanically significant natural areas and herbarium collections is of special interest. The governance is provided by a Board of Directors currently consisting of 15 members, and the various activities are conducted within five Sections: Ecology and Conservation; Mycology; Systematics, Evolution and Biodiversity; Plant Development: Molecules, Cells, and Systems; and Teaching.



Examples of Activities in 2023-2024

The IDEA (Inclusion, Diversity, Equity and Accessibility) Committee (established in 2021) focused on (a) guidance for conference local organizing committees on including local First Nations and other underrepresented groups and reducing barriers to participation, (b) developing and improving a best practices code for conferences and meetings to ensure safe and welcoming environments, (c) a survey of member diversity, (d) a workshop together with CSEE during the annual conference in Winnipeg about open science funding as avenues for improving accessibility and equity in science. The committee meets regularly.

The Association published three issues of the Bulletin [56 (2, 3), 57 (1)], which documented and profiled the awards and winners from the 2023 conference, detailed the activities of members and committees, as well as included book reviews, researcher or student profiles, and a wide diversity of articles on different botanical themes. The website was updated to include a page that gathered a comprehensive collection of ca. 150 articles previously published in the Bulletin: "Portraits of native, alien/invasive, and ornamental plants in Canada".

In the past year, CBA/ABC has strongly supported the preservation of the Kew herbarium at its current location and advocated against the decision to close DUKE herbarium. Resolutions were adopted by the Board of Directors and lobbying was conducted with the administrations of these institutions and other governing bodies.

ANNUAL AWARDS PRESENTED 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 best 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 (Proposal and Results stages $500 and $250) **Lionel Cinq-Mars Award** for the best oral presentation and **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 and **Travel Award** for undergraduate students.

- for undergraduate research, **Undergraduate Awards** ($100), best poster and best presentation at undergraduate conferences/meetings taking place in all the major regions of Canada: Atlantic region, Québec, Ontario, Prairies and Territories, and British Columbia.

- for research in Canada's north, **Laurie Consaul Northern Research Scholarship** ($1,500).
  In 2023-2024, the total value of student awards was ca. $15,000.

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 2023-2024

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Webmaster	Mélissande Nagati, Université du Québec en Abitibi-Témiscamingue

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Co-Chairs: Elizabeth Schultz, University of Lethbridge
Shelley Hepworth, Carleton University

ECOLOGY AND CONSERVATION
Chair: Jenny McCune, University of Lethbridge

MYCOLOGY
Chair: Allison Walker, Acadia University

SYSTEMATICS EVOLUTION AND BIODIVERSITY
Co-Chairs: Julissa Roncal, Memorial University of Newfoundland
Jeffery M. Saarela, Canadian Museum of Nature

TEACHING
Chair: Laura Super, University of British Columbia

Canadian Phytopathological Society | La Société Canadienne de Phytopathologie

The Canadian Phytopathological Society (CPS) will reach its centennial year in 2029; its main objective is to promote research, education and Knowledge dissemination on the nature, cause and control of plant diseases. The society has more than 350 members in Canada and abroad, including graduate students, postdoctoral fellows/research associates, technical assistants, extension plant pathologists, research scientists and university professors with expertise ranging from fundamental/molecular plant-pathogen interactions to field research on crop disease management. Additionally, several grower organizations and private companies are sustaining members. The society's operations are guided a Board of Directors and several committees. For 2024-2025, the CPS Board consists of:

President: **Gary Peng**
Past-President: **Sheau-Fang Hwang**
President Elected: **Guillaume Bilodeau**
Vice-President: **Maria-Antonia Henriquez**
Secretary: **Tom Fetch**
Treasurer: **Michelle Hubbard**
Membership Secretary: **Sara Stricker**
Senior Director: **Wen Chen**
Junior Director: **Gurcharn Brar**
CJPP Editor-in-Chief: **Linda Jewell**
CPS Website Editor: **Michael Holtz**

The CPS publishes the Canadian Journal of Plant Pathology (CJPP) and the Canadian Plant Disease Survey (CPDS), both of which have transitioned to online-only publication. CJPP has adopted a hybrid publication model, allowing authors to choose between immediate open access for a fee or conventional publication with only a page charge. However, all issue will become open access one year after its initial publication. The editorial board of CJPP, led by Editor-in-Chief Dr. Linda Jewell, remains pivotal in maintaining the journal's high standards. The CPS also publishes a quarterly newsletter. This year, the CPS has been diligently working to publish the fourth edition of "Diseases of Field Crops in Canada," which includes significant updates from the previous 2003 edition. A sample book is planned for display at the Plant Canada 2024 Conference, and preorders will be available at a discounted price...

The society presents several awards, including the prestigious Award for Outstanding Research, the Outstanding Young Scientist Award, and several awards for graduate students. Dr. Tom Hsiang, a professor from the University of Guelph, received the 2023 Award for Outstanding Research. Equally deserving of recognition, Dr. Gurcharn Brar, an assistant professor at UBC (now at the University of Alberta), received the 2023 Outstanding Young Scientist Award. The 2023 CPS John Yorston Graduate Student Scholarship Awards went to Sarah Drury, Vinuri Weerasinghe, and Yishan Zhang, while the 2023 CPS Graduate Student Travel Awards were given to Razan Malla, Rasha Salih, and Emilee Storfie. The achievements of these young scientists are a testament to the bright future of plant pathology in Canada.

CPS was the hosting society for the 2023 Tri-society Joint Conference in Ottawa, involving CPS, the Canadian Society of Agronomy (CSA), and the Canadian Society for Horticultural Science (CSHS). This meeting brought together researchers under the theme “Agroecosystem Resiliency Under a Changing Climate,” including two symposiums, 14 sessions of talks, and two sessions of posters, covering a wide range of topics on agronomy, disease, and horticultural crops. The Local Arrangements Committee (LAC) was led by Dr. Guillaume Bilodeau, and the conference was a huge success. CPS also sponsored the Glenn Anderson Lectureship, awarded to Dr. Bram Govaerts, the current Director General of the International Maize and Wheat Improvement Center (CIMMYT) in Mexico, during the 12th International Congress of Plant Pathology held in Lyon, France (Aug 20-25, 2023). Dr. Lone Buchwaldt introduced Dr. Govaerts on behalf of the CPS. Additionally, CPS invited and sponsored Dr. Fiona Doohan from University College Dublin, Ireland, to give a talk in the same session.

CPS will again be the hosting society for the Plant Canada Conference, to be held in Winnipeg from July 7-10, 2024. The LAC, led by Drs. Tom Fetch, Barry Saville, and Dilantha Fernando, with participation from all Plant Canada societies, has been working tirelessly to put together an incredible program for the conference. This year, CPS will celebrate its 95th anniversary during the Plant Canada meeting. We will have an awards banquet on Tuesday evening (July 9th), where our 2024 major award winners will be recognized. CPS will be organizing the following workshops/symposia/activities during the conference:

1. Sun, July 7: Workshop: Metabarcoding for Phytopathogens (2:30 - 4:30pm)
2. Mon, July 8: ALL SOCIETY Student Social (8:30 – 10:30pm)
3. Tues, July 9: CropLife Symposia: Resistance Management (11:15am - 1:00pm)
4. Tues, July 9: CPS 95th Anniversary and Awards Banquet -York 2-3 (7:00 - 11:00pm)
5. Wed, July 10: CPS Plenary Session 3 - Emerging Technologies in Plant Health Hall C (East) with three invited speakers: Drs. Jan Leach, Colorado State University, Martina Stromvik, McGill University and Brent McCallum, AAFC Morden Research and Development Center (8:30 -11:00am).

We look forward to meeting colleagues and students from all Plant Canada societies at the conference in Winnipeg. For more information on the CPS, including membership, publications, awards and committees, please visit our website at https://phytopath.ca/.

Canadian Society of Agronomy
La Société Canadienne d'Agronomie

Canadian Society of Agronomy Annual Report 2023-2024

agronomycanada.com | @agronomycanada

The Canadian Society of Agronomy (CSA) is a non-profit, educational and scientific society affiliated with the Agricultural Institute of Canada. The CSA was formed in 1954, building on the historic Western Canadian Society of Agronomy (established 1919) and the Eastern Canadian Society of Agronomy (established 1949). The CSA is dedicated to enhancing cooperation and coordination among agronomists, to recognizing significant achievements in agronomy and to providing the opportunity to report and evaluate information pertinent to agronomy in Canada. Our goals are to provide opportunities for interaction among members and to act as a conduit for interacting with members of other professional organizations, to provide our members with a united voice for making agronomic concerns known to the public and to other organizations, and to provide opportunities for members to communicate news and scientific findings to the scientific community. More information can be found at agronomycanada.com.

2023-2024 CSA Executive Committee

Harpinder Singh Randhawa
President

Jamie Larsen
Past-President

Kui Liu
President-Elect

Kathleen Glover
Secretary/Treasurer

Hiroshi Kubota
Western Director

Linda Gorim
Western Director

Laura Van Eerd
Eastern Director

Joshua Nasielski
Eastern Director

Jagroop Gill Kahlon
Industry Representative

Ben Thomas
CJPS Representative

Alexa Peterson
Student Representative

CSA Activities

The CSA executive met five times over the last year. Key highlights of this year include: The “Green Bagger” virtual lunch session started in October 2020 running once each month to May. An initiative brought to the CSA by Amy Mangin, Laurel Thompson and Sheri Strydhorst with the goal of building the CSA student community and helping to prepare students for live oral presentations. The four students who presented in these sessions are well-represented among our student award winners. This initiative will continue in 2023-2024.

Our annual conference, the CPS-CSA-CSHS tri-society conference was held June 17-20, 2023 and was a major success. There were over 250 registrants, about 20% of whom were CSA members. There were 14 technical sessions composed of 106 oral presentations, and 3 invited keynote speakers. A total of 101 posters were presented. The Canadian Society of Agronomy also hosted a workshop on “Practical Carbon Capture GHG Emission Measurements: Methods, Implementation and Uses” which also linked with a field tour of environmental science research at the CFIA-Fallowfield station and plant breeding and environmental science research at the Ottawa Research and Development Centre. There was a panel discussion on Equality, Diversity, and Inclusion which was well attended by the participants. CSA also finalized and singed the MOU with Canadian Science Publication. With the sincere efforts of Kathleen Glover, multiple crop specific graduate student awards were build which will be awarded at the annual meeting of 2024.

CSA members Jamie Larsen Mumtaz Cheema, Harpinder Randhawa, Kathleen Glover, Gurcharn Singh Brar, Leonardo Galindo, André Lévesque, Jagroop Gill Kahlon, Hiroshi Kubota, Nate Ort, Jaswinder Singh, Andrew Burt, Simon Lackey, Kui Liu Kui, Milad Eskandari and

Marcie Wilson have all made large donations of their time and effort to get everything from the scientific program, session moderators, to sponsorships, to awards, and to student events organized.

CSA Membership

The Canadian Society of Agronomy provides its members with a variety of benefits:

- Editorial functions of world class scientific journal.
- Meeting and interacting with other agronomists across Canada
- Recognition by peers through awards program.
- Presentation of scientific results at annual meeting.
- Forum for making scientific information available to the public.
- Competitive awards for graduate students.
- Participation in international projects.
- Enhanced career opportunities.
- Deep discounts on the CJPS journal. CSA members pay $50.00 for the electronic version (regular rate $526.00) and $125.00 for the print and electronic versions (regular rate $634.00).
- Representation on various national Expert Committees

The Canadian Society of Agronomy currently has about 160 members.

CSA Awards 2023

CSA Professional Awards

The CSA professional awards are an important peer recognition benefit. Professional Awards include:

- **Early Career Agronomist** is intended for individuals actively engaged in research, teaching, extension or administration within 10 years of starting their career or earning their last degree.
- **CSA Fellow** is intended for individuals actively engaged in research, teaching, extension or administration for at least 10 but less than 20 years of their career.
- **Distinguished Agronomist** is intended for individuals actively engaged in research, teaching, extension or administration for more than 20 years of their career.

Nominations for the above awards can be made by any active member of CSA who has had continuous active membership in CSA for at least five years.

Below are the Professional Award winners for 2023

2023 Distinguished Agronomist

- Dr. Pierre Hucl

2023 Fellow Award

- Dr. Laura Van Eerd

2023 Early Career Agronomist Award

- Dr. Gurcharn Brar

CSA Graduate Student Awards
The Canadian Society of Agronomy Graduate Student Awards include:

- **Ali Navabi Grad 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 Student Travel Award is $500 with a maximum of 5 awarded annually.
- **Pest Management Award** includes an award of $500 available to a graduate student enrolled at a Canadian University with research programs relevant to pest management. The award is accompanied by a grant to cover registration at the CSA Virtual Annual General Meeting and present on his/her research project.
- **Student Presentation and Poster Awards -** A number of awards are awarded at the CSA Annual General Meeting for the best oral and poster presentations given by graduate student members. The awards are presented after an assessment conducted by a panel of judges. Up to $2,000.00 total is awarded for graduate student oral and poster presentations.

Graduate students must be a member of CSA to apply for the above awards.

Below are the Graduate Student Award Winners for 2023.

2023 Ali Navabi Student Travel Awards
- Natalie LaForest
- Yutong Jiang
- Mohammed Antar
- Sharandeep Singh
- Syed Jahanzaib Rasool Bukhari

2023 Pest Management Award
- Vincent Fetterley

2023 Student Presentation and Poster Awards:

Oral Awards
1st - $700, Yutong Jiang: Water-conducting roots responsible for nitrogen uptake in maize (Zea mays)
2nd - Natalie LaForest: Investigating the role of Pterostichus melanarius in agricultural pest predation in wheat (Triticum aestivum) and hemp (Cannabis sativa L.) in Alberta
3rd - Riley McConachie: Winter wheat genotype-Fusarium graminearum isolate interactions using the detached wheat head bioassay method

Poster Awards
1st, Syed Jahanzaib Rasool Bukhari: Agronomic performance of inter-seeded legume-cereal Cover crops mixtures in silage corn in boreal climate
2nd, Fernando Guerrero Zurita: Identifying superior photosynthetic traits in canola Brassica napus gene pool
3rd - Farzana Yasmin: Integrating bio-strip tillage into overwintering cover crop mixtures prior to grain corn (Zea mays L.)

The CSA would like to recognize 2023 Outstanding Reviewers for the Canadian Journal of Plant Science

Shaun Sharpe
Dilshan Benaragama
Linda Y. Gorim

The CSA would like to recognize the 2023 Outstanding Associate Editor for the Canadian Journal of Plant Science

Malinda Thilakarathna

2023 Photo Contest (sponsored by BASF)

Crops & Biological Interactions

1st - Morgan McNeil
2nd - Jujhar Gill
3rd - Gurcharn Brar

Agronomy in Action

1st - Alexa Peterson
2nd - Sumedha Nallanthighal
3rd - Naveen Kumar

Landscapes & Fieldscapes

1st - Zhanghan Zhanghan
2nd - Jujhar Gill
3rd - Nate Ort

Acknowledgements
Bayer Canada provides financial support for the Pest Management Award. The CSA is grateful to Bayer for their support.

The 2023 CSA awards committee members were: Jamie Larsen, Mumtaz Cheema, Kui Liu.

Contact Information
For more information on CSA Membership or our awards program contact Marcie Wilson 204-228-8508, CSAgronomy@gmail.com or visit our website at agronomycanada.com and follow us on X (formerly Twitter) @agronomycanada, Facebook and LinkedIn.

Canadian Society of Agronomy
La Société Canadienne d'Agronomie

The Canadian Society of Agronomy would like to thank the sponsors of our 2024 Student Awards

Gold Sponsors

Manitoba Pulse Soybean Growers

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Sask Wheat Development Commission

Bronze Sponsors

Alberta Canola

BCRC Beef Cattle Research Council

Crop Development Centre USASK

Manitoba Canola Growers

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 (2023-2025)

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. The current Secretary is covering the roles of Secretary and Northern representing regions of Canada. Therefore, the CSHS Executive board is looking for a Northern Representative to cover the Northern regions of Canada.

President
Bourlaye Fofana, PE
Agriculture and Agi-Food Canada

Past-President
Youbin Zheng, ON
University of Guelph

Vice-President
Lord Abbey, NS
Dalhousie University

Treasurer
Beatrice Amyotte, NS
Agriculture and Agi-Food Canada

Secretary
Julie Lajeunesse
Agriculture and Agi-Food Canada

Western Representative
Simone Castellarin, BC
University of British Columbia

Prairie Representative
Jazeem Wahab, SK
Agriculture and Agi-Food Canada

Communication Officer
Qinglu Ying, ON
Vineland Research and Innovation Centre

Student Representative
Sarah Drury, QC
Université de Sherbrooke

Quebec Representative & Web-master, QC
Shahrokh Khanizadeh
ELM Consulting

Ontario Representative
Melanie Kalischuk, ON
University of Guelph

Atlantic Representative
Vasantha Rupasinghe, NS
Dalhousie University

Northern Representative
TBD

While we practice a progression within the board based on need, our members are encouraged to submit their candidacy to any currently position available. **In fact, CSHS will renew its board members in summer 2025, and we are currently recruiting for a representative for the Northern region.** Terms are for 2 years with the possibility of 2 consecutive terms in the same position. Please contact the CSHS secretary (Julie.lajeunesse@agr.gc.ca) if you are interested in the Northern Representative position or any upcoming vacant positions in 2025.

CSHS Annual Conferences

The CSHS also prioritizes travelling around the country for its annual meetings. Due to the Covid19 pandemic, the CSHS held a virtual student conference on August 27, 2020 and a virtual Joint tri-societies (CPS-CSA-CSHS) conference on July 5-9, 2021. These meetings were followed by a first post-pandemic in-person conference in Halifax on August 18-20, 2022, chaired by Dr. Fofana and was a real success. This past year, the CSHS held its conference in Ottawa, Ontario, as part of the Tri-Society Conference with the Canadian Phytopathological Society and the Canadian Society of Agronomy, from June 17-21, 2023. The conference covered the topic “Agroecosystem resiliency under changing climate”,and was chaired by Dr Guillaume Bilodeau. CSHS organized and chaired a symposium on controlled environment agriculture, a concurrent session on disease management of horticultural crops, and its members presented at and chaired many other sessions. Dr. Fofana actively contributed to the Scientific Paper Worshop organized by the Canadian Journal of Plant Science for students.

CSHS – Halifax 2022

Tri-Society (CSHS-CPS-CSA) – Ottawa 2023

The CSHS is proud to be part of the **2024 Plant Canada Conference in Winnipeg, MB**. The CSHS will organize 5 concurrent sessions targeting topics including a Cannabis symposium (sessions 1 & 2), Root Crops (session 3), Fruits (session 4) and Vegetables (session 5) sessions.

In 2025, our annual meeting will be held in the west coast region, with Dr. Beatrice Amyotte and Dr. Simone Castellarin as the chairs. **If you are interested in participating in the organization of the conference, please contact the CSHS secretary** (Julie.laleunesse@agr.gc.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 so far been very busy.

Sarah Drury (Current CSHS Student Representative and Student Committee Chair) and past student committee chairs have organized and will organize the student social event for CSHS and all of the societies attending the Plant Canada Conferences. **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!**




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, Sarah Drury (sarah.drury@usherbrooke.ca).

Becoming a member of the CSHS offers numerous benefits including:
• Significantly reduced registration fees at CSHS and Plant Canada conferences
• Reduced page charges to publish in the Canadian Journal of Plant Science
• Timely direct mail alerts to jobs, grant opportunities, etc.
• Eligibility for the CJPS Best Paper Award for horticulture, which comes with an invitation to be a conference speaker

In addition, for students, benefits also include:
• Eligibility for Presentation Awards for the best oral and poster presentations
• Eligibility for Travel Awards to annual conferences
• Community & Extension Funding, which supports student activities in their communities
• Networking opportunities between members, and sharing the experience of study and research

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

The Canadian Society of Plant Biologists
La Société Canadienne de Biologie Végétale

The Canadian Society of Plant Biologists/ La Société Canadienne de Biologie Végétale
Report submitted by Marcus Samuel: CSPB/SCBV President, Jun 2024

About the CSPB-SCBV

The Canadian Society of Plant Biologists/ La Société Canadienne de Biologie Végétale (CSPB-SCBV) was founded in 1958 as the Canadian Society of Plant Physiologists. In 2012, the Society adopted its present name to include the various facets of Plant Biology 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 a member of the **Partnership Group for Science and Engineering**. Our membership is close to 600 with over 300 student members and more than 60 PDFs along with research associates, professional scientists, scientists from government organizations, and a few corporate members. We are close partners with the American Society of Plant Biologists and host joint meetings every four years. We consistently strive toward improving our organization to be a welcoming, inclusive, and resourceful one.

Upcoming CSPB/SCBV Annual General Meetings:
2025 Annual General Meeting: Halifax, Nova Scotia
2026 Plant Biology 2026 (Joint ASPB/CSPB-SCBV), TBD

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: Over 10k per year is given to students and postdoctoral fellows to support travel to the annual summer meeting.

Becoming a member of the CSPB-SCBV
CSPB-SCBV is a diverse, welcoming, and highly inclusive organization. If you are interested in joining our dynamic community, please feel free to contact either myself (president@cspb-scbv.ca) or our Senior Director, Mehran Dastmalchi (seniordirector@cspb-scbv.ca). We are always looking for new members to get involved with the society and for volunteers to engage in the various CSPB/SCBV committees. Benefits of membership include reduced registration fees at our conferences and meetings; access to the education, student/pdf funding links, ECR resources and employment pages of our website; and eligibility for the various awards, scholarships and bursaries listed.

CSPB Inside

CSPB / SCBV Executive Committee Membership 2024

TOP **President:** Marcus Samuel, **Vice-President:** Hugo Zheng, **Secretary:** David Bird, **Treasurer:** Rongmin Zhao, **Communications Director:** Lauren Erland, **Western Regional Director:** Barbara Hawkins BOTTOM **Eastern Regional Director:** Sophia Stone, **Senior Director:** Mehran Dastmalchi, **Science Policy Director:** Gopal Subramaniam, **Education Director:** Miranda Meents, **PDF Representative:** Mark Minow, **Student Representative:** Sean Ritter, **Past President:** Robin Cameron

At Plant Canada 2024

Our student and post-doctoral representatives, Dr. Mark Minow and Sean Ritter, have organized a workshop on "Survival in the jungle of scholarly publishing: Building authorship and peer review skills" to demystify the world of scholarly publishing. It is scheduled on July 7th, 2024, from 12:00-2:00 PM in Meeting Room 17. Our CSPB-SCBV executive committee members Drs. Miranda Meents, David Bird, Lauren Erland, along with Drs. Robin Young and Solmaz Irani, are organizing a workshop on **"**Developing a Community of Practice for Plant Biology Teaching,**"** scheduled for July 8th, 2024, from 11:15 AM-1:00 PM. The workshop will help build an online community to provide new ideas for teaching and lay the foundation to develop new resources and connections that make your creative ideas a reality. CSPB-SCBV is also organizing 14 concurrent sessions with several of them as joint sessions with other societies on various themes, providing the opportunity for a highly diverse group of exceptional researchers to showcase their work.

The CSPB-SCBV Annual Business Meeting will be held on Wednesday, July 10th at 11:15 AM, during which we will announce our Presidents Awards and all our 2024 major award winners. Our Society Social event will be held from 7-9 PM on Monday in the Pan Am room; we will also be joining the other participating societies and associations in the multi-society social event on Monday evening. Two of our 2023-24 Awardees feature in the plenary talks: our 2023 C.D. Nelson Award winner Gavin Chen and our 2024 Carl Douglas Prize winner Dr. Mark Minow will deliver their seminars as the two final plenary speakers on Wednesday, July 10th. For more information, please visit http://cspb-scbv.ca/

CSPB-SCBV Report for 2023

Our 2023 Annual General Meeting (AGM) was held at Laval University, Quebec City, from June 18th to 21st, organized by Dominque Michaud, Edel Pérez Lopez and Marie-Claire Goulet. Laval University was certainly a great venue for the conference. The conference was well attended as it was the first Canadian CSPB-SCBV conference after the COVID interruption. The organizing committee chose a diverse and excellent group of inspiring plenary speakers. Our 2023 Carl Douglas Post-doctoral award winner, Dr. Devang Mehta, delivered an engaging seminar that included an EDI section in addition to his research highlights. The banquet at the Musée National des Beaux-Arts du Québec was delightful and entertaining.

During the AGM at Laval University, the 2023 CSPB-SCBV awards were given to several exceptional people. Dr. Guanqun Gavin Chen was awarded the C.D. Nelson award for outstanding research contributions to plant biology. Dr. Peter Moffet was awarded the Mary Spencer award for outstanding research in plant biology and active public service to the plant biology community by a mid-career researcher. The Carl Douglas post-doctoral award for outstanding contributions to plant biology based on originality of research, productivity and leadership was awarded to Dr. Devang Mehta. The Ragai Ibrahim Award for excellence in publication by a graduate student was awarded to Mendel Perkins for his paper, “Monolignol export by diffusion down a polymerization-induced concentration gradient,” in Plant Cell (2022). The Student Presentation Competition included over 90 student presentations for which several awards were given for oral and poster presentations.

The Western Regional Meeting was held at the University of Victoria on May 1-2, 2023, in conjunction with the UVic Centre for Forest Biology Research Symposium. Our Western Regional Director, Dr. Barabara Hawkins, organized the event along with other volunteers. Over 100 people attended from BC and Alberta universities, provincial ministries, and federal forestry and agriculture research institutions. With 31 talks and a score of posters, many interesting findings were presented and discussed; several awards were given out for oral and poster presentations.

The 2023 Eastern Regional Meeting was held at Concordia University on December 1-2. The organizing committee chaired by Dr. Jin Suk Lee, with colleagues Drs. Patrick Gulick, Selvadurai Dayanandan, and William Zerges, who put together an exciting meeting agenda under the guidance of our Eastern Regional Director Dr. Sophia Stone. Highlights included plenary sessions by Dr. Mehran Dastmalchi (McGill University), Dr. Thomas DeFalco (University of Western Ontario), and Dr. Shelley Hepworth (Carleton University). Over 140 attendees participated in six concurrent sessions on various topics including abiotic stress, agriculture and biotechnology, and plant-pathogen interactions. Student trainees delivered exceptional oral and poster presentations. The 2024 Eastern Regional Meeting will be held later this year virtually, it is being organized by Dr. Yang Qu at the University of New Brunswick.

We have re-vitalized our education and communication committees under the leadership of Dr. Miranda Meents and Dr. Lauren Erland. Several new initiatives have been implemented and we are in the process of constantly coming up with new ideas to be a resourceful organization to all the students and ECRs. Our presence on social media platforms has significantly improved. In April, an online workshop was organized for grad students, post docs, and other ECRs exploring Teaching Careers in Higher Education. Dr. Meents and Dr. Solmaz Irani organized and moderated this event. The group explored the diversity of teaching and teaching-related careers available, tips for building teaching experience, and tools and resources to help get the job.

As a society, we continue to strongly promote Equity, Diversity and Inclusion. Some of our recent accomplishments that have been implemented are,

Enhanced diversity of CSPB-SCBV Executive: Compared to the composition of our executive committee in 2021 (42% women and 0% members of a visible minority), our current Executive (50% women) is quite diverse and is made up of a mix of BIPOC (33%) and Caucasian (67%) members. We have changed from 0% representation of visible minorities to 33%. Our aim was to achieve 22% representation from members of visible minorities by 2030, and we have been able to exceed the 22% target in less than one year. Representation of BIPOC in the 12 committees of CSPB-SCBV has also increased from 17% to 28%, exceeding our proposed 22% target by 2030.

French versions of the CSPB-SCBV bulletin, emails and conference communications: Through the Executive's efforts, new opportunities for graduate students and post-doc involvement in CSPB-SCBV were created by introducing a column dedicated to their voices in the bi-annual bulletin, offered in both official languages. The bulletin is in both French and English and we are also striving to send out emails and conference communications in both languages as well.

New EDI-informed conference handbook that includes a collection of guidelines and resources to promote more inclusive conference planning. This handbook will be posted on the CSPB-SCBV webpage and will also be provided to the conference organizers during the planning stages.

New inclusive guidelines for judging posters and oral presentations at both national and regional conferences to reduce any potential bias while judging. These guidelines were implemented in the 2021 ERM, WRM meetings, 2022 joint ASPB/CSPB-SCBV PB22 meeting, the 2023 CSPB-SCBV AGM at Laval University, WRM 2023 and ERM 2023 meetings.

Reformed nomination process for several society awards, so that candidates are also able to self-nominate without a need for seeking their nomination by another member of the society.

First ever EDI plenary session at Plant Biology 22: At PB22, CSPB-SCBV actively participated in the first ever Joint CSPB-SCBV- ASPB EDI Plenary session entitled, *Science Without Borders.* Our CSPB-SCBV speakers, Edel Pérez-López (Laval) and Allison MacDonald (Laurier) certainly made us proud with their exceptional EDI-focussed seminars. CSPB-SCBV EDI committee chair, Marcus Samuel, chaired the plenary session which also included other science-based talks from ASPB members on species migration, domestication, and culture.

Canadian Weed Science Society
Société canadienne de malherbologie

The Canadian Weed Science Society-Société canadienne de malherbologie (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, 3) ensure good governance.

Current Board of Directors of the CWSS-SCM is as follow:


President
Jeanette Gaultier
BASF


Past President
Harold Wright
Retired


1st Vice President
Robert Nurse
AAFC


2nd Vice President
Andrew McKenzie-Gopsill
AAFC


Treasurer
Deanna McLennan
FMC


Secretary
Sara Martin
AAFC


Regulatory Representative
Wendy Asbil
CFIA


Regulatory Representative
Michael Downs
PMRA


Governance Director
Shaun Sharpe
AAFC

Publications Director
Jichul Bae
AAFC


Research Representative
Leonard Galindo González
CFIA


Crop Life Representative (East)
Meghan Dilliot Belchim


Crop Life Representative (West)
Tyler Gullen
Nufarm


Member at Large (East)
Martin Laforest
AAFC


Member at Large (West)
Dilshan Benaragama
University of Manitoba


Graduate Student Representative
William Kramer
Colorado State University

Board membership is open to all CWSS-SCM members in good standing and is by election. Term length varies by position but is generally three years with an option for renewal. If you are interested in submitting your name for nomination to a board position, please reach out to a member at large.

Annual Meetings

Following two years of on-line only meetings, the CWSS-SCM co-hosted its 76th annual meeting jointly with the Canadian Society of Agronomy-Société canadienne d'agronomie (CSA-SCA) in Halifax Nova Scotia in November 2022. An exciting plenary session on precision agriculture technologies featured Drs. Arnold Schumann, Louis Longchamps, Athyna Cambouris, Aitazaz Farooque, Steven Fennimore, and Travis Esau. In addition, we hosted two workshops, one on statistical analysis of non-normal data and another from Canadian Science Publishing. This first conference post-COVID was a great success and co-chaired by Drs. Scott White and Andrew McKenzie-Gopsill (CWSS-SCM), as well as Drs. Kathleen Glover, Andrew Burt, and Mumtaz Cheema (CSA-SCA).

The 77th annual meeting of the CWSS-SCM was hosted in Winnipeg, MB in November 2023. This meeting co-chaired by Dr Rob Gulden and Kim Brown-Livingston hosted an exciting plenary session on next generation weed management from genomics to seedbank

management and featured Drs. Eric Patterson, Martin Laforest, Michael Flessner, and Breanne Tidemann. Dr. Patterson hosted a workshop on getting started with analyzing weed genomics data which was incredibly well received and attended.

The CWSS-SCM will host its next AGM virtually in November 2024 followed by an international joint meeting with the Weed Science Society of America in Vancouver, BC in February 2025. The CWSS-SCM will meet again in November 2025 in Ottawa ON. For more information, please contact the CWSS-SCM secretary at sara.martin@agr.gc.ca

Graduate Students

Graduate students are a highlight of the CWSS-SCM and its annual meetings. Over the past several years the graduate students have organized networking and social events at each meeting. In addition, in collaboration with the Weed Science Society of America, the graduate students have hosted several workshops throughout the past year on a wide range of topics such as the transition from graduate school to industry or academia.

The CWSS-SCM supports graduate students through various scholarships, travel enrichment awards, and provides oral presentation awards at each meeting. We would like to congratulate all of our graduate students and recent scholarship and award winners. For more information and a list of past winners please see, https://weedscience.ca/student-awards/.

Other activities

Herbicide-resistant weeds are a challenging problem for farmers globally, and Canada is no exception. Recent estimates for the prairie region alone suggest that herbicide-resistant weeds cost farmers an estimated CAD $530 million annually in decreased crop yields and quality and increased weed control expenses. There is an immediate need to forge new paths to mitigate and manage herbicide-resistant weeds in Canada. The CWSS-SCM recently published a special collection in the *Canadian Journal of Plant Science* on “Forging New Paths to Manage Herbicide-Resistant Weeds”. This issue contains five articles on managing herbicide resistant weeds in Canadian production systems.

Nearly three-quarters of wild oat populations across the Canadian prairies are herbicide resistant. In response to this increasing challenge, the CWSS-SCM formed the Resistant Wild Oat Action Committee to provide information on testing and management advice to producers and researchers. A variety of excellent resources have been and continue to be produced and are available at https://weedscience.ca/wild-oat-action-committee/

Become a member of the CWSS-SCM today!

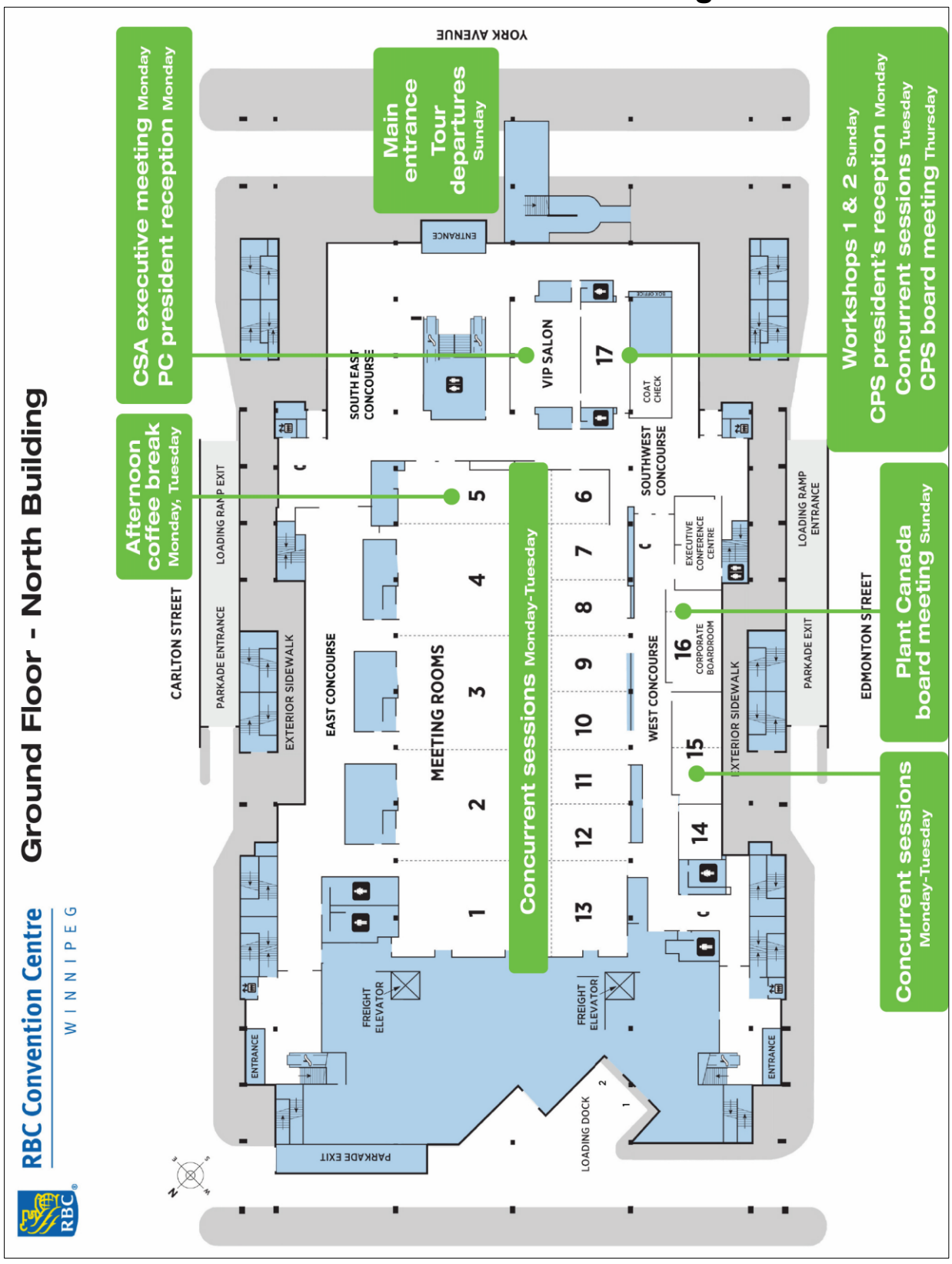
- Reduced registration fees for CWSS-SCM annual meetings
- Reduced page charges to publish in the Canadian Journal of Plant Science
- Subscription access to the Canadian Journal of Plant Science
- Eligibility for the CJPS Best Paper Award – Weed Science

For students membership includes:

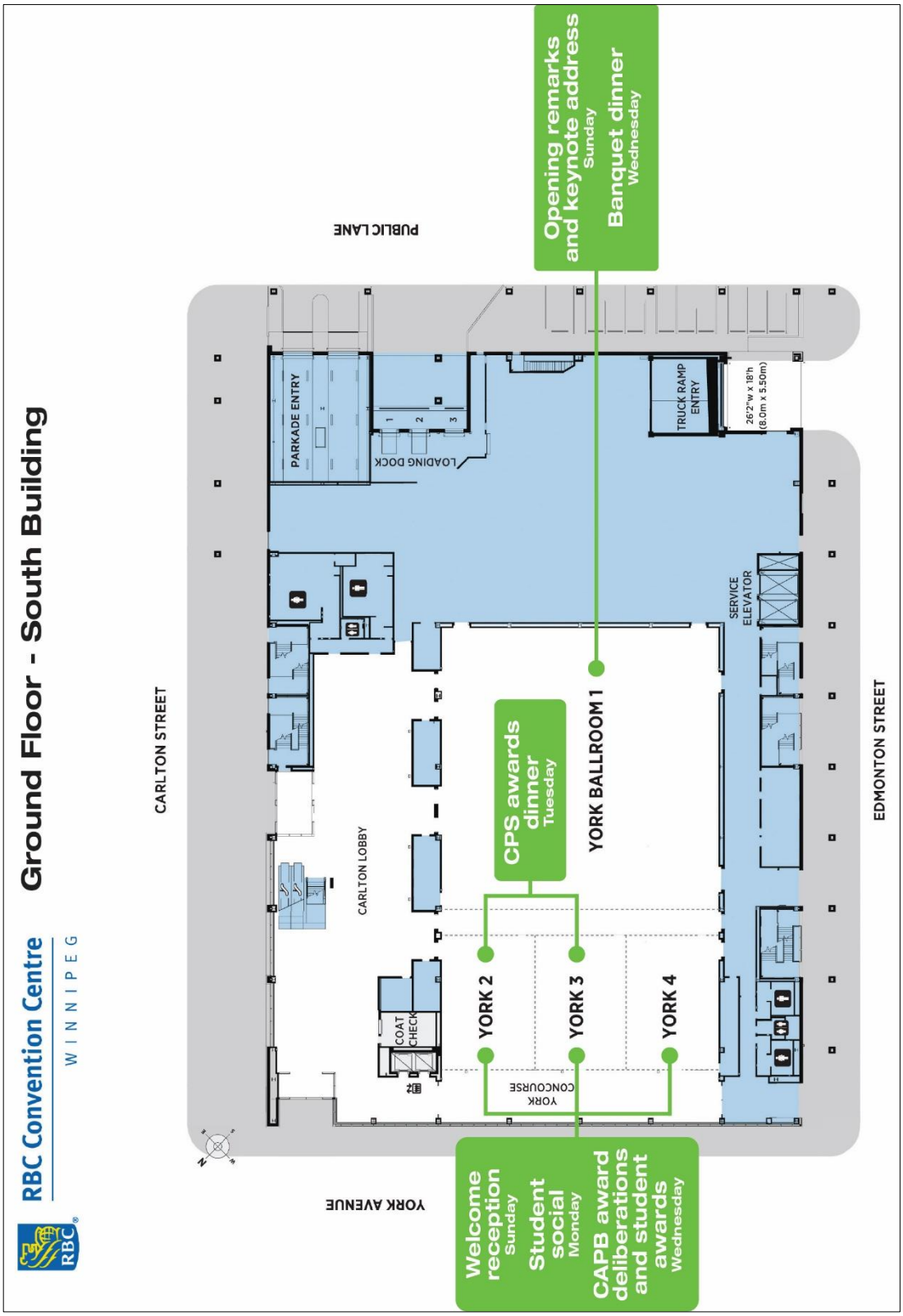
- Eligibility for oral presentation awards
- Eligibility for scholarships & the travel enrichment award
- Networking opportunities

See www.weedscience.ca for more information and to become a member.

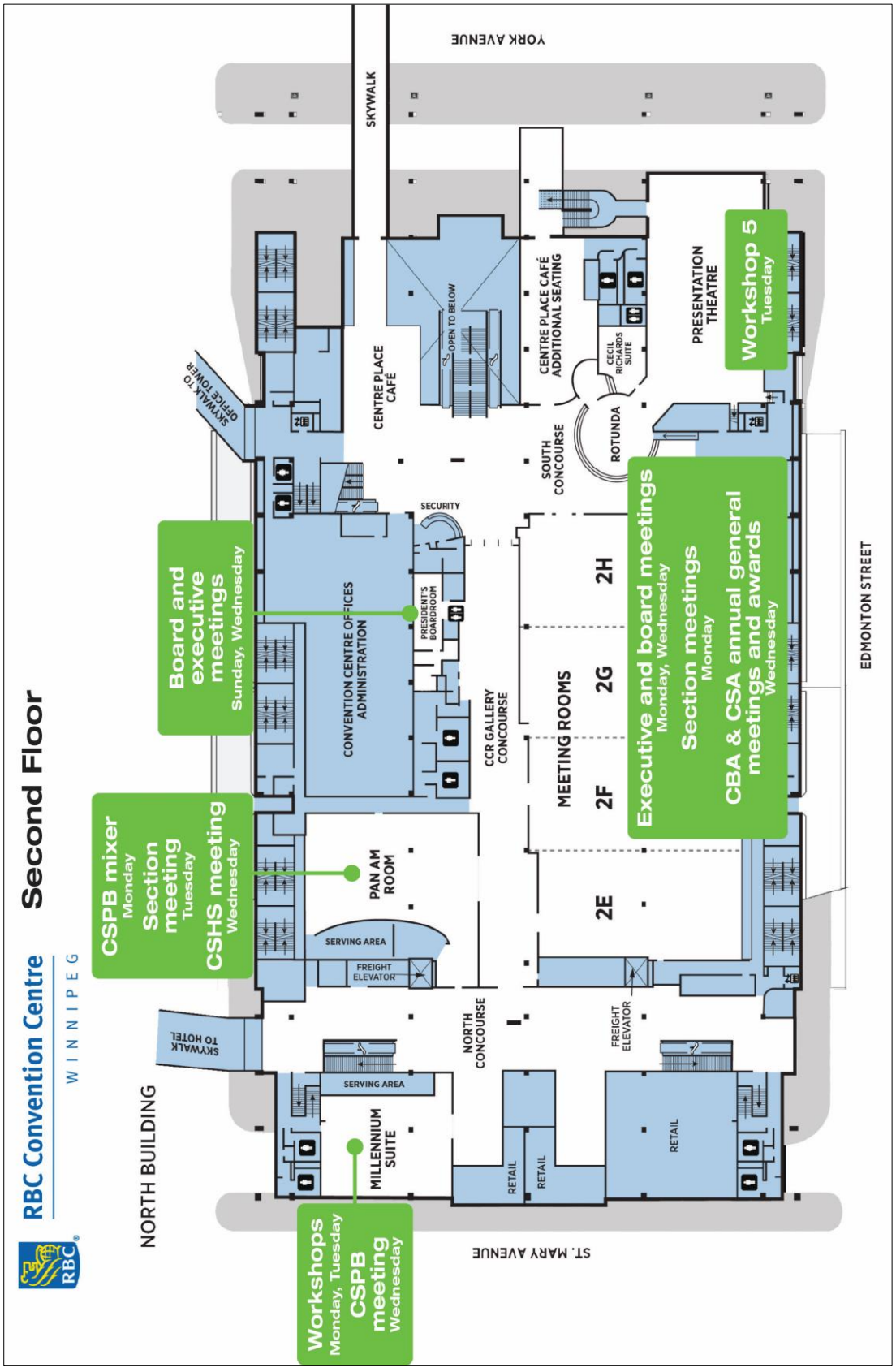
Ground Floor – North Building



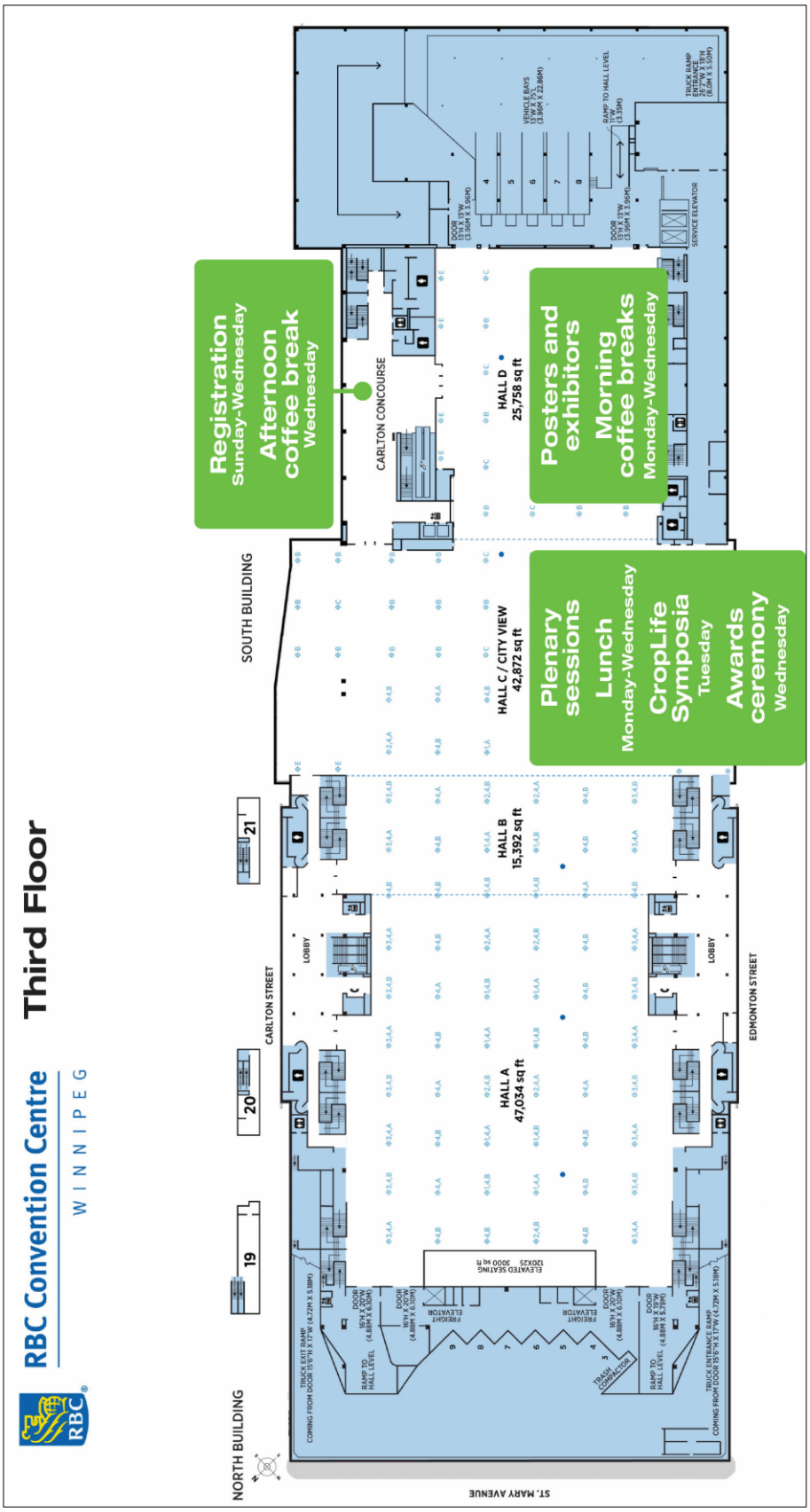
Ground Floor – South Building



Second Floor

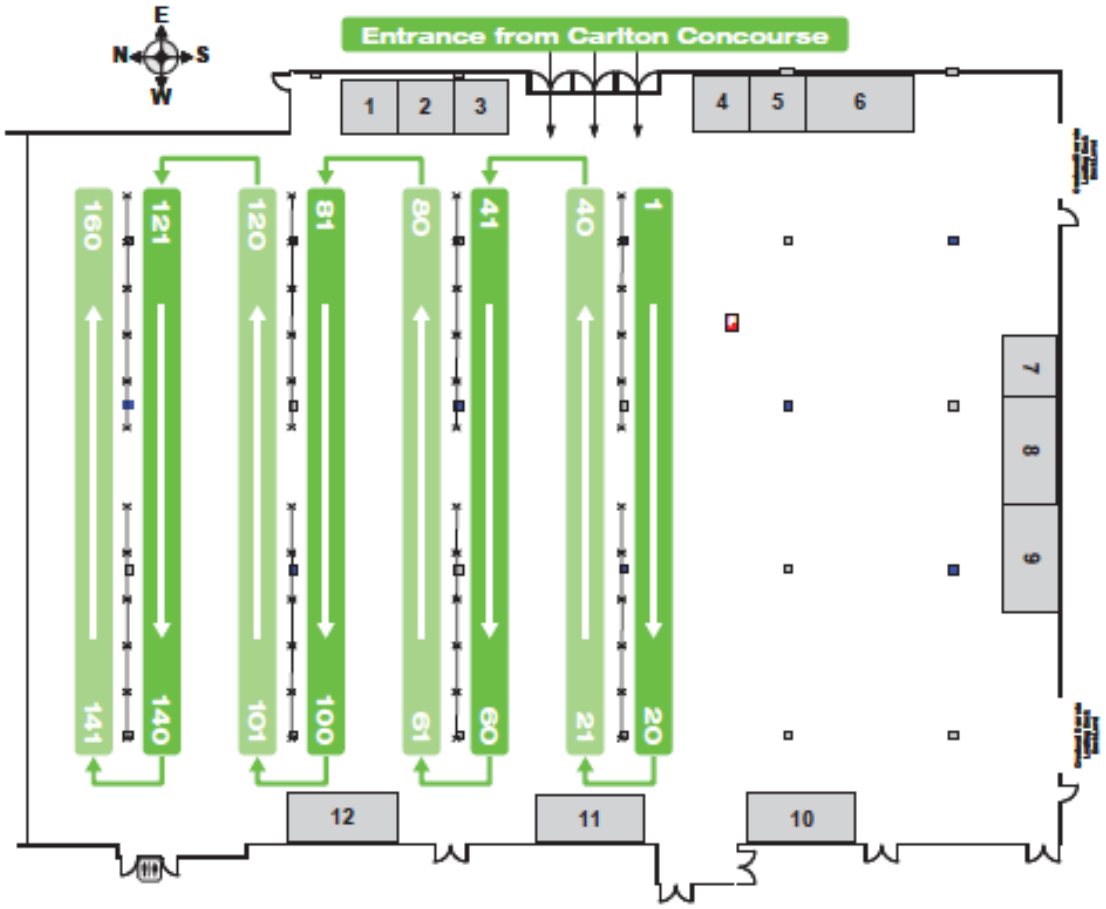


Third Floor


RBC Convention Centre
WINNIPEG
Third Floor
Registration
Sunday-Wednesday
Afternoon coffee break
Wednesday
Posters and exhibitors
Morning coffee breaks
Monday-Wednesday
Plenary sessions
Lunch
Monday-Wednesday
CropLife Symposia
Tuesday
Awards ceremony
Wednesday
HALL A
47,034 sq ft
HALL B
15,392 sq ft
HALL C / CITY VIEW
42,872 sq ft
HALL D
25,758 sq ft
CARLTON CONCOURSE
CARLTON STREET
EDMONTON STREET
ST. MARY AVENUE
SOUTH BUILDING
NORTH BUILDING
LOBBY
SERVICE ELEVATOR

Plant Canada 2024
Poster and Exhibitor Area

RBC Convention Centre – Hall D



Plant Canada 2024
Exhibitors

1 Elementar
2 MB Assoc. Plant Biologists
3 New England Biolabs
4 PhytoAB
5 Royal Society Publishing
6 Conviron
7 CropLife Canada
8 Hoskin/LiCor
9 ATS Scientific/Aralab
10 BioChambers
11 ThermoFisher
12 University of MB Departments

PROGRAM SCHEDULE OVERVIEW FOR SATURDAY JULY 6, 2024

EXHIBITOR SET-UP: Starting from noon until 6:00 pm **Hall D**

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

PROGRAM SCHEDULE OVERVIEW FOR SUNDAY JULY 7, 2024

8:00 am – 9:00 pm Registration in the Carlton Concourse

	POSTER VIEWING and EXHIBITS in Hall D from 8:00 am – 7:00 pm	
Time	**TOURS DEPARTURE from RBC Convention Centre, York Avenue Main Entrance**	
9:00 am	**TOUR 1: The Leaf Tour and Conviron Plant Tour with Lunch**	
9:30 am	**TOUR 2: The Leaf Tour and Assiniboine Park Tour (on your own)**	
8:00 -2:00 pm	**CPS FAC and Outgoing Board Meeting**	**President's Boardroom**
12:00-2:00 pm	**Workshop 1 (CSPB) Survival in the jungle of scholarly publishing**	**Meeting Room 17**
1:00-3:00 pm	**Plant Canada Outgoing Board and Annual General Meetings**	**Meeting Room 16**
3:30-5:00 pm	**CAPB Outgoing General Meeting**	**President's Boardroom**
2:30-4:30 pm	**Workshop 2 (CPS) Metabarcoding for Phytopathogens**	**Meeting Room 17**
5:30-5:45 pm	**Opening Remarks** **York 1** • Plant Canada 2024 Co-Chairs Dr. Tom Fetch / Dr. Dilantha Fernando • Mr. Timi Ojo, Manitoba Agriculture, Government of Manitoba • Dr. Geoff Wasteneys, President Plant Canada • Dr. Guillaume Bilodeau, Chair Scientific Program Committee, Plant Canada 2024	
5:45-6:45 pm	**Keynote Address by Dr. Sylvain Charlebois** **York 1**	
6:45-7:30 pm	**Major Society Awards** (presented by the Presidents of each Society)	
7:30-10:00 pm	***Plant Canada Welcome Reception** **York 2 – 4**	

*Hearty appetizers will be served.

PROGRAM SCHEDULE OVERVIEW FOR MONDAY JULY 8, 2024

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

Time	POSTER VIEWING and EXHIBITS in Hall D from 8:00 am – 7:00 pm								
8:00 – 8:30	**Coffee Break in Hall D** sponsored by **DL Seeds**								
Loading talks at 8	**Plenary Session 1-Plant Biotechnology for a Changing World (CAPB) Hall C East** *Chair: Dominique Michaud (Laval University, president of CAPB)*								
8:30 – 9:20 **PS1**	**Dr. Louis-Philippe Hamel, Medicago Inc.** ***Understanding plant molecular responses to the production of enveloped VLPs leads to the improvement of a molecular farming expression platform***								
9:20 – 10:10 **PS2**	**Dr. Dan Voytas, University of Minnesota** ***Overcoming Bottlenecks in Plant Gene Editing***								
10:10 – 11:00 **PS3**	**Dr. Nicola Patron, University of Cambridge** ***Synthetic biology for metabolic pathway engineering in photosynthetic organisms***								
11:00 – 1:00	**LUNCH in Hall C West** sponsored by **ThermoFisher Scientific**								
11:15 – 1:00	**Workshop 3 (CAPB) Developing a community for plant biology teaching Millennium Suite**								
11:15 – 1:00	**CPS Annual Business Meeting Room 2G**								
11:15 – 1:00	**CAPB Annual General Meeting Room 2F**								
11:15 – 1:00	**CBA Section Meetings: Ecology, Systematics, Development Room 2E**								
11:30 – 1:00	**CSA Executive Meeting VIP Salon**								
Rooms→	MR 1	MR 15	MR 3	MR 4	MR 7+8	MR 9+10	MR 11+12	MR 13	MR 2
Loading talks will be inside corresponding rooms at 1:00-1:15 pm for CS1 and at 3:00-3:15 pm for CS2									
Concurrent Session 1	**CSPB-I**	**CSA-I**	**CAPB/ CSPB-II**	**CSPB-III**	**CSHS-I/ CPS-J1**	**CBA-I**	**CPS-I**	**CPS-II**	**CPS-III**
1:15 - 1:30	O1	O7	O13	O18	O23	O29	O34	O40	O46
1:30 - 1:45	O2	O8	O14	O19	O24	O30	O35	O41	O47
1:45 - 2:00	O3	O9	O15	O20	O25	O31	O36	O42	O48
2:00 - 2:15	O4	O10	O16	O21	O26	O32	O37	O43	O49
2:15 - 2:30	O5		O17	O22	O27	O33	O38	O44	O50
2:30 - 2:45	O6				O28			O45	
2:45 - 3:15	**Coffee Break in Meeting Room 5** sponsored by **FMC**								
Concurrent Session 2	**CSA-II**	**CSA-III**	**CSPB-IV**	**CBA/ CSPB-V**	**CSHS-II/ CPS-J2**	**CSA-IV**	**CPS-IV**	**CPS-V**	**CPS-VI**
3:15 - 3:30	O51	O57	O62	O67	O72	O77	O81	O88	O94
3:30 - 3:45	O52	O58	O63		O73	O78	O82	O89	O95
3:45 - 4:00	O53	O59	O64	O68	O74	O79	O83	O90	O96
4:00 - 4:15	O54	O60	O65	O69	O75	O80	O84	O91	O97
4:15 - 4:30	O55	O61	O66		O76		O85	O92	O98
4:30 - 4:45	O56			O70			O86	O93	O99
4:45 – 5:00				O71			O87		
5:00 – 7:00	**POSTER SESSION 1 (odd #s) in Hall D** sponsored by **Manitoba Crop Alliance**								
5:30 – 7:30	PC President's Reception in VIP Salon (invitation only)								
7:00 – 9:00	CPS President's Reception in MR 17				CSPB Mixer in Pan Am Room (members only)				
8:30 – 10:30	**ALL SOCIETY Student Social York 2-4**								

PROGRAM SCHEDULE OVERVIEW FOR TUESDAY JULY 9, 2024

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

Time	POSTER VIEWING and EXHIBITS in Hall D from 8:00 am – 7:00 pm									
8:00 – 8:30	**Coffee Break in Hall D** sponsored by **Saskatchewan Pulse Growers**									
Loading talks at 8am	**Plenary Session 2-Emerging Technologies to Enhance Production in a Changing Environment** *Chairs: Harpinder Randhawa and Andrew McKenzie-Gopsill* **Hall C East**									
8:30 – 9:20 **PS4**	**Dr. Matthew Reynolds, CIMMYT, Mexico** ***Crop Physiology, Genomics, and Cropping Systems***									
9:20 – 10:10 **PS5**	**Dr. Eric Patterson, Michigan State** ***Building weed genomic resources through international collaboration and exciting new discoveries from the genomics frontier***									
10:10-11:00 **PS6**	**Dr. Sara Martin, AAFC, Ottawa** ***Changing Environment, Changing Genes: Insights from Weed Genetics and Genomics***									
11:00-1:00	**LUNCH in Hall C West** sponsored by **CropLife Canada**									
11:15 – 1:00	**Workshop 4 (CSPB) Bioinformatics 101: First steps into 'omics' data**							**Millennium Suite**		
11:15 – 1:00	**Workshop 5 (CAPB) Brief overview of gene editing landscape in Canada**							**Presentation Theatre**		
11:15 – 1:00	**CBA Meeting – Teaching Section**							**Pan Am Room**		
11:45 – 1:00	**CropLife Symposia: Resistance Management**							**Hall C East**		
Rooms→	MR 1	MR 2	MR 3	MR 4	MR 7+8	MR 17	MR 11+12	MR 13	MR 15	MR 9+10
Loading talks will be inside corresponding rooms at 1:00-1:15 pm for CS3 and at 3:00-3:15 pm for CS4										
Concurrent Session 3	**CAPB/ CSPB-VI**	**CAPB/ CSPB-VII**	**CSPB-VIII**	**CPS-J4/ CAPB/ CSPB-IX**	**CSHS-III/CPS-J3**	**CBA-II**	**CSPB-X**	**CPS-VII**	**CSA-V**	**CPS-VIII**
1:15 - 1:30	O100	O105	O110	O114	O120	O126	O130	O134	O140	O145
1:30 - 1:45	O101	O106	O111	O115	O121	O127	O131	O135	O141	O146
1:45 - 2:00	O102	O107	O112	O116	O122	O128	O132	O136	O142	O147
2:00 - 2:15	O103	O108	O113	O117	O123	O129a	O133a	O137	O143	O148
2:15 - 2:30	O104	O109		O118	O124	O129b	0133b	O138	O144	O149
2:30 - 2:45				O119	O125	O129c		O139		
2:45 - 3:15	**Coffee Break in Meeting Room 5** sponsored by **AgQuest**									
Concurrent Session 4	**CSPB-XI**	**CSHS-IV**	**CSHS-V**	**CAPB/ CSPB-XII**	**CSA-VI**	**CPS-IX**	**CPS-X**	**CSPB-XIII**	**OPEN**	**CSPB-XIV Gene Editing**
3:15 - 3:30	O150	O154	O160	O166	O173	O177	O185	O189		O195
3:30 - 3:45	O151	O155	O161	O167	O174	O178	O186	O190		O196
3:45 - 4:00	O152	O156	O162	O168	O175	O179	O187	O191		O197
4:00 - 4:15	O153	O157	O165a	O169	O176a	O180	O188	O192		O198
4:15 - 4:30		O158	O165b	O170	O176b	O182		O193		O199
4:30 - 4:45		O159		O171		O183		O194		
5:00 – 7:00	**POSTER SESSION 2 (even #s) In Hall D** sponsored by **Hoskin Scientific/LI-COR**									
7:00 – 11:00	**CPS Awards Dinner in York 2-3**									

PROGRAM SCHEDULE OVERVIEW FOR WEDNESDAY JULY 10, 2024

8:00 am until 1:00pm Registration in the Carlton Concourse

Time	POSTER VIEWING and EXHIBITS in Hall D from 8:00 am – 11:00 am
8:00 – 8:30	**Coffee Break in Hall D** sponsored by **Alberta Grains**
Loading talks at 8am	**Plenary Session 3-Emerging Technologies in Plant Health** **Hall C East** *Chairs: Bourlaye Fofana (AAFC, Charlettetown)*
8:30 – 9:20 **PS7**	**Dr. Jan Leach, University Distinguished Professor, Colorado State University** ***Intergenic spaces: A new frontier to improving plant health***
9:20 – 10:10 **PS8**	**Dr. Martina Stromvik, McGill University** ***The Petota super-pangenome and potato wild relatives***
10:10 – 11:00 **PS9**	**Dr. Brent McCallum, AAFC Morden, MB** ***Combating a Dynamic Wheat Rust Population in Canada***
11:00 - 1:00	**LUNCH in Hall C West** / loading talks 1:00-1:30pm
1:00-4:00	Please take down Posters and Exhibits in Hall D
11:15 – 1:15	**CSHS Annual Business Meeting** **Pan Am Room**
11:15 – 1:30	**CSPB Annual Business Meeting** **Millennium Suite**
11:30 – 1:30	**CBA Annual General Meeting and Awards** **Room 2F**
11:30 – 1:00	**CSA Annual General Meeting and Awards** **Room 2E**
11:30 – 12:30	**CAPB Award Deliberations** **York 2-3**
12:30 – 1:30	**CAPB Student Presentation Awards** **York 2-3**
Loading talks at 1pm	**Plenary Session 4- Understanding and exploiting cell wall biosynthesis and signaling to promote sustainability** **Hall C East** *Chairs: Marcus Samuel and Hugo Zheng*
1:30- 2:20 **PS10**	**Dr. Lacey Samuels, University of British Columbia** ***Building plant biomass: secondary cell wall biosynthesis***
2:20 – 3:10 **PS11**	**Dr. Heather McFarlane, University of Toronto** ***Modifying the plant cell wall from the inside out***
3:10 – 3:40	**Coffee Break in Carlton Concourse** sponsored by **Dept of Biology, Univ of Winnipeg**
3:40 – 4:15 **PS12**	**C.D. Nelson Award talk - Dr. Guanqun Chen, University of Alberta** ***Producing Specialty Oil with Unusual Fatty Acids for Sustainable Growth in Agriculture and Fermentation***
4:15 - 4:45 **PS13**	**Carl Douglas Award talk - Dr. Mark Minow** ***The heritability of chromatin accessibility in Zea mays***
4:45 – 5:15	**AWARDS CEREMONY and CLOSING REMARKS** **Hall C East**
5:30 – 6:30	**Plant Canada Incoming Board** **President's Boardroom**
6:00 – 11:00	**ALL SOCIETY FINAL COCKTAIL RECEPTION & BANQUET - FEATURING CHRIS FUNK York 1**

PROGRAM SCHEDULE OVERVIEW FOR THURSDAY JULY 11, 2024

8:30 – 11:00 **CPS Incoming Board meeting in MR 17**

Dr. Sylvain Charlebois

Keynote Speaker

"Cultivating Tomorrow: Agri-Food Trends in Canada"

Sunday, July 7 @ 5:45 pm
York 1

Join **Dr. Sylvain Charlebois, Director of the Agri-Food Analytics Lab at Dalhousie University**, as he delves into the dynamic landscape of the Canadian food industry. From farmgate innovations to dining tables across the nation, Dr. Charlebois will address the most significant challenges faced by food sector players in their quest to feed the world.

This thought-provoking keynote will explore sustainability not just as a buzzword, but through concrete case studies that highlight its practical applications. Dr. Charlebois will also discuss the intricacies of the supply chain, providing participants with a deeper understanding of current opportunities and challenges in the food sector. Topics will include the state of GM crops, vertical agriculture, climate change, and more. This engaging session promises valuable insights for anyone involved in or interested in the future of food.

Bio: *Dr. Sylvain Charlebois is a professor in food distribution and policy in the Faculty of Management at Dalhousie University in Halifax. He is also the Senior Director of the Agri-food Analytics Lab, also located at Dalhousie University. Known as "The Food Professor", his current research interest lies in the broad area of food distribution, security and safety. He is one of the world's most cited scholars in food supply chain management, food value chains and traceability. He co-hosts The Food Professor podcast, discussing issues in the food, foodservice, grocery and restaurant industries and which is the most listened Canadian management podcast in Canada. Every year since 2012, he has published the now highly anticipated Canadian Food Price Report, which provides an overview of food price trends for the coming year. Furthermore, his research has been featured in several newspapers and media groups, nationally as well as internationally. He has testified on several occasions before parliamentary committees on food policy-related issues as an expert witness. He has been asked to act as an advisor on food and agricultural policies in many Canadian provinces and other countries.*

SCHEDULE OF PLENARY SPEAKERS

Time	Monday July 8th	Tuesday July 9th	Wednesday July 10th
Place	**Hall C East**	**Hall C East**	**Hall C East**
8:00 am	Coffee break in Hall D	Coffee break in Hall D	Coffee break in Hall D
Session	**#1 Plant Biotechnology for a Changing World**	**#2 Emerging Technologies to Enhance Production in a Changing Environment**	**#3 Emerging Technologies in Plant Health**
Chair(s)	Dr. Dominique Michaud	Dr. Harpinder Randhawa and Dr. Andrew McKenzie-Gopsill	Dr. Bourlaye Fofana
8:30 am	**Dr. Louis-Philippe Hamel** Medicago Inc. *Understanding plant molecular responses to the production of enveloped VLPs leads to the improvement of a molecular farming expression platform*	**Dr. Matthew Reynolds** CIMMYT, Mexico *Crop Physiology, Genomics and Cropping Systems*	**Dr. Jan Leach** University of Alberta, AB *Intergenic spaces: A new frontier to improving plant health*
9:20 am	**Dr. Dan Voytas** University of Minnesota, MN *Overcoming Bottlenecks in Plant Gene Editing*	**Dr. Eric Patterson** Michigan State University, MI *Building weed genomics resources through international collaboration and exciting new discoveries from the genomics frontier*	**Dr. Martina Strömvik** McGill University, QC *The Petota super-pangenome and potato wild relatives*
10:10 am	**Dr. Nicola Patron** University of Cambridge, UK *Synthetic biology for metabolic pathway engineering in photosynthetic organisms*	**Dr. Sara Martin** AAFC Ottawa, ON *Changing Environment, Changing Genes: Insights from Weed Genetics and Genomics*	**Dr. Brent McCallum** AAFC Morden, MB *Combating a Dynamic Wheat Rust Population in Canada*
11 am	Lunch in Hall C West	Lunch in Hall C West	Lunch in Hall C West
Session			**#4 Understanding and Exploiting Cell Wall Biosynthesis**
Chair(s)			Dr. Marcus Samuel and Dr. Hugo Zheng
1:30 pm			**Dr. Lacey Samuels** University of British Columbia, BC *Building plant biomass: secondary cell wall biosynthesis*
2:20 pm			**Dr. Heather McFarlane** University of Toronto, ON *Modifying the plant cell wall from the inside out*
3:10 pm			Coffee break in Carlton Concourse
3:40 pm			**Dr. Guanqun (Gavin) Chen** University of Alberta ***C.D. Nelson Award talk**:* *Producing Specialty Oil with Unusual Fatty Acids for Sustainable Growth in Agriculture and Fermentation*
4:15 pm			**Dr. Mark Minow** University of Georgia, GA ***Carl Douglas Award talk:*** *The heritability of chromatin accessibility in Zea mays*

PLENARY SPEAKERS

Dr. Guanqun (Gavin) Chen University of Alberta	PS12	Producing Specialty Oil with Unusual Fatty Acids for Sustainable Growth in Agriculture and Fermentation
Dr. Louis-Philippe Hamel Medicago Inc.	PS1	Understanding plant molecular responses to the production of enveloped VLPs leads to the improvement of a molecular farming expression platform
Dr. Jan Leach University of Alberta	PS7	Intergenic spaces: A new frontier to improving plant health
Dr. Sara Martin AAFC Ottawa	PS6	Changing Environment, Changing Genes: Insights from Weed Genetics and Genomics
Dr. Brent McCallum AAFC Morden	PS9	Combating a Dynamic Wheat Rust Population in Canada
Dr. Heather McFarlane University of Toronto	PS11	Modifying the plant cell wall from the inside out
Dr. Mark Minow University of Georgia	PS13	The heritability of chromatin accessibility in Zea mays
Dr. Nicola Patron University of Cambridge	PS3	Synthetic biology for metabolic pathway engineering in photosynthetic organisms
Dr. Eric Patterson Michigan State University	PS5	Building weed genomics resources through international collaboration and exciting new discoveries from the genomics frontier
Dr. Matthew Reynolds CIMMYT	PS4	Crop Physiology, genomics and cropping systems
Dr. Lacey Samuels University of British Columbia	PS10	Building plant biomass: secondary cell wall biosynthesis
Dr. Martina Strömvik McGill University	PS8	The Petota super-pangenome and potato wild relatives
Dr. Dan Voytas University of Minnesota	PS2	Overcoming Bottlenecks in Plant Gene Editing

Monday, July 8

Dr. Louis-Philippe Hamel

"Understanding plant molecular responses to the production of enveloped VLPs leads to the improvement of a molecular farming expression platform"

Abstract: In plants, the production of COVID-19 vaccines can be achieved via transient expression of the Spike (S) protein from Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). Relying on bacterial vector *Agrobacterium tumefaciens*, this process is favored by co-expression of silencing suppressor P19. During expression, the S protein is produced and matured through the secretory pathway of plant cells, before being trafficked to the plasma membrane where it induces formation of coronavirus-like particles (CoVLPs). Using time course sampling, we characterized molecular responses of *Nicotiana benthamiana* leaf cells expressing P19 only, or co-expressing P19 and a recombinant S protein. This revealed expression of the latter to trigger early but transient activation of the unfolded protein response, in addition to distinct waves of transcription factor genes involved in immunity. Accordingly, defense genes were induced with different kinetics, including those promoting oxidative stress and cell wall lignification. Crosstalk between stress hormone pathways was also denoted, including rapid repression of jasmonic acid biosynthesis genes after agroinfiltration, and later dampening of salicylic acid responses upon S protein accumulation. Further analysis of the data revealed CoVLP production to induce leaf senescence, as revealed by up-regulation of transcription factor and senescence-associated genes, accumulation of the senescence-specific protease SAG12, and concomitant down-regulation of genes involved in photosynthesis and nitrogen assimilation. In a molecular farming context, these combined responses were hypothesized to restrain foreign protein accumulation and strategies were thus developed to improve molecular farming efficacy. This includes the co-expression of helper proteins that reduce stress symptoms or that improve yields *in planta*.

Bio: *Dr. Louis-Philippe Hamel is an expert of the plant innate immune system with a unique expertise in the biopharmaceutical industry and in the field of plant molecular farming. Formerly employed by Medicago, his most recent work aims at understanding plant's responses to* Agrobacterium*-mediated expression of recombinant proteins in plants, including for the production of plant-made vaccines and antibodies. In addition to these fundamental aspects, his research focuses on the development of genetic and non-genetic approaches to improve plant molecular farming practices. During his Ph.D and as a postdoc fellow at the University of Sherbrooke and at Harvard University, Dr. Hamel worked on intracellular signaling pathways that lead to the activation of plant defense, including downstream of resistance proteins and mitogen-activated protein kinase cascades. His work highlighted several defense activation routes, including through the degradation of defense repressors that inhibit resistance mechanisms in the absence of stress.*

Monday, July 8

Dr. Nicola Patron

University of Cambridge

"Synthetic biology for metabolic pathway engineering in photosynthetic organisms"

Abstract: Over the past decade, synthetic biology has significantly advanced the reconstruction of biosynthetic pathways for high-value natural products in "chassis" organisms. In our lab, we integrate genomics, metabolomics, and bioactivity assays to identify the molecules responsible for the bioactivities of medicinal plants and to elucidate the genetic basis of these natural products. This comprehensive approach enables us to understand the mechanisms of metabolic diversification and to explore innovative methods for biomanufacturing. Additionally, we develop plants as photosynthetic biomanufacturing platforms, engineering synthetic circuits and tailoring plant genomes to optimize yield.

Bio: *Nicola Patron is an Associate Professor in Plant Synthetic at the University of Cambridge, UK. Nicola has a PhD in plant molecular biology and pursued postdoctoral research at The John Innes Centre and The University of British Columbia. In 2015, she was identified as an emerging leader in synthetic biology and awarded a SynBioLEAP fellowship. She started her research group at the Earlham Institute in 2016 to apply engineering approaches to plant biology. Her group relocated to Cambridge in February 2024 and is focused on understanding how phenotypes emerge from network functions and exploring and utilising metabolic diversity.*

Monday, July 8

Dr. Dan Voytas

University of Minnesota

"Overcoming Bottlenecks in Plant Gene Editing"

Abstract: Plant gene editing is usually carried out by delivering reagents such as Cas9 and sgRNAs to explants in culture. Edited cells are then induced to differentiate into whole plants by exposure to various hormones. Creating edited plants through tissue culture is often inefficient, requires considerable time, only works with limited species and genotypes and causes unintended changes to the genome and epigenome. We have been pursuing alternative approaches for plant gene editing that minimize or obviate the need for tissue culture. In one approach, we generate gene edited dicotyledonous plants through *de novo* meristem induction. Developmental regulators and gene editing reagents are delivered to somatic cells on whole plants. Meristems are induced that produce shoots with targeted DNA modifications, and gene edits are transmitted to the next generation. In a second approach, we use RNA viruses to deliver sgRNAs through infection to transgenic plants that express Cas9. The sgRNAs are augmented with sequences that promote cell-to-cell mobility and movement into the meristem. Gene edited shoots are thus generated that transmit gene edits to the next generation. Because both approaches minimize the need for tissue culture, they promise to help overcome this bottleneck in plant gene-editing.

Bio: *Dr. Dan Voytas is a Professor in the Department of Genetics, Cell Biology and Development and the Director of the Center for Precision Plant Genomics at the University of Minnesota. Dr. Voytas graduated from Harvard College in 1984 and received his Ph.D. from Harvard Medical School in 1990. He conducted postdoctoral research at Johns Hopkins University School of Medicine. Prior to joining the University of Minnesota in 2008, Dr. Voytas was a professor at Iowa State University. Dr. Voytas' research focuses on developing methods to edit plant genomes. Dr. Voytas' lab is currently optimizing methods for efficiently making targeted genome modifications in a variety of plant species to advance basic biology and develop new crop varieties. In addition to his position at the University of Minnesota, Dr. Voytas co-founded Calyxt, an agricultural biotechnology company that used gene editing for crop improvement. In 2019, Dr. Voytas was elected to the National Academy of Sciences.*

Tuesday, July 9

Dr. Matthew Reynolds

CIMMYT

"Crop Physiology, genomics and cropping systems"

Abstract: Spring wheat breeding at CIMMYT continues to underpin food security in the Global South, especially by avoiding disease epidemics while increasing profit margins through steady genetic gains ~1%p.a. Modern tools like genomic selection combined with speed breeding function best with restricted gene-pools. However, analysis of historical international nursery big-data sets show a significant trend for reduced wide-adaptation under warmer temperatures. This has two major implications: 1) Centralized breeding with restricted gene-pools, while highly cost-effective for relatively-simply inherited strategic traits (having global or regional impact), will boost yields at fewer sites due to restricted genetic backgrounds of advanced lines; 2) Breeding will require access to wider genetic diversity to cater for a more diverse set of target environments. This will require refining genetically complex-trait expression. To achieve this, the IWYP-HeDWIC translational research Hub at CIMMYT, identifies novel genetic variation for key performance traits, including from exotic material, like amphiploids encompassing entire genomes of wild relatives. (The latter have evolved through millions of years of environmental flux while our crops were isolated from those gene-pools upon domestication.) The Hubs test combinations of promising traits and alleles through crossing and evaluating best progeny internationally as physiological pre-breeding (PPB) nurseries. While on average PPB lines track yield gains of elite breeding lines globally, at the site and cluster level, specific PPB lines express outstanding yield over checks. This suggests that wide genetic variation within PPB nurseries may be providing a range of favorable trait/allele combinations that will help adapt to new and generally harsher environmental norms.

Bio: *Matthew Reynolds (m.reynolds@cgiar.org) leads Wheat Physiology at CIMMYT, developing breeding technologies for climate resilience and yield improvement. He has fostered global collaborations to tap expertise and emerging technologies in basic plant sciences for translation to breeding. Networks initiated include the International Wheat Yield Partnership* ***https://iwyp.org/****, and the Heat and Drought Wheat Improvement Consortium* ***https://hedwic.org/-*** *, whose products provide breeders globally with unique pre-breeding material with new combinations of complex physiological traits and their haplotypes. He has published widely in crop physiology, genomics and pre-breeding and since 2018 is listed among top 1% of world's researchers in plant & animal science (Web of Science). He was recently invited to compile as wheat textbook as editor, which was published open access in 2022* ***https://link.springer.com/book/10.1007/978-3-030-90673-3****. He co-supervises PhD thesis projects through his links with universities worldwide and has developed physiological manuals for use by national programs which have been translated into several languages.*

Tuesday, July 9

Dr. Eric Patterson

Michigan State University

"Building weed genomics resources through international collaboration and exciting new discoveries from the genomics frontier"

Abstract: The classic dogma of herbicide resistance evolution stats that random genetic variation in wild weed populations contains initially rare resistance alleles that then increase in time with herbicide selection pressure. A fundamental question then becomes, where does genetic variation come from? One source of variation is random small polymorphisms that occur during DNA replication. Classic target site mechanisms from SNPs most likely start this way; however, thanks the advent of cheap, third generation sequencing and chromosome level genome assemblies, we are discovering that genomic rearrangements are also frequently sources of herbicide resistance traits. This phenomenon is most obvious in the case of glyphosate, where at least 8 species have developed some sort of target site copy number variation. Each species evolves glyphosate resistance independently and utilizes different rearrangement mechanisms, but the end result is the same. Recently, target site copy number variation was also cited as providing glufosinate resistance in Amaranthus palmeri and ACCase resistance in Digitaria sanguinalis. In separate, extraordinary case of genomic rearrangements, a transposable element inserted into an intron and changed splicing of a target site. These discoveries are only the beginning of the insights that weed genomes have to offer.

Bio: *Eric Patterson is an Assistant Professor in Weed Science in the Department of Plant, Soil, and Microbial Sciences at Michigan State University where he teaches weed science to Undergraduate and Graduates. His research focuses on more basic aspects of weed science including weed genomics, molecular biology of resistance mechanisms, rapid molecular weed diagnostics, and herbicide mode of action discovery. His lab is especially interested in how genome rearrangements (i.e. transposable elements and copy number variation) form and are utilized as novel sources of genetic variation for weed adaptation to abiotic stresses.*

Tuesday, July 9

Dr. Sara Martin

Agriculture and Agri-Food Canada

"Changing Environment, Changing Genes: Insights from Weed Genetics and Genomics"

Abstract: We are privileged to be living through this era of biology. Our ability to sequence genomes is tantamount to a superpower that allows us to reconstruct an organism's evolutionary history, and even to observe as it continues to evolve. This was very publicly illustrated during the COVID-19 pandemic when evolutionary questions such as "where did the virus originate? what do these mutations in a genomes mean?" were of intense public interest. Our ability to rapidly sequence genomes meant that scientists were able to answer the first question, and the massive amount of data collected will help us answer the second. The genomic data clearly showed the diversity of SARS-CoV-2 variant changing in response to inadvertent selection stemming from changes in human behavior, such as the rollout of vaccines and anti-viral treatments. What we see resulting from these kinds of treatments generally, however, is growing resistance to chemical control in bacteria, fungi, arthropods and plant species. Compared to the acute challenge of the SARS-CoV-2 virus, these are chronic challenges that receive less attention, but that are likely to be more costly in the long term. For example, estimates have suggested that a loss of chemical controls could halve agricultural production. While weed genomics doesn't yet have the epistemic foundation that virologists can rely on, we are building this foundation quickly. Sequencing genomes allows us to help address the chronic challenge of herbicide resistance by improving our ability to: detect target site mutations; determine the genetic basis of non-target site mutations; and predict future evolution by understanding past evolution and current connections among populations. These genomes will provide the foundational data for new tools that will allow us to understand the consequences of mutations and of key genetic pathways that could be disrupted by new chemical controls. Plant genome sequences are the key to making progress in the face of the chronic challenge of herbicide resistance, just as the sequencing of the SARS-CoV-2 genome was key to overcoming the pandemic.

Bio: *Dr. Sara L. Martin is a research scientist at Agriculture and Agri-Food Canada's Ottawa Research and Development Centre. She holds a B.Sc in Botany from the University of Toronto and a Ph.D. in Integrated Biology from the University of Guelph. Her research program's mandate is to develop our understanding of how gene flow between crop and wild species could lead to transgene escape, with a secondary focus on the evolution and spread of herbicide resistance in weeds. As a result, her work ranges from field work to document the current geographic range of species, to greenhouse work creating hybrids, to the assembly, analysis and use of plant genomes. Her work has investigated kochia, fleabane, ragweed, wild mustard, cleavers, and the wild relatives of Camelina.*

Wednesday, July 10

Dr. Jan Leach

Colorado State University

"Intergenic spaces: A new frontier to improving plant health"

Abstract: Adaptation of plants to both biotic and abiotic stresses involve changes in expression patterns of genes in diverse defense and tolerance pathways. These expression changes are controlled by short sequences in promoter regions known as cis-regulatory elements (CRE) or combinations of CRE organized as modules (called cis-regulatory modules or CRM). Conserved CRE/CRMs are shared among stress response genes, and genetic polymorphisms in CRE/CRMs significantly impact gene expression. We have shown the presence of shared sets of CRMs in promoters of genes conferring broad-spectrum disease resistance (BSDR) to multiple diseases in rice. In addition, conserved CRE and CRM are common to genes co-activated in plants with enhanced tolerance to different types of stresses, such as thermotolerance and disease. We propose a strategy to simultaneously increase heat and disease tolerance in crop plants through the development of breeding markers that are based on conserved CRE/CRMs associated with functional candidate genes. Our goal is to enable genome-wide selection of complex traits with a reduced number of markers, allowing for efficient, critical solutions to enhance sustainable food production for a growing global population.

Bio: *Jan Leach is a molecular plant pathologist who studies the basis of plant disease susceptibility and resistance and how these responses are influenced by interactions within the phytobiome. She is a University Distinguished Professor in the Department of Agricultural Biology at Colorado State University. Leach is the Immediate Past President of the International Society of Plant Pathology and is a Fellow and a past President of the American Phytopathological Society (APS). Leach was elected to the US National Academy of Sciences in 2021.*

Wednesday, July 10

Dr. Martina Strömvik

McGill University

"The Petota super-pangenome and potato wild relatives"

Abstract: Potato wild relatives are a source of genetic diversity for improving traits in modern cultivars to meet climate challenges. There are over 100 species the *Solanum* section *Petota*, with ploidy ranging from diploid to hexaploid. A *Petota* super pan-genome was constructed using 296 accessions including both diploid and polyploid cultivars, clones, landraces and wild relatives representing a total of 60 species. The phylogeny based on presence/absence variation within the super pan-genome shows clade-specific core genes, and the impact of transposable element in potato evolution. As a tool to help understand cold adapted potato species, an allotetraploid wild potato species was sequenced and compared with a common autotetraploid cultivar that is not cold climate adapted. The allotetraploid *Solanum acaule* Bitter has long been used to introgress cold tolerance into potato breeding germplasm. The present study includes the sequenced and phased subgenomes of *Solanum acaule* placed in a phylogenetic context with other potato wild relatives.

Bio: *Dr. Strömvik leads a bioinformatics research program focusing on complex polyploid genomes of plants (e.g. arctic and temperate* Oxytropis *sp., and potato wild relatives). She completed a Ph.D. in Crop Sciences (plant molecular genetics of soybean) at University of Illinois at Urbana-Champaign (USA), and a B.A. in Theoretical Philosophy as well as a M.Sc. in Biology (tissue culture and transformation in* Picea abies*) at Stockholm University (Sweden). She carried out postdoctoral studies in Bioinformatics and Computational Genomics at University of Minnesota, Minneapolis (USA) working on genomics projects in soybean,* Medicago truncatula *and loblolly pine. In 2003 she joined McGill's Department of Plant Science where she pioneered the development of university-wide graduate bioinformatics programs and courses. She serves on national and international grant panels, as Associate Editor for several journals, and as Chair of the Department of Plant Science since 2015.*

Wednesday, July 10

Dr. Brent McCallum

Agriculture and Agri-Food Canada

"Combating a dynamic wheat rust population in Canada"

Abstract: Wheat is the largest crop in Canada. Wheat leaf rust, caused by *Puccinia triticina* Eriks., is one of the most common and destructive diseases of wheat. The population of *P. triticina* primarily arrives each year from the United States, carried by wind currents. Due to the absence of the alternate host in North America, which eliminates sexual recombination, the *P. triticina* population is characterized by clonally reproducing groups that diversify through step-wise mutations. All members of each group have the same mating type alleles and are similar in their genomes and virulence spectra. Two clonal groups are dominant and comprise the majority of the population in Canada, while many other smaller groups contribute to diversity. Each growing area in Canada has different compositions of these groups, which changes annually. To combat this dynamic population genetic resistance has been effectively deployed in the wheat cultivars grown in Canada. The common resistance genes in Canadian wheat in order of frequency are *Lr2a*, *Lr34*, *Lr21*, *Lr16*, *Lr46*, and *Lr14a*. Since 2013 *Lr2a*, *Lr21* and *Lr34* were all deployed in over 50% of the seeded area for the largest wheat class Canadian Western Red Spring. Of these *Lr34* has had the biggest impact because of its ability to combine additively with other leaf rust resistance genes and its multi-pest resistance that contributes to resistance to other wheat diseases such as stem rust, stripe rust, and Fusarium head blight. *Lr34* also produces leaf tip necrosis, primarily on flag leaves at normal growing temperatures. This necrosis and leaf rust resistance can be observed on seedling plants when they are grown at cold temperatures (8ºC to 10ºC). Both *Lr46* and *Lr67* have also been shown to act similarly to *Lr34*, in conditioning multi-pest resistance and combining additively with other resistance genes. While *Lr46* is in some Canadian wheat cultivars, *Lr67* has not been deployed to date. Modern Canadian bread wheat cultivars often have combinations of many resistance genes, such as those found in Carberry (*Lr2a*, *Lr13*, *Lr16*, *Lr23*, *Lr34*, *Lr46*), which act together to impart the high levels of durable resistance that characterize these cultivars.

Bio: *Dr. Brent McCallum is a research scientist with Agriculture and Agri-Food Canada working at the Morden Research and Development Centre in Morden Manitoba. He received his Ph.D in Plant Pathology from the University of Minnesota in 1995 and started working at AAFC in 1996. His research focus is on wheat leaf rust disease in Canada. He conducts an annual national virulence survey in Canada to track changes in the pathogen population that could affect the wheat crop in Canada. He is involved in identifying and developing sources of resistance to use in future wheat cultivars and to understand the genetics of disease resistance. This includes mapping and marker development for genes of interest, host-parasite interactions, and understanding interactions between resistance genes. He is also involved in research projects on the causal rust,* Puccinia triticina*, to understand its pathogenesis, diversity and evolution.*

Wednesday, July 10

Dr. Lacey Samuels

University of British Columbia

"Building plant biomass: secondary cell wall biosynthesis"

Abstract: The bulk of the plant biomass is made up of secondary cell wall materials, including cellulose, hemicelluloses, and lignin. With our changing climate and requirement to reduced dependence on fossil fuels, renewable biopolymers of plant secondary cell walls represent a promising source of bioproducts and biofuels. Using a combination of molecular genetics and advanced biological imaging, we can manipulate the cellular and molecular machinery responsible for producing secondary cell wall components. Beyond considering each component individually, understanding how different components can influence each other's biosynthesis provides new insights into the coordination of secondary cell wall biosynthesis. For example, cellulose production is sensitive to changes in the surrounding hemicelluloses (glucuronoxylan). After polysaccharide deposition, the secondary cell wall is lignified when monolignol precursors are exported to the cell wall where laccases and peroxidases produce monolignol radicals that polymerize with radical coupling. Our understanding of the lignification process is changing from active transport of monolignols by unknown xylem cells, to a coordinated activity in which monolignols diffuse from defined cell populations during xylem development. Diffusion is driven down a concentration gradient, when monolignols are consumed by laccases and peroxidases in the cell wall. Within secondary cell walls, regions like cell corners and middle lamella have unique chemistries and functions, as well as distinct subsets of laccases and peroxidases. Knocking out these combinations of laccases and peroxidases changes lignification patterns. In addition to advancing basic biology, defining these cell populations and oxidative enzymes that contribute to lignification opens new opportunities for lignin manipulation.

Bio: *Professor Samuels has a B.Sc. in Neurobiology from McGill University in Montreal, and a Ph.D. in Botany, from the University of British Columbia in Vancouver, BC., Canada. She did post-doctoral studies at the University of Colorado, Boulder, USA and at UBC Vancouver, where she has been a faculty member since 2000. Professor Samuels initiated the UBC node of the graduate teaching training network called the Centre for the Integration of Research, Learning, and Teaching (CIRTL). She is Academic Director of the Bioimaging Facility, a campus-wide light and electron microscopy shared research facility, and a member of the UBC Bioproducts Institute. The goal of Samuels' research is to integrate plant cell biology and biochemistry to discover how plant cells produce valuable renewable resources.*

Wednesday, July 10

Dr. Heather McFarlane

University of Toronto

"Modifying the plant cell wall from the inside out"

Abstract: The plant cell wall is a polysaccharide-based extracellular matrix that surrounds and protects all plant cells. Since plants are constantly growing and developing within the confines of their cell walls, plant cells must be in constant communication with their cell walls. Furthermore, cell walls are a critical line of defense between plant cells and their environment; changes to the cell wall are often early warning signs of pathogen attack or abiotic stress, and plants fortify their cell walls in response to these stresses. This ongoing communication between the plant cells and their cell walls is collectively called "cell wall signaling". Attempts to modify plant cell walls for improved materials or biofuels have exposed a critical gap in our understanding: inadvertent activation of cell wall signaling typically cause yield penalties that render these cell wall "improvements" agriculturally/economically unviable. The McFarlane Lab at The University of Toronto studies the molecular mechanisms of cell wall signaling and responses, including cell wall secretion and remodeling. Using a combination of live cell imaging, high-resolution electron microscopy, genetics, proteomics, and biochemistry, we have recently uncovered new molecular components of cell wall signaling and provided insights into what types of modifications the plant cell wall can tolerate without triggering yield losses.

Bio: *Dr. Heather E. McFarlane is an Assistant Professor and Canada Research Chair in Plant Cell Biology in the Department of Cell & Systems Biology at the University of Toronto. She earned her PhD at the University of British Columbia (Canada) where she studied the transport of lipids that form the protective plant cuticle. After her PhD, she joined the Max Planck Institute for Molecular Plant Physiology (Germany) to study cell wall synthesis as an EMBO postdoctoral fellow. She then moved to University of Melbourne (Australia) where she was awarded an Australian Research Council Discovery Early Career Researcher Award to initiate her work on cell wall signaling. Heather joined the Department of Cell and Systems Biology at the University of Toronto July 2019. The McFarlane Lab studies cell wall synthesis, secretion, signaling, and remodeling with a view to improving plant biomass for food, materials, and energy.*

Wednesday, July 10

Dr. Guanqun (Gavin) Chen

University of Alberta

"Acids for sustainable growth in agriculture and fermentation"

Abstract: Some plant and microalgae species can produce high levels of unusual fatty acids (UFAs), which are valuable in the food, feed, and oleochemical industries. Understanding the mechanisms of their biosynthesis and regulation, as well as developing novel genetic engineering strategies to increase their production, is an exciting area of research in lipid biotechnology. This presentation will cover our work on the biochemical characterization of proteins associated with several UFAs in plants and their production through biotechnology. The UFAs we will discuss include long-chain n-3 polyunsaturated fatty acids, hydroxyl fatty acids, and conjugated fatty acids, with punicic acid as a representative example.

Punicic acid is primarily sourced from pomegranate seed oil, but its productivity is very low. Therefore, it is attractive to establish its production in engineered oilseed crops and yeasts. By expressing cDNAs encoding pomegranate fatty acid conjugase and Δ12 desaturase, we achieved the accumulation of 11% of total fatty acids as punicic acid in canola seeds. In *Saccharomyces cerevisiae*, we created recombinant libraries by directly shuffling candidate genes within its genome using Ty retrotransposon-targeted random gene integration. Subsequent library screening and bioprocess development identified a recombinant strain that accumulated 26.7% of total fatty acids as punicic acid. We also engineered an oleaginous yeast strain, *Rhodosporidium toruloides*, which accumulated 12% of its total fatty acids as punicic acid with glucose as the carbon source and 6.4% with wood hydrolysate as the feedstock.

The presentation will conclude with a general discussion of the challenges and future perspectives in this research field.

Bio: *Dr. Guanqun (Gavin) Chen is an Associate Professor and Canada Research Chair in Plant Lipid Biotechnology in the Department of Agricultural, Food, and Nutritional Science at the University of Alberta, Canada. His research interests include expanding our understanding of storage lipid biosynthesis and developing biotechnological approaches to enhance oil yield and quality in both plants and microorganisms. This knowledge platform will further enable him to redesign lipid biosynthesis in these organisms, producing unusual fatty acids for applications in food, nutraceuticals, and industrial settings.*

Wednesday, July 10

Dr. Mark Allan Alexander Minow

University of Georgia

"The heritability of chromatin accessibility in Zea mays"

Abstract: Transcription factors bind specific DNA sequences, known as cis-regulatory elements, to regulate the transcription of nearby genes. In eukaryotic genomes, the accessibility of these cis-regulatory elements is controlled by the chromatin environment, with accessible, nucleosome-free DNA needed for most transcription factor binding. Cis-regulatory element accessibility changes precede transcriptional ones, and differentially tune gene expression in diverse cell-types. Single-cell Assay for Transposase Accessible Chromatin sequencing (scATAC-seq) measures chromatin accessibility at a cell-type resolved level. Here, we applied scATAC-seq to 172 diverse maize inbred genotypes to discover how genetic diversity influences chromatin accessibility, and thus transcriptional regulation, in seedling cell types. Using this panel, we uncovered varying conservation of chromatin accessibility, while finding genetic variants that associate with altered local chromatin accessibility, revealing cell type level chromatin accessibility quantitative trait loci (caQTL). These caQTL encompass known and novel variants, and evidence suggests these variants modify transcription factor binding which then impacts local chromatin states. Bulk ATAC-seq was also conducted on maize F1-parent pairs to learn more about the heritability of chromatin accessibility. Calculating narrow sense heritability for chromatin accessibility revealed good concordance between high heritability at a region and caQTL detection in our panel. Heritability was high for most accessible chromatin regions but was higher in promoters or intergenic regions than accessible genic regions. Finally, we exploited our parent-offspring pairs to find accessible chromatin regions that had the hallmarks of trans regulation – these candidate regions can be combined with our diversity panel to empower the detection of trans caQTL, potentially discovering new regulatory relationships within the maize genome.

Bio: *Dr. Mark Allan Alexander Minow received his PhD in plant molecular biology and genetics in the department of Molecular and Cellular Biology at the University of Guelph in 2020 for his study of plant small RNA biology and the regulation of the maize floral transition. He is currently a Postdoctoral Research Associate at the University of Georgia under the supervision of Dr. Robert Schmitz, exploring maize biology through molecular genetics and single-cell genomics. An avid plant lover, when not in the lab, Dr. Minow is usually found landscaping his 2.5-acre property, nestled in the abandoned cotton terraces of rural North Georgia.*

WORKSHOPS IN PLANT CANADA 2024

Plant Canada 2024 brings an exciting program of workshops led by both professional and academic scientists.

These are open to all registered attendees of Plant Canada 2024 and are free with no reservations required – only exception is W2 with a fee and limited attendance.

The times and locations for each Workshop are provided below.

#	Date	Time	Location	Title
W1	Sunday, July 7	12:00-2:00 pm	Meeting Room 17	**Survival in the jungle of scholarly publishing: Building authorship and peer review skills**
W2	Sunday, July 7	2:30-4:30 pm	Meeting Room 17	**R for biovigilance of phytopathogens based on metabarcoding approach**
W3	Monday, July 8	11:15-1:00 pm	Millennium Suite	**Developing a community of practice for plant biology teaching**
W4	Tuesday, July 9	11:15-1:00 pm	Millennium Suite	**Bioinformatics 101: Your first steps into the world of 'omics' data analysis**
W5	Tuesday, July 9	11:15-1:00 pm	Presentation Theatre	**A brief overview of the gene editing landscape in Canada**

WORKSHOP #1

Survival in the jungle of scholarly publishing: Building authorship and peer review skills
July 7, 2024, from 12:00-2:00 pm in Meeting Room 17

The world of publication may look like a jungle for graduate students. Join Botany Co-Editors-in-Chief Dr. Liette Vasseur and Dr. Shelley Hepworth and journal staff for an interactive workshop designed to demystify the world of scholarly publishing. From selecting the right journal to preparing your submission, learn how to set up your manuscript for success. We will walk you through the peer review process and give tips for handling a variety of different situations, whether you are encountering them as an author or a peer reviewer. We will discuss Open Science, equity and inclusion in publishing, and other topics of interest. This workshop will include breakout activities for an opportunity to participate in hands-on exercises and receive real-time feedback from journal editors and staff. Join us and learn how to map your path to success in publishing your research.

WORKSHOP #2

R for biovigilance of phytopathogens based on metabarcoding approach
July 7, 2024, from 2:30-4:30 pm in Meeting Room 17

Metabarcoding combines DNA barcoding with high-throughput sequencing (HTS) technologies for rapid and high-throughput identification of multiple species from environmental samples, offering a powerful tool for biodiversity studies and ecosystem monitoring. It has transformed our ability to profile complex microbial communities and track plant pathogens in various environments.

This workshop will provide hands-on experience in metabarcoding-based community analysis using R, a versatile programming language and environment for statistical computing and graphics. You will learn about various R packages and tools that are essential for community data analysis, enabling you to effectively analyze and interpret metabarcoding data.

This workshop is designed to demonstrate how you may use metabarcoding for plant pathogen monitoring and tracking. This is crucial for early detection and management of plant diseases and for agriculture and biodiversity conservation. We will explore case studies and practical applications, highlighting how metabarcoding, combined with R analysis, becomes a potential diagnostic tool for Biovigilance of phytopathogens.

WORKSHOP #3

Developing a community of practice for plant biology teaching
July 8, 2024, from 11:15 am-1:00 pm in the Millennium Suite

Join us to discuss the ins and outs, ups and downs, and tips and tricks for teaching plant biology. You'll leave the session with new ideas for your teaching and new resources and connections to help make your ideas a reality. Beyond that, you'll be part of a team laying the groundwork and planting the seeds for an online community of like-minded colleagues across the country who believe in plant education and supporting the people who teach it. Participants of all career and experience levels are welcome! **No registration required for conference attendees!** https://cspb-scbv.ca/Education-Committee-Events

WORKSHOP #4

Bioinformatics 101: Your first steps into the world of 'omics' data analysis
July 9, 2024, from 11:15 am–1:00 pm in the Millennium Suite

Join us to discuss the basic bioinformatics skills researchers need to begin working in 'omics'. The workshop will come in two parts. In the first, we will provide a hands-on training that showcases basic command-line coding that will illustrate the power of BASH for data handling and processing of immensely large omics datasets. In the second part we will discuss RNA-seq, the various steps involved and considerations when setting up your first RNA-seq experiment. Ultimately, this workshop is intended to be a first introduction to bioinformatics and as a forum to ask any questions you may have if you intend to have bioinformatics as part of your future research. For Mac/Linux users, you are ready to start command-line tomorrow! For PC/Windows users, consider downloading 'MobaXterm' before attendance so that you are ready for working in a Unix environment (https://mobaxterm.mobatek.net/)!

WORKSHOP #5

A brief overview of the gene editing landscape in Canada
July 9, 2024, from 11:15 am–1:00 pm in the Presentation Theatre

Moderator: Dominique Michaud (Laval U)
Panelists: Stacy Singer (AAFC), Hannah Clouthier (CFIA), Jennifer Hubert (CropLife Canada), Steve Webb (GIFS), Pankaj Bhowmik (NRC)

Plant Biotechnology is at the forefront of scientific innovation in Canada, harnessing diverse tools and technologies to enhance plant genetics and yield products of agricultural, environmental or industrial value. The Plant Biotechnology sector significantly contributes to Canada's economy, providing 15,000 jobs and over $2 billion to the GDP each year. Beyond scientific and economic prowess, its influence also permeates regulatory frameworks and societal perspectives, shaping its impact on society, the economy and the environment. As a trailblazer in the realm of Plant Biotechnology, Canada is now witnessing a compelling chapter in its scientific narrative, strongly influenced by evolving guidelines amidst the rapid development of genome editing technologies and the adoption of gene-edited crops. Please join us for an open discussion about the gene editing landscape in Canada. Different aspects of the question will be addressed by the panelists, from the basic concepts of gene editing to the regulation, IP protection and commercialization of gene-edited crops and products.

CROPLIFE SYMPOSIA: RESISTANCE MANAGEMENT

SPONSORED BY CROPLIFE CANADA

Tuesday July 9, Hall C East at 11:45 am

Resistant insects, diseases, and weeds have the potential to affect all crops in Canada. Herbicide resistance alone costs Canadian growers an estimated $1.3 billion annually due to increased input use and decreased yield and quality. CropLife Canada invites Plant Canada attendees to be part of this discussion and learn the challenges and opportunities in the resistance field. The panel will focus on how researchers, industry and government can collaborate to ensure science-based policies best support innovation and secure farmers' access to the tools that help combat resistance.

PANELISTS

- **Jocelyn Smith**, University of Guelph, Ridgetown Campus
- **Curtis Rempel**, Canola Council of Canada
- **Albert Tenuta**, OMAFRA
- **Brittany Lacasse**, CropLife Canada

MODERATOR

- **Luis Luque**, CropLife Canada

Oral Presentations

Oral presentations are grouped by society and topic – refer to the concurrent session list to find the number for your talk. The presenter's name is underlined. Student presentations for competition are identified by an asterisk.

MONDAY AFTERNOON Concurrent Session 1

Meeting Room 1		CSPB-I Plant Reproduction *Chair: Teagen Quilichini*
1:15	*O1	A CELL ATLAS OF MALE AND FEMALE REPRODUCTIVE STRUCTURES IN POPULUS REPRESENTING MULTIOME DATA; Oscar Felipe Nunez-Martinez, Stefan Heinen, Raju Soolanayakanahally, and Katharina Bräutigam
1:30	O2	WITHDRAWN
1:45	O3	A FUNCTIONALLY REDUNDANT MAPK PATHWAY CONTROLS STIGMA RECEPTIVITY IN ARABIDOPSIS; Muhammad Jamshed, Subramanian Sankaranarayanan, Kumar Abhinandan, and Marcus A. Samuel
2:00	*O4	CHARACTERIZING THE ROLES OF MECHANOSENSITIVE ION CHANNEL GENES MSL7 AND MSL8 IN THE BASAL COMPATIBLE POLLEN RESPONSE IN A. THALIANA; Paula Beronilla and Daphne R. Goring
2:15	O5	SHOWCASING THE POWER OF SYNCHROTRON X-RAY IMAGING TOOLS FOR CROP SEED RESEARCH; Paula Ashe, Kaiyang Tu, Jarvis A. Stobbs, Jay Dynes, Miranda Vu, Hamid Shaterian, Sateesh Kagale, Karen K. Tanino, Janitha P.D. Wanasundara, Chithra Karunakaran, and Teagen D. Quilichini
2:30	O6	FLOWER OPENING; ARF2-MYB6 MODULE MEDIATES AUXIN-REGULATED PETAL EXPANSION IN ROSA HYBRIDA; Nisar Hussain, Changxi Chen, Xiaoming Sun, and Junping Gao
Meeting Room 15		**CSA-I Breeding and Genetics (Graduate Students)** *Chairs: Jamie Larsen and Simranjeet Kaur*
1:15	*O7	NESTED ASSOCIATION MAPPING TO IDENTIFY STRIPE RUST RESISTANCE LOCI AND THEIR MARKERS IN SPRING WHEAT; Simranjeet Kaur, Raman Dhariwal, Gurcharn Singh Brar, and Harpinder Singh Randhawa
1:30	*O8	GENOMIC PREDICTION FOR IMPROVING WINTER HARDINESS AND FUSARIUM HEAD BLIGHT RESISTANCE IN WINTER DURUM WHEAT; Ritesh K. Yadav, Raja Ragupathy, Gavin Humphreys, Demissew S. Desta, André Laroche, Harmeet S. Chawla, Marcos Cordeiro, Akshaya Vasudevan, Harpinder S. Randhawa, and Curt A. McCartney
1:45	*O9	ENHANCEMENT OF TOTAL SHOOT LIPID CONTENT (TSLC) IN PERENNIAL LEGUME FORAGES USING CHEMICAL MUTAGENESIS; Mohammed Musthafa Mukthar, Tharangani Somarathna, Bin Shan, Guanqun (Gavin) Chen, Stacy Singer, and Hari Poudel
2:00	*O10	IDENTIFYING KEY PHENOTYPIC AND GENOTYPIC TRAITS LINKED TO TRANSPIRATION EFFICIENCY AGAINST INDIVIDUAL AND COMBINED HEAT AND DROUGHT STRESSES IN CONTRASTING WHEAT GENOTYPES; Abdul Halim, Raju Soolanayakanahally, and Karen Tanino

Meeting Room 3		**CAPB/CSPB-II Abiotic Stress #1 Resilience to Climate Extremes** *Chair: Jean-Benoit Charron*
1:15	*O13	A SINGLE NUCLEUS ATLAS OF TRANSCRIPTIONAL RESPONSES TO GROWTH-ALTERING STRESS: DROUGHT, SALINITY, AND FLOODING; **Sean Robertson** and Olivia Wilkins
1:30	*O14	COMBINED EXPOSURE TO LOW PHOSPHATE AND SALT ELICITS DIFFERENT PHENOTYPIC AND TRANSCRIPTIONAL RESPONSES FOR TWO EXTREMOPHILE ECOTYPES; **Haoran Jia**, Solmaz Irani, Isabel Johnson, Maheshi Dassanayake and Elizabeth Weretilnyk
1:45	O15	DISSOCIATED FLOWERING AND COLD ACCLIMATION IN BRACHYPODIUM HYBRIDUM PROVIDE INSIGHTS INTO THE ADAPTIVE RESPONSES TO LOW TEMPERATURES IN CEREALS; **Jean-Benoit Charron**, Luc Ouellette, and Boris Mayer
2:00	*O16	TRANSCRIPTIONAL REPRESSION OF *MSWOX13-2* IN ALFALFA ENHANCES TOLERANCE TO WATERLOGGING STRESS; **Udaya Subedi**, Kimberley Burton Hughes, Madeline Lehmann, Gaganpreet Dhariwal, Guanqun(Gavin) Chen, Surya Acharya, and Stacy Singer
2:15	*O17	PLANT GROWTH-PROMOTING PHYTOMICROBIOME BACTERIA: ENHANCED CROP PERFORMANCE UNDER SALINITY STRESS AND FOR GREENHOUSE GAS MANAGEMENT; **Rania Alrasheed**, Sowmyalakshmi Subramanian, Michael Fefer, and Donald L. Smith
Meeting Room 4		**CSPB-III Molecular Host-Pathogen Interaction #1** *Chair: David Chiasson*
1:15	*O18	*TETRANYCHUS URTICAE* METABOLIC RESPONSES TO *ARABIDOPSIS THALIANA* DEFENSIVE PHENYLPROPANOIDS; **A. Harrison**, C. Sharma, K. Bruinsma, J. Maglov, M. Bernards, and V. Grbic
1:30	*O19	THE IMPACT OF ELEVATED TEMPERATURE ON NPR1 PROTEIN REGULATION IN PIPECOLIC ACID-MEDIATED IMMUNITY IN ARABIDOPSIS THALIANA; **Spencer Tout** and Christian Danve M. Castroverde
1:45	*O20	FER KINASE AND CELL WALL SENSORS LRX1/2 REGULATE MICROBIOME IN A PHOSPHATE-DEPENDENT MANNER; **Siyu Song**, Keegan J. McDonald, Melissa Y. Chen, Zayda Morales Moreira, and Cara H. Haney
2:00	*O21	DISTINCT PLANT IMMUNE RESILIENCE MECHANISMS IN DIVERSE ACCESSIONS OF *ARABIDOPSIS THALIANA*; **Christina AM. Rossi**, Dhrasti N Patel, and Christian Danve M. Castroverde
2:15	*O22	AGE-RELATED RESISTANCE REQUIRES SALICYLIC ACID SIGNALING VIA NPR PROTEINS AND RESULTS IN THE MODEST ACCUMULATION OF N-HYDROXYPIPECOLIC ACID IN LEAVES; **G.M. Nunn**, Jacob Lund, Natalie Belu, Rowan Brookman, and R.K. Cameron
Meeting Rooms 7+8		**CSHS-I / CPS-J1 Cannabis** *Chair: Dr. Youbin Zheng, University of Guelph*
1:15	O23	BOTTOM COOLING DURING CULTURE INITIATION INCREASES SURVIVAL AND REDUCES HYPERHYDRICITY IN MICROPROPAGATED CANNABIS PLANTS; **Rambod Abiri**, Declan O'Reilly, and Andrew Maxwell Phineas Jones

1:30	*O24	OPTIMIZING *EX-VITRO* ONE-STEP RUBY-EQUIPPED HAIRY ROOT TRANSFORMATION IN DRUG- AND HEMP-TYPE CANNABIS; Ladan Ajdanian, Mohsen Niazian, and Davoud Torkamaneh
1:45	*O25	SPECTRUM MATTERS: THE IMPACT OF RED LIGHT ON MORPHOLOGY, POTENCY, AND PHOTOBLEACHING IN *CANNABIS SATIVA*; Karine Jarzecki and Susan J. Murch
2:00	*O26	FUNGAL, OOMYCETE AND BACTERIAL MICROBIOME COMMUNITIES IN ROOTS OF GREENHOUSE CULTIVATED *CANNABIS SATIVA* ARE INFLUENCED BY GROWTH SUBSTRATE, HOST GENOTYPE, AND PLANT GROWTH STAGE; Heather H Tso and Zamir K Punja
2:15	*O27	CHARACTERIZATION OF INDIGENOUS POPULATIONS OF CANNABIS IN IRAN: A MORPHOLOGICAL AND PHENOLOGICAL STUDY; Mehdi Babaei and Davoud Torkamaneh
2:30	*O28	PROFILING THE TRANSCRIPTOMIC AND CELLULAR RESPONSE OF *CANNABIS SATIVA* TO INFECTION BY *SCLEROTINIA SCLEROTIORUM* THROUGH SPACE AND TIME; Natalie L. Cale, Rylee E. Swiderek, and Mark F. Belmonte
Meeting Rooms 9+10		**CBA-I General Botany** *Chair: Jenny McCune*
1:15	O29	RADIOMETRIC INVESTIGATION DUE TO NATURALLY OCCURRING RADIONUCLIDES IN SOILS OF IGBOKODA, A COASTAL AREA IN ONDO STATE, NIGERIA. A; Funmilola Mabel Ojo, Abiola Olawale Ilori and Kayode Olayele Karigidi
1:30	O30	PLANT AND SOIL COMMUNITIES GIVEN NITROGEN DEPOSITION, WARMING, HARVESTING AND SOIL CONDITIONS; Laura Super
1:45	*O31	PREVALENCE AND CONSEQUENCES OF INTERSPECIFIC POLLEN TRANSFER IN A MONTANE COMMUNITY; Jacalyn Grey and Anne Worley
2:00	*O32	EVOLUTIONARY ANALYSIS OF INDIAN & SRI LANKAN WOODY TREES; Harsimran Kaur, Sachin Medigeshi Harish, Semini Nawalage, and Selvadurai Dayanandan
2:15	O33	ECOLOGICAL PROCESSES DETERMINING WEED SPECIES DISTRIBUTION ACROSS NOVA SCOTIAN WILD BLUEBERRY FIELDS; Andrew McKenzie-Gopsill, Hugh Lyu, Scott White, and Sheldon Hann
Meeting Rooms 11+12		**CPS-I Advances in Plant Pathology 1** *Chair: Dr. Tom Hsiang (U of Guelph) & Dr. Lone Buchwaldt (AAFC Saskatoon)*
1:15	O34	CONTRIBUTIONS OF METABARCODING AND POPULATION GENETICS TO FUSARIUM HEAD BLIGHT EPIDEMIOLOGY; Toan Bao Hung Nguyen, Marie Foulongne-Oriol, Amandine Henri-Sanvoisin, Sylvie Treguer, Gaétan Le Floch, and Adeline Picot
1:30	O35	ADVANCED MOLECULAR DIAGNOSTICS REVEAL SHIFTS IN *FUSARIUM* POPULATIONS ASSOCIATED WITH WHEAT IN WESTERN CANADA: A FIVE-YEAR STUDY; Mohamed Hafez, Nicola Schatz, Khouloud Ayari, Rhodesia Celoy, Mouldi Zid, Ryan Gourlie, Dianevys GonzalezPenaFundora, Thomas Kelly Turkington, and Reem Aboulhaddour
1:45	O36	GENOME MINING OF PHYTOPATHOGENIC FUNGI FOR PHARMACOLOGICAL PRODUCTS; Tom Hsiang, Xueting Liu, Jingyu Zhang, Lixin Zhang, Lan Jiang, Xinye Wang, and Guoliang Zhu
2:00	O37	*EXECUTER1* IS TRIGGERED BY SINGLET OXYGEN AND CONFER RESISTANCE TO *SCLEROTINIA SCLEROTIORUM* VIA PROGRAMMED CELL DEATH IN BOTH CANOLA AND SOYBEAN; Lone Buchwaldt, Helen Lui, Alan Davies, Jonathan Durkin, and Fuyou Fu

2:15	O38	VIRAL DIVERSITY IN A MIXED TREE FRUIT PRODUCTION SYSTEM DETERMINED THROUGH BEE-MEDIATED POLLEN METAGENOMICS; **Raj Vansia, Guillaume J. Bilodeau, Stephen F. Pernal, M. Marta Guarna, Michael Rott, and Jonathan S. Griffiths**
Meeting Room 13		**CPS-II Advances in Plant Pathology, Surveillance, and Diagnostics (Competition)** *Chairs: Ryan Gourlie (AAFC Lethbridge) & Dr. Nora Foroud (AAFC Lethbridge)*
1:15	*O40	POTENTIAL FOR BEES AND POLLEN AS BIOMONITORS OF AGRICULTURAL PATHOGENS THROUGH A METABARCODING HIGH THROUGHPUT SEQUENCING (HTS) APPROACH; **C. M. Hewapathirana, M.E. Rott, M.M. Guarna, S.F. Pernal, J.S. Griffiths, and G.J. Bilodeau**
1:30	*O41	IDENTIFICATION AND CHARACTERIZATION OF *PODOSPHAERA APHANIS* CAUSING POWDERY MILDEW ON SALMONBERRY AND THIMBLEBERRY PLANTS IN BRITISH COLUMBIA; **Chidrupa Podile, Rishi R. Burlakoti, Amy Novinscak, Miao Liu, Zamir K. Punja, Davis Iritani, and Yoichiro Watanabe**
1:45	*O42	ESTIMATING EARLY INFECTION OF ONIONS BY *STEMPHYLIUM VESICARIUM* BASED ON SPORE TRAPPING AND INFECTION OF BARLEY; **Julia Scicluna, Bruce D. Gossen, and Mary Ruth McDonald**
2:00	*O43	IDENTIFICATION OF NOVEL AND DIVERSE MYCOVIRUSES IN THE PHYTOPATHOGENIC FUNGUS, BOTRYTIS CINEREA; **Sarah C. Drury, Naser Poursalavati, Peter Moffett, and Mamadou Lamine Fall**
2:15	*O44	COLLECTION AND IDENTIFICATION OF *PLASMODIOPHORA BRASSICAE* PATHOTYPES COLLECTED IN WESTERN CANADA OVER THE LAST TEN FIELD SEASONS (2014-2023); **Emilee Storfie, Victor Manolii, Yoann Aigu, Michael Harding, Sheau-Fang Hwang, and Stephen Strelkov**
2:30	*O45	UTILITY OF CONTROLLED ENVIRONMENT AGRICULTURE IN THE PRODUCTION OF MEDICINAL FUNGI; **Jacqueline Nguyen, Nykole Crevits, Jeff Huber, Mike Dixon, and Thomas Graham**
Meeting Room 2		**CPS-III Disease Resistance** *Chair: Dr. Lipu Wang (U of Saskatchewan) & Malini Jayawardana (U of Manitoba)*
1:15	O46	A HIGH THROUGHPUT PHENOTYPING PLATFORM FOR CEREAL RESEARCH AND BREEDING PROGRAMS TO IDENTIFY FUSARIUM DAMAGED KERNELS AND FUSARIUM PRODUCED MYCOTOXINS; **Lipu Wang, Deborah Michel, Keyhan Najafian, Mackenzie Hladun, Alejandra M. Oviedo-Ludena, Sheila M P Andrade, Anas El-Aneed, Ruijiao Kang, Yuefeng Ruan, Lingling Jin, Ian Stavness, and Hadley R. Kutcher**
1:30	O47	A NEW MODEL: FUNCTIONAL GENES CONTRIBUTING TO ADULT PLANT RESISTANCE FROM CANOLA-BLACKLEG PLAYBOOK; **Zhongwei Zou, and W. G. Dilantha Fernando**
1:45	O48	CANADIAN DURUM WHEAT CULTIVAR STRONGFIELD EXHIBITS MODERATE SUSCEPTIBILITY TO MEXICAN LEAF RUST (*PUCCINIA TRITICINA*) RACES; **Firdissa E. Bokore, Kerry Boyle, Yuefeng Ruan, Curt A. McCartney, Colin W. Hiebert, Ron E. Knox, Xiangyu Pei, Elsa Reimer, Karim Ammar, Wentao Zhang, Pierre Fobert, Richard D. Cuthbert, Samia Berraies, and Brent D. McCallum**
2:00	O49	IDENTIFYING RESISTANCE (R) GENES TO BLACKLEG *LEPTOSPHAERIA MACULANS* IN ACCESSIONS OF CANOLA; **Oluwafemi Lawal and Dilantha Fernando**
2:15	O50	THE EFFECT OF *R* GENE ROTATION ON MITIGATION OF CANOLA BLACKLEG DISEASE IN WESTERN CANADIAN PRAIRIES; **Malini Anudya Jayawardana, Zhongwei Zou, and Dilantha Fernando**

MONDAY AFTERNOON Concurrent Session 2

Meeting Room 1		**CSA-II Breeding and Genetics** *Chairs: Harpinder Randhawa and Ritesh Yadav*
3:15	O51	DEVELOPMENT OF SALT TOLERANT ALFALFA (*MEDICAGO SATIVA* L.): FROM LAB TO FIELD; **Bill Biligetu**, Shanna Quilichini, and Surendra Bhattarai
3:30	O52	LEAF WATER RELATIONS AND OSMOTIC ADJUSTMENT OF CANADA WESTERN RED SPRING WHEAT CULTIVARS SUBJECTED TO DROUGHT; Gopal Sharma, Thorsten Knipfer, and **Gurcharn S. Brar**
3:45	O53	ENHANCING PROTEIN CONTENT IN *BRASSICA NAPUS*: GENETIC INSIGHTS AND BREEDING IMPLICATIONS; **Harmeet S. Chawla**, Mohamed S. Youssef, Sean Walkowiak, and Robert W. Duncan
4:00	O54	PARTICIPATORY PLANT BREEDING TO INCREASE DIVERSITY AND RESILIENCE: A CASE STUDY OF CANADIAN WHEAT; **Michelle Carkner** and Martin Entz
4:15	O55	EXAMINING THE RELATIONSHIP BETWEEN BACTERIAL BROWN SPOT AND COMMON BACTERIAL BLIGHT IN COMMON BEAN; Caio Correa, Emily Morneau, Owen Wally, Chris Gillard, and **Jamie Larsen**
4:30	O56	PROGRESS IN OAT BREEDING IN NORTH CHINA; **Junyong Ge**, Xingyu Wang, Yunxia Li, Zhanhong Dong, Haige Zhao, Huadong Zang, Yadong Yang, Zhaohai Zeng
Meeting Room 15		**CSA-III Agronomy I – Cropping Systems** *Chairs: Malinda Thilakarathna and Ahmad Sharjeel*
3:15	O57	DETERMINING OPTIMUM SEEDING RATIOS AND PEA-BRASSICA INTERCROP COMBINATIONS FOR MAXIMIZING AGRONOMIC BENEFITS; **Yunfei Jiang** and Claude Caldwell
3:30	O58	AN INTEGRATED STRATEGY TO IMPROVE PROFITABILITY OF BARLEY PRODUCTION IN WESTERN CANADA: AN INTRODUCTION OF GROW BARLEY PROGRAM; **Hiroshi Kubota**
3:45	O59	IMPLEMENTING DIVERSIFIED CROP ROTATIONS ENHANCES ECOSYSTEM SERVICES; **Liu K**, Wen G, Chau H, Kubota H, Mohr R, Peng G, Semach G, Lokuruge P, Entz M, Lemke M, Khakbazan M, Kim YM, Sharpe S, Town J, Hernandez G, Iheshiulo E, Ferrari Machado P, Glenn A, Zhang H, Qian B, Jing Q, Kroebel R, and Bourgault M
4:00	O60	EFFECT OF ECOTEA™ SEED TREATMENT ON SPRING CROPS AT THUNDER BAY; **Tarlok Singh Sahota**
4:15	O61	COVER CROPPING AND NITROUS OXIDE EMISSIONS IN THE RED RIVER VALLEY; **Mario Tenuta**, Shannon Mustard, Katie Webb, Junaid Afzal, Rida Sabirova, and Brad Sparling
Meeting Room 3		**CSPB-IV Molecular Host-Pathogen Interaction #2** *Chair: Christian Danve Castroverde*
3:15	O62	MOLECULAR ANALYSES OF DIFFERENTIAL RESISTANCE IN LODGEPOLE AND JACK PINE TO CRONARTIUM HARKNESSII, THE CAUSAL AGENT OF WESTERN GALL RUST; **Janice Cooke**, Samson Osadolor, Rhiannon Peery, Laura Manerus, Marion Mayerhofer, L. Irina Zaharia, and Chandra McAllister
3:30	*O63	DO GINSENOSIDES ALTER THE PATHOGENICITY OF *ILYONECTRIA*? **Anka Colo** and Mark A. Bernards

3:45	O64	PLANT IMMUNE RESILIENCE: FROM GENE REGULATORY NETWORKS TO BIOMOLECULAR CONDENSATES; Christian Danve M. Castroverde, Jong Hum Kim, Alyssa Shields, Lingya Yao, Shuai Huang, Eric J.R. Marchetta, Richard Hilleary, Adam Seroka, John D. MacMicking, Xiu-Fang Xin, and Sheng Yang He
4:00	*O65	BACK TO THE ROOTS: EXPLORING PLANT-INSECT INTERACTIONS IN CULTIVATED AND WILD TOMATOES; Andreea Bosorogan, Osmond Hui, and Eliana Gonzales-Vigil
4:15	O66	PAPERCLIP RNA STRUCTURES REDUCE DISEASE SYMPTOMS CAUSED BY SCLEROTINIA SCLEROTIORUM THROUGH HOST INDUCED GENE SILENCING; Mark F Belmonte, Bliss M. Beernink, and Steve Whyard
Meeting Room 4		**CBA/CSPB-V Cellular Conversations: Decoding Plant Signals and Developmental Responses** *Chair: Shelley Hepworth*
3:15	O67	VOICES FROM BOTH SIDES: A MOLECULAR DIALOGUE BETWEEN TRANSCRIPTIONAL ACTIVATORS AND REPRESSORS IN SEED AND SEEDLING DEVELOPMENT; Liang Song
3:45	*O68	SOMETHING SWEET: SUGAR MEDIATED CHANGES IN CELL PROLIFERATION VIA TOR-BRASSINOSTEROID SIGNALLING REQUIRE THE MICROTUBULE ASSOCIATED PROTEIN *CLASP;* Sean P.A. Ritter, Dr. Laryssa Halat, and Dr. Geoffrey Wasteneys
4:00	O69	HOW INTERNAL GROWTH CONTROLS PLANT MORPHOGENESIS? Sylvia R. Silveira, Loann Collet, Sahil M. Haque, Luc Lapierre, Agnieszka Bagniewska-Zadworna, Frederick P. Gosselin, Richard S. Smith, Anne-Lise Routier-Kierzkowska, and Daniel Kierzkowski
4:30	O70	A UNIVERSAL MODEL OF EMBRYO DEVELOPMENT IN LAND PLANTS (EMBRYOPHYTES) AND THEIR POTENTIAL APPLICATIONS FOR CROP IMPROVEMENT; Prakash Venglat, Perumal Vijayan, Timothy F. Sharbel, Abidur Rahman, and Karen Tanino
4:45	*O71	ADAPTIVE ROOT MORPHOLOGY AND ARCHITECTURE AS A DROUGHT RESPONSE IN *BROMUS* INERMIS; Nora Kroeger and Rafael Otfinowski
Meeting Rooms 7+8		**CSHS-II / CPS-J2 Cannabis** *Chair: Dr. Youbin Zheng (University of Guelph)*
3:15	*O72	QUANTIFICATION OF BIO-STIMULANTS (MICROBES AND BACILLIN-20) AND THEIR INTERACTIONS FOR ENHANCED CANNABIS GROWTH AND QUALITY IN TERMS OF SECONDARY METABOLITE COMPOSITION; Ambreen, A. Geitmann, and D.L.Smith
3:30	*O73	BIOCONTROL ACTIVITY OF *BACILLUS SP*. OF PHYTOMICROBIOME AGAINST *BOTRYTIS CINEREA* IN *CANNABIS* SATIVA; Haleema Tariq, Anja Geitmann, and Donald Smith
3:45	O74	GENETIC CONTROL OF FLOWERING IN *CANNABIS SATIVA*; Soheil S. Mahmoud
4:00	O75	HOW TO DETERMINE THE OPTIMAL FLOWERING-STAGE PHOTOPERIOD FOR CANNABIS PRODUCTION; Youbin Zheng
4:15	*O76	OPTIMIZATION OF SOLVENT-BASED EXTRACTION USING A CENTRIFUGE ON THE BASIS OF PARTICLE SIZE AND THE AGITATION TIME; Ritul Jyani, Philip Wiredu Addo, Sarah MacPherson, Nichole Taylor, Michelle Shearer, Fredrick Gallant, Maxime Paris, Valerie Orsat, and Mark Lefsrud
4:30		PANEL DISCUSSION

Meeting Rooms 9+10		**CSA-IV Nutrient Management (Graduate Students)** *Chairs: Hiroshi Kubota and Emma McIlveen*
3:15	*O77	*EFFECT OF ENHANCED EFFICIENCY NITROGEN FERTILIZERS AND **ANVOL™** ON SPRING WHEAT PRODUCTION AND SOIL HEALTH;* Harsh Bagria , Tarlok Singh Sahota, and Brian McLaren
3:30	*O78	**CAN STARTER POTASH APPLICATIONS IMPROVE THE YIELD AND CROP HEALTH OF CHICKPEA, MUSTARD, AND DURUM WHEAT IN THE BROWN SOIL ZONE OF SASKATCHEWAN? Tristan Chambers, Jeff Schoenau, Ryan Hangs, Michelle Hubbard, Alejandra Oviedo-Ludeña, and Randy Kutcher**
3:45	*O79	**THE EFFECT OF VARYING FERTILITY MANAGEMENT REGIMES N THE YIELD AND QUALITY OF VARIOUS FORAGE SPECIS/MIX; Puja Lamichhane and Kimberley Schneider**
4:00	*O80	**EFFECT OF ENHANCED EFFICIENCY NITROGEN FERTILIZERS ON AGRONOMIC AND ENVIRONMENTAL PERFORMANCE IN GRAIN CORN; Baillie Lynds and Yunfei Jiang**
Meeting Rooms 11+12		**CPS-IV Molecular Host-Pathogen Interactions (Competition)** *Chair: Dr. Jim Menzies (AAFC Morden) & Dr. Mohamed Abdel-Fattah (AAFC Lethbridge)*
3:15	*O81	**MECHANISMS OF DEMETHYLATION INHIBITOR RESISTANCE IN *CLARIREEDIA JACKSONII*; E. McNab and T. Hsiang**
3:30	*O82	**FUNCTION OF THE CONCANAMYCIN PHYTOTOXINS IN THE POTATO COMMON SCAB PATHOGEN STREPTOMYCES SCABIEI; Corrie V. Vincent and Dawn R. D. Bignell**
3:45	*O83	**TRANSGENIC EXPRESSION OF PROTEIN-BASED INHIBITOR AGAINST TURNIP YELLOW MOSAIC VIRUS IN ARABIDOPSIS THALIANA; J K Anuradha De Silva, Kihun Kim, Jacky Chung, John Weiland, Jihyun Hwang, Melvin Bolton, Mohammed Mira, Claudio Stasolla, Sachdev Sidhu, and Brian Mark**
4:00	*O84	**DECIPHERING *TETRANYCHUS URTICAE - ARABIDOPSIS THALIANA* INTERACTIONS: UNVEILING DETOXIFICATION MECHANISMS AND PLANT RESISTANCE STRATEGIES; Michele Antonacci, Jorden Maglov, Julia Pastor Fernandez, Chetan Sharma, Vladimir Zhurov, Brendan Abiskaroon, Maksymilian Chruszcz, and Vojislava Grbic**
4:15	*O85	**PROTEOMIC ANALYSIS REVEALS NEW INSIGHTS RELATED TO THE INTERACTION BETWEEN *XANTHOMONAS PHASEOLI PV PHASEOLI* AND *PHASEOLUS VULGARIS* L.; Mylene Corzo-Lopez, Jason McAlister, Boyan Liu, Jennifer Geddes-McAlister, and K. Peter Pauls**
4:30	*O86	**INSIGHTS FROM NEXT GENERATION SEQUENCING: NOVEL VIRUSES AND VARIANTS IN HIGHBUSH BLUEBERRIES OF BRITISH COLUMBIA; Sachithrani Kannangara, Juan Rodriguez, Adam Gilewski, Gerda de Villiers, Megan Ellis, Peter Ellis, Eric Erbrandt, and Jim Mattsson**
4:45	*O87	**A CLUBROOT PATHOGEN EFFECTOR DISRUPT AUXIN HOMEOSTASIS TO PROMOTE COLONIZATION; Melaine González García, Marina Silvestre Vano, Soham Mukhopadhyay, Ian Major, and Edel Pérez López**

Meeting Room 13		**CPS-V Advances in Fusarium Management (Competition)** *Chairs: Dr. Adam Foster, AAFC Charlettetown & Dr. Ahmed Abdelmagid (AAFC Morden)*
3:15	*O88	RNASEQ STUDY OF PARTIALLY RESISTANT AND SUSCEPTIBLE PEA GENOTYPES UPON *FUSARIUM AVENACEUM* INFECTION; Sijan Pandit, Eoin O'Hara, Robert Gruninger, and Syama Chatterton
3:30	*O89	METABARCODING REVEALS BACTERIAL ENDOPHYTES FROM BARLEY GRAINS ARE SIGNIFICANTLY ASSOCIATED WITH FUSARIUM HEAD BLIGHT, BARLEY GENOTYPE, AND TIME OF SAMPLING; Vinuri Weerasinghe, Matthew Bakker, James Tucker, Dilantha Fernando, Ana Badea, and Champa Wijekoon
3:45	*O90	COMMERCIAL FORMULATIONS CONTAINING *BACILLUS* SPECIES REDUCE THE DEVELOPMENT AND SURVIVAL OF *FUSARIUM OXYSPORUM* IN SOIL-LESS GROWTH MEDIA; Denna N. Dalrymple and Zamir K. Punja
4:00	*O91	GENETIC MAPPING OF RESISTANCE TO FUSARIUM HEAD BLIGHT AND DON ACCUMULATION IN WATKINS LANDRACE WAT.1190580; Sharandeep Dhaliwal, Maria Antonia Henriquez, Curt McCartney, Samuel Holden, and Gurcharn Singh Brar
4:15	*O92	THE EVOLUTIONARY DYNAMICS OF AZOLE RESISTANCE IN *FUSARIUM GRAMINEARUM*; Kelsey Wog, Matthew. G. Bakker, and Aleeza C. Gerstein
4:30	*O93	THE ROLE OF HYD5 PROTEIN IN *FUSARIUM*-BARLEY INTERACTIONS; Anuradha U. Jayathissa, W. G. Dilantha Fernando, Raymond He, David N. Langelaan, and Matthew G. Bakker
Meeting Room 2		**CPS-VI Soilborne Diseases and Pathogens** *Chairs: Dr. Michelle Hubbard (AAFC Swift Current) & Dr. Owen Wally (AAFC Harrow)*
3:15	O94	PREVALENCE OF *VERTICILLIUM* SPP. AND *PRATYLENCHUS* SPP. IN COMMERCIAL POTATO FIELDS IN EASTERN CANADA; Dahu Chen, Ryan Barrett, Benjamin Mimee, Tanya Arseneault, Louis-Pierre Comeau, Kamrun Nahar, Sebastian Ibarra Jimenez, and Bernie J. Zebarth
3:30	O95	IMPACT OF CROP ROTATION ON THE MICROBIOMES OF SUDDEN DEATH SYNDROME (SDS) AND SOYBEAN CYST NEMATODE (SCN) SUPPRESSIVE SOILS OF SOYBEANS IN SOUTHERN ONTARIO, CANADA; R. Malla, L.A. Phillips, K.E. Dunfield, B.Seuradge, A. Wragg, and O.S. Wally
3:45	O96	PREVALANCE STUDY AND EVALUATION OF COMMERCIAL CULTIVARS AS AN IMMEDIATE MEASURE TO FIND VERTICILLIUM MANAGEMENT OPTIONS ON CANOLA; Venkat Chapara, Anitha Chirumamilla, Amanda Arens, and Larissa Jennings
4:00	O97	GINSENOSIDE MOBILITY IN GINSENG GARDEN SOIL; Andrew Rabas and Mark A. Bernards
4:15	O98	INTERACTIONS BETWEEN *APHANOMYCES EUTEICHES* AND *FUSARIUM AVENACEUM* AND *GRAMINEARUM*; Michelle Hubbard, Olivia Zajac, Anas Eranthodi, Syama Chatterton, David Overy, and Nora Foroud
4:30	O99	PRESCREENING AND MONITORING EVALUATION USING SEQUENCING TECHNOLOGIES FOR *PHYTOPHTHORA* AND OOMYCETES; Guillaume J. Bilodeau and Hervé Van der Heyden

5:00 – 7:00 pm **Poster Session 1 in Hall D**

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

Light refreshments will be served.

Sponsored by

MANITOBA CROP ALLIANCE

TUESDAY AFTERNOON Concurrent Session 3

Meeting Room 1		**CAPB/CSPB-VI Plant Metabolomics** *Chair: Barbara Hawkins*
1:15	*O100	PROFILING ENVIRONMENTAL AND SEASONAL VARIATIONS IN CONDENSED TANNINS AND METABOLITES OF BIRDSFOOT TREFOIL (*LOTUS CORNICULATUS* L.) CULTIVARS; Solihu Kayode Sakariyahu, Tim McDowell, Justin Renaud, Yousef Papadopoulos, Kathleen Glover, Rebecca Brown, Mike Peel, Heathcliffe Riday, Susanne Kohalmi, and Abdelali Hannoufa
1:30	O101	METABOLIC ENGINEERING-INDUCED TRANSCRIPTOME REPROGRAMMING ENHANCES OIL COMPOSITION IN OAT (*AVENA SATIVA* L.); Zhou Zhou, Rajvinder Kaur, Thomas Donoso, Jae-Bom Ohm, Rajeev Gupta, Mark Lefsrud, and Jaswinder Singh
1:45	*O102	THE RELATIONSHIPS AMONG PHYTOHORMONES AND BENZYLISOQUINOLINE ALKALOIDS DURING EARLY DEVELOPMENT OF *PAPAVER RHOEAS* L.; Zeynab Azimychetabi, Anna B. Kisiala, Scott C. Farrow, and R. J. Neil Emery
2:00	O103	PROANTHOCYANIDINS IN POPLAR ROOTS: EFFECTS ON MYCORRHIZAL COLONIZATION AND NITROGEN UPTAKE; Daisuke Yamakawa, C. Peter Constabel, and Barbara J. Hawkins
2:15	*O104	A PROMOTER FOR THE METABOLIC ENGINEERING OF GLANDULAR TRICHOMES IN LAVENDER; Reza Sajaditabar and Soheil Mahmoud
Meeting Room 2		**CAPB/CSPB-VII Plant Lipids** *Chair: Eliana Gonzales-Vigil*
1:15	*O105	SOYBEAN CYTOCHROME P450S AND THE MAKING OF ALIPHATIC SUBERIN MONOMERS; Lorena S. Yeung, Delicia Wong, Sangeeta Dhaubhadel, and Mark A. Bernards
1:30	*O106	BUILDING OF SUBERIN - THE IMPORTANCE OF TIMING AND A STRONG FOUNDATION; Jessica L. Sinka and Mark A. Bernards
1:45	*O107	SUBERIN PRODUCTION IN SOYBEAN IS MICROBIOME-RESPONSIVE; Alicia Halhed, Isabel Molina, and Owen Rowland
2:00	O108	GONE WITH THE WIND: CUTICULAR WAXES AS PRECURSORS OF VOLATILE ORGANIC COMPOUNDS; Jeff Y. Chen, Aswini Kuruparan, Mahbobeh Zamani-Babgohari, and Eliana Gonzales-Vigil
2:15	*O109	IDENTIFICATION OF QUANTITATIVE TRAIT LOCI (QTL) FOR ERUCIC ACID CONTENT IN *BRASSICA NAPUS* L.; Yong Liu, Genyi Li, Harmeet S Chawla, Robert W. Duncan, and Curt McCartney
Meeting Room 3		**CSPB- VIII Plant Organelle Biology** *Chair: Peter Constabel*
1:15	*O110	TOC159 RECEPTORS: THE ROLE OF PLASTID MEMBRANE GALACTOLIPIDS IN TARGETING TO THE CHLOROPLAST OUTER ENVELOPE; Michael Fish, George Saudan, Simon Chuong, Masoud Jelokhani-Niaraki, and Matthew Smith
1:30	O111	THE REGULATORY FUNCTION OF PLASTID CHAPERONE HSP90C C-TERMINAL EXTENSION; Bona Mu, Adheip Monakan Nair, and Rongmin Zhao
1:45	*O112	IDENTIFICATION AND CHARACTERIZATION OF OEP6 MOTIFS AND THEIR ROLE IN TARGETING TO THE CHLOROPLAST OUTER MEMBRANE; Holly Ferguson, Matthew Smith, and Simon Chuong

2:00	*O113	**PLASTID MOLECULAR CHAPERONE HSP90C INTERACTS WITH THE SECA1 SUBUNIT OF SEC TRANSLOCASE FOR THYLAKOID PROTEIN TRANSPORT;** Adheip Monikantan Nair, Tim Jiang, Bona Mu, and Rongmin Zhao
Meeting Room 4		**CPS-J4/CAPB/CSPB-IX Plant Pathogenesis and Protection** *Chair: Shuanglong Hong*
1:15	O114	**ADVANCING CANOLA PROTECTION: QPCR SCREENING AND MARKER DEVELOPMENT FOR VERTICILLIUM STRIPE DISEASE RESISTANCE;** Mohamed Samir Youssef, W. G. Dilantha Fernando, Robert Duncan, Sally Vail, Isobel A. P. Parkin, and Harmeet Singh Chawla
1:30	*O115	**IDENTIFICATION OF MICROORGANISMS WITH CLUBROOT BIOCONTROL POTENTIAL AND INVESTIGATION OF MECHANISMS OF THEIR ACTION;** Ananya Sarkar, Anna Kisiala, Vedanti Ghatwala, Neil Emery, Habibur Rahman, and Nat N.V. Kav
1:45	O116	**MODULATION OF PLASTIDIAL PROTEIN TURNOVER BY *PB*PAE, A *PLASMODIOPHORA BRASSICAE* PLASTID-ASSOCIATED EFFECTOR THAT FACILITATES CLUBROOT DISEASE PROGRESSION IN ARABIDOPSIS;** Musharaf Hossain, Christopher D. Todd, Yangdou Wei, and Peta C. Bonham-Smith
2:00	*O117	**CLUBROOT RESISTANCE OF *BRASSICA NAPUS* INTROGRESSED FROM *BRASSICA OLERACEA;*** Sonia Navvuru, Nat N.V. Kav, and Habibur Rahman
2:15	O118	**MULTI-OMICS ANALYSIS OF MECHANISMS BEHIND THE "GAME OF HIDE AND SEEK" IN THE *BRASSICA NAPUS - LEPTOSPHAERIA MACULANS* PATHOSYSTEM;** Shuanglong Huang, Peng Gao, Dilantha Fernando, and Gary Peng
2:30	O119	**DECIPHERING THE MOLECULAR EVENTS BEHIND SYSTEMIN-INDUCED RESISTANCE AGAINST *BOTRYTIS CINEREA* IN TOMATO PLANTS;** Julia Pastor-Fernández, Neus Sanmartín, Maria Manresa, Cédric Cassan, Pierre Pétriacq, Yves Gibon, Jordi Gamir, Beatriz Romero Rodriguez, Araceli G. Castillo, Miguel Cerezo, Victor Flors, and Paloma Sánchez-Bel
Meeting Rooms 7+8		**CSHS-III / CPS-J3 Root Crops** *Chair: Dr. Wahab Jazeem (AAFC, Saskatoon) and Dr. Bourlaye Fofana (AAFC, Charlottetown)*
1:15	O120	**BLACKLEG PREVENTION IN POTATO BY PATHOGEN AND BACTERIOPHAGE IDENTIFICATION;** Binod Pageni, Michele Konschuh, Jonathan Neilson, Melanie Kalischuk, and Lawrence Kawchuk
1:30	*O121	**SOIL MICROBIOME AND SOIL PROPERTIES ASSOCIATED WITH THE RISK OF CAVITY SPOT ON CARROTS IN HIGH ORGANIC MATTER SOILS;** Umbrin Ilyas, Lindsey J. du Toit, M. Kalischuk, and Mary Ruth McDonald
1:45	O122	**PERFORMANCE OF SWEET POTATO UNDER HIGH-TUNNEL PRODUCTION SYSTEM IN SASKATCHEWAN;** Jazeem Wahab, Reynald Lemke, Raju Soolanayakanahally, Champa Wijekoon, Edmund Mupondwa, Erl Svendsen, Dale Tomasiewicz, and Evan Derdall
2:00	O123	**CULTURAL PRACTICES INFLUENCE WEED COMMUNITY AND SEEDBANK DYNAMICS IN THE LIVING LABS ATLANTIC;** McKenzie-Gopsill A, Nyiraneza J, and Fillmore S
2:15	O124	**GLOBAL REGULATION OF PLANT PATHOGENICITY IN THE COMMON SCAB PATHOGEN STREPTOMYCES SCABIEI;** Wanyue Li, Aaron Rees, and Dawn R. D. Bignell
2:30	O125	**DROUGHT-RESILIENT DIPLOID POTATOES FOR SHORT AND LONG GROWING SEASON AGROCLIMATES AS DEPICTED THROUGH GENOME-WIDE ASSOCIATION STUDIES;** Bourlaye Fofana, David Main, Moshin Zaidi, and Benoit Bizimungu

Meeting Room 17		**CBA-II General Botany** *Chair: John Markham*
1:15	O126	GENOMIC DISSECTION OF ISLAND SYNGAMEONS: ARBORESCENT ASTERACEAE FROM ST HELENA (SOUTH ATLANTIC OCEAN); **Quentin Cronk**, Andreas Kolter, and Mikko Paajanen
1:30	O127	NUTRIENT LIMITATION IN SUBARCTIC TERRESTRIAL PLANT COMMUNITIES; **John Markham** and Emily Klapprat
1:45	O128	TESTING ECOWOOL PELLET APPLICATION AS AN ENVIRONMENTALLY FRIENDLY AMENDMENT IN GREENHOUSES; **Liette Vasseur**, Avalon Halgreen, Natasha Hearn, Reem Mahamoud, and Vaughn Mangal
2:00	O129a	DESIGNING AND IMPLEMENTING A USER-FRIENDLY PLANT COMMUNITY SURVEY PROTOCOL TO HELP CONSERVATION ORGANIZATIONS SELECT REINTRODUCTION SITES FOR AN ENDANGERED PRAIRIE BUTTERFLY IN MANITOBA; **Katherine Dearborn** and Richard Westwood
2:15	*O129b	CHARACTERIZING DEFENSE MECHANISMS IN *ARABIDOPSIS THALIANA* AGAINST *TETRANYCHUS URTICAE* HERBIVORY; **Jorden Maglov**, Julia Pastor-Fernandez, Michele Antonacci, Alexander Harrison, Emilie Widemann, Vladimir Zhurov, and Vojislava Grbic
2:30	O129c	BRAWLING WEEDS AND THE FIGHT FOR CROP SURVIVAL; **Clarence Swanton**, Sasan Amirsadeghi, Nicole Berardi, William Kramer, and Andrew McKenzie-Gopsill
Meeting Rooms 11+12		**CSPB-X Plant Signaling** *Chair: Hong Wang*
1:15	O130	DECIPHERING THE ROLE OF ER-LOCALIZED HSP90 FAMILY HEAT SHOCK PROTEIN IN PLANT DEVELOPMENT AND STRESS RESPONSES; **Rongmin Zhao**, Jenan Noureddine, and Morvenley Mamenta
1:30	O131	ARABIDOPSIS ICK/KRP CYCLIN-DEPENDENT KINASE INHIBITORS ARE INTRINSICALLY DISORDERED PROTEINS AND REGULATED BY BOTH UBIQUITIN-DEPENDENT AND UBIQUITIN-INDEPENDENT MECHANISMS; Shengjian Ye, Sheng Wang, Ron Chan, Ling Cao, and **Hong Wang**
1:45	*O132	EXPLORING SPECIFICITY OF PLANT RLCK-VII SIGNALLING; **Eleanor Khochaba** and Thomas A. DeFalco
2:00	*O133a	DOWNSTREAM SIGNALING RESULTING FROM DAMAGED RIBOSOMAL RNA BY POKEWEED ANTIVIRAL PROTEIN (PAP); **Tanya Prashar** and Katalin A. Hudak
2:15	O133b	*ASCOPHYLLUM NODOSUM*-DERIVED FUCOIDAN INDUCES FLOWERING BY REGULATING THE *MIR156*-MEDIATED AGE PATHWAY IN ARABIDOPSIS; **Ramin Bahmani**, Pramod Rathor, and Balakrishnan Prithiviraj
Meeting Room 13		**CPS-VII Resistance Genetics and Host-Pathogen Interactions (Competition)** *Chairs: Dr. Rudolph Fredua-Agyeman (U of Alberta) & Mary Ruth McDonald (U of Guelph)*
1:15	*O134	THE IDENTIFICATION AND FUNCTIONAL ASSESSMENT OF *PLASMODIOPHORA BRASSICAE* EFFECTORS; **Emilee Storfie**, Leonardo Galindo-González, Sheau-Fang. Hwang, and Stephen Strelkov
1:30	*O135	GENOMIC ANALYSIS OF THE PUCCINIA STRIIFORMIS F.SP TRITICI POPULATIONS CAUSING STRIPE RUST IN CANADA; **Bohan Wei**, Ryan Gourlie, Rodrigo Ortega Polo, Nathaniel Zhin-Loong Lim, Rhodesia Celoy, Stephen Strelkov, and Reem Aboukhaddour

1:45	*O136	DEVELOPMENT OF A KASP ASSAY FOR DETECTION OF SUCCINATE DEHYDROGENASE MUTATIONS ASSOCIATED WITH SDHI RESISTANCE IN *STEMPHYLIUM VESICARIUM*; Julia Scicluna, Emily McFaul, Afsaneh Sedaghatkish, Bruce D. Gossen, and Mary Ruth McDonald
2:00	*O137	GENOME-WIDE ASSOCATION STUDY (GWAS) OF STEM RUST RESISTANCE IN WESTERN CANADIAN WINTER WHEAT; Kaitlyn A. Pidherny, Jim G. Menzies, Colin W. Hiebert, Harwinder S. Sidhu, and Curt A. McCartney
2:15	*O138	GENETIC ANALYSIS AND GENOMIC SELECTION MODELS FOR LEAF RUST RESISTANCE IN CANADA WESTERN RED WINTER WHEAT; Anirup Sengupta, Brent D. McCallum, Colin W. Hiebert, Harwinder S. Sidhu, and Curt A. McCartney
2:30	*O139	UNVEILING A DNA VIRUS SECRETS: *DE NOVO* METHYLATION PROFILING OF GRAPEVINE RED BLOTCH VIRUS VIA LONG-READ SEQUENCING; Vahid J Javaran, Pierre Lemoyne, Dong Xu, Dave T Ste-Croix, Peter Moffett, and Mamadou L Fall
Meeting Room 15		**CSA-V Agronomy II (Graduate Students)** *Chair: Bill Biligetu and Baillie Lynds*
1:15	*O140	PURPOSE-GROWN BIOMASS CROPS IN NOVA SCOTIA: STATISTICAL PREDICTIVE YIELD MODELLING AND REAL-WORLD VERIFICATION; Emily G. Mantin, Laura K. Weir, Yousef A. Papadopoulos, and J. Kevin Vessey
1:30	*O141	A SEED TREATMENT FOR THE MANAGEMENT OF SOYBEAN CYST NEAMTODE ON DRY BEANS; Emma McIlveen, Chris Gillard, and Owen Wally
1:45	O142	EFFECT OF HUMIC-BASED SOIL AMENDMENT ON PLANT GROWTH, YIELD AND SYMBIOTIC NITROGEN FIXATION OF FIELD PEA (*Pisum sativum* L.); Pramod Rathor, Thomas D. Warkentin, and Malinda S. Thilakarathna
2:00	*O143	ON-FARM ASSESSMENT OF YIELD RESPONSE OF GRAIN CROPS TO SOIL PH AND LIMING IN CENTRAL ALBERTA; Chirchir Jedida, Dyck Miles, Enesi Rebecca, and Gorim Linda
2:15	*O144	THE EFFECT OF INTEGRATED CROP MANAGEMENT PRACTICES ON WEED GROWTH AND PERSISTENCE TRAITS; Uthpala Ekanayake, Rob Gulden, Chris Willenborg, Jonathan Rosset, and Dilshan Benaragama
Meeting Rooms 9 + 10		**CPS-VIII Advances in Plant Pathology 2** *Chair: Drs. Mamadou Fall (AAFC) and Afsaneh Sedaghatkish (U. of Guelph)*
1:15	O145	THE EFFECT OF BORON ON CLUBROOT SEVERITY AND DEFENSE MECHANISMS IN *BRASSICA NAPUS*; A. Sedaghatkish, S. Chesney, B. D. Gossen, and M. R. McDonald
1:30	O146	BACTERIAL LEAF STREAK SURGE ON THE CANADIAN PRAIRIES: INSIGHTS AND MANAGEMENT STRATEGIES; Shaheen Bibi, Malini Jayawardana, and Dilantha Fernando
1:45	O147	A SURVEY FROM 2006-2023 TO STUDY THE STATE AND PREVALENCE OF FUSARIUM HEAD BLIGHT DISEASE ON WHEAT IN ALBERTA; Monika Dayarathne, Michael Harding, and Dilantha Fernando
2:00	O148	ARE NEMATODES INVOLVED IN THE EMERGING CHICKPEA HEALTH ISSUE IN SASKATCHEWAN? Fernanda Gouvea Pereira, Mario Tenuta, Michelle Hubbard, and Sarah Anderson
2:15	O149	ADVANCEMENT OF B2-BASED DSRNA EXTRACTION METHOD: COST-EFFECTIVENESS COMPARISON OF HTS-BASED VIRUS DETECTION METHODS; Mamadou L. Fall, Dong Xu, and Pierre Lemoyne

TUESDAY AFTERNOON Concurrent Session 4

Meeting Room 1		**CSPB-XI Plant Cell Biology** *Chair: Katharina Braeutigam*
3:15	*O150	PECTIN DYNAMICS DICTATES ANISOTROPIC CELL GROWTH DURING MESOPHYLL MORPHOGENESIS; **Diksha Bhola** and Anja Geitmann
3:30	*O151	SNAKE CHARMMING: UNDERSTANDING COBRA THROUGH BIOINFORMATICS AND MUTATIONAL ANALYSIS; **Kamryn Diehl** and Geoffrey Wasteneys
3:45	O152	FROM SINGLE CELLS TO COMPLEX TISSUES - THE MOLECULAR DECODING OF PLANT SEXUAL REPRODUCTION AT SINGLE CELL RESOLUTION; **Katharina Bräutigam**
4:00	O153	FORMATION OF A STABLE TUBULAR ER NETWORK REQUIRES A LOCALIZED PHOSPHATIDYLCHOLINE SYNTHESIS IN ARABIDOPSIS; **Weina Wang**
Meeting Room 2		**CSHS-IV Fruits** *Chair: Dr. Melanie Kalischuk (University of Guelph)*
3:15	O154	TESTING THREE ALTERNATIVE TECHNOLOGIES AGAINST POWDERY AND DOWNY MILDEWS ON WINE GRAPE, GREENHOUSE CUCUMBER, FIELD ZUCCHINI AND STRAWBERRY; **Andrew C. Wylie**, Irina Perez-Valdes, and Rose Buitenhuis
3:30	O155	DEVELOPING 'STONY HARD' PEACH TO MITIGATE CLIMATE CHANGE EFFECTS AND LONGER SHELF LIFE; **Jayasankar Subramanian** and Naincy Sharma
3:45	O156	CRANBERRY RESPONSES TO IN-FIELD EXPERIMENTAL WARMING; **Lauren A E Erland**
4:00	O157	EPIDEMEOLOGY OF *NEOPESTALOTIOPSIS* SPP. IN STRAWBERRY; Justin McNally, Adam Dale, Erica Pate, and **Melanie Kalischuk**
4:15	*O158	THE DIVERSITY OF BIOACTIVE COMPOUND PROFILES IN CANADIAN PRAIRIE SMALL FRUITS AND THEIR ANTIOXIDANT AND ANTI-HYPERTENSIVE POTENTIAL AS FUNCTIONAL FOODS; **Chamali Kodikara**, Sura Srinivas, Nandika Bandara, Thomas Netticadan, Sijo Joseph, and Champa Wijekoon
4:30	*O159	EXOGENOUS APPLICATIONS OF DOUBLE-STRANDED RNA TO INDUCE RNA INTERFERENCE FOR THE CONTROL OF THE NOVEL FUNGAL PATHOGEN *NEOPESTALOTIOPSIS* SP. AFFECTING STRAWBERRY; **Sarah Koeppe** and Melanie Kalischuk
Meeting Room 3		**CSHS-V Vegetables** *Chair: Dr. Lord Abbey (Dalhousie University)*
3:15	O160	LEAFY GREEN VEGETABLE PRODUCTION IN SASKATCEWAN; **Jazeem Wahab,** Janitha Wanasundara, Edmund Mupondwa, Erl Svendsen, Raju Soolanayakanahally, and Evan Derdall
3:30	*O161	OPTIMIZATION OF LIGHT INTENSITY FOR GROWTH OF MINT (*MENTHA* SPP.) IN CONTROLLED ENVIRONMENTS; **Andrew Burns**, Mike Dixon, Mike Stasiak and Youbin Zheng
3:45	*O162	HARNESSING CONTROLLED ENVIRONMENT SYSTEMS FOR ENHANCED PRODUCTION OF MEDICINAL PLANTS; **Ajwal Dsouza**, Mike Dixon, Mukund Shukla, and Thomas Graham

4:00	O165a	**TEMPERATURE IMPACT ON PLANT GROWTH AND DEVELOPMENT OF SELECTED VEGETABLES;** Peter A. Ofori, Raphael Ofoe, Efoo B. Nutsukpo, and Lord Abbey
4:15	*O165b	**EXPLORING THE IMPACT OF FAR-RED AND BLUE LED LIGHT RATIOS ON *BOTRYTIS CINEREA*'S MORPHOGENESIS;** Abheet Aulakh, William Jordan, and Valerie Gravel
Meeting Room 4		**CAPB/CSPB-XII Plant Genomics** *Chair: David Konkin*
3:15	O166	**COMPARING PHENOTYPIC SELECTION WITH GENOMIC SELECTION WHEN BREEDING FOR NEW VARIETIES OF COMMON BEAN (PHASEOLUS VULGARIS): AN EMPIRICAL STUDY;** Robert McGee, Isabella Chiaravalotti, Marysia Zaleski-Cox, Evan Wright, Karen Cichy, Diego Jarquin D, and Valerio Hoyos-Villegas
3:30	O167	**A MULTISPECIES AMPLISEQ APPROACH TO ASSESS INTRA- AND INTER-SPECIFIC DIVERSITY OF *SPHAGNUM* AND ASSIST RESTORATION EFFORTS;** Mélanie Bourque, François-Olivier Hébert, and David L. Joly
3:45	*O168	**GENOME-WIDE ASSOCIATION ANALYSIS OF LODGING-RELATED CULM TRAITS IN DIVERSE SPRING WHEAT (*TRITICUM AESTIVUM* L.) POPULATION;** Ginelle Grenier, Muhammad Iqbal, Curt McCartney, Gavin D. Humphreys, Dean Spaner, and Belay T. Ayele
4:00	O169	**PAN-GENOME AND LONG-READ STRUCTURAL VARIANT LANDSCAPE OF 51 BRASSICA NAPUS GENOMES UNVEIL CANOLA'S HIDDEN GENETIC DIVERSITY FOR CROP IMPROVEMENT;** Sampath Perumal, Kevin Koh, Raju Chaudhary, Peng Gao, Isobel Parkin, and Andrew Sharpe
4:15	*O170	**GENOME-WIDE ASSOCIATION AND GENOMIC SELECTION FOR OIL AND FATTY ACID PROFILE IN RAPESEED (*BRASSICA NAPUS* L.);** Jared Bento, Jia Sun, Sakaria Liban, Curt McCartney, Harmeet Chawla, and Robert Duncan
4:30	O171	**CROSS-SPECIES COMPARATIVE SEQUENCE-BASED GENE EXPRESSION MODELLING IN LEGUMES;** Nicolas Raymond, Sheikh Jubair, Jordan Ubbens, Xi Zhang, Fatima Davelouis, Ruchika Verma, David Staszak, Dustin Cram, Halim Song, Yongguo Cao, Christine Sidebottom, Yasmina Bekkaoui, Morgan Kirzinger, Deborah Akaniru, and David Konkin
Meeting Rooms 7+8		**CSA-VI Plant-Soil health** *Chair: Kui Liu and Jedida Chirchir*
3:15	O173	**HUMIC PRODUCTS: TO USE OR NOT TO USE IN YOUR FIELD;** Linda Y. Gorim
3:30	O174	**GROWTH-PROMOTING RHIZOBACTERIA MITIGATES SALT STRESS IN RICE THROUGH THE ENHANCEMENT OF ANTIOXIDANT DEFENSE, ION HOMEOSTASIS, AND PHOTOSYNTHETIC PARAMETERS;** Ayesha Siddika, Alfi Anjum Rashid, Shakila Nargis Khan, Amena Khatun, Muhammad Manjurul Karim, PV Vara Prasad, and Mirza Hasanuzzaman

3:45	O175	**EFFECTS OF DEFOLIATION ON ROOT TRAITS, NITROGEN FIXATION, SOIL NITROGEN AVAILABILITY, SOIL ENZYME ACTIVITIES AND SOIL BACTERIAL COMMUNITIES OF FORAGE LEGUMES; Malinda Thilakarathna, Danielito Dollete, Rhea Amor Lumactud, Cameron Carlyle, and Krzysztof Szczyglowski**
4:00	O176a	**EFFECT OF ROW SPACINGS/GEOMETRY AND RATES OF S APPLICATION ON ALFALFA YIELD AND QUALITY IN NORTHERN ONTARIO; Tarlok Singh Sahota, Harmeet Singh, Mikala Parr, David Thompson, and Kim Jo Bliss**
4:15	O176b	**CLIMATE CONDITIONS IN THE NEAR-TERM, MID-TERM AND DISTANT FUTURE FOR GROWING SOYBEANS IN CANADA; Budong Qian, Ward Smith, Qi Jing, Yong Min Kim, Guillaume Jégo, Brian Grant, Scott Duguid, Ken Hester, and Alison Nelson**
Meeting Room 17		**CPS-IX OMICS** *Chair: Dr. Wen Chen (AAFC Ottawa) & Dr. Sandra Velasco-Cuervo (U of Alberta)*
3:15	O177	**DE NOVO WHOLE-GENOME ASSEMBLIES AND A COMPARATIVE PANGENOME ANALYSIS OF THE SOILBORNE PLANT PATHOGEN PLASMODIOPHORA BRASSICAE; Sandra M. Velasco-Cuervo, Yoann Aigu, Leonardo Galindo-Gonzailez, Sheau-Fang Hwang, and Stephen E. Strelkov**
3:30	O178	GENOMIC INVESTIGATION OF WESTERN CANADIAN *APHANOMYCES EUTEICHES* ISOLATES FROM MULTIPLE HOST LEGUME CROPS; Zelalem Taye, Jamuna Paudel, Lou Kun, Cormier Trista, Ethan Done, Jennifer Town, Syama Chatterton, Michelle Hubbard, Hossein Borhan and Nicholas Larkan
3:45	O179	**SINGLE-CELL DNA SEQUENCING OF *PLASMODIOPHORA BRASSICAE* REVEALS CLONAL CHARACTERISTICS; A. Sedaghatkish, B. D. Gossen, and M. R. McDonald**
4:00	O180	**METAGENOMICS-BASED MICROBIAL COMMUNITY PROFILING IN THE QUEST FOR POTATO WART BIOLOGICAL CONTROL AGENTS; Ishraq Akbar, Yichao Shi, Bart. T. L. H. van de Vossenberg, Theo A. J. van der Lee, Sean Li, Linda Jewell, Hai D.T. Nguyen, and Wen Chen**
4:15	O182	**ALLELIC DIVERSITY AND EVOLUTIONARY PATTERNS OF TOXB GENE IN PYRENOPHORA TRITICI-REPENTIS AND RELATED SPECIES: A GLOBAL PERSPECTIVE; Mohamed Hafez, Ryan Gourlie, Megan McDonald; Melissa Telfer, Marcelo A. Carmona, Francisco J. Sautua, Caroline S. Moffat, Paula M. Moolhuijzen, Pao Theen See, and Reem Aboukhaddour**
4:30	O183	**ENDOGENOUS RUST PEPTIDES FROM PUTATIVE SHORT OPEN READING FRAMES IDENTIFIED USING PEPTIDOMICS AND DE NOVO SEQUENCING STRATEGIES; Christof Rampitsch, Slavica Djuric-Ciganovic, Zhen Yao, and Mark Lubberts**

Meeting Rooms 11+12		**CPS-X Disease Management (Competition)** *Chairs: Maxime Delisle-Houde (U of Laval) & Dr. Bruce Gossen (AAFC Saskatoon)*
3:15	*O185	**CHANGES IN SENSITIVITY OF *CLARIREEDIA JACKSONII* TO THE DEMETHYLATION INHIBITOR FUNGICIDE PROPICONAZOLE AFTER 30 YEARS OF USE; Andrea Rether, Mikaela Ryan, Nava Brimble, Alexa Nguyen, and Tom Hsiang**
3:30	*O186	**IMPROVING BACTERIAL LEAF STREAK MANAGEMENT IN WHEAT: DEVELOPMENT OF A RAPID LOOP-MEDIATED AMPLIFIATION (LAMP) PROTOCOL FOR SEED TESTING; Valentina Anastasini, Heting Fu, Jie Feng, T. Kelly Turkington, Michael Harding, Constanza Fleitas, and Randy Kutcher**
3:45	*O187	**EVALUATING THE INFLUENCE OF NITROGEN ON ROOT ARCHITECTURE AND CLUBROOT RESPONSE IN *BRASSICA* GENOTYPES; Danna Rotariu, Yoann Aigu, Rudolph Fredua-Agyeman, Sheau-Fang Hwang, and Stephen Strelkov**
4:00	*O188	**EFFECTS OF FREEZE AND THAW TEMPERATURE CYCLES ON THE SURVIVAL OF PLASMODIOPHORA BRASSICAE RESTING SPORES; K. Holy, B. D. Gossen, and M. R. Mcdonald**
Meeting Room 13		**CSPB-XIII Plant Biochemistry** *Chair: Neha Vaid*
3:15	*O189	**UNRAVEL TO BUILD: PTEROCARPAN BIOSYNTHESIS FROM LEGUMES TO HETEROLOGOUS HOSTS; Audrey Cote, Brandon Saltzman, and Mehran Dastmalchi**
3:30	*O190	**CHARACTERIZATION OF A CYSTEINE PROTEASE FROM PHYTOLACCA AMERICANA AND ITS ASSOCIATION WITH POKEWEED ANTIVIRAL PROTEIN; Annabelle Audet and Katalin A. Hudak**
3:45	O191	**GLUTAMINE ACTIVATION OF TOR REGULATES PROTEIN SYNTHESIS IN DEVELOPING PEAS; Brendan O`Leary, Vinti Kumari, and Christoph Rampitsch**
4:00	*O192	**EXPLORING THE ALKENE BIOSYNTHETIC PATHWAY IN POPULUS TRICHOCARPA; Jessica Hu, Jeff Chen, Bianca Ortiz,, and Eliana Gonzales-Vigil**
4:15	O193	**POPLAR LEAF BUD RESIN BIOCHEMISTRY: SEASONAL PATTERNS AND ENZYMES FOR RESIN SYNTHESIS IN BLACK COTTONWOOD (POPULUS TRICHOCARPA); C. Peter Constabel, David Ma, and Eerik-Mikael Piirtola**
4:30	O194	**REGIOSELECTIVE O-METHYLATION OF STILBENES IN SACCHARINAE GRASSES; Nan Lin, Andy CW Lui, Kah Chee Pow, Zhuming Fan, Chen Jing Khoo, Quan Hao, and Clive Lo**
Meeting Rooms 9 + 10		**CSPB-XIV All Societies Gene Editing Session** *Chair: Andriy Bilichak*
3:15	*O195	**MODULATION OF CLOCK IN WHEAT VIA DIPLOID AND HAPLOID GENE EDITING; Sandhya Gautam, Fengying Jiang, Chelsi Harvey, Andre Laroche, Guanqun Chen, John Laurie**
3:30	*O196	**SPEED EDITING: HIGH THROUGHPUT GENE EDITING USING CRISPR/CAS9 SYSTEM IN *BRASSICA NAPUS*; Rajbir Kaur, Mohamed Samir Youssef, Robert Duncan, and Harmeet Singh Chawla**

3:45	O197	FUNCTIONAL VALIDATION OF A CANDIDATE GENE CONTROLLING SOYBEAN ROOT SYSTEM ARCHITECTURE BY CRISPR-CAS9 TECHNOLOGY; **Benjamin Karikari**, Waldiodio Seck, Davoud Torkamaneh, and François Belzile
4:00	O198	GENE EDITING-ASSISTED FUNCTIONAL GENOMICS STUDIES IN WHEAT (TRITICUM AESTIVUM L.); **Andriy Bilichak**, Louie Lopos, Emanpreet Kaur, and Natalia Bykova
4:15	O199	CRISPR/CAS9 BASED LOSS-OF-FUNCTION GENE EDITING CONFERS BROAD-SPECTRUM CLUBROOT TOLERANCE IN CANOLA; **L. Wang**, R. Wen, B. Luo, K. Yang, X. Liu, T. Dumonceaux, G. Peng, and W. Xiao

5:00 – 7:00 pm Poster Session 2 in Hall D

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

Light refreshments will be served.

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Poster Presentations

Poster presentations are grouped by society in the following order: CPS, CWSS, CBA, CSHS, CAPB, CSPB, CSA, and non-affiliated. The presenter's name is underlined. Student presentations for competition are identified by an asterisk. Poster sessions will be held in Hall D from 5:00 pm – 7:00 pm on Monday July 8 (odd numbers) and Tuesday July 9 (even numbers).

CPS (Posters P1-P51, P148)

P1	**FIRST REPORT OF *FUSARIUM SPOROTRICHIOIDES* AND *FUSARIUM CEREALIS* CAUSING ROOT ROT OF SOYBEAN IN CANADA, WITH POTENTIAL IMPLICATIONS FOR CROP ROTATION STRATEGIES;** Ahmed Abdelmagid, Mohamed Hafez, and Fouad Daayf
P2	**THE OCCURRENCE AND SPREAD OF CLUBROOT IN ALBERTA (2005-2023);** Y. Aigu, V.P. Manoli, S.F. Hwang, and S.E. Strelkov
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Abstracts for Oral Presentations

***[O1] A CELL ATLAS OF MALE AND FEMALE REPODUCTIVE STRCTURES IN POPULUS REPRESENTING MULTIOME DATA.** Oscar Felipe Nunez-Martinez[1,2], Stefan Heinen[2], Raju Soolanayakanahally[3], and Katharina Bräutigam[1,2]. [1]Cell and Systems Biology, University of Toronto, Toronto, ON, Canada; [2]Department of Biology, University of Toronto Mississauga, Mississauga, ON, Canada; and [3]Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, Saskatoon, Saskatchewan, Canada
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Reproductive development in long-lived plants such as trees is initiated from vegetative meristems on an annual basis. Shoots carry uncommitted meristems, stem cells undergo extensive reprogramming, take on reproductive identity, and eventually form mature reproductive organs. Here, we study reproductive development in trees of the genus *Populus*, an established model for tree species and promising model for floral development. Intriguingly, *Populus* is dioecious with individuals either forming male or female reproductive structures. There is currently no lineage map or cell type inventory for reproductive organs in woody plants.

Therefore, we set out to create the first cell atlas for male and female reproductive structures in *Populus*. Classical analyses utilize bulk tissue that represent the heterogeneous cell populations that make up the complex tissues and organs. Here, we apply modern single-nuclei multiome sequencing comprising the joint analysis of single-nuclei RNA sequencing and single-nuclei ATACseq (assay for transposase accessible chromatin) for an integrated characterization of transcriptomes chromatin patterns at single cell resolution.

Our work identified 34 cell clusters in female and 24 cell clusters in male reproductive organs representing 13 and 14 different cell types, respectively. For each cell type, we identified unique markers and compiled an inventory of cell-type specific marker genes for reproductive structures in *Populus*. In addition, trajectory analyses were performed to characterize differentiation pathways towards female and male reproductive tissue types. This characterization of sex-specific cell-type differentiation now allows detailed insights into molecular paths that lead cells to transition from uncommitted to specialized reproductive cell fates. Our work provides a valuable resource for investigating the principles underlying cell differentiation and characterization of reproductive structures in a woody plants, and it provide a basis for targeted reproductive engineering.

[O3] A FUNCTIONALLY REDUNDANT MAPK PATHWAY CONTROLS STIGMA RECEPTIVITY IN ARABIDOPSIS. Muhammad Jamshed[1], Subramanian Sankaranarayanan[2], Kumar Abhinandan[3], and Marcus A. Samuel[1]. [1]University of Calgary, BI 391, Department of Biological Sciences, 2500 University Dr. NW. Calgary, Alberta T2N 1N4, Canada; [2]Department of Biological Science and Engineering, Indian Institute of Technology 7 Gandhinagar, Palaj, Gujarat - 382355, India; and [3]2020 Seed Labs Inc, 507 – 11 Avenue Nisku, Alberta T9E 7N5, Canada
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In Angiosperms, pollination is a highly coordinated process, which relies on proper cell to cell communication and intricate signaling between the pollen grain and the stigmatic papillae. Successful pollination is achieved when pollen germinates on stigmatic surface and efficiently penetrates through the papillary cell to reach the ovule, where it fertilizes the egg cell. In Brassicaceae, a compatible mate (pollen), triggers the stigmatic machinery to release necessary resources required for its germination and penetration. Despite the identification of a number of stigmatic proteins that facilitate pollination responses, the early signaling machinery that regulates pollination has remained elusive. Through

combinatorial genetics and cell biological approached, we show that, in Arabidopsis, an extremely functionally redundant mitogen-activated protein kinase (MAPK) cascade is required for maintaining stigma receptivity to accept compatible pollen. Our genetic analyses demonstrate that in stigmas, five MAPK kinases (MKKs), MKK1/2/3/7/9 are required to transmit upstream signals to two MPKs, MPK3/4, to mediate compatible pollination. Compromised functions of these five *MKKs* in the quintuple mutant (*mkk1/2/3RNAi/mkk7/9*) phenocopied pollination defects observed in the *mpk4RNAi/mpk3* double mutant. We further show that this MAPK nexus converges on Exo70A1, a previously identified stigma receptivity factor essential for pollination. Given that pollination is the crucial initial step during plant reproduction, understanding the mechanisms that govern successful pollination could lead to development of strategies to improve crop yield.

***[O4] CHARACTERIZING THE ROLES OF MECHANOSENSITIVE ION CHANNEL GENES MSL7 AND MSL8 IN THE BASAL COMPATIBLE POLLEN RESPONSE IN A. THALIANA.** Paula Beronilla and Daphne R. Goring. Department of Cell and Systems Biology, University of Toronto
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In the Brassicaceae family, reproductive success is determined by the molecular dialogue between the female pistil and the male pollen. The characteristic dry stigmas of the Brassicaceae family provide a highly selective environment, where upon pollination, pollen grains must undergo compatibility checks through molecular interactions with the stigma for the acceptance of compatible pollen or the rejection of self-incompatible pollen. In the early stages of this dialogue, the basal compatible pollen response pathway facilitates the transfer of water from the stigma to the pollen, resulting in pollen hydration and pollen germination. Several regulators of pollen hydration in the stigma have been identified, but the loss of function of the identified factors only result in a mild hydration defect, signifying the involvement of other unidentified factors in this process. The objective of this research is to investigate the role of mechanosensitive ion channels of small conductance-like genes (MSLs), MSL7 and MSL8, in the basal compatible pollen response pathway in Arabidopsis thaliana. The pollen-specific MSL8 is characterized as a regulator of osmotic stress during pollen hydration and germination, and interestingly, MSL8 is tandemly-linked to the stigma-specific MSL7. We hypothesize that MSL7 functions in the transport of ions facilitating turgor pressure homeostasis in the stigma during compatible pollen responses, which may in turn impact pollen hydration. Utilizing the CRISPR/Cas9 technology, gene deletion mutants of MSL7 were generated and the role of MSL7 was investigated with other pollen hydration regulators including the pollen PCP-B ligands, and the stigma RKF1/RKFLs to gain a better understanding of the mechanism underlying pollen hydration control. The msl7 mutation resulted in a mild hydration defect upon pollination with wildtype or pcp-bα/β/γ pollen. Furthermore, this mild hydration defect was consistent in higher order mutants when msl7 was combined with msl8 or rkfΔ, suggesting that MSL7 and the RKF1/RKFLs in the stigma function in the same signaling event as the pollen PCP-Bs in regulating pollen hydration. The slower pollen hydration rates elicited by the mutant stigmas did not impact pollen germination and pollen tube growth, highlighting the role of MSL7 in the pollen hydration stage. Together, these findings support the requirement of MSL7 in the basal compatible pollen response pathway and contributes to the growing understanding of the mechanism underlying hydration control in A. thaliana.

[O5] SHOWCASING THE POWER OF SYNCHROTRON X-RAY IMAGING TOOLS FOR CROP SEED RESEARCH. Paula Ashe[1], Kaiyang Tu[2], Jarvis A. Stobbs[2], Jay Dynes[2], Miranda Vu[2], Hamid Shaterian[1], Sateesh Kagale[1], Karen K. Tanino[3], Janitha P.D. Wanasundara[4], Chithra Karunakaran[2], Teagen D. Quilichini[1]. [1]Aquatic and Crop Resource Development, National Research Council Canada, 110 Gymnasium Place, Saskatoon, Saskatchewan S7N 0W9, Canada; [2]Canadian Light Source Inc., 44 Innovation Boulevard, Saskatoon, Saskatchewan S7N 2V3, Canada; [3]Department of Plant Sciences, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada; and [4]Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, Saskatchewan S7N 0X2, Canada
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Seed-bearing plants package each embryo with nutrient reserves and a protective sheath to support survival of the next generation. The wide spectrum of light provided by synchrotron radiation illuminates internal structure and chemical composition across scales, making it an ideal, but underutilized tool for plant and seed research. This study features an array of methodologies spanning five beamlines at the

Canadian Light Source located in Saskatoon, Canada, to demonstrate the breadth of structural and chemical insights that are made possible by synchrotron-based research. Synchrotron micro-computed tomography (S-µCT) imaging revealed the three-dimensional internal structural landscape of seeds in exquisite detail. Synchrotron X-ray methods that probe chemical landscapes, including X-ray absorption spectroscopy (XAS), X-ray fluorescence (XRF) imaging and spectroscopy in the infrared spectrum, were used to spatially map the distribution of micronutrients (for elemental distributions and speciation data) and macronutrients (e.g., proteins, carbohydrates and lipids) across seed subcompartments. Spectromicroscopy (SM), employing synchrotron-based soft X-rays, probed sample biochemistry with nano-scale resolutions. Seed datasets presented span a range of valued food and crop species, including *Citrullus* sp. (watermelon), *Pisum sativum* (pea), *Brassica* sp. (canola), and *Triticum durum* (wheat), to showcase the broad potential for synchrotron imaging to inform plant and agricultural research.

[O6] FLOWER OPENING; ARF2-MYB6 MODULE MEDIATES AUXIN-REGULATED PETAL EXPANSION IN *ROSA HYBRIDA*. Nisar Hussain[1,2], Changxi Chen[1], Xiaoming Sun[1], and Junping Gao[1]. [1]Beijing Key Laboratory of Development and Quality Control of Ornamental Crops, China Agricultural University, Beijing, 100193, China, and [2]Department of Production Technology, Kunming 24Hua Modern Agricultural Technology, Kunming, China
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Flower opening is a complex biological process that promotes pollination and determines the market value of flowers. Most cut roses are supplied by long-distance transportation, which disturbs proper flower opening and diminishes the ornamental period. Elucidating the mechanism of flower opening would benefit both plant science and commercial horticulture. This study aims to explore the regulatory networks of transcription factors (TFs) involved in flower opening and their role in petal cell expansion. Here, we identified an auxin-inducible transcription factor gene *RhMYB6*, whose expression level is high during the early stages of flower opening. Silencing of *RhMYB6* delayed flower opening by controlling petal cell expansion through downregulation of cell expansion–related genes. Furthermore, we demonstrated that the auxin response factor RhARF2 directly interacts with the promoter of *RhMYB6* and represses its transcription. Silencing of *RhARF2* resulted in larger petal size and delayed petal movement. We also showed that RhARF2 plays a role in petal movement by regulating the expression of ethylene biosynthesis and signaling pathway genes. Our results indicate that auxin-regulated RhARF2 is a critical player that controls flower opening by governing *RhMYB6* expression and mediating the crosstalk between auxin and ethylene signaling. This study reveals the molecular mechanism of petal expansion and provides theoretical sustenance for the molecular breeding of ornamental crops.
Keywords: rose, flower opening, auxin, petal expansion, RhARF2, RhMYB6

***[O7] NESTED ASSOCIATION MAPPING TO IDENTIFY STRIPE RUST RESISTANCE LOCI AND THEIR MARKERS IN SPRING WHEAT.** Simranjeet Kaur[1,2], Raman Dhariwal[2], Gurcharn Singh Brar[1], and Harpinder Singh Randhawa[2]. [1]University of Alberta, 116 St & 85 Ave, Edmonton, AB, Canada, AB T6G 2R3; and [2]Lethbridge Research Centre, Agriculture and Agri-Food Canada, 5403 1 Ave S, Lethbridge, AB, Canada, AB T1J 4B1
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Stripe rust of wheat, caused by *Puccinia striiformis* f. sp*. tritici* (*Pst*), categorized as the "priority one" disease for Western Canadian breeding programs, is one of the most threatening diseases to wheat production. Genetic resistance is the most effective approach among all the management strategies. However, the evolving pathogen defeats the genetic resistance and contributes to the geographical expansion of the infection sites. Thus, we developed a large, nested association mapping (NAM) population of more than 2900 recombinant inbred line (RIL) families involving 16 resistance donors to identify stripe rust-resistance genes. This multiparent population approach combines the advantages of linkage and association mapping to achieve high-resolution and high-mapping power. We screened these RIL families at three locations (Edmonton, Lethbridge, and Creston) to obtain coefficient of infection (CI) values and further processed CI values to improve the normality followed by single nucleotide polymorphism (SNP) genotyping. We processed the genotypic data of all individual populations and developed SNP genetic maps. We are conducting the QTL mapping across all RIL families in the NAM population separately to identify quantitative trait loci and markers for resistance to stripe rust in individual NAM populations.

***[O8] GENOMIC PREDICTION FOR IMPROVING WINTER HARDINESS AND FUSARIUM HEAD BLIGHT RESISTANCE IN WINTER DURUM WHEAT.** Ritesh K. Yadav[1,2], Raja Ragupathy[2], Gavin Humphreys[3], Demissew S. Desta[2], André Laroche[1], Harmeet S. Chawla[2], Marcos Cordeiro[4], Akshaya Vasudevan[5], Harpinder S. Randhawa[1], and Curt A. McCartney[2]. [1]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada (AAFC), 5403 1st Avenue South, Lethbridge, Alberta, Canada T1J 4B1; [2]Department of Plant Science, University of Manitoba (Fort Garry Campus), 66 Dafoe Road, Winnipeg, MB, Canada, R3T 2N2; [3]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada (AAFC), 960 Carling Avenue, Ottawa, Canada, ON K1A 0C6; [4]Department of Animal Science, University of Manitoba (Fort Garry Campus), 12 Dafoe Road, Winnipeg, MB, Canada, R3T 2N2; and [5]Department of Plant Breeding, Hochschule Geisenheim University, Geisenheim, 65366 Hesse, Germany
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Fusarium head blight (FHB) disease resistance and winter hardiness are the two priority traits in the Canadian winter durum wheat breeding program. These traits, influenced significantly by polygenic factors and environmental conditions, are crucial given the ongoing climate change challenges in Western Canada, such as rising temperatures and escalating drought risks. There is only a single winter durum cultivar (OAC Amber) registered in Eastern Canada in 2010, which remains uncommercialized. At present, no winter durum wheat candidates are available for testing in Western Canada. Recently, joint Genome-Wide Association Study-Genomic Selection (GWAS-GS) and haploblock based GS approach have shown great potential for deciphering the genetic basis of complex traits, facilitating more accurate prediction of breeding values and enhancing genetic gains for difficult-to-phenotype and complex traits, such as FHB resistance and winter hardiness. In our study, we assembled a diverse panel of 292 winter durum accessions from Canada, Europe, and the USA, including in-house winter hexaploid wheat x durum cross derivatives. The panel was phenotyped for FHB resistance and winter hardiness at multi-location trials in Winnipeg, Carman, and Ottawa during the 2021-23 seasons, with ongoing trials in 2023-24. Genotyping was performed using Genotyping-by-Sequencing, and SNPs were called against the durum cv Svevo.v1 reference assembly. Genetic structure analyses (phylogenetic, principal component and ancestry analyses) clustered the accessions into six sub-populations. We utilized multi-locus GWAS models, including FarmCPU, mrMLM, FASTmrEMMA, ISIS EM-BLASSO, pKWmEB, pLARmEB, and a haploblock-based multi-locus analysis (RTM-GWAS), to identify loci associated with the target traits. A total of 14,486 haploblocks were constructed, using criteria such as a minimum minor haplotype frequency of 0.05, a maximum block length of 100 kb, and a informative strong linkage disequilibrium threshold of 0.95. Our analysis detected 121 QTNs associated with FHB resistance traits and 15 QTNs for winter hardiness. Of these, 25 QTNs for FHB resistance and 4 for winter hardiness were detected by two or more multi-locus models. Additionally, haplotype-based GWAS identified significant singletons (independent blocks) on chromosomes 5B and 2A and a notable haploblock on chromosome 2B for winter hardiness, along with critical haploblocks on 5A and 7B and singletons on 1A, 1B, 7B, 5B, and 6B for FHB resistance. Further we will employ a joint GWAS-GS approach using the identified SNPs, haploblocks, and singletons as fixed effects in various genomic prediction models, including parametric methods (GBLUP and RRBLUP), Bayesian approaches, non-parametric methods like Random Forest and RKHS, and haploblock-based genomic prediction.

***[O9] ENHANCEMENT OF TOTAL SHOOT LIPID CONTENT (TSLC) IN PERENNIAL LEGUME FORAGES USING CHEMICAL MUTAGENESIS.** Mohammed Musthafa Mukthar[1,2], Tharangani Somarathna[2], Bin Shan[2], Guanqun (Gavin) Chen[2], Stacy Singer[1,2], and Hari Poudel[1]. [1]Lethbridge Research and Development Center, Agriculture and Agri-Food Canada, Lethbridge, AB; and [2]Department of Agricultural, Food, and Nutritional Science, University of Alberta, Edmonton, AB
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Inefficient enteric fermentation in ruminants accounts for 28% of anthropogenic methane emissions, potentially reducing the feed efficiency by up to 15%. Increasing the amount of lipids in the vegetative tissues of forages can reduce such methane emissions. While this has been achieved through lipid supplementation in ruminants' diet, it is often costly and sometimes impractical. Alfalfa (*Medicago sativa* L.), is a notable legume forage crop in terms of ruminant rations and export value, and sainfoin

(*Onobrychis viciifolia*), which is a condensed tannin-producing forage, is gaining considerable interest in Western Canada because of its bloat-free status and compatibility with alfalfa. However, available cultivars of both of these crops contain < 3% lipid, where ruminants can utilize forages with up to 7 – 8% TSLC (dry weight basis) without impairing their performance. As such, the objective of this study is to generate chemically mutagenized alfalfa and sainfoin populations with increased TSLC, and further our understanding of the mechanisms driving improvements in lipid accumulation using RNA-Seq. For each alfalfa (cv. AC Blue J) and sainfoin (cv. AAC Mountainview) cultivar, approximately 500 mutant plants generated through treatment with 0.5-1% ethyl methane sulfonate (EMS), as well as 100 water-treated (control) plants, were established in the greenhouse. TSLC was predicted using standard equations developed by the NIRS consortium, allowing for subsequent downsizing to 50 individuals in high-lipid and low-lipid pools with 10 random individuals in the control pool. The downsized population was then evaluated for TSLC using Gas Chromatography-Mass Spectrophotometry (GC-MS), which not only validated the NIRS method but also served as a selection criteria. Based on the GC-MS results, 16-18 genotypes were selected in each pool for each species. The selected high lipid pool exhibited a 13% relative increase and the low lipid pool exhibited an 11% relative decrease in TSLC compared to water-treated controls for both alfalfa and sainfoin. The selected genotypes (M2) were crossed to generate 16-18 high and low lipid M3 half-sib (HS) families representing each selected plant. Stem cuttings of these selected genotypes were utilized for morphological assessments to identify differences in agronomic performance that could potentially be caused by random mutations. Two genotypes from each category of alfalfa were used for RNA-Seq to identify genes related to lipid biosynthesis and accumulation. The application of chemical mutagenesis breeding to develop new germplasm with high TSLC may contribute to the provision of sustainable ruminant feed that lowers greenhouse gas emissions from agricultural production.

***[O10] IDENTIFYING KEY PHENOTYPIC AND GENOTYPIC TRAITS LINKED TO TRANSPIRATION EFFICIENCY AGAINST INDIVIDUAL AND COMBINED HEAT AND DROUGHT STRESSES IN CONTRASTING WHEAT GENOTYPES.** Abdul Halim[1], Raju Soolanayakanahally[2], and Karen Tanino[1]. [1]College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada
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Environmental changes especially increasing global warming and desertification have already thrown a challenge to global food security. Traditionally, researching the effects of environmental stress on plants has been conducted either under growth chamber or under field conditions in multiple locations over multiple years. With increasing annual variability in our climate, controlling environmental factors such as temperature and soil moisture are the main challenges to conduct this type of research under field conditions. With a view to overcome this challenge, for the first time we introduced an automated Hi-Tunnel system in Canada which can impose not only drought or heat stress individually, but also applies the combined stress of heat x drought, along with the control. We built a series of 12 Hi-Tunnels (4 treatments x 3 replications) with a motorized plastic roll-up/down system that regulates day temperature and automatically serves as a rain shelter. Under the present study, 47 spring wheat genotypes from diverse sources (Canada, Australia, and Mexico) were collected, grown in these Hi-Tunnels, and screened under the stress treatments to identify the most tolerant and susceptible contrasting genotypes. Among wheat, the CIMMYT genotypes from Mexico showed the most consistent tolerance across all stresses with stable grain yield whereas certain other genotypes including the founder line, Red Fife, showed the most susceptibility with highly variable yields across the treatments. A set of six contrasting genotypes will be used for further in-depth studies on Transpiration efficiency (TE). The role of stomata and cuticular wax on TE will be examined at both the physiological and molecular levels including the AP2/ERF TF gene family.

***[O13] A SINGLE NUCLEUS ATLAS OF TRANSCRIPTIONAL RESPONSES TO GROWTH-ALTERING STRESS: DROUGHT, SALINITY, AND FLOODING.** Sean Robertson[1] and Olivia Wilkins[1]. [1]Department of Biological Sciences, University of Manitoba, Winnipeg, MB R3T 2N2, Canada
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Single-nuclear RNA-sequencing allows for in-depth characterization of transcriptome differences between plant cell types and states during cell fate specification and maturation. This technology can be used to profile stress responses of individual cells in developing leaves at a resolution not possible with bulk RNA

sequencing. Here, we perturbed the growth and development of emerging leaves in rice seedlings by applying different severities of osmotic stressors: mild and severe drought, mild and severe salinity, and 12- and 24-hour waterlogging. These conditions were sufficient to reduce: leaf initiation, elongation rate, and length; length of the division zone within the leaf growth zone; and gas exchange measures of carbon assimilation, stomatal conductance, and transpiration. Given the altered developmental and physiological states of plants grown in each condition, we measured the transcriptomes of individual nuclei harvested from emerging leaves to investigate osmotic stress responses during leaf development.

With a dataset of >100,000 high-quality nuclei, we identified transcriptome signatures of a developmental gradient of cell states for each of the major tissue systems, from their origin as dividing cells in the shoot apical meristem to mature cells in epidermal, mesophyll, and vascular tissues. We show that there is extensive heterogeneity between cell types with respect to their responses to different stressors. Mild drought, mild salinity, and both waterlogging treatments induce minor transcriptomic changes across most cell populations, while severe drought and salinity induce substantial, yet similar, changes of developmental trajectories, especially in the development of mesophyll cells. Generally, cells in early stages of cell fate specification have stronger transcriptomic responses to stress than dividing and mature cells. Additionally, the majority of stress-responsive genes are only differentially expressed in a single cell type or state.

Overall, our results indicate that osmotic stressors induce highly specific responses in distinct cell populations of developing leaves, dependent on the cell type and stage of development. This knowledge can guide rational engineering of crops for enhancing stress tolerance by highlighting cell state-specific responses that are indiscernible in bulk analyses.

***[O14] COMBINED EXPOSURE TO LOW PHOSPHATE AND SALT ELICITS DIFFERENT PHENOTYPIC AND TRANSCRIPTIONAL RESPONSES FOR TWO EXTREMOPHILE ECOTYPES.**

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Salt cress, *Eutrema salsugineum,* is a highly stress-tolerant, halophytic relative of *Arabidopsis thaliana* and the oilseed crop, canola. *E. salsugineum* found in the Yukon, Canada, tolerates low inorganic phosphate (Pi) with seedlings displaying similar root architecture when grown on low-Pi (0.05 mM) or Pi-supplemented (0.5 mM) agar. In contrast, an ecotype from Shandong, China, has shortened primary roots when grown on low-Pi vs Pi-supplemented medium. We also tested the impact of adding 150 mM NaCl to the medium and on both low-Pi and high-Pi agar, Yukon seedlings had significantly larger shoots and longer lateral roots compared to Shandong plants. Transcriptomes from plants grown on low-Pi and Pi-supplemented media in the absence or presence of 150 mM NaCl were compared. We used two software platforms (DESeq2 and NOISeq) to detect differentially expressed genes (DEGs) and found around 100 low-Pi responsive genes, a number representing less than 1% of the coding capacity of the *E. salsugineum* genome. Pairwise comparisons between transcriptomes showed that the fewest DEGs, 0 to 20 depending on the software used, were between Yukon plants grown on low-Pi agar without salt vs 150 mM NaCl. In a similar comparison, Shandong plants on low-Pi had five thousand salt-responsive DEGs providing evidence that this treatment combination generates substantively different ecotype-specific reprogramming. We hypothesize that Yukon plants may be advantaged relative to Shandong plants by needing fewer DEGs and perhaps lower associated costs to support growth under low Pi when salt is present. Among the DEGs were genes encoding Pi transporters, notably members of the *EsPHT1;3* family, and the lipid remodeling enzyme *glycerophosphodiester phosphodiesterase* **(***EsGDPD*). RT-qPCR analysis of the *PHT1;3* family members predicts a greater low-Pi response and higher induction of *EsPHT1;3s* transcript levels for Shandong relative to Yukon plants, an observation that does not adequately explain the better growth observed for Yukon plants on low Pi. We also investigated the reuse of Pi in lipid remodeling between the ecotypes. Preliminary comparisons between polar lipids of both ecotypes grown with low or supplemented-Pi indicates relative phospholipid content is reduced by about 10% for plants grown on low relative to supplemented-Pi level. The similar decrease in relative phospholipid content seems unlikely an explanation for the differential low-Pi tolerance between the

ecotypes. Identifying traits that confer low-Pi tolerance using plants adapted to extreme environments can guide efforts to improve crop productivity on global soils experiencing declining fertility and increased salinity.

[O15] DISSOCIATED FLOWERING AND COLD ACCLIMATION IN BRACHYPODIUM HYBRIDUM PROVIDE INSIGHTS INTO THE ADAPTIVE RESPONSES TO LOW TEMPERATURES IN CEREALS.
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Understanding how plants adapt to environmental changes is increasingly critical for designing more resilient agricultural systems. In cereals, flowering time and cold acclimation are typically interconnected, with cold periods often triggering flowering while simultaneously preparing the plant to withstand low temperatures. This is the case in the temperate grass model Brachypodium distachyon, where cold acclimation and vernalization are linked via VERNALIZATION1 and mechanisms of transcriptional memory. Finding Brachypodium accessions that undergo cold acclimation without simultaneous vernalization would therefore facilitate the characterization of cold acclimation in temperate grasses, but this has so far been elusive. Here, we report the isolation of a B. hybridum accession, an allotetraploid of B. distachyon and B. stacei parents, in which cold exposure confers high freezing tolerance but has no effect on flowering time. Results show that B. hybridum expresses the cold acclimation traits of B. distachyon, including the increase of VERNALIZATION1 expression, which, however, has no influence on FLOWERING LOCUS T expression and flowering. Moreover, B. hybridum showed a high adaptability compared to B. distachyon, highlighting possible mechanisms for its radiation into new environments. This research not only sheds light on the evolutionary advantages of such dissociation in B. hybridum but also opens new avenues for developing cold-resistant cereal varieties.

***[O16] TRANSCRIPTIONAL REPRESSION OF *MSWOX13-2* IN ALFALFA ENHANCES TOLERANCE TO WATERLOGGING STRESS.**
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Soil waterlogging events are expected to increase worldwide due to climate change, posing a major threat to the sustainability of alfalfa and livestock production in coming years. To cope with abiotic stresses, plants utilize sophisticated adaptive mechanisms, reprogramming their transcriptional networks through the modulation of transcription factors (TFs). WUSCHEL-related homeobox (WOX) TFs are known for their involvement in various developmental processes and abiotic stress responses; however, their role in waterlogging resilience has yet to be examined. In this study, we characterized the alfalfa *MsWOX13-2* gene, which we found to be expressed preferentially in roots and differentially under waterlogging stress. While the RNAi-mediated down-regulation of *MsWOX13-2* in alfalfa had no significant effects on growth or morphological characteristics under control conditions, under waterlogged conditions, *MsWOX13-2* RNAi plants exhibited enhanced performance, as evidenced by a reduced impact of stress on morphology and greater survivability compared to empty vector (EV) control genotypes. In addition, *MsWOX13-2* RNAi genotypes exhibited an apparent reduction in leaf chlorosis under waterlogging, which correlated with higher chlorophyll retention and maximum quantum efficiency of photosystem II (F_v/F_m), compared to EV genotypes. This reduction in stress symptoms may be linked, at least in part, with the fact that *MsWOX13-2* RNAi leaves accumulated less malondialdehyde (MDA), which is a marker for oxidative stress, and displayed higher superoxide dismutase (SOD) activity. RNA-Seq analysis confirmed alterations in transcript levels of genes related to photosynthesis, antioxidant activities, anaerobic respiration, cell wall modulation, phytohormones and transcription factors. Taken together, our results indicate that *MsWOX13-2* functions as a negative regulator of waterlogging stress response in alfalfa, providing a novel putative target gene for downstream gene editing and/or breeding efforts in this species.

***[O17] PLANT GROWTH-PROMOTING PHYTOMICROBIOME BACTERIA: ENHANCED CROP PERFORMANCE UNDER SALINITY STRESS AND FOR GREENHOUSE GAS MANAGEMENT.** Rania Alrasheed[1], Sowmyalakshmi Subramanian[1], Michael Fefer[2], and Donald L. Smith[1]. [1]Department of Plant Science, McGill University, Montreal, QC, Canada; and [2]Suncor AgroScience, Mississauga, ON, Canada
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This review explores the role of plant growth-promoting bacteria (PGPB), specifically individual strains from the genera *Bacillus, Pseudomonas,* and *Mucilaginibacter*, in increasing crop resilience to salinity stress, potentially exacerbated by ongoing climate change and soil degradation. We detail mechanisms such as hormonal regulation and nutrient solubilization that enhance stress tolerance. Studies show PGPB application improves salinity tolerance in crops such as canola, soybean, and wheat, enhancing yield and soil health. The integration of PGPB into agricultural systems is discussed, highlighting application methods (including use of microbe-to-plant signals), timing, and compatibility with conventional farming. Benefits extend beyond reducing salt stress, including decreased reliance on chemical fertilizers and improved agricultural sustainability. The review identifies gaps in understanding PGPB-plant interactions under stress and suggests further research areas, including genetic engineering and application techniques. Advocating extensive research, this paper highlights PGPB roles in sustainable agriculture, addressing climate change and food security challenges.

***[O18] *TETRANYCHUS URTICAE* METABOLIC RESPONSES TO *ARABIDOPSIS THALIANA* DEFENSIVE PHENYLPROPANOIDS.** A. Harrison, C. Sharma, K. Bruinsma, J. Maglov, M. Bernards, and V. Grbic.
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Tetranychus urticae – the two spotted spider mite – is a global pest that poses a threat to hundreds of economically important agricultural crops. *T. urticae* possess a strong xenobiotic detoxification capability and short generational cycle that enables them to develop rapid resistance to pesticides and quickly establish high performance on initially unfavorable hosts. Additionally, the genome of *T. urticae* reveals a large arsenal of detoxification enzymes that may attribute to host promiscuity and overall composite generalist capacity, such as: cytochrome P450s (CYPs), glutathione-S-transferases (GSTs), and UDP-glucuronosyltransferases (UGTs). Little is known about the underlying mechanisms that allow *T. urticae* to overcome plant defenses, or the roles that individual plant metabolites play in plant-mite interactions. Therefore, this study aims to (1) establish the role phenylpropanoids, a large family of secondary metabolites, play in *Arabidopsis thaliana* defense to mite herbivory, and (2) uncover the metabolic responses of *T. urticae* following exposure to Arabidopsis defensive phenylpropanoids. To achieve these goals, *T. urticae* reared on *Arabidopsis thaliana* and an ancestral population reared on *Phaseolus vulgaris* were exposed to Arabidopsis phenylpropanoids to assess chemical toxicity and effect on mite fecundity. Moreover, the metabolic profiles of both mite populations following exposure to Arabidopsis phenylpropanoids were compared to determine mechanisms of mite metabolism that may drive increased generational performance on initially unfavorable hosts. Recent results indicate sinapoyl malate as a non-differentially toxic Arabidopsis phenylpropanoid to both bean-reared and Col-reared mites, but exclusively reduces the fecundity of bean-reared mites. Further analysis of mite metabolomic data should reveal the mechanisms behind differential population response to this Arabidopsis phenylpropanoid. This research could broaden our understanding of the roles phenylpropanoids play in plant defense to herbivory, as well as the mechanisms that allow *T. urticae* to act as a composite generalist.

***[O19] THE IMPACT OF ELEVATED TEMPERATURE ON NPR1 PROTEIN REGULATION IN PIPECOLIC ACID-MEDIATED IMMUNITY IN *ARABIDOPSIS THALIANA*.** Spencer Tout[1] and Christian Danve M. Castroverde[1]. [1]Department of Biology, Wilfrid Laurier University, 75 University Ave W, Waterloo, ON, Canada, N2L 3C5
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Healthy plant development requires balancing both climatic and pathogen challenges, which intercept important signaling responses in plants. For example, climate change-associated elevated temperature can negatively modulate various aspects of plant immunity, including the production of central immune signals salicylic acid (SA) and N-hydroxypipecolic acid (NHP). Since SA and NHP signaling both require the master immune co-activator NON-EXPRESSOR OF PATHOGENESIS-RELATED GENES 1 (NPR1),

we are investigating NPR1 as a potentially temperature-regulated molecular hub. Although the *NPR1* gene is not transcriptionally downregulated at elevated temperatures (28°C vs. 23°C), little is known about the translational and/or post-translational regulation of NPR1 by Pip treatment under warmer temperature conditions. In this study, we have investigated the effect of exogenous Pip treatment on NPR1 protein levels, nuclear localization and phosphorylation under changing temperatures in the model species *Arabidopsis thaliana*. Immunoblot analysis of total protein extracts was performed to evaluate temperature-regulated changes in NPR1 protein levels after Pip treatment. Laser confocal microscopy of Arabidopsis leaves was conducted to observe Pip-mediated NPR1 nucleocytoplasmic dynamics at both ambient and warm temperatures. Lastly, variations in Pip-induced NPR1 phosphorylation under different temperatures were analyzed using Phos-tag™ gel electrophoresis and immunoblotting, which can distinguish between phosphorylated and non-phosphorylated NPR1 proteins. Experiments are being replicated to make robust conclusions, but preliminary observations suggest a thermosensitive trend in NPR1 protein induction, subcellular localization and post-translational regulation. Collectively, this research aims to build on our conceptual understanding of NPR1-mediated immune signaling and to identify molecular nodes that are vulnerable to changing environmental factors, such as elevated temperature. Understanding these molecular mechanisms provides an organizing framework for future genome engineering to develop more climate-resilient and disease-resistant plants.

***[O20] FER KINASE AND CELL WALL SENSORS LRX1/2 REGULATE MICROBIOME IN A PHOSPHATE-DEPENDENT MANNER.** Siyu Song[1], Keegan J. McDonald[1], Melissa Y. Chen[1], Zayda Morales Moreira[1], and Cara H. Haney[1,2]. [1]Department of Microbiology and Immunology, University of British Columbia, Vancouver, BC, Canada; and [2]Department of Biological Sciences, The University of Pittsburgh, Pittsburgh, PA, USA
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Plants establish beneficial associations with rhizosphere microbiota through fine-tuning immune responses and metabolic processes, thereby promoting growth and enhancing resilience to biotic and abiotic stresses. However, the detailed genetic mechanisms by which plants determine the functional outcomes of the rhizosphere microbiome community structure and function remain largely unknown. Here, through screening Arabidopsis leucine-rich repeat extensins (LRXs) mutants for altered rhizosphere Pseudomonas growth, we identified lrx1/2 mutants with enriched rhizosphere P. fluorescens in natural soil that phenocopies previously described feronia (fer) loss-of-function mutants. 16S rRNA microbiome sequencing demonstrated that lrx1/2 and fer-4 exhibited similar microbiome shifts with an overall microbial diversity decrease in natural soil. Microbiome functional analysis suggests a connection between altered microbial composition and the observed stunted plant growth of lrx1/2 and fer-4, indicative of a dysbiotic state. FER has been reported to regulate the microbiome in adaptation to environmental phosphate changes. Microbiome sequencing under both naturally limiting and sufficient phosphate conditions revealed that lrx1/2 and fer-4 exhibit distinct microbiome structures with supplemented phosphate: while the fer-4 mutant exhibits a phosphate-responsive microbiome, the lrx1/2 mutant remained unchanged regardless of phosphate availability. These observations suggest that FER and LRX1/2 may jointly contribute to microbiome regulation under phosphate-limiting conditions, but not when phosphate is abundant. In conclusion, our research sheds light on the crucial roles of LRX1/2 and FER in preventing microbiome dysbiosis and adapting to environmental phosphate changes. These results lay the foundation for future studies to decipher the genetic pathways underlying plant regulation of the rhizosphere microbiome, and develop methods to cultivate beneficial microbiomes to bolster plant resilience under environmental stress.

***[O21] DISTINCT PLANT IMMUNE RESILIENCE MECHANISMS IN DIVERSE ACCESSIONS OF *ARABIDOPSIS THALIANA*.** Christina AM. Rossi[1], Dhrasti N Patel[1], and Christian Danve M. Castroverde[1]. [1]Department of Biology, Wilfrid Laurier University, 75 University Ave W, Waterloo, ON, N2L 3C5
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Previous research has demonstrated that elevated temperatures suppress the biosynthesis and signaling of the central plant defence hormone salicylic acid (SA) in diverse plant species, including both monocots and dicots. In the model dicot species *Arabidopsis thaliana*, temperature-regulated immunity studies have focused on the reference accession Columbia-0 (Col-0), which exhibits reduced disease resistance under

warmer conditions. However, the natural variation of Arabidopsis immunity at elevated temperature remains a major knowledge gap, representing a critical roadblock to our understanding of the plant disease triangle facing climate change. Using a previously published collection of natural accessions, we have identified temperature-resilient and -sensitive Arabidopsis accessions based on disease resistance to the important pathogen *Pseudomonas syringae* pv. *tomato* (*Pst*) DC3000, which belongs to a bacterial species that infects numerous plant species. Temperature-sensitive or -resilient immunity did not correlate with DNA or protein sequence polymorphisms in BASIC HELIX LOOP HELIX 059 (bHLH059), a recently discovered thermosensitive SA regulator at non-stress temperatures. In agreement, *bhlh059* mutants exhibited temperature-sensitive defences (i.e. higher *Pst* pathogen loads at warm temperature), suggesting that bHLH059 does not regulate immune suppression at elevated temperature. To further elucidate the mechanistic basis of temperature-resilient immunity in certain Arabidopsis accessions, we performed gene expression analysis of *CBP60g* and *SARD1*, which control the temperature-vulnerability of SA-mediated plant immunity in the Col-0 accession. Intriguingly, we found that different temperature-resilient accessions exhibit both thermoresilient and thermosensitive *CBP60g* and *SARD1* expression profiles, suggesting the existence of both CBP60g/SARD1-dependent and independent mechanisms of plant immune resilience to warming temperature. Collectively, we have shed light on the intraspecific diversity of Arabidopsis immune responses under warm temperatures, which is bHLH059-independent but differentially mediated by the master immune transcription factors CBP60g and SARD1. Our dissection of mechanisms underlying temperature-modulated plant immunity could aid in predicting plant responses to climate change and provide foundational knowledge for climate-resilient crop engineering.

***[O22] AGE-RELATED RESISTANCE REQUIRES SALICYLIC ACID SIGNALING VIA NPR PROTEINS AND RESULTS IN THE MODEST ACCUMULATION OF N-HYDROXYPIPECOLIC ACID IN LEAVES.**

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In *Arabidopsis thaliana*, leaves of young plants are susceptible to the bacterial pathogen *Pseudomonas syringae* pv. *tomato* (*Pst*) while leaves of mature plants display Age-Related Resistance (ARR). RNA-sequencing was used to investigate how mature plants become competent for ARR. This analysis revealed that Systemic Acquired Resistance (SAR)-associated genes were upregulated during ARR. SAR is a defense response in which a local infection in one leaf leads to the production of signals that spread to distant leaves and induce an immune ready/primed state in the distant naïve leaves. This immune ready state in SAR results in modest expression of cell-surface receptors and genes responsible for the biosynthesis of N-hydroxypipecolic acid (NHP). We demonstrated that NHP biosynthesis was required for ARR, modest expression of NHP biosynthesis genes was associated with an ARR-competent state in mature naïve leaves and NHP genes were highly expressed following inoculation with *Pst*. To confirm that NHP is produced in ARR-competent and ARR-responding leaves, NHP was quantified by LC-MS/MS of leaf samples collected from untreated or *Pst*-inoculated young ARR-incompetent and mature ARR-competent plants. NHP was observed to accumulate to modest levels in leaves of mature ARR-competent naïve plants. Similar to observations of SAR-induced distant leaves, naïve ARR-competent leaves expressed cell-surface receptors *RLP23* and *RLP28*, suggesting that ARR includes an immune ready/primed state similar to SAR. To obtain further evidence of the similarities between ARR and SAR, the role of the SA receptors NPR1 and NPR4 were examined in the *npr1-1 npr4-4D* mutant, which is defective in SA perception, SAR, and NHP-induced systemic immunity. The *npr1-1 npr4-4D* mutant was fully ARR-defective suggesting that ARR requires SA signaling via NPR proteins. To determine if NPR proteins are downstream of NHP biosynthesis gene regulation, the expression of *ALD1* and *FMO1* was examined in naïve leaves from young and mature *npr1-1 npr4-4D* mutants. Expression of *ALD1* and *FMO1* was unaffected in *npr1-1 npr4-4D* however, expression of the cell-surface receptor *RLP23* was reduced in the mature leaves of *npr1-1 npr4-4D* suggesting that during ARR, NPR signaling is downstream of NHP but upstream of the ARR immune ready/primed state.

[O23] BOTTOM COOLING DURING CULTURE INITIATION INCREASES SURVIVAL AND REDUCES HYPERHYDRICITY IN MICROPROPAGATED CANNABIS PLANTS. Rambod Abiri[1], Declan O'Reilly[1], and Andrew Maxwell Phineas Jones[1]. Department of Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1, Canada
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Hyperhydricity is a common disorder during micropropagation of cannabis, typified by morphological abnormalities, reduced vigour and multiplication rates, poor rooting, and low survival during acclimatization. The present investigation aimed to prevent hyperhydricity and promote healthy growth of cannabis by utilizing a bottom cooling system during stage 1 of micropropagation (culture initiation). Nodal explants from two clonal triploid cultivars known to exhibit hyperhydricity in vitro, Higher Education 1 (HEd1) and Higher Education (HEd2), were surface sterilized and placed in culture tubes using standard methods. The culture tubes were then cultured in the following three treatment groups:(i) On metal pads with hydronic bottom cooling, ii) On metal pads without bottom cooling (first control), and (iii) directly on the metal shelving unit without bottom cooling (second control). To assess the effect of bottom cooling, various morphological and physiological traits including a detached leaf water loss assay to assess cuticle and stomatal function, leaf dry mass, chlorophyll fluorescence ratio, chlorophyll content, survival rate, number of leaflets per explant, number of primary serrations of the central leaflet, plant height (mm), and length of the central leaflet were measured. Plants cultured with bottom cooling had a higher survival rate and were healthier with vibrant green coloration, firm and turgid shoots, normal leaf morphology, better leaf to tissue ratio, and vigorous growth. In comparison, a large portion of explants initiated without bottom cooling were hyperhydric, with translucent brittle leaves and abnormal growth. Quantitative data indicated significant positive effects of bottom cooling on fresh and dry weight, chlorophyll fluorescence ratios, chlorophyll content, and cuticle/stomate function for both cultivars. This study confirmed that bottom cooling helps reduce the rate and impacts of hyperhydricity in cannabis and significantly improves survival and quality of in vitro plants.
Keywords: Cannabis; hyperhydricity; oxidative stress; micropropagation; bottom cooling

***[O24] OPTIMIZING *EX-VITRO* ONE-STEP RUBY-EQUIPPED HAIRY ROOT TRANSFORMATION IN DRUG- AND HEMP-TYPE CANNABIS.** Ladan Ajdanian, Mohsen Niazian, and Davoud Torkamaneh. Département de phytologie, Université Laval, Québec City, QC, Canada, Institut de Biologie Intégrative et des Systèmes (IBIS), Université Laval, Québec City, QC, Canada, Centre de recherche et d'innovation sur les végétaux (CRIV), Université Laval, Québec City, QC, Canada, Institute Intelligence and Data (IID), Université Laval, Québec City, QC, Canada
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Cannabis (*Cannabis sativa* L.), once concealed by the veil of prohibition, is now emerging as a versatile and promising plant species, riding the wave of recent legalization. This transformation has unlocked unprecedented opportunities for both medical research and industry growth, positioning cannabis on a trajectory to reach a projected market size of USD 444.34 Billion by 2030. Despite the plant's capability to produce more than 545 potentially bioactive secondary metabolites, its legal categorization in Canada, the USA, and Europe hinges on the concentration of a solitary cannabinoid, Δ^9-tetrahydrocannabinol (THC), found in female flowers. In recent decades, hairy root (HR) culture, an established method facilitated by *Agrobacterium rhizogenes*-mediated transformation techniques, has gained significant attention by academic research teams, biotechnology companies and pharmaceutical industries as a convenient and viable approach to produce target metabolites due to its rapid growth and stability in terms of both biochemistry and genetics. Obtaining suitable HRs from *A. rhizogenes* represents the pivotal the initial step in producing secondary metabolites from transformed HRs. While a method for the *in-vitro* HR induction of cannabis has been proposed, there is currently no reported *ex-vitro* method. Here, we optimized an *ex-vitro* one-step HR transformation of the *RUBY* system in both drug- and hemp-type cannabis, shedding light on its potential applications in secondary metabolite production. Ten-day-old seedlings were diagonally excised from the apical portion of the hypocotyl using a sterile scalpel and subsequently inoculated with three different *A. rhizogenes* strains (A4, ARqual, and K599). Inoculated seedlings were enclosed in paper bags and placed in a growth chamber. HRs emerged 10 days post-inoculation, at the cutting place, and putative transgenic HRs (characterized by the expression of the *RUBY* gene, observed as red HRs) appeared 14 days post-inoculation. Mature putative transgenic HRs were observed on the 20th day of the experiment. Overall, drug-type seedlings exhibited the highest HR induction, increasing by 58.8% compared to hemp-type seedlings. The A4 strain consistently demonstrated the highest TE (75%) irrespective of genotype,

while the ARqual strain yielded the lowest TE (8.33%). Notably, the K599 treatment did not result in the formation of transformed roots. In conclusion, our study presents the first *ex vitro* one-step transformation in both hemp- and drug-type cannabis. Compared to the *in vitro* method, our *ex-vitro* method offers simplicity, speed, and reduced contamination risk, making it an optimal choice for the efficient production of secondary metabolites using CRISPR/Cas system in cannabis.

***[O25] SPECTRUM MATTERS: THE IMPACT OF RED LIGHT ON MORPHOLOGY, POTENCY, AND PHOTOBLEACHING IN *CANNABIS SATIVA*.** Karine Jarzecki[1] and Susan J. Murch[1]. [1]University of British Columbia Okanagan, 3333 University Way, Kelowna, BC, Canada, V1V 1V7
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Photobleaching is an emerging phenomenon in the indoor cannabis industry in which the tips of apical inflorescences are white in colour. Very little is known about its cause nor prevention, which can reduce viable yield in an already competitive market. Currently, it is thought that high fractions of red light within an LED fixture are responsible for photobleaching. A variety of spectrum combinations ranging from 39.3% to 88.7% red were implemented across ten segmented plots within a standard cultivation indoor grow room, each equipped with their own tunable LED rail lighting. Treatments with exceptionally high fractions of red light (greater than 50% red) did not photobleach the high THC cannabis cultivar used for this trial ("Black Cherry Punch #2"). Our chemical analysis results show that differing light spectra recipes influenced final plant potency, at times in conflict or in agreement with other observations reported in the literature. Our results do not support the hypothesis that an absolute, certain threshold of red light - in terms of an absolute photosynthetic photon flux density (PPFD) value, a percentage value out of total PPFD, or as a daily light integral value - exists for all cultivars where photobleaching is guaranteed to occur. Rather, our data indicate variability by chemotype and further investigation is necessary to fully understand the combination(s) of factors that induces photobleaching in Cannabis.

***[O26] FUNGAL, OOMYCETE AND BACTERIAL MICROBIOME COMMUNITIES IN ROOTS OF GREENHOUSE CULTIVATED *CANNABIS SATIVA* ARE INFLUENCED BY GROWTH SUBSTRATE, HOST GENOTYPE, AND PLANT GROWTH STAGE.** Heather H Tso[1] and Zamir K Punja[1]. [1]Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC, Canada, V5A 1S6
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Cannabis (*Cannabis sativa* L.) is grown commercially using hydroponic methods of cultivation in greenhouses across Canada. Some producers have opted to use organic production systems in soil. Root pathogens are a major challenge in both production systems and their interactions with other microbes in the root zone are not well understood. Using a metagenomics approach, this study evaluated the microbiome of cannabis roots and how it may be influenced by growth substrate (hydroponic rockwool or organic soil), cannabis genotype, and plant growth stage (vegetative vs. flowering). Root samples were obtained from vegetative and flowering plants cultivated using hydroponic (8 genotypes) or organic (2 genotypes) methods. Total DNA was extracted and subjected to 16S rRNA bacterial and ITS fungal sequencing to assess microbial species diversity and abundance. A difference was observed between growth substrates. Bacterial species made up 95% of the total microbial sequencing reads in organic roots but accounted for 75% of microbial reads in hydroponically grown roots. There were also differences among cannabis genotypes in microbial composition, with 'Pink Kush' showing the lowest microbial diversity and abundance relative to other genotypes. In both growth substrates, the predominant fungi/oomycetes identified, in order of decreasing frequency, were *Pythium dissotocum*, *Metarhizium acridum*, *Fusarium oxysporum*, *Paracoccidioides brasiliensis*, *Aspergillus terreus*, *Neoarthrinium moseri*, and *Sordaria macrospora*. Additionally, *Fusarium odoratissimum*, *Fusarium proliferatum*, *Ramularia collo-cygni*, and various members of *Debaryomyces* and *Penicillium* were uniquely present in organic roots. *P. dissotocum* accounted for 57% of the total fungal/oomycete reads in hydroponic roots and 29% in organic roots. In comparing vegetative with flowering plants, the biocontrol fungus *M. acridum* made up 14% of the total fungal reads in vegetative plants but was essentially absent in flowering plants. In contrast, *F. oxysporum* represented 6% of the total fungal reads in flowering plants but was present at <1% in vegetative plants. The most common bacterial species present were *Rhizobium esperanzae, Mycobacterium canettii*, and various species of *Pseudomonas* and *Enterobacter*. In addition, *Stenotrophomonas maltophilia* and various species of *Acinetobacter* were unique to organic roots. Our findings show that a range of microbial species are present on healthy-appearing cannabis roots and can

vary depending on plant growth stage. Growth substrate impacts the bacterial component of the root microbiome. These results offer a glimpse into the microbial communities of cannabis roots, which are comprised of plant pathogens, potentially beneficial microbes, as well as species with undetermined functions that may be interacting in the rhizosphere.

***[O27] CHARACTERIZATION OF INDIGENOUS POPULATIONS OF CANNABIS IN IRAN: A MORPHOLOGICAL AND PHENOLOGICAL STUDY.** Mehdi Babaei and Davoud Torkamaneh. Département de Phytologie, Université Laval, Rue de l'Université, Québec City, G1V 0A6, Québec, Canada ; Institut de Biologie Intégrative et des Systèmes (IBIS), Université Laval, Rue de l'Université, Québec City, G1V 0A6, Québec, Canada; Centre de recherche et d'innovation sur les végétaux (CRIV), Université Laval, Rue de l'Agriculture Québec City, G1V 0A6, Québec, Canada; Institute Intelligence and Data (IID), Université Laval, Rue de l'Agriculture Québec City, G1V 0A6, Québec, Canada
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Cannabis is a historically, culturally, and economically significant crop in human societies, owing to its versatile applications in both industry and medicine. Over many years, native cannabis populations have acclimated to the various environments found throughout Iran, resulting in rich genetic and phenotypic diversity. Examining phenotypic diversity within and between indigenous populations is crucial for effective plant breeding programs. This study aimed to classify indigenous cannabis populations in Iran to meet the needs of breeders and breeding programs in developing new cultivars. Here, we assessed phenotypic diversity in 25 indigenous populations based on 12 phenological and 14 morphological traits in male and female plants. The extent of heritability for each parameter was estimated in both genders, and relationships between quantitative and time-based traits were explored. Principal component analysis (PCA) identified traits influencing population distinctions. Overall, populations were broadly classified into early, medium, and late flowering groups. The highest extent of heritability of phenological traits was found in Start Flower Formation Time in Individuals (SFFI) for females (0.91) Flowering Time 50% in Individuals (50% of bracts formed) (FT50I) for males (0.98). Populations IR7385 and IR2845 exhibited the highest commercial index (60%). Among male plants, the highest extent of Relative Growth Rate (RGR) was observed in the IR2845 population (0.122 $g.g^{-1}.day^{-1}$). Finally, populations were clustered into seven groups according to the morphological traits in female and male plants. Overall, significant phenotypic diversity was observed among indigenous populations, emphasizing the potential for various applications. Early-flowering populations, with their high RGR and Harvest Index (HI), were found as promising options for inclusion in breeding programs. The findings provide valuable insights into harnessing the genetic diversity of indigenous cannabis for diverse purposes.

***[O28] PROFILING THE TRANSCRIPTOMIC AND CELLULAR RESPONSE OF *CANNABIS SATIVA* TO INFECTION BY *SCLEROTINIA SCLEROTIORUM* THROUGH SPACE AND TIME.** Natalie L. Cale, Rylee E. Swiderek, and Mark F. Belmonte. Department of Biological Sciences, University of Manitoba, 50 Sifton Road, Winnipeg, MB, Canada, R3T 2N2
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Known to infect more than 600 plant species worldwide, *Sclerotinia sclerotiorum* is a necrotrophic fungal pathogen, and the causative agent of white mold. With its wide host range and capacity to overwinter in the soil, *Sclerotinia* is a pathogen of immense agricultural importance. *Cannabis sativa* is one of the many plant species known to be susceptible to *Sclerotinia* infection, with infection reports recently having been documented in both field and greenhouse conditions. As one of the most widely cultivated crops worldwide, *C. sativa* is grown for its fibre in addition to its medicinal/psychoactive properties. As a result of legal constraints associated with growing *C. sativa* in various countries, little is known about the *C. sativa -S. sclerotiorum* pathosystem, especially with regard to how the plant responds to pathogen attack at the cellular and molecular levels. Anatomical studies revealed initial infection and degradation of the epidermis and cortical parenchyma, followed by widespread infection of the vascular phloem tissues that allowed *S. sclerotiorum* to travel into the main stem of the plant. Dual RNA sequencing of both *S. sclerotiorum* and *C. sativa* in the floral stem over a seven-day period provided a detailed transcriptomic profile of this pathosystem directly at the site of infection. Differential gene expression analysis revealed large-scale transcriptional changes in both *C. sativa* and *S. sclerotiorum* as a result of rapid infection. Differential gene expression (DEG) analysis identified the up regulation of 65 DEGs at 1 day post

inoculation (dpi) and 11656 DEGs 5 dpi in *C. sativa,* while 3082 DEGs were identified in *S. sclerotiorum* 7 dpi. Gene ontology term enrichment identified biological processes associated with plant defense and signal transduction cascades during *C. sativa* infection while biological processes associated with redox control and sugar catabolism were enriched in *S. sclerotiorum*. Taken together, global mRNA sequencing of the *C. sativa*-*S. sclerotiorum* pathosystem reveals extensive transcriptional reprogramming in both the host plant and fungal pathogen that is associated with the degradation of host cortical and vascular phloem tissues.

[O29] RADIOMETRIC INVESTIGATION DUE TO NATURALLY OCCURRING RADIONUCLIDES IN SOILS OF IGBOKODA, A COASTAL AREA IN ONDO STATE, NIGERIA. Abiola Olawale Ilori[1], Funmilola Mabel Ojo[2], and Kayode Olayele Karigidi[3]. [1]Department of Physical Sciences, Olusegun Agagu University of Science and Technology, Okitipupa, Ondo State, Nigeria. [2]Department of Biological Sciences, Olusegun Agagu University of Science and Technology, Okitipupa, Ondo State, Nigeria; [3]Department of Chemical Sciences, Olusegun Agagu University of Science and Technology, Okitipupa, Ondo State, Nigeria
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This study measured the activity concentration of natural radionuclides (238U, 232Th, and 40K) in soil samples taken from Igbokoda, a coastal area of Ondo state, Southwest Nigeria, using a thallium-doped sodium iodide (NaI(TI)) gamma-ray spectrometry system. The study's results have found significant differences in the activity of naturally occurring radionuclides in the study area's soil. 238U, 232Th, and 40K concentrations in the soils have mean values of 37.63 ± 3.82, 23.20 ± 2.55, and 657.17 ± 45.15 $Bq.kg^{-1}$, respectively. The results were compared with values for other coastal regions and the worldwide recommended limits. The calculated mean radiological risks are as follows: radium equivalent: 121.413 $Bq.kg^{-1}$; absorbed gamma dose rate: 57.684 $nGyh^{-1}$; annual effective dose rate: 70.744 $\mu Sv, y^{-1}$; and representative level index: 0.921. According to the results of this study, the population's radiation exposure as a consequence of the measured radionuclide concentration in the soil of the study area is less than the globally recommended limits. Therefore, the soil in the study region will not seriously endanger the public. Nonetheless, more research is required to estimate the radionuclide concentration in the agricultural produce cultivated in the study area.
Keywords: Igbokoda, NaI(TI), Natural radionuclide, radiological risk, soil

[O30] PLANT AND SOIL COMMUNITIES GIVEN NITROGEN DEPOSITION, WARMING, HARVESTING AND SOIL CONDITIONS. Laura Super. University of British Columbia
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Earth is under simultaneous human-caused disturbances, which can have devastating impacts on biological communities. Understanding how biotic communities respond to multiple factors in forest ecosystems is crucial to management, basic science and conservation planning. Recently published research in clear-cuts and forest edges suggested that warming, but not nitrogen deposition, increased tree seedling performance in clear-cuts in the University of British Columbia's Malcolm Knapp Research Forest (MKRF), British Columbia, Canada. The present MKRF research, in the same study, focuses on the associated understory plant and soil communities in clear-cuts and forest edges. The number of species of plants increased in clear-cuts compared to forest edges. Fungi and prokaryote taxa numbers did not differ across habitats, but there were more soil nematode taxa in clear-cuts than forest edges. More complex results are forthcoming including diversity in relation to soil conditions, cross-taxa comparison and simulated nitrogen and warming in forest edges and clear-cuts. This research has important implications for forest management, conservation and basic science.

***[O31] PREVALENCE AND CONSEQUENCES OF INTERSPECIFIC POLLEN TRANSFER IN A MONTANE COMMUNITY.** Jacalyn Grey[1] and Anne Worley[2]. [1]Department of Biological Sciences, University of Manitoba, 66 Chancellors Circle, Winnipeg, MB, Canada, R3T 2N2; and [2]Department of Biological Sciences, University of Manitoba, 66 Chancellors Circle, Winnipeg, MB, Canada, R3T 2N2
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Many pollinators visit multiple plant species, causing pollinators to carry and deposit diverse pollen loads. Research on how pollen load composition and donor identity affect seed set is needed to understand how changes in floral communities may affect plant fitness. Pollen from close relatives may decrease reproductive success due to their ability to germinate, clog pistils and usurp ovules, whereas pollen from distantly related donors may have negligible effects. However, when pollinator activity is low, flowering neighbours may enhance pollinator visitation and cause a positive relationship between conspecific and heterospecific pollen deposition. I investigated the fitness consequences of pollen donor-recipient relatedness and pollinator sharing within two populations of *Polemonium brandegeei*, a montane herb with diverse pollinators, and its co-flowering communities. First, I conducted experimental hand pollinations including mixes of conspecific pollen and heterospecific pollen from a closely and distantly related species. I used general linear mixed models to test the prediction that congeneric donors decrease *P. brandegeei* pollen germination and seed set. Distantly related donors had no effect on *P. brandegeei* reproduction, although closely related donors decreased pollen germination, seed set and seed weight. Second, I collected open pollinated stigmas from all abundant co-flowering species in the communities. I used pollen transfer networks and major axis regressions to test the prediction that pollinator sharing within communities (pollen loads containing heterospecific pollen) results in increased conspecific pollen deposition and germination. Pollinator sharing was common between co-flowering species in both of my study communities. All sampled species received or donated heterospecific pollen. However, most species received little heterospecific pollen in each pollen load and heterospecific pollen was typically from distantly related species, resulting in neutral and facilitative relationship between co-flowering species. This study suggests that pollinator sharing between native co-flowering species can be common and beneficial in plant communities. However, competition may occur if closely related species begin to co-flower due to range changes or phenological shifts.

***[O32] COMMUNITY PHYLOGENETICS OF FOREST TREES IN INDIA AND SRI LANKA.** Harsimran Kaur, Sachin Medigeshi Harish, Semini Nawalage, and Selvadurai Dayanandan. Department of Biology, Concordia University, 7141 Sherbrooke St. W., Montreal, QC, Canada, H4B 1R6
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The origin and maintenance of high biological diversity in species-rich tropical forest communities has long been a subject of much controversy. Understanding the relative roles of several evolutionary forces, including speciation, dispersal, random drift, and selection, in shaping the assembly of tree species in these communities is crucial for gaining insights into the origin and maintenance of biodiversity in these ecosystems. We reconstructed the phylogeny of 2208 species of forest trees belonging to 47 orders and 143 families distributed in India and Sri Lanka (covering most of the Indian subcontinent) using the nucleotide sequences of the *rbc*L, *mat*K, and *psb*A-*trn*H regions of the chloroplast, and the ITS region of the nuclear genome. We are using these phylogenetic trees as a framework to analyze the data on the distribution patterns of trees in forest census plots to infer the relative roles of speciation, dispersal, stochastic drift, and selection in shaping the assembly of tree species in forest communities.

[O33] ECOLOGICAL PROCESSES DETERMINING WEED SPECIES DISTRIBUTION ACROSS NOVA SCOTIAN WILD BLUEBERRY FIELDS. Andrew McKenzie-Gopsill[1], Hugh Lyu[2], Scott White[2], and Sheldon Hann[3]. [1]Agriculture and Agri-Food Canada, Charlottetown Research and Development Centre; [2]Dalhousie University Department of Plant, Food, and Environmental Sciences; and [3]Agriculture and Agri-Food Canada, Fredericton Research and Development Centre
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Ecological gradients and processes are known to play a key role in determining weed community composition in agroecosystems. The present study investigated whether climatic, topographical, and soil edaphic factors were associated with weed species occurrences and abundances in wild blueberry fields. A plant survey of 165 wild blueberry fields in the Canadian province of Nova Scotia was conducted and

combined with climatic, topographical, and soil edaphic data collected from Federal databases. Linear mixed models and multivariate analyses were used to disentangle the relationship between weed species occurrences, species-species interactions, and environmental covariates in wild blueberry fields. The surrounding weed species diversity in fields had the largest effect on wild blueberry stem density with increasing species richness driving a decrease in stem density regardless of weed density. Weed diversity was affected by accumulated growing degree days, topographical position index, and topographical wetness index. The occurrence and abundance of many common weed species was positively associated with wild blueberry management intensity and accumulated growing degree days. The relative importance of niche-based assembly rules for overall weed species composition in wild blueberry fields, however, was minimal. Yet several species showed high correlation with environmental cofactors. These results stress the importance of local stochasticity and species-species interactions in determining weed communities in wild blueberry fields and the challenge with predicting weed communities in perennial agroecosystems.

[O34] CONTRIBUTIONS OF METABARCODING AND POPULATION GENETICS TO FUSARIUM HEAD BLIGHT EPIDEMIOLOGY. Toan Bao Hung Nguyen[1], Marie Foulongne-Oriol[2], Amandine Henri-Sanvoisin[1], Sylvie Treguer[1], Gaétan Le Floch[1], and Adeline Picot[1]. [1]Laboratoire Universitaire de Biodiversité et Ecologie Microbienne, INRAE, Technopôle Brest-Iroise, 29280, Plouzané, France; and [2]Mycologie et Sécurité des Aliments, INRAE, CS 20032, 33882, Villenave d'Ornon, France
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Fusarium Head Blight is a devastating disease of cereals mainly caused by a complex of *Fusarium* species (Fspp). Despite being primary inoculum sources, Fspp diversity and dynamics in soils and residues have been less studied than in grains. Besides, the importance of long-distance airborne spores *vs.* soil and residue-borne spores in inoculum dispersal is still under debate. Yet, understanding Fspp population diversity and the origin of inoculum is crucial to gain insight into the FHB epidemiology and elaborate efficient management strategies. In this context, the objectives of this study were to i) decipher Fspp diversity and dynamics in maize residues, soil and wheat heads over the wheat cycle; and ii) determine the extent to which strains isolated from residues contribute to head contamination. Six minimal tillage wheat fields, with maize as previous crop, were monitored for two years. The soils, maize residues, and wheat grains were collected at four stages throughout the wheat cycles. Metabarcoding sequencing of the EF1α region, enabling species-level resolution of Fspp, revealed that differences in *Fusarium* composition were primarily influenced by the substrate type (36% of explained variance), followed by sampling locations (21%) and sampling times (13%). Among the 31 species identified, grains were dominated by *F. poae* (Fp, mean relative abundance: 47%) and *F. graminearum* (Fg, 29%) while residues were mainly contaminated by Fg with low presence of Fp (as also confirmed by species-specific qPCR). More precisely, under high FHB pressure, such as in 2021, Fg dominated grains whereas Fp outcompeted Fg the following year, leading to reduced disease pressure, aligning with Fp lower pathogenicity. A Source Tracker analysis also showed that residues more importantly contributed to wheat contamination in 2021 than in 2022, suggesting that Fg in heads of 2021 mainly originated from residues while Fp most likely originated from airborne spores. To further investigate inoculum transfer from residues to heads, the diversity and structure of the Fg population was then studied on 122 and 137 isolates from residues and grains respectively, using a SSRseq approach targeting 22 markers. Of these isolates, 156 were unique haplotypes, with most genetic diversity distributed within populations of a single field (99%) rather than between geographical regions (1%). Surprisingly, 40-76% of closely-related residue genotypes were found in grains but without preferential flow from residues to grains collected from the same field, suggesting a region-wide dispersal. Altogether, our *High Throughput Sequencing* (HTS)-based approaches provided interesting insights into FHB epidemiology at both community and population levels, taking into account Fspp diversity and interactions while investigating inoculum source and monitoring pathogens at the field scale.

[O35] ADVANCED MOLECULAR DIAGNOSTICS REVEAL SHIFTS IN *FUSARIUM* POPULATIONS ASSOCIATED WITH WHEAT IN WESTERN CANADA: A FIVE-YEAR STUDY. Mohamed Hafez[1], Nicola Schatz[1], Khouloud Ayari[1], Rhodesia Celoy[1], Mouldi Zid[1], Ryan Gourlie[1], Dianevys GonzalezPenaFundora[1], Thomas Kelly Turkington[2], and Reem Aboulhaddour[1]. [1]Agriculture and Agri-Food Canada, Lethbridge Research and Development Center, Lethbridge, AB, Canada, T1J 4B1; and [2]Agriculture and Agri-Food Canada, Lacombe Research and Development Center, Lacombe, AB, Canada, T4L 1W1
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Due to the complex and dynamic nature of *Fusarium* populations associated with wheat, it is imperative to regionally detect and quantify these pathogens to implement appropriate research activities and management strategies. Recent reports have highlighted changes in the composition of these populations and their associated trichothecene chemotypes, both in Canada and globally. Many *Fusarium* species exhibit high similarity and are challenging to distinguish, even at the molecular level. Existing molecular markers lack the necessary sensitivity for specific detection of targeted *Fusarium* species, particularly those closely related. In this study, we developed molecular diagnostic tools for precise detection and quantification of the most prevalent wheat-associated *Fusarium* species in Canada. These tools were utilized to screen wheat grain and node samples collected from representative sites across the western Canadian prairies over a five-year period (2018-2022). This analysis aimed to characterize the major *Fusarium* species associated with wheat in these regions. Our findings revealed infrequent detection of *F. graminearum*, highlighting the need for greater attention to other *Fusarium* species that were commonly recovered and detected in significant quantities using culture- and molecular-based methods, such as *F. avenaceum*, *F. culmorum*, and *F. poae*. Trichothecene genotyping demonstrated that the 3ADON genotype predominated, followed by type-A trichothecenes, while the 15ADON genotype exhibited lower prevalence, and the NIV genotype was not detected. Analyzing fungal populations within wheat node and grain tissues from diverse regions can offer valuable insights, and aid in predicting diseases that may impact subsequent crops, and the development of effective disease management strategies.

[O36] GENOME MINING OF PHYTOPATHOGENIC FUNGI FOR PHARMACOLOGICAL PRODUCTS. Tom Hsiang[1], Xueting Liu[2], Jingyu Zhang[2], Lixin Zhang[2], Lan Jiang[2], Xinye Wang[2], and Guoliang Zhu[2]. [1]Environmental Sciences, University of Guelph, Guelph, ON, Canada, N1G 2W1; and [2]State Key Laboratory of Bioreactor Engineering, East China University of Science and Technology, Shanghai 200237, China
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Since 2014, Tom Hsiang of the University of Guelph (Ontario, Canada) has been cooperating with scientists at ECUST (East China University of Science and Technology, Shanghai, China). The expertise of the collaborators at ECUST includes drug discovery from microbials. For example, they have worked with actinomycetes (deep sea, high mountains) for novel natural products. They started genome mining actinomycetes (over 12,000 in mixed batches) for potential pharmacological products. In 2014, they attended a seminar given by Tom Hsiang on fungal genome sequencing, and they became interested in mining fungal genomes. In 2015, T. Hsiang shared the draft genome sequences of two dozen phytopathogenic fungi with them initially, and they found some biosynthetic gene clusters (BGCs) of interest. The researchers discussed further, and then over 450 draft phytopathogenic fungal genomes were shared. Phytopathogenic fungi are in a constant state of warfare with their hosts, and the numerous secondary metabolites they produce, such as terpenoids, may have potent anti-microbial and anti-cancer activity. This presentation details some of the methods and major findings from that work starting with fungal genome sequencing and assembly, and highlighting some novel compounds from a wide range of phytopathogenic fungi which may be of pharmacological interest.

[O37] *EXECUTER1* IS TRIGGERED BY SINGLET OXYGEN AND CONFER RESISTANCE TO *SCLEROTINIA SCLEROTIORUM* VIA PROGRAMMED CELL DEATH IN BOTH CANOLA AND SOYBEAN. Lone Buchwaldt, Helen Lui, Alan Davies, Jonathan Durkin, and Fuyou Fu. Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, 107 Science Place, Saskatoon, SK, S7N0X2
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Singlet oxygen ($^1O_2$) is a byproduct of photosynthesis (PSI and PSII) and the most abundant reactive oxygen species in plant cells. Although $^1O_2$ is highly reactive it is quenched by antioxidants (carotenoids and vitamin E) during steady-state metabolism. However, during pathogen infection, elevated $^1O_2$ levels trigger release of Executer1 from the thylakoid membrane, resulting in retrograde signaling to the nucleus. Here the protein activates transcription factors, primarily WRKYs, leading to a range of responses from cellular acclimation, synthesis of pathogenesis-related proteins (PR1 and PR5), to programmed cell death (PCD). The EX1 gene was identified at QTLs conferring resistance to the fungal pathogen *Sclerotinia sclerotiorum* in both canola (*Brassica napus*) and soybean (*Glycine max*) using genome wide association studies (GWAS) of 192 diverse lines of each crop species. In preparation for GWAS, *Sclerotinia* phenotyping was conducted by attaching fungal mycelium to the stem when plants were at early to full flower, followed by measurement of lesion length and stem collapse 21 days after inoculation (dai). Genotyping was carried out with a 6K *B. napus* SNP and a 90K *G. max* SNP array (Illumina), respectively. Data analysis showed EX1 was located on chromosome A3 in canola and on 13 in soybean. To take advantage of EX's ability to trigger PCD, the gene was cloned from the resistant *B. napus* line PAK54 (Pakistan) and transformed into a susceptible line under the constitutive gene promotor, CaMV35S. Three *B. napus* lines, with a single gene-inserted in a homozygous state, were generated and phenotyped for *Sclerotinia* resistance as described above. One line was completely resistant showing only small necrotic stem lesions, while two lines showed 50% reduction in disease traits. PCR primers, designed to only amplify the inserted EX1 gene copy, were used in a time course study 0-21 dai. The protein was present at the time of *Sclerotinia* infection and throughout the test period. Although the amounts were low relative to a standard gene, TIP41, it induced PCD and contained the necrotrophic pathogen *S. sclerotiorum*. An amino acid substitution (proline to serine) in the cloned gene, could also have affected its binding to D1 protein thereby affecting PSII directly. We conclude that the EX1-$^1O_2$ interaction is an important link between steady-state photosynthesis and pathogen defense. Importantly, constitutive expression of the selected EX1 gene has the potential to reduce crop loss caused by *S. sclerotiorum* and maybe other fungal pathogens.

[O38] VIRAL DIVERSITY IN A MIXED TREE FRUIT PRODUCTION SYSTEM DETERMINED THROUGH BEE-MEDIATED POLLEN METAGENOMICS. Raj Vansia[1,2], Guillaume J. Bilodeau[3], Stephen F. Pernal[4], M. Marta Guarna[4], Michael Rott[5], and Jonathan S. Griffiths[1]. [1]Agriculture and Agri-food Canada, London Research and Development Centre, Agriculture and Agri-Food Canada, 4902 Victoria Ave N, Vineland Station, ON L0R 2E0, Canada; [2]Department of Biological Sciences, Brock University, 1812 Sir Isaac Brock Way, St. Catharine's, ON L2S 3A1, Canada; [3]CFIA Canadian Food Inspection Agency, Ottawa Plant Laboratory, 3851 Fallowfield Rd, Ottawa, ON K2J 4S1, Canada; [4]Agriculture and Agri-food Canada, Beaverlodge Research Farm, P.O. Box 29, Beaverlodge, AB T0H 0C0; and [5]Canadian Food Inspection Agency, Centre for Plant Health, Sidney Laboratory, 8801 East Saanich Rd, North Saanich, BC V8L1H3, Canada
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Commercially cultivated *Prunus* species are commonly grown in adjacent or mixed orchards, and can have unique or commonly shared viral pathogens. Apple (*Malus domestica*), another member of the *Rosacea* and distantly related to *Prunus*, can share the same growing regions and some common viral infections. Pollen can be a major route for virus transmission, and analysis of the pollen virome in tree fruit orchards can provide insights into these virus pathogen complexes from mixed production sites. Commercial honey bee (*Apis melifera*) pollination is essential for improved fruit set and yield in tree fruit production systems. Honey bees collect small amounts of pollen from multiple flowering individuals in the immediate area, providing mixed samples that can be conveniently collected from a bee hive location. Here we describe the metagenomics-based detection of plant viruses through bee and pollen samples collected during the spring bloom period from a mixed *Prunus* and *Malus* orchard. Twenty-one unique viruses were detected in samples collected during apricot (*Prunus armeniaca*), sweet cherry (*Prunus*

avium), peach (*Prunus persica*), and apple (*Malus domestica*) blooms. *Ilarviruses* prune dwarf virus (PDV) and prunus necrotic ringspot virus (PNRSV), *Secoviridae* family members tomato necrotic ringspot virus, tobacco necrotic ringspot virus, and prunus virus F, and C*apillovirus* cherry virus A (CVA) were detected in all time points, while other viruses were detected with more restricted ranges. Pairwise nucleotide sequence analysis suggests two major groups of PDV and PNRSV CP nucleotide sequences present at this site, supported by phylogenetic relationships. A wide variety of individual viruses and nucleotide sequence diversity was identified at this site, demonstrating the benefits of area-wide monitoring through bee pollination activities and providing new insights into the pollen-associated virome in tree fruit production ecosystems.

***[O40] POTENTIAL FOR BEES AND POLLEN AS BIOMONITORS OF AGRICULTURAL PATHOGENS THROUGH A METABARCODING HIGH THROUGHPUT SEQUENCING (HTS) APPROACH.** C. M. Hewapathirana[1], M.E. Rott[2], M.M. Guarna[3], S.F. Pernal[3], J.S. Griffiths[4], and G.J. Bilodeau[1]. [1]Canadian Food Inspection Agency (CFIA), 3851 Fallowfield Road, Ottawa, ON, K2H 8P9, Canada; [2]Canadian Food Inspection Agency (CFIA), 8801 East Saanich Road, North Saanich, BC, V8L 1H3, Canada; [3]Agriculture and Agri-Food Canada (AAFC), 1 Research Road, Beaverlodge, AB, T0H 0C0, Canada; and [4]Agriculture and Agri-Food Canada (AAFC), 4902 Victoria Avenue North, Vineland Station, ON, L0R 2E0, Canada; Correspondence to: Minuka.Hewapathirana@inspection.gc.ca

The European honeybee (*Apis mellifera*) is a vital component of agricultural systems and recent research suggest it could be used as a tool for biomonitoring. During foraging activities, bees can come into contact with plant pathogens through their interactions with pollen and fungal spores. This project aims to evaluate the potential and limitations in using honeybees as a biomonitoring species for pre-screening and identifying major pathogenic threats to beekeeping and the Canadian agricultural sector. Over 220 samples including - Hive and Forager bees, Pollen and Bee Bread were collected from *A. mellifera* hives in experimental tree fruit farms across British Colombia and Ontario. HTS technologies (ION Torrent) are utilized to sequence barcode regions - Internal Transcriber Spacer 1 (ITS1) region for fungal identification and 16S ribosomal DNA for bacterial identification for a total of 90 million reads sequenced for ITS1 and 35 million reads for 16S. Bioinformatics workflows including - QIIME and Phyloseq packages were used to assess read quality and generate taxonomic profiles. The UNITE fungal database classified up to 7,148 Operational Taxonomic Units (OTUs) while the SILVA bacterial database classified up to 986 OTUs. Results present pollen and forager bees to be a rich source for fungal pathogen detection, for example with the identifications such as *Podosphaera leucotricha* (Powdery mildew - apples) and *Blummeria gramminis* (Powdery mildew- grasses). The *Monilinia* genus is considered a high-risk pathogen genus by the CFIA as it contains species that pose a threat to stone fruit and berry plants in Canada. Through Phyloseq subset analysis several *Monilinia* species was detected in the sample sets. Fungal bee pathogens identified in the samples include - *Ascophaera apis* (Chalkbrood disease) and Bacterial pathogen - *Melissococcus plutonius* (European foulbrood disease). Multiple Sequence Alignment analysis was deployed to validate the initial hits and phylogenetic trees generated consistent confidence scores, suggesting accurate taxonomic classification through QIIME. Although a number of high risk plant and bee pathogens were identified using the fungal workflow, the bacterial taxonomic classification classified most OTUs at the genus level and was limited to resolving bee pathogens. An alternate sequencing platform such as the Oxford Nanopore system may produce a higher resolution of the 16S bacterial region or full genome sequencing. These results illustrate the potential and limitations of using honeybees as a pre-screening tool for the identification of pathogenic threats to beekeeping and the Canadian agricultural sector.

***[O41] IDENTIFICATION AND CHARACTERIZATION OF *PODOSPHAERA APHANIS* CAUSING POWDERY MILDEW ON SALMONBERRY AND THIMBLEBERRY PLANTS IN BRITISH COLUMBIA.** Chidrupa Podile[1,3], Rishi R. Burlakoti[1], Amy Novinscak[1], Miao Liu[2], Zamir K. Punja[3], Davis Iritani[4], and Yoichiro Watanabe[4]. [1]Science and Technology Branch, Agassiz Research and Development Centre, Agriculture and Agri-Food Canada, Agassiz, BC V0M 1A0, Canada; [2]Science and Technology Branch, Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa, ON K1A 0C6, Canada; [3]Department of Biological Sciences, Simon Fraser University, Burnaby, BC V5A 1S6, Canada; and [4]Science and Technology Branch, Summerland Research and Development Centre, Agriculture and Agri-Food Canada, Summerland, BC V0H 1Z0, Canada
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Salmonberry and thimbleberry are important native plants to Indigenous communities because of their traditional, cultural and medicinal importance. In 2022, powdery mildew was observed on salmonberry and thimbleberry plants in research plots of the Agassiz Research and Development Centre, British Columbia. Although powdery mildew is a common fungal disease on cultivated berry crops, including strawberry, raspberry, blackberry and blueberry, very little information is available on the diseases affecting salmonberry and thimbleberry. This research was focused on the identification and characterization of the pathogen causing powdery mildew on these native berry plants. Symptoms and signs of diseases including curling of younger leaves and white powdery patches on leaves were observed on the infected plants. Compound and scanning electron microscopy of the infected leaves showed the presence of conidia, conidiophores, foot cells and fibrosin bodies. The shape of conidia ranged from ovo-ellipsoid to citriniform and the conidial size ranged 24.1 to 36.5 µm in length and 12.7–27.5 µm in width. These morphological features were similar to that of *Podosphaera aphanis*. For molecular characterization, DNA was extracted directly from the infected leaf samples taken from each host. For the amplification and sequencing of the internal transcribed spacer region (ITS), polymerase chain reaction was performed for the two samples using fungal-specific primers ITS1F and ITS4. Powdery mildew-specific primers PMITS1 and PMITS2 were also utilized. NCBI BLAST (basic local alignment search tool) analysis for the sequences from salmonberry and thimbleberry samples showed maximum similarity (> 99%) to *Podosphaera aphanis*. For pathogenicity tests, healthy salmonberry and thimbleberry plants in the greenhouse were inoculated with inoculum from infected leaves of salmonberry and thimbleberry, respectively. Further, cross-pathogenicity tests were performed by inoculating salmonberry plants with infected thimbleberry leaves and inoculating thimbleberry plants with infected salmonberry leaves. One month after inoculation, all inoculated plants started producing white powdery patches on the upper leaf surface which started spreading to the adjacent leaves. Therefore, cross-pathogenicity to each host was demonstrated. Further research is required to manage powdery mildew on these native berries.

***[O42] ESTIMATING EARLY INFECTION OF ONIONS BY *STEMPHYLIUM VESICARIUM* BASED ON SPORE TRAPPING AND INFECTION OF BARLEY.** Julia Scicluna[1], Bruce D. Gossen[2], and Mary Ruth McDonald[1]. [1]Department of Plant Agriculture, University of Guelph, 50 Stone Rd E, Guelph, ON, Canada, N1G 2W1; and [2]Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK, Canada, S7N 0X2
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Stemphylium leaf blight (SLB) caused by *Stemphylium vesicarium* is an important foliar disease of onion in Ontario. Symptoms usually appear at the 3-4 true leaf stage, but inoculum is found on spore traps earlier in the growing season. Senesced barley, which is a wind abatement crop planted with onions, can be infected by *S. vesicarium*. Quantifying infection of barley has been used to forecast SLB in Eastern Canada. Penflufen, a succinate dehydrogenase inhibitor (SDHI) seed treatment, has provided protection against *S. vesicarium* infection at early growth stages, but resistance to this fungicide is developing. Seeded onions, transplanted onions and barley were sampled from field plots in the Holland Marsh, Ontario from the flag leaf to the 3-4 true leaf stage and assessed for sporulation in humid chambers. Rotorod and Burkard spore traps were placed in onion fields in April 2023 and 2024. Onion cv. Traverse, with or without penflufen seed treatment, was inoculated with isolates of *S. vesicarium* from 2023 at the 1st and 3-4 true leaf stages in two controlled environment studies. In field trials, infection was detected in seeded onions beginning at the 2nd true leaf stage. There was a strong positive correlation ($r = 0.72$, $P = 0.03$) between the 7-day average of conidia captured by the Rotorod trap and infection of seeded onions. Infection of barley was detected at a low frequency and was not correlated with infection of seeded or transplanted onions. There was no effect of penflufen seed treatment on SLB severity in the controlled environment studies. The Rotorod trap was more effective at capturing conidia than the Burkard trap and may be useful for predicting the initial infection of onions by *S. vesicarium*. This could contribute to disease forecasting models for SLB. Infection of barley is unlikely to accurately forecast the severity of SLB in Ontario.

***[O43] IDENTIFICATION OF NOVEL AND DIVERSE MYCOVIRUSES IN THE PHYTOPATHOGENIC FUNGUS, BOTRYTIS CINEREA.** Sarah C. Drury[1,2], Naser Poursalavati[1,2], Peter Moffett[2], and Mamadou Lamine Fall[2]. [1]Saint-Jean-sur-Richelieu Research and Development Centre, Agriculture and Agri-Food Canada, 430 Boulevard Gouin, Saint-Jean-sur-Richelieu, QC J3B 3E6, Canada; and [2]Centre SÈVE, Département de Biologie, Université de Sherbrooke, 2500 Boulevard de l'Université, Sherbrooke, QC J1K 2R1, Canada
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Botrytis cinerea is a necrotrophic fungal pathogen that causes significant economic losses to a wide variety of crops. To date, over 100 mycoviruses have been reported in Botrytis spp., some of which induce reduced virulence (hypovirulence). Hypovirulence-inducing mycoviruses can be used as biocontrol agents, offering alternative methods to synthetic fungicides for managing B. cinerea. This research aimed to explore the mycovirome of B. cinerea and identify potential hypovirulence-inducing mycoviruses. B. cinerea isolates were collected from different horticultural crops in Quebec. Fitness and pathogenicity criteria, including conidiation, radial growth, and morphotype, were evaluated. A double-stranded RNA (dsRNA)-based extraction method was developed to sequence 42 low-performing and three higher performing isolates. A customized bioinformatics workflow, Soil Virome Analysis Pipeline, was used for analysis. Mycoviruses were detected in 44 out of 45 isolates. These mycoviruses belonged to 19 families and to unclassified dsRNA, positive-strand RNA (+ssRNA), and negative-strand RNA (-ssRNA) genome types, demonstrating that B. cinerea has an evolutionarily diverse mycovirome. Most mycoviruses had +ssRNA and dsRNA genomes, and a small number had -ssRNA, single-stranded DNA, and reverse transcriptase RNA genomes. Several mycovirus species positively and/or negatively co-occurred with each other or with being in B. cinerea isolates collected from specific hosts. Additionally, 62 novel contigs belonging to novel strains of mycovirus species were identified through RNA-dependent RNA polymerase analysis and motif identification. Further, this method was used to identify four putative novel mycovirus species belonging to Endornaviridae, Botybirnaviridae, Peribunyaviridae, and Bunyavirales taxa. Hypovirulence-inducing mycoviruses including Botrytis cinerea mitovirus 1, Botrytis cinerea fusarivirus 1, and Botrytis porri botybirnavirus 1 were also detected. This study provides valuable insights into the taxonomy and diversity of mycoviruses in B. cinerea which will be useful for subsequent evaluations of select mycoviruses as biocontrol agents.

***[O44] COLLECTION AND IDENTIFICATION OF *PLASMODIOPHORA BRASSICAE* PATHOTYPES COLLECTED IN WESTERN CANADA OVER THE LAST TEN FIELD SEASONS (2014-2023).** Emilee Storfie[1], Victor Manolii[1], Yoann Aigu[1], Michael Harding[2], Sheau-Fang Hwang[1], and Stephen Strelkov[1]. [1]Department of Agriculture, Food, and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada; and [2]Crop Diversification Centre South, Alberta Agriculture and Irrigation, Brooks, AB T1R 1E6, Canada
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Canola (oilseed rape; *Brassica napus*) is the second-most important oilseed crop worldwide. In the Canadian Prairies, canola production can be severely impacted by clubroot disease, caused by the obligate soilborne parasite *Plasmodiophora brassicae.* Initially controlled by first-generation clubroot-resistant (CR) canola cultivars, shifts in the virulence of *P. brassicae* populations have led to an increasing number of resistance-breaking pathotypes. As this disease continues to spread and novel pathotypes emerge on CR cultivars, it becomes increasingly important to collect field isolates with clubroot symptoms for downstream pathotype characterization. During annual field surveys from 2021 to 2023, a total of 210 field isolates were collected: 198 in Alberta, eight in Saskatchewan, and four in Manitoba. Each isolate represented one field and its pathotype designation was evaluated on the Canadian Clubroot Differential (CCD) set. Thirty-one unique pathotypes were found across all tested isolates, which included eight novel resistance-breaking pathotypes (1D, 1G, 3F, 3J, 5D, 6F, 8K, and 9G) and one pathotype (1H) still controlled by first-generation clubroot resistance. Pathotypes 3A, 3D, and 3H were identified at the highest frequencies among the field isolates assessed, and their geographic distribution in Alberta was mapped. In an effort to refine the CCD set, an automated approach was investigated to improve the accuracy and speed of pathotype designation, which is currently determined manually. A meta-analysis of virulence patterns across isolates collected over the past 10 field seasons (2014-2023) revealed over 50 unique pathotypes in western Canada, with more than half confirmed as resistance breaking. The majority of these pathotypes are rare, identified at frequencies of less than 2%,

while 3A, 3D, and 3H have remained predominant over the years. Numerous new canola cultivars enter the market every year, often advertised as carrying novel resistance capable of controlling resistance-breaking pathotypes. Monitoring the performance of these cultivars and evaluating the pathotype composition of isolates recovered from infected plants will help farmers and agronomists determine which commercial cultivars should be planted in the future.

***[O45] UTILITY OF CONTROLLED ENVIRONMENT AGRICULTURE IN THE PRODUCTION OF MEDICINAL FUNGI.** Jacqueline Nguyen[1], Nykole Crevits[2], Jeff Huber[3], Mike Dixon[1], and Thomas Graham[1]. [1]Controlled Environment Systems Research Facility, School of Environmental Sciences, University of Guelph, Guelph, ON, N1G 2W1, Canada; [2]Informatics and Life Sciences, School of Health and Life Sciences, Kitchener - Doon Campus, Conestoga College, Kitchener, ON N2G 4M4, Canada; and [3]Agri-Business Management, School of Engineering and Technology, Guelph Campus, Conestoga College, Guelph, ON N1H 0A8, Canada
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Fungal-derived drugs have revolutionized the landscape of pharmaceuticals. There is an increasing interest in medicinal fungi as nutraceutical products but as demand rises, supply chain issues have emerged. Medicinal and culinary varieties of fungi are often grown in hoop houses or indoor growing facilities with limited environment controls. This can lead to biological and chemical contamination, including environmental pollutants. Growth conditions vary between producers, and there is limited information available on the effect of environment controls on the physicochemical properties of fungi. Other issues including quality control, contamination, and efficacy of nutraceuticals in general have become more prevalent due to unregulated cultivation, postharvest processing, and wild harvesting. The lack of oversight in the nutraceutical market can lead to serious health risks for consumers. To address these issues, we propose the cultivation of medicinal fungal species under controlled environment conditions. Controlled Environment Agriculture (CEA) medicinal mushroom production allows for control over all key environmental growth parameters (e.g., CO2, humidity, temperature, etc.). Advancements in this biotechnology approach will ensure conditions are optimal and homogenized at all stages of growth. Standardizing cultivation protocols can improve overall quality and uniformity, while reducing contamination. Conditions can be altered to express desired traits from crops such as their size, shape, bioactive content, and growth rate. Current literature regarding the use of CEA is focused on plant production; there is a paucity of data for fungi cultivation. The limited variety of cultivated mushrooms has also contributed to a lack of transferable knowledge across different fungal species presenting challenges in progressing the cultivation of medicinal fungi. The state and future of CEA medicinal mushroom production will be discussed along with research underway at the University of Guelph.

[O46] A HIGH THROUGHPUT PHENOTYPING PLATFORM FOR CEREAL RESEARCH AND BREEDING PROGRAMS TO IDENTIFY FUSARIUM DAMAGED KERNELS AND FUSARIUM PRODUCED MYCOTOXINS. Lipu Wang[1], Deborah Michel[2], Keyhan Najafian[3], Mackenzie Hladun[1], Alejandra M. Oviedo-Ludena[1], Sheila M P Andrade[1], Anas El-Aneed[2], Ruijiao Kang[1], Yuefeng Ruan[4], Lingling Jin[3], Ian Stavness[3], and Hadley R. Kutcher[1]. [1]Department of Plant Sciences/Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8; [2]College of Pharmacy and Nutrition, University of Saskatchewan, 2D10 HSB, 107 Wiggins Rd., Saskatoon, SK, Canada, S7N 5E5; [3]Department of Computer Science, University of Saskatchewan, Thorvaldson Building, 110 Science Place Saskatoon, SK, Canada, S7N 5C9; and [4]Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, P.O. Box 1030, Swift Current, SK, Canada, S9H 3X2
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Fusarium head blight (FHB), caused by *Fusarium* spp., is a destructive disease of wheat. FHB affects kernel development, resulting in lightweight, chalky white, shrunken kernels covered with white or pink mycelia; these are known as Fusarium damaged kernels (FDKs). Infected kernels are frequently contaminated with Fusarium produced mycotoxins, especially deoxynivalenol (DON). FHB significantly reduces grain yield and quality, resulting in hundreds of millions of dollars in losses annually in Canada. Breeding cultivars with high disease resistance and low mycotoxin contamination is a priority for wheat breeders. However, traditional FDK and DON measurement methods are time-consuming, labor-intensive, and of variable accuracy; improvements are needed for large-scale screening in breeding

programs. In this study, two high throughput phenotyping tools were developed for FDK and DON measurement. A fast chromatography (FC) - tandem mass spectrometry (MS/MS) method was developed for DON quantification. It employs a one-step acetonitrile extraction protocol with a short guard column to reduce complexity, cost and analysis time. In addition, a high-throughput single-kernel screening tool was developed to assess FDK through automated image acquisition and analysis. It non-destructively images and analyzes samples composed of several hundred seeds, taking close-up top and side images of individual kernels. Meanwhile a customized convolutional neural network (CNN) model was developed and trained to process, count, and analyze vast amounts of scanned sample images. Preliminary results with the CNN model are promising; it can automatically determine the percentage of FDK in much less time than visual assessment.

[O47] A NEW MODEL: FUNCTIONAL GENES CONTRIBUTING TO ADULT PLANT RESISTANCE FROM CANOLA-BLACKLEG PLAYBOOK. Zhongwei Zou[1] and W. G. Dilantha Fernando[2]. [1]Department of Biology, Wilfrid Laurier University, 75 University Ave W, Waterloo, ON, Canada, N2L 3C5; and [2]Department of Plant Science, University of Manitoba, 66 Dafoe Rd, Winnipeg, MB, Canada, R3T 2N2 Correspondence to: zzou@wlu.ca

Blackleg, primarily caused by the fungal pathogen *Leptosphaeria maculans*, is one of the most devastating diseases in canola (*Brassica napus*), resulting in significant yield loss worldwide. Recent management strategies to minimize infection include of using resistant varieties based on the R-Avr interaction between canola and blackleg, crop rotation, rotation of resistance sources, seed treatments, disease scouting, and forecasting. Besides the *R* gene-determined resistance (qualitative or seedling resistance), quantitative resistance or adult plant resistance controlled by minor or functional genes is another option that can be incorporated into the canola for breeding against diseases. *BnNCED3* (9-cis-epoxycarotenoid dioxygenease), is an essential gene in ABA biosynthesis, can enhance adult plant resistance to blackleg infection in overexpressed transgenic lines. However, BnTX1 (trithorax-like factor), which interacts with the promoter region of *BnNCED3*, plays a negative role, as overexpressed transgenic plants exhibit decreased adult plant resistance to blackleg pathogen infection. Moreover, overexpression of another transcription factor, *BnNAC19*, has enhanced adult plant resistance against blackleg pathogen in transgenic canola plants. Our study unveils a new model illustrating how functional genes enhance adult plant disease resistance by regulating ABA biosynthesis and transcription factor activity in plant signaling pathways. These findings may pave the way for the characterization of minor/quantitative genes in the *B. napus–L. maculans* interaction.

[O48] CANADIAN DURUM WHEAT CULTIVAR STRONGFIELD EXHIBITS MODERATE SUSCEPTIBILITY TO MEXICAN LEAF RUST (*PUCCINIA TRITICINA*) RACES. Firdissa E. Bokore[1], Kerry Boyle[2], Yuefeng Ruan[1], Curt A. McCartney[3], Colin W. Hiebert[4], Ron E. Knox[1*], Xiangyu Pei[3], Elsa Reimer[4], Karim Ammar[5], Wentao Zhang[2], Pierre Fobert[2], Richard D. Cuthbert[1], Samia Berraies[1], and Brent D. McCallum[4]. [1]Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, 1 Airport Road, P.O. Box 1030, Swift Current, *SK*, Canada. S9H 3X2; [2]Aquatic and Crop Resource Development, National Research Council Canada, 110 Gymnasium Pl, Saskatoon, SK, Canada. S7N 0W9; [3]Department of Plant Science, University of Manitoba, *66 Dafoe Road University of Manitoba (Fort Garry campus) Winnipeg, MB,* Canada. R3T 2N2; [4]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Rte. 100 #100, Morden, MB R6M 1Y5 Canada; and [5]International Maize and Wheat Improvement Center (CIMMYT), Texcoco, Mexico ([*]Retired) Correspondence to: firdissa.bokore@agr.gc.ca; brent.mcallum@agr.gc.ca

Leaf rust, caused by *Puccinia triticina* (*Pt*) Eriks., is a major disease of durum wheat (*Triticum turgidum* L. var. *durum*) in the world. Canadian durum wheat has traditionally been very resistant to *Pt* isolates from Canada, but races that specifically attack durum wheat in Mexico are virulent on Canadian durum cultivars. A multi-parental population comprised of six subpopulations with the backbone Canadian durum cultivar Strongfield as a common parental line was used to uncover the genetic resistance to Canadian and Mexican leaf rust races. The six populations were evaluated at the seedling plant stage with different Canadian *Pt* races at Morden Research and Development Centre. Of these populations, Strongfield/Blackbird was evaluated for adult plant leaf rust infection near Morden and Carman, Canada and El Batan, Mexico, and Strongfield/RL6089 was evaluated at Morden, Canada and Obregon, Mexico. Strongfield was evaluated against nine Mexican leaf rust races during seedling stage. All six populations were genotyped with the Illumina iSelect 90K SNP array. Genome wide association study, stepwise

regression joint linkage QTL mapping and analysis by MapQTL were performed. Strongfield displayed a resistance response across all the tests in Canada, but an intermediate to susceptible response at El Batan, and a resistant response at Obregon, Mexico. Strongfield contributed seven QTL revealed by the field data, and nine QTL conditioning seedling resistance. A major QTL was discovered on chromosome 3A of Strongfield. The 3A QTL showed resistance to all the tested Canadian *Pt* races during the seedling stage and all the field tests in Canada; however, it was not effective in Mexico. A QTL on 1B from Strongfield corresponded with the multi-pest resistance gene *Lr46*/*Yr29*. In addition to 1B, Strongfield contributed one QTL at El Batan and two QTL at Obregon all revealed by single environments. Notably, we found three new QTL donated from Blackbird or RL6089 that conferred resistance in the Mexican field tests. The major QTL on 3A and most of the other QTL identified in Canada were not effective in Mexico, suggesting the need for pre-emptive resistance breeding to fight against the imminent incursion of Mexican races to Canadian wheat growing areas. The minor effect QTL identified in Mexico show the potential power of pyramiding QTL to build on the existing foundation of Canadian durum wheat to protect against these new leaf rust races in Mexico.

[O49] IDENTIFYING RESISTANCE (R) GENES TO BLACKLEG *LEPTOSPHAERIA MACULANS* IN ACCESSIONS OF CANOLA. Oluwafemi Lawal[1] and Dilantha Fernando[1]. [1]Department of Plant Science, University of Manitoba, Winnipeg, Manitoba, Canada
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Canola (*Brassica napus*), as one of the most economically important crops in Canada, is challenged by a constant arms race with *Leptosphaeria maculans*-blackleg causative agent. This led to the breakdown of resistant (R) genes in most canola cultivars grown in Canada particularly in the Prairie, where canola is mainly grown, leading to more than 30% yield reduction. Identifying the R gene is a precursor in breeding for resistance to blackleg disease, which is the most effective method of protecting canola plants against blackleg disease and its yield loss. Although resistant genes have been explored from other Brassica species, their blackleg resistance potential and stability have not been exploited in the cultivars grown on the farmers' field. Therefore, this research sought to identify R genes from some B. napus accessions sourced from China, where canola is believed to be resistant to blackleg disease, though caused predominantly by *L. biglobosa* in China. To date, 60 Chinese accessions of canola have been screened against 12 IBCN (International Blackleg of Crucifers Network) differential isolates of *L*. *maculans*. The cotyledons of six plants were infected with each of the isolates at seven days post inoculation (dpi), and rated at 10dpi and 14dpi on a scale of 1-9. With 1-3 = resistant, 5 = moderately susceptible, and 7-9 = susceptible. Less than 1% of the Chinese accessions had good resistant scores. Although most accessions were susceptible to *L. maculans,* there is still the high potential for identifying novel R genes among Chinese accessions, as this is essential in breeding for blackleg resistance in canola. Furthermore, the identified accessions were vernalized, grown to the booting stage, and crossed with Westar. The F1 seeds of Chinese lines x Westar will be selfed to F2, screened with differential isolates of *L*. *maculans*, and then subjected to bulk segregant analysis (BSA) to identify putative R gene. Together, the identified R gene will provide more sources of R genes available in the pool to canola breeding program for possible introgression and gene pyramiding towards improving sustainable resistance to blackleg disease, enhancing canola yield, and alleviating the trade barriers usually imposed by importing countries towards curtailing the spread of blackleg disease.

[O50] THE EFFECT OF *R* GENE ROTATION ON MITIGATION OF CANOLA BLACKLEG DISEASE IN WESTERN CANADIAN PRAIRIES. Malini Anudya Jayawardana[1], Zhongwei Zou[2] and Dilantha Fernando[1]. [1]Department of Plant Science, University of Manitoba, Winnipeg, MB, R3T2N2 Canada; and [2]Department of Biology, Wilfrid Laurier University, Waterloo, Ontario, N2L 3C5 Canada
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Blackleg caused by the fungal pathogen *Leptosphaeria maculans* is one of the devastating diseases in western Canada. Host resistance plays a major role among the management strategies currently available to control blackleg. Host resistance in canola against blackleg is governed by both qualitative (*R* genes) and quantitative resistance. However, the continuous exposure of the same *R* gene to the pathogen over the years leads to the breakdown of its resistance. This is called *R* gene resistance breakdown. To understand the delay in the *R* gene resistance breakdown, we have introduced a 4-year *R* gene rotation study in three provinces Manitoba, Saskatchewan, and Alberta. We have included 11

rotation types including single, two, and more than two *R* genes without rotation or rotation with maximum *R* gene diversity. Disease scores from each province were used to calculate the disease severity index (DSI) and disease incidence (DI). In addition, canola stubble samples were used to isolate *L. maculans* isolates for each year from 2019-2022 in Manitoba. The race structures of the *L. maculans* population were determined by phenotyping with the differential set of Brassica species and genotyping by PCR. DSI in all the rotations were significantly lower than the susceptible check Westar in Manitoba and Alberta. In addition, the DSI and DIs for rotations of canola varieties with maximum *R* gene diversity was significantly lower than two *R* genes (*Rlm3/X* or *RlmLepR3/3*) with no rotation in Manitoba and Alberta. Saskatchewan followed the same DSI pattern except for no significant difference among susceptible control and canola varieties *LepR3/Rlm3* and *Rlm3/RlmX* with no rotation. Moreover, DSIs and DIs for rotations of canola varieties with maximum *R* gene diversity were significantly lower than two *R* genes (*Rlm3/X*) with no rotation in Saskatchewan. Interestingly, any rotation that included canola varieties exhibiting *Rlm4* had significantly lower DSIs and DIs with or without rotation. This was further supported by the pathogen race structure where the abundant pathogen races all included *AvrLm4*. Although the data supports for a *Rlm3* resistance breakdown in Canada, the impact can be reduced when *Rlm3* is rotated with *Rlm4*. Overall, this study demonstrates that the *R* gene rotation strategy is effective not only on delaying *R* gene resistance breakdown, but also in reusing ineffective *R* genes in Canada.

[O51] DEVELOPMENT OF SALT TOLERANT ALFALFA (*MEDICAGO SATIVA* L.): FROM LAB TO FIELD. Bill Biligetu[1], Shanna Quilichini[2], and Surendra Bhattarai[3]. [1]Crop Development Center, College of Agriculture and Bioresources, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK, S7N 5A8; [2]Salinity Laboratory, Agriculture and Agri-Food Canada, 1 Airport Road, Swift Current, SK S9H 3X2; and [3]SARDA Ag Research, Donnelly, AB Canada T0H 1G0
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Development of salt tolerant alfalfa cultivars has a significant value to reclaiming saline areas and increasing forage production for animal feed. The objectives of this study were to understand morphological, physiological, and molecular changes of alfalfa in response to salt stress and to develop novel populations with improved salt tolerance. A series of experiments have been carried out over last decade using Synchrotron beam lines, transcriptome analysis, salt lab tests, and field trials. Salt tolerant populations showed greater germination percentage and seed vigor at 16 dS m^{-1} E.C, and out-performed the check cultivars, especially under a high salinity of 20 dS m^{-1} E.C, which indicated effectiveness of direct selection under high salt stress. Salt tolerant selection increased alfalfa leaf protein concentration, and reduced fiber concentration, which was a favorable change in term of forage value. The pattern of chlorine accumulation showed reduced ion accumulation in leaf tissues in the tolerant populations. In root tissue, salt tolerant populations maintained greater number of differently expressed genes (DEGs) during the first 27 h of salt stress, while the number of DEGs decreased for a susceptible population. We developed KASP assay for the SNPs linked to the highly expressed genes. Our results showed that four cycles of recurrent selection have accumulated certain salt resistant related favorable alleles in the alfalfa breeding populations. Taken together, salt tolerance in alfalfa is a complex trait, and morphological, genomic, and physiological indicators have been developed for future breeding use.

[O52] LEAF WATER RELATIONS AND OSMOTIC ADJUSTMENT OF CANADIAN WHEAT CULTIVARS SUBJECTED TO DROUGHT. Gopal Sharma[1], Thorsten Knipfer[1], and Gurcharn S. Brar[1,2].
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For wheat (*Triticum aestivum*), in previously published literature, sustained crop yield at limited soil water has been linked to osmotic adjustment (OA) as one of the main drivers to minimize drought-induced reductions in leaf hydration status and growth. Canada Western Red Spring (CWRS) cultivars are typically grown in rainfed areas in northern plains region with milder climates, but ongoing climate change has increased the frequency and intensity of drought event questioning how successful they are in tolerating drought. The extent of OA and its relation to stomatal behavior, leaf roll, and kernel development under periods of drought remain elusive for CWRS. For several commercially used Canada Western Red Spring (CWRS) wheat cultivars ('Superb', 'Stettler', 'AAC Viewfield'), OA was not found to be a mechanism contributing to drought tolerance. In contrast, we found that sustained kernel weight

during periods of relatively low soil water content was linked to 'tight' stomatal behavior (i.e., efficient transition from onset to full stomatal closure) and 'early' leaf roll (i.e., reductions in flag leaf width). Moreover, leaf hydration status (Θ_{RWC}) marked the onset of drought-induced losses in kernel weight in all three cultivars. Among cultivars, 'Superb' was most successful in employing these strategies which also prolonged the onset of severe leaf dehydration under drought to a soil relative water content (i.e., % of field capacity) as low as 36% (defined as threshold Θ_{RWC}); 'Stettler' at a Θ_{RWC} of 48%, and 'AAC Viewfield' at a Θ_{RWC} of 51%. Moreover, Θ_{RWC} marked the onset of drought-induced losses in kernel weight in all three cultivars. Leaf epicuticular waxes exhibited differences in chemical composition between cultivars, which will be discussed in the context of leaf water loss beyond stomatal regulation under drought. In conclusion, Canadian hard red spring wheat lacks OA but both leaf stomatal behavior and leaf rolling aid in securing leaf hydration status and kernel weight under drought.

[O53] ENHANCING PROTEIN CONTENT IN *BRASSICA NAPUS*: GENETIC INSIGHTS AND BREEDING IMPLICATIONS. Harmeet S. Chawla[1], Mohamed S. Youssef[1], Sean Walkowiak[2], and Robert W. Duncan[1]. [1]Department of Plant Science, University of Manitoba, Winnipeg, Manitoba, R3T 2N2, Canada; and [2]Canadian Grain Commission, Winnipeg, MB R3T 6C5, Canada
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Brassica napus, commonly known as canola, is a vital oilseed crop extensively cultivated for its high-quality canola oil. However, oil extraction generates approximately 1.2 million tons of canola meal annually as a by-product. Despite the increasing popularity of plant-based protein and the rising demand for alternative protein sources, the breeding of canola cultivars with enhanced protein content has been limited, primarily due to the lack of financial incentives. Understanding the genetic factors that influence protein content in *B. napus* is crucial for meeting this growing demand. This study aimed to identify genetic polymorphisms associated with protein content in *B. napus*. We focused on pinpointing the critical candidate genes, as well as the single nucleotide polymorphisms (SNPs) and structural variations (SVs) that play significant roles in regulating protein content in this crop species. Our research identified 24 quantitative trait loci (QTL) associated with protein content across two double haploid mapping populations. Notably, a QTL located on chromosome C09 was consistently detected in three different environments within both populations. By anchoring the genetic markers flanking this QTL region onto the Westar genome assembly, we identified a 7 Mb region on chromosome C09 containing 1079 protein-coding transcripts. Integrating QTL data with long-read PacBio HiFi sequencing data from the parental lines of the two bi-parental populations, we discovered a potential candidate gene that may significantly contribute to protein synthesis in *B. napus*. Our findings underscore the complexity of the genetic regulation of protein content in *B. napus* and provide valuable insights for future research aimed at expanding the end-use of this essential crop. The integration of genetic data with advanced sequencing technologies presents a powerful approach to unravelling the genetic basis of complex traits in crops, paving the way for more targeted and efficient crop breeding programs.

[O54] PARTICIPATORY PLANT BREEDING TO INCREASE DIVERSITY AND RESILIENCE: A CASE STUDY OF CANADIAN WHEAT. Michelle Carkner[1] and Martin Entz[1]. [1]Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB, Canada, R3T 2N2
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Numerous studies have shown that greater biodiversity enhances functioning in cropping ecosystems, yet modern breeding programs focus on uniformity. This contradiction raises the question "Will uniform crop varieties be resilient in the face of increasingly unpredictable weather events and seasonal extremes brought on by climate change?" Our project is based on the premise that diversity offered by populations of plants will lend greater climate resilience than genetically uniform genotypes in contrast to the current Canadian crop registration system and global market demands for uniformity. Secondly, we hypothesized that engaging Canadian farmers in the early selection phase of plant breeding will increase the level of "effective diversity" within wheat genotypes.

In this work, we adopted a decentralized/target environment approach where early generation selection (F3 to F6) took place on farms with farmers directly involved in the selection. By working specifically with organic farmers, we ensured that nutrients would be supplied biologically (legumes, manures, etc.) rather than synthetic fertilizers that exacerbate agriculture's reliance on fossil fuels.

This approach, called 'Participatory Plant Breeding' (PPB) has gained momentum in the last 30 years under low-input, challenging environments in developing countries. However, PPB programs are now expanding across the Global North to meet the needs of the underserved organic industry. Canada's first PPB program in wheat was established in 2011 in partnership with plant breeders with Agriculture and Agri-Food Canada, and the University of Manitoba's Natural Systems Agriculture Research Group. The program worked with over 75 farmers across Canada, generating over 50 wheat genotypes on a diversity of farms. We will report experimental data from trials testing spring wheat 'farmer genotypes' vs. checks under organic management in 12 environments. Average environment yields ranged from 714 to 4382 kg ha^{-1}. Multiple farmer genotypes performed just as well and, in many cases, better than check cultivars. Using three yield stability models demonstrated that 3 farmer genotypes and one check were top performers and most adapted to organic conditions. Another farmer genotype demonstrated high yield, but also superior stability according to the Finlay-Wilkinson test and GGE Biplot analysis. AAC Brandon, one of the most popular commercial cultivars in Manitoba, was found to have low yield and poor adaptation to organic environments. In addition to performance data, we will also share successes and logistical challenges we experienced running the program, as well as future opportunities for Canadian agriculture.

[O55] EXAMINING THE RELATIONSHIP BETWEEN BACTERIAL BROWN SPOT AND COMMON BACTERIAL BLIGHT IN COMMON BEAN. Caio Correa[1,2], Emily Morneau[2], Owen Wally[2], Chris Gillard[1], and Jamie Larsen[2]. [1]Department of Plant Agriculture, University of Guelph-Ridgetown Campus, Ridgetown, ON, Canada, N0P 2C0; [2]Harrow Research and Development Centre, Agriculture and Agri-Food Canada, Harrow, ON, Canada, N0R 1G0
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Bacterial Blights caused by *Xanthomonas axonopodis* var. *phaseoli* (Common Bacterial Blight; CBB) and *Pseudomonas syringae* pv. *syringae* (Bacterial Brown Spot; BBS) are important dry bean (*Phaseolus vulgaris* L.) diseases. These pests are challenging to deal with as they are known to be endemic to most dry bean growing regions and are seedborne, limiting the ability to control disease transmission in seed produced in humid regions like Ontario. Producers are impacted by increased cost of production due to disease-free pedigreed seed production being completed in semi-arid regions, a 20%-45% yield reduction due to impacts on plant health in field outbreaks and a reduction in seed coat quality leading to 'pick' loss when sorted by seed handlers after harvest. Previously, it was thought that CBB was the primary cause of bacterial blights in Ontario, however BBS had not been explored to determine if this disease is present and what impact it has on dry bean varieties grown in Ontario.

Dry bean disease surveys of leaves and seed harvest samples indicated that both CBB and BBS pathogens are found across Ontario, with BBS being most prevalent. Through the use of artificially inoculated CBB and BBS nurseries over 400 cultivars were tested from multiple market classes for reaction to these pathogens. Analysis of data found a significant positive correlation for disease reaction between these two diseases in white bean and small seeded coloured beans, but not for large seeded coloured beans. A subset of 70 cultivars were assayed using molecular markers linked to CBB resistance. A significant molecular marker association was found for both diseases, indicating that resistance to one pathogen was generally associated with resistance to the other, meaning that CBB resistance genes are effective for both diseases. To explore bacterial blight resistance in large seeded coloured beans, three kidney bean populations of 125 recombinant inbred lines each were developed using USDK CBB-15 as a CBB resistant common parent. The three populations were screened for BBS and CBB severity in field-based nurseries and a restricted two stage multi-locus genome-wide association study (RTM-GWAS) was performed using genotype by sequencing molecular marker data to detect single nucleotide polymorphisms potentially linked to resistance genes. In total, 26 and 23 major QTL for BBS and CBB, respectively were identified. These results provide key information on genomic regions that could be selected to improve bacterial blight resistance in kidney beans.

[O56] PROGRESS IN OAT BREEDING IN NORTH CHINA. Junyong Ge[1], Xingyu Wang[1], Yunxia Li[1], Zhanhong Dong[1], Haige Zhao[1], Huadong Zang[2], Yadong Yang[2], and Zhaohai Zeng[2]. [1]Zhangjiakou Academy of Agricultural Sciences (Hebei Alpine Crops Institute), 2 Huitong Street, Zhangjiakou City, Hebei Province, 075000, China; and [2]College of Agronomy and Biotechnology, China Agricultural University, 2 Yuanmingyuan West Road, Haidian District, Beijing, 100193, China
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Oats are commonly grown in North China, and the naked (hulless) type of oats are predominant in the region. In the past ten years, our breeding program have carried out research activities to focus on two major issues affecting seed yield of naked oats. The first breeding objective is to increase ear size of oats and improve grain harvest index. The second breeding objective is to reduce plant height and increase resistance to lodging, thereby achieving increased density and high yield potential. The number of spikelets in some large-ear type oat breeding progeny materials has reached 70-131, and the number of grains per panicle can reach 140-264, which are more than 20% higher than the control varieties. One of the stable offsprings of the strain, Bayou No. 21, had the seed yield of 6935 kg ha^{-1} in 2023, which was more than 15% higher than the same type of control varieties. The offspring of dwarf naked oat breeding materials have a plant height of 70~90 cm, which is more than 30% shorter than existing varieties, and compared with the same type of control varieties, the yield increase is 2300 kg ha^{-1}, with the yield increase rate of more than 35%. These advances have laid some material reserves for the next step in dealing with the rapidly changing climate and an increasing population.

[O57] DETERMINING OPTIMUM SEEDING RATIOS AND PEA-BRASSICA INTERCROP COMBINATIONS FOR MAXIMIZING AGRONOMIC BENEFITS. Yunfei Jiang and Claude Caldwell**.**
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Evidence from both natural ecosystems and agroecosystems reveal that species richness increases plant reproductive potential and productivity. This is mechanistically linked to biodiversity and enhanced resource acquisition due to species complementarity, competition, cooperation, and compensation. Intercropping allows for simultaneous cultivation of multiple crop species or genotypes in the same field during a growing season or a part of the growing season, which is a promising strategy for ecological intensification for improving sustainability. Local adoption of intercrops depends on defining the optimum combinations of crops for maximizing environmental and economic benefits. The objective of this study was to evaluate intercrop performance of two brassica species [camelina (*Camelina sativa*) and brown mustard (*Brassica juncea*)] with peas (*Pisum sativum*) to determine the optimum intercrop mix for maximizing Land Equivalent Ratio (LER) for seed yield profitability in Maritime Canada. Combinations of three seeding rates of peas with three seeding rates of either camelina or mustard at 0.5, 1.0, 1.5 times of the recommended seeding rate for each species were evaluated. In addition, each species was grown separately to determine its sole yield at its recommended seeding rate – 100, 600, and 100 seeds/m^2 for pea, camelina, and brown mustard, respectively. Our results showed that these brassica and pea intercrops were consistently providing LER greater than 1, indicating greater land use efficiency compared to the sole crop. Despite different growing conditions in 2020 and 2022, the most effective seeding rate ratios appear consistent - 600/150 seeds/m^2 for camelina-pea intercrops and 50/150 seeds/m^2 for mustard-pea intercrops. Consistent positive LERs resulting from most of the combinations indicate there is promise for this approach in Maritime agriculture. Our findings will be used to strategically design plant mixtures to improve environmental and economic sustainability.

[O58] AN INTEGRATED STRATEGY TO IMPROVE PROFITABILITY OF BARLEY PRODUCTION IN WESTERN CANADA: AN INTRODUCTION OF GROW BARLEY PROGRAM. Hiroshi Kubota.
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Barley cultivation in Canada has seen a decline in seeded acres from 11.5 million to 7.1 million between 2000 and 2024, causing it to rank third due to the increase in canola acreage. Climate changes may lead to the expansion of corn and soybean production in western Canada, potentially transitioning from barley to more corn or soybean acres, especially if the net revenue of barley production remains less competitive with other crops. Unfortunately, the commodity price fluctuates and is somehow uncontrollable to barley producers. Therefore, producers need to increase barley grain yield while maintaining or reducing production costs to increase net revenue. To respond to this, several challenges need to be addressed.

Barley is more prone to lodging compared to other cereals, thus developing a decision-making tool for PGR applications will benefit producers by reducing the chance of unnecessary PGR applications. Secondly, there is an urgent need to improve the efficiency in adopting newly registered varieties to take advantage of their high yield potential. Providing ready-to-use agronomy packages for newly registered varieties can help speed up their adoption, although factors such as target market, grain buyer, and end-user requirements need to be considered. With the increasing nitrogen fertilizer price and the necessity of reducing greenhouse gas (GHG) emissions from fertilizer, biological nitrification inhibition (BNI) traits in Canadian barley germplasms could also help increase nitrogen use efficiency in barley. Agronomy research related to BNI will be needed. Information regarding the effects of barley and other crops in rotations on nitrogen cycling and pest management can also help producers reduce input costs, resulting in profitable and sustainable barley production. The GROW Barley program is a 7-year research program that will address the most relevant needs in the barley industry, aiming to close the gaps in barley agronomy and maintain its competitiveness and profitability in western Canada.

[O59] IMPLEMENTING DIVERSIFIED CROP ROTATIONS ENHANCES ECOSYSTEM SERVICES. Liu K[1], Wen G[2], Chau H[3], Kubota H[4], Mohr R[5], Peng G[6], Semach G[7], Lokuruge P[8], Entz M[9], Lemke M[6], Khakbazan M[5], Kim YM[5], Sharpe S[6], Town J[6], Hernandez G[10], Iheshiulo E[3], Ferrari Machado P[1], Glenn A[5], Zhang H[1], Qian B[2], Jing Q[2], Kroebel R[3], and Bourgault M[11]. Agriculture and Agri-Food Canada: [1]Swift Current, SK; Ottawa, ON; [3]Lethbridge, AB; [4]Lacombe, AB; [5]Brandon, MB; [6]Saskatoon, SK; [7]Beaverlodge, AB; and [8]Scott, SK; University: [9]U of Manitoba, [10]U of Alberta, [11]U of Saskatchewan
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Agriculture faces significant challenges in the face of climate change, necessitating innovative strategies to enhance the resilience of cropping systems to biotic and abiotic stresses. Crop diversification plays a vital role in improving the ecosystem services that underpin the production function of cropping systems, thereby fostering climate-smart agriculture. Despite being recognized as a cornerstone of adaptive agricultural practice, crop diversification encounters challenges in the current canola-wheat dominant cropping systems on the Canadian Prairies. This presentation will explore novel avenues for diversifying the existing cropping systems. These findings, based on multiple ecosystem service indicators such as production, resource use efficiency, soil health, economic returns, and carbon footprint assessments, indicate that diversifying cropping systems, particularly through the integration of pulse crops, is an effective strategy to improve the sustainability of cropping systems.

[O60] EFFECT OF ECOTEA™ SEED TREATMENT ON SPRING CROPS AT THUNDER BAY. Tarlok Singh Sahota[1]. [1]LUARS, 5790 Little Norway Road, Thunder Bay, ON, P7J 1G1
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EcoTea™ is a biological product combining a wide array of plant-supporting microorganisms and is fortified with added biostimulants to enhance soil quality and nutrient function. A field experiment with combinations of two EcoTea™ seed treatments (no seed treatment and seed treatment with EcoTea™ @ 4 gram kg^{-1} seed) and four spring crops (wheat, barley, canola and soybean) replicated four times in RCBD was conducted during 2021-'23 at Thunder Bay, NWO to evaluate the effect of EcoTea™ on the yield of spring crops. Averaged over 2021-2023, EcoTea™ considerably increased grain (by 1.22 Mg ha-

^{1}), straw (by 1.32 Mg ha^{-1}) and biomass (by 2.49 Mg ha^{-1}) yields of only wheat. Yields of barley, canola and soybean weren't affected by EcoTea™ seed treatment. Among crops, barley produced the highest grain (3.59 Mg ha^{-1}), straw (6.66 Mg ha^{-1}) and biomass (9.80 Mg ha^{-1}) yields. *Farmers are recommended to treat wheat seed with EcoTea™ for increasing grain, straw and biomass yields of wheat.*

[O61] COVER CROPPING AND NITROUS OXIDE EMISSIONS IN THE RED RIVER VALLEY. Mario Tenuta, Shannon Mustard, Katie Webb, Junaid Afzal, Rida Sabirova, and Brad Sparling. Department of Soil Science, University of Manitoba, Winnipeg, Manitoba, Canada R3T 2N2
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Achieving crop production that is net zero for greenhouse gas emissions involves reducing the losses of nitrous oxide (N_2O) from nitrogen fertilizer applied to soils. Nitrification inhibitors, DCD and nitrapyrin with urea (46-0-0) and UAN (28-0-0) fertilizers, can reduce emissions of N_2O by 30-50%. However, commercial nitrification inhibitors such as pronitridine and DMPP are recently available in commercial products and if they reduce emissions is not well known. Here we examined in 2023 and 2024 in two farm studies spring and fall application of a pronitridine (Centuro) product with anhydrous ammonia (82-0-0). We also conducted four field trials with DMPP and urea applied in spring to canola. 2023 was a dry year with low emissions. Centuro did not reduce emissions at either farm site and DMPP did not reduce emissions at all four trial sites. 2024 is off to a much wetter start and results available for one site indicate Centuro is reducing emissions so far. The laboratory results showed Centuro or DMPP with UAN to also not reduce emissions though nitrapyrin (eNtrench) and, to a lesser extent, DCD, to reduce emissions. Here, we discuss some possible reasons why the newer products were not be effective in reducing N_2O emissions.

[O62] MOLECULAR ANALYSES OF DIFFERENTIAL RESISTANCE IN LODGEPOLE AND JACK PINE TO *CRONARTIUM HARKNESSII*, THE CAUSAL AGENT OF WESTERN GALL RUST. Janice Cooke[1], Samson Osadolor[1], Rhiannon Peery[1,3], Laura Manerus[1], Marion Mayerhofer[1], L. Irina Zaharia[2], and Chandra McAllister[1,4]. [1]Department of Biological Sciences, University of Alberta, Edmonton, AB T6G 2E9, Canada; [2]National Research Council of Canada, Aquatic and Crop Resource Development Research Centre, Saskatoon, SK S7N 0W9 Canada; [3]Present address: Natural Resources Canada, Canadian Forest Service, Pacific Forestry Centre, Victoria BC V8Z 1M5 CANADA; and [4]Present address: Entos Pharmaceuticals, San Diego CA 92121 UNITED STATES
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Forest health is profoundly impacted by pests and pathogens. In Canada, the forest area affected by pests and pathogens each year exceeds the annual harves, and is predicted to increase under climate change [2]. Western gall rust is a disease of pines caused by the fungal pathogen *Cronartium harknessii* Meinecke (syn. Endocronartium harknessii (Moore) Hiratsuka). *C. harknessii* causes tree stunting and deformation, and can result in seedling mortality. The most economically and environmentally important hosts for *C. harknessii* are lodgepole pine (*Pinus contorta* Dougl. ex Loud. var. *latifolia* Engelm.) and jack pine (*Pinus banksiana* Lambert) [6]. Lodgepole pine is found in the mountain regions of western North America, while jack pine spans the boreal forest from Alberta to the Maritimes. *C. harknessii* belongs to Class Puccinales (Basidiomycota), members of which are considered to be obligate biotrophs. We have demonstrated that lodgepole pine is more susceptible to *C. harknessii* than jack pine. RNA-Seq of mock-inoculated vs. *C. harknessii*-inoculated lodgepole and jack pine seedlings revealed that jack pine mounts a quicker, more intense response at the level of gene expression than does lodgepole pine. Simultaneous quantification of *C. harknessii* transcripts – sometimes called dual RNA-Seq – indicates that jack pine's concerted gene expression defense strategy is more effective at limiting pathogen colonization than that of lodgepole pine. Mining of functional annotation categories that were significantly enriched in jack pine but not lodgepole pine suggests that jack pine effectively constrains *C. harknessii* colonization via cell wall remodeling together with increased terpenoid and phenolic defense metabolite synthesis. RNA-Seq data suggested that this response is regulated at the transcriptional level as well as at the level of post-translational modification. Several transcription factors belonging to families with well-established roles in plant immunity were upregulated early in jack pine's response to *C. harknessii* inoculation, but not in lodgepole pine. Given that salicylate is canonically implicated in plant responses to biotrophs, we had predicted that salicylate would be invoked in pine responses to *C. harknessii*.

However, RNA-Seq and hormone profiling data revealed that jasmonate rather than salicylate biosynthesis is upregulated in *C. harknessii*-inoculated lodgepole and jack pine. Interestingly, levels of jasmonate-isoleucine, the active form of jasmonate, did not increase in these plants. Drawing from recent research in angiosperm pathosystems, we speculate that *C. harknessii* may act to upregulate jasmonate biosynthesis, possibly as a means to suppress salicylate signalling and thereby decrease host immunity against this biotroph.

***[O63] DO GINSENOSIDES ALTER THE PATHOGENICITY OF *ILYONECTRIA*?** Anka Colo[1] and Mark A. Bernards[1]. [1]Department of Biology, Western University, 1151 Richmond Street, London, ON, Canada, N6A 3K7
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American ginseng, *Panax quinquefolius* L., is an economically valuable crop used in Traditional Chinese Medicine; however, yield of ginseng is negatively impacted by ginseng replant disease (GRD). GRD is characterized by a severe root rot, primarily caused by the fungus *Ilyonectria mors-panacis (Imp)* (formerly *Cylindrocarpon destructans*), in ginseng planted in a former-ginseng garden. While *Imp* is typically present in ginseng garden soils during the first cultivation of a ginseng crop, *Imp*-associated root rot is more extensive during subsequent crop plantings. Furthermore, the bioactive ginsenoside compounds produced by ginseng accumulate in ginseng garden soils during cultivation and are known to be fungitoxic toward some soil-borne fungi, while growth stimulants of others, including *Imp*. Presently, it is not clear if (1) prior exposure to ginsenosides enhances *Ilyonectria* virulence, (2) different *Ilyonectria* isolates can metabolize ginsenosides equally effectively, and (3) there is a relationship between *Ilyonectria* virulence and the metabolism of ginsenosides. To address these issues, twelve independent *Ilyonectria* isolates that differ in their geographic and host plant origins, were screened for their pathogenicity toward American ginseng. For this, one-year old American ginseng seedlings were inoculated separately with twelve *Ilyonectria* isolates and monitored for disease onset using non-invasive chlorophyll fluorescence detection over 28-days. Disease load was scored at 28-days. Five *Ilyonectria* isolates displayed low virulence while seven *Ilyonectria* isolates displayed high virulence. To address the question of whether prior exposure to ginsenosides affects *Ilyonectria* virulence on ginseng, two-year old American ginseng roots were inoculated with different isolates of *Ilyonectria* from both the low and high virulence groups that had been cultivated on media with and without ginsenosides. After 16-days, lesions were measured. Two low virulent isolates showed increased virulence (i.e., greater lesion size) after being grown on ginsenoside containing media for a minimum of four transfers, while the virulence of high virulent isolates remained unchanged by ginsenoside treatment. These data suggest that exposure to ginsenosides increase the virulence of *Ilyonectria* toward American ginseng. Lastly, to determine whether *Ilyonectria* isolates can metabolize ginsenosides equally effectively, we are currently growing *Ilyonectria* isolates in liquid minimal media supplemented with ginsenosides and will use liquid chromatography–mass spectrometry (LCMS) used to quantify the ginsenosides remaining after seven days. Understanding whether exposure to ginsenosides enhances virulence will further our understanding of *Ilyonectria* and its implications in GRD.

[O64] PLANT IMMUNE RESILIENCE: FROM GENE REGULATORY NETWORKS TO BIOMOLECULAR CONDENSATES. Christian Danve M. Castroverde[1], Jong Hum Kim[2], Alyssa Shields[1], Lingya Yao[3], Shuai Huang[4], Eric J.R. Marchetta[1], Richard Hilleary[5], Adam Seroka[5], John D. MacMicking[6], Xiu-Fang Xin[3], and Sheng Yang He[5]. [1]Department of Biology, Wilfrid Laurier University, Waterloo, ON, Canada, N2L 3C5; [2]Department of Life Sciences, Pohang University of Science and Technology, Pohang, 37673, Republic of Korea; [3]National Key Laboratory of Plant Molecular Genetics, CAS Center for Excellence in Molecular Plant Sciences, Institute of Plant Physiology and Ecology, Chinese Academy of Sciences, Shanghai 200032, China; [4]Department of Molecular Genetics, The Ohio State University, Columbus, OH, USA 43210; [5]Howard Hughes Medical Institute, Department of Biology, Duke University, Durham, NC, USA 27708; and [6]Howard Hughes Medical Institute, Departments of Immunobiology and Microbial Pathogenesis, Yale University School of Medicine, New Haven, CT, USA 06477
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Climate warming negatively affects diverse aspects of plant life, including effective immune signaling and responses. Two central plant immune-activating signals are salicylic acid (SA) and *N*-hydroxypipecolic

acid (NHP), which synergistically potentiate both basal immunity and systemic acquired resistance to numerous pathogens. The SA and NHP pathways are particularly vulnerable to suppression by elevated temperatures simulating heat waves above the normal growth range. However, the mechanistic basis for heat-mediated suppression of SA and/or NHP has remained elusive, representing a significant concern for crop protection amidst a warming climate. In our recent work, we identified a novel thermosensitive mechanism governing the SA and NHP pathways via the *CALMODULIN-BINDING PROTEIN 60-LIKE G* (*CBP60g*) and *SYSTEMIC ACQUIRED RESISTANCE DEFICIENT 1* (*SARD1*) genes. *CBP60g* and *SARD1* encode master transcription factors regulating SA and NHP biosynthetic genes, as well as other drivers of the plant immune system. While ambient temperature conditions led to immune-responsive *CBP60g* and *SARD1* gene transcription, elevated temperature largely suppressed this induced expression. Further investigations led to the discovery that thermosensitive *CBP60g/SARD1* transcription is controlled by GUANYLATE-BINDING PROTEIN-LIKE 3 (GBPL3), an intrinsically disordered region-containing GTPase protein that can form membraneless nuclear assemblies called GBPL defence-activated condensates (GDACs). These GDACs concentrate essential transcriptional regulators (e.g. Mediator complex) and enzymes (e.g. RNA polymerase II) during plant immune elicitation. We observed that GDAC formation is dynamically regulated by temperature, with a notable decrease in condensate formation in planta at higher temperatures. This resulted in reduced recruitment of the Mediator complex and RNA polymerase II to the *CBP60g* and *SARD1* promoter regions, which decreased downstream gene transcription and worsened disease susceptibility of plants under warm conditions. Genetically engineering this temperature-vulnerable *CBP60g/SARD1* transcriptional node effectively restored SA/NHP biosynthesis and strengthened plant immune resilience. Taken together, we successfully identified the GBPL3-CBP60g/SARD1 regulatory network that governs the thermosensitivity of the plant immune landscape. This promises a broadly applicable roadmap to safeguard plant disease resistance for a warming climate.

***[O65] BACK TO THE ROOTS: EXPLORING PLANT-INSECT INTERACTIONS IN CULTIVATED AND WILD TOMATOES.** Andreea Bosorogan[1,2], Osmond Hui[2], and Eliana Gonzales-Vigil[1,2]. [1]Department of Cell and Systems Biology, University of Toronto, Toronto, ON, Canada, M5S 3G5; and [2]Department of Biological Sciences, University of Toronto - Scarborough, Scarborough, ON, Canada, M1C A14
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Conventional breeding has improved several agronomic traits in tomato (*Solanum lycopersicum)*, yet herbivore resistance remains a critical challenge in tomato production. Plants use a plethora of strategies including specialized structures (e.g., cuticles containing epicuticular waxes) and a diversity of metabolites (e.g., terpenes) to reduce insects' feeding ability and development. However, cultivated tomatoes lack the chemical diversity of wild relatives, like *S. habrochaites.* Despite *S. habrochaites'* rich chemical variation, little is known about its contribution of the chemical diversity to herbivore resistance traits. In this study, we examined the variation in epicuticular waxes and terpenes among 17 accessions of *S. habrochaites* and *S. lycopersicum*, and evaluated their resistance to herbivory by exposing the plants to *Trichoplusia ni* (Lepidoptera) larvae. Large differences in insect mortality and weight gain were seen across the 17 accessions. Specifically, five *S. habrochaites* accessions were highly resistant, causing over 80% mortality and reduced mass gain in *T. ni.* The significant differences in insect performance among cultivated and wild tomatoes were followed up by chemical characterization. Terpene diversity and abundance varied significantly across the accessions, yet the epicuticular wax profiles of *S. habrochaites* were similar to those of cultivated tomatoes. Accessions with elevated levels of several terpenes, including bergamotene, santalene, and elemene, showed high resistance to insect damage, suggesting potential repellent or toxic effects on *T. ni.* Yet, it is still to be determined whether chemical diversity or quantity has the largest effect on herbivory, as increased quantities of total terpenes and epicuticular waxes were negatively correlated with insect performance. Overall, this study provides a critical step in understanding insect interactions with complex specialized metabolites in *S. habrochaites,* which will inform the development of resilient tomato cultivars with enhanced resistance to Lepidopteran herbivores.

[O66] PAPERCLIP RNA STRUCTURES REDUCE DISEASE SYMPTOMS CAUSED BY *SCLEROTINIA SCLEROTIORUM* THROUGH HOST INDUCED GENE SILENCING. Mark F Belmonte, Bliss M. Beernink, and Steve Whyard. University of Manitoba, Department of Biological Sciences, 50 Sifton Road, Winnipeg, Manitoba, Canada
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Sclerotinia sclerotiorum, the causal agent of white mold, infects over 600 species of plants worldwide. *Sclerotinia* is a persistent problem for global food production that has traditionally been managed using broad-spectrum fungicides. However, current fungicide strategies have proven less effective and crop rotations fail due to the promiscuous host range of Sclerotinia and the formation of durable resting structures known as sclerotia. Thus, there is an immediate need to manage Sclerotinia using novel species-specific control methods. Our strategy exploits the inherent cellular defense process known as RNA interference (RNAi). Upon encountering a double stranded RNA (dsRNA) molecule like a paper clip (pc)RNA, the cell processes the pcRNA specifically targeting transcripts with sequence homology. Using long dsRNAs and pcRNA structures produced *in planta*, we identified *Sclerotinia*-specific target genes capable of host induced gene silencing via RNAi knockdown thus reducing the disease pressure of Sclerotinia on transgenic Arabidopsis. These Sclerotinia gene targets and pcRNA structures shown to work in Arabidopsis can be quickly translated into other plant species for improved fungal control in economically important crops.

[O67] VOICES FROM BOTH SIDES: A MOLECULAR DIALOGUE BETWEEN TRANSCRIPTIONAL ACTIVATORS AND REPRESSORS IN SEED AND SEEDLING DEVELOPMENT. Liang Song.
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High-quality seeds ensure successful seedling establishment and provide valuable nutrients to human society. The phase switch from seed to seedling is crucial for plant survival and success. During seed germination, the embryonic programs regulating storage reserve accumulation and dormancy must be shut down, involving epigenetic modifications and feedback regulation among transcriptional regulators. Recent works have reported Arabidopsis thaliana SEED DORMANCY 4-LIKE (AtSDR4L) and its homolog Dynamic Influencer of Gene Expression 1 (DIG1) are targeted by ABA INSENSITIVE 3 (ABI3), a master transcription factor in seed development. AtSDR4L and DIG1 function as transcriptional co-repressors of the seed maturation programs during Arabidopsis seedling establishment. We established a link between AtSDR4L/DIG1 and the Polycomb Repressive Complex (PRC)-associated protein VIVIPAROUS1/ABI3-LIKE 2 (VAL2) by demonstrating their physical interactions and genome-wide binding similarities. We present evidence that AtSDR4L and DIG1 likely use PRC2-mediated H3K27me3 deposition to regulate target genes, including master regulators of seed maturation as well as AtSDR4L and its homologous loci, to promote the embryonic-to-vegetative transition. Lastly, SDR4 and its orthologs appear to have opposite functions in regulating seed germination in representative dicotyledonous and monocotyledonous species, warranting further characterization of this family in various species.

***[O68] SOMETHING SWEET: SUGAR MEDIATED CHANGES IN CELL PROLIFERATION VIA TOR-BRASSINOSTEROID SIGNALLING REQUIRE THE MICROTUBULE ASSOCIATED PROTEIN *CLASP*.** Sean P.A. Ritter, Dr. Laryssa Halat, and Dr. Geoffrey Wasteneys. The University of British Columbia
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To survive, all organisms must coordinate energy intensive processes, such as growth, with environmental conditions to prevent over-exertion in challenging situations. In plants, sugars are the major energy source utilized to power cellular processes. Thus, plants must be able to both perceive and enact appropriate cellular responses to sugar levels. TARGET OF RAPAMYCIN (TOR) is a conserved protein kinase activated by growth factors and inactivated by energy deprivation, thereby acting as a master regulator of metabolic pathways in all eukaryotes. In plants, TOR has been shown to alter meristem activity, and thereby cell proliferation and growth, in response to changing light levels and sugar availability. While numerous targets of TOR kinase activity have been identified, such as the brassinosteroid (BR) responsive transcription factor BRASSINAZOLE RESTISTANT 1 (BZR1), how TOR kinase activity is translated into altered growth at the cellular level is less clear. A candidate for one such crucial link between TOR signaling and growth is the microtubule-associated protein CLIP-ASSOCIATED

PROTEIN (CLASP). CLASP expression is altered by both BZR1 activity and light availability, thereby fine-tuning cell proliferation in response to environmental conditions through modulation of microtubule dynamics. In addition, CLASP also modulates meristem activity through an interaction with SORTING NEXIN 1 (SNX1) which sustains the auxin transporter PIN2, a known target of TOR, at the plasma membrane. I propose that CLASP acts as a crucial component of the TOR signaling pathway, providing a mechanism by which sugar affects root meristem activity and growth. My research shows *CLASP* null mutant plants display reduced sensitivity to pharmacological inhibition of TOR at the organ, cellular and subcellular levels. Plants lacking functional *CLASP* fail to increase cell proliferation in response to sugar, suggesting it is required for this process. Both PIN2 expression and auxin distribution are unaltered by TOR inhibition in the absence of CLASP. This effect is mediated by the brassinosteroid signalling pathway, as both constitutively active BZR1 and mutation of the BZR1 binding site within the *CLASP* promoter prevents TOR dependant changes in root growth and CLASP expression. Through characterization of the interaction between CLASP, TOR and plant hormones, this work provides insight on how the sugar provision is translated into altered root development, thereby furthering our understanding of how plants perceive their changing environment.

[O69] HOW INTERNAL GROWTH CONTROLS PLANT MORPHOGENESIS? Sylvia R. Silveira[1], Loann Collet[1], Sahil M. Haque[1], Luc Lapierre[1], Agnieszka Bagniewska-Zadworna[2], Frederick P. Gosselin[3], Richard S. Smith[4], Anne-Lise Routier-Kierzkowska[1], and Daniel Kierzkowski[1]. [1]Institut de Recherche en Biologie Végétale, Département de Sciences Biologiques, Université de Montréal, 4101 Sherbrooke St E, Montréal, QC, H1X 2B2, Canada; [2]Department of General Botany, Institute of Experimental Biology, Faculty of Biology, Adam Mickiewicz University, Uniwersytetu Poznańskiego 6, 61-614 Poznań, Poland; [3]Laboratory of Multiscale Mechanics (LM2), Department of Mechanical Engineering, Polytechnique Montréal, Montréal, QC H3C 3A7, Canada; and [4]Department of Computational and Systems Biology, John Innes Centre, Norwich NR4 7UH, UK
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The differential growth between connected plant tissues generates mechanical conflicts which are thought to regulate organogenesis. The roles of outer and inner layers in this process remains a matter of debate. Using the anther as a model system we explore how mechanical interactions control the acquisition of complex three-dimensional organ shapes. By combining live-cell imaging, 3D growth analysis, osmotic treatment, genetics, and mechanical modeling, we demonstrate that lobe outgrowth is driven by a fast localized growth in internal cells. Additionally, we show that at later stages, the mechanical load shifts to the endothecium, contributing to the proper shaping of the anther. Our findings reveal how mechanical interactions between tissue layers control 3D morphogenesis.

[O70] A UNIVERSAL MODEL OF EMBRYO DEVELOPMENT IN LAND PLANTS (EMBRYOPHYTES) AND THEIR POTENTIAL APPLICATIONS FOR CROP IMPROVEMENT. Prakash Venglat[1], Perumal Vijayan[1], Timothy F. Sharbel[1], Abidur Rahman[1,2], and Karen Tanino[1]. [1]College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada; and [2]Department of Plant Biosciences, Faculty of Agriculture, Iwate University, Morioka, Iwate 0208550, Japan
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The evolution of land plants (embryophytes) is marked by a series of adaptations enabling their colonization of diverse terrestrial habitats. This involved a stepwise evolution of the embryonic program, allowing for successful reproduction and dispersal in challenging environments. Similarly, the root program in early embryophytes underwent progressive development, facilitating nutrient acquisition and anchorage. A key aspect of plant adaptation is their regenerative capacity, a trait deeply integrated into plant development and asexual propagation throughout evolution. The traditional model of embryo development, centered on a bipolar apical-basal axis, as observed in Arabidopsis, may not fully encompass the diversity of mechanisms across land plants. An alternative evolutionary model, taking into account the stepwise evolution of embryogenesis, root development, and regenerative capacity, to be discussed in this presentation, offers a more comprehensive understanding of plant embryo development. This proposed universal model of embryo development in land plants would provide a valuable framework for studying various species, revealing commonalities and unique adaptations. Such knowledge could be harnessed for crop improvement by manipulating key developmental pathways to enhance traits like root development, nutrient use efficiency, and yield potential. Understanding the regenerative capacity

embedded within the embryonic programs could lead to the development of new propagation techniques and crop varieties with improved stress resilience.

***[O71] ADAPTIVE ROOT MORPHOLOGY AND ARCHITECTURE AS A DROUGHT RESPONSE IN *BROMUS* INERMIS.** Nora Kroeger[1] and Rafael Otfinowski[1]. [1]Department of Biology, University of Winnipeg, 515 Portage Avenue, Winnipeg, MB, Canada, R3B 2E9
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Grassland ecosystems across the globe are increasingly threatened by climate change, which is predicted to exert different pressures on native and invasive plants. Plant responses to changing environmental conditions are often measured or predicted using their morphological and anatomical traits, however, few studies account for the intraspecific trait plasticity that plants exhibit in response to environmental stressors, including drought. In this study, we examined whether six years of experimentally induced extreme drought altered plant species composition and diversity in a grassland in western Manitoba, Canada, and whether smooth brome (*Bromus inermis*), an invasive perennial grass, exhibited differential root morphology and architecture as a result of drought. We conducted a plant inventory, harvested aboveground biomass, and collected, washed, and scanned roots of twenty smooth brome individuals sampled from five drought frames and five frames exposed to ambient precipitation. Long-term drought increased the alpha diversity but not the beta diversity of experimental grasslands. For smooth brome, drought increased the number of crown buds that produced rhizomes, and the total length and surface area of roots. Focal plants also increased their allocation of root length and surface area to very fine roots under drought, indicating a phenotypically plastic strategy of water acquisition in smooth brome. Understanding how smooth brome responds to drought is critical to predicting how the structure, composition, and function of grasslands across North America will be shaped by climate change and will help to control the spread of invasive species both now and in the future.

***[O72] QUANTIFICATION OF BIO-STIMULANTS (MICROBES AND BACILLIN-20) AND THEIR INTERACTIONS FOR ENHANCED CANNABIS GROWTH AND QUALITY IN TERMS OF SECONDARY METABOLITE COMPOSITION.** Ambreen[1], A. Geitmann[1], and D. L. Smith. [1]Department of Plant Science, Macdonald Campus, McGill University, Montreal, QC, Canada
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Cannabis has proven to be a promising medicinal plant, effective in relieving pain, relaxing muscles, and treating neurological disorders. With its potential benefits becoming better documented, it has earned a place of interest in the scientific community and several governments have legalized it because of its wide range of uses, such as fiber, oil, medicinal treatments, and recreational use. CBD (cannabidiol) and THC (tetrahydrocannabinol) are the most important secondary metabolites, involved in controlling pain and recreational use, respectively. Small fluctuations in growth conditions can change the production of these metabolites and hence the medicinal value and quality of the plant. This study investigates the potential of bio-stimulants, microbes, and a microbe-to-plant peptide signal molecule, Bacillin-20, to affect cannabis growth, cannabinoid, and terpene levels by augmenting nutrient uptake or enhancing resistance against biotic and abiotic factors by triggering plant stress/defence responses. The study also addresses the effects of bio-stimulants at the proteomic level. Scanning electron microscopy was used to document root colonization by bacterial strains (U35, U49, U50) on the surface and inside roots. Image analysis with winRhizo showed increased root length, root diameter, and root volume in plants inoculated with strains U35, U47, U48, U50 whereas, U49 resulted in a decrease in these parameters. The 5 microbial strains are also being tested for their bio control activity against *Botrytis* sp. and *Fusarium* sp. Cannabis plants in the flowering stage are going to be tested for cannabinoids and terpene levels using LC-UV, LC-MS, and GC-FID-MS to determine the effect of microbial treatment. The results will facilitate a switch to biological inputs to reduce the use of synthetic chemicals and pesticides, for more sustainable crop-plant growth.
Keywords: Cannabinoids, Terpenes, Bio-stimulants, Root colonization, Quantification

***[O73] BIOCONTROL ACTIVITY OF *BACILLUS SP*. OF PHYTOMICROBIOME AGAINST *BOTRYTIS CINEREA* IN *CANNABIS* SATIVA.** Haleema Tariq[1], Anja Geitmann[1], and Donald Smith[1]. [1]Department of Plant Science, Macdonald Campus, McGill University, Montreal, QC, Canada
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Cannabis is a promising medicinal plant that is used for relieving pain, relaxing muscles, improving sleep, and treating many neurological disorders. Cannabinoids such as cannabidiol (CBD) and tetrahydrocannabinol (THC) are important secondary metabolites produced by *Cannabis* and have been used as analgesics. *Botrytis cinerea* is a fungal pathogen that affects a wide range of crops worldwide including *Cannabis*. It compromises the ability of *Cannabis* producers to achieve the desired secondary metabolite profiles and overall productivity. Controlling this fungus using fungicides costs more than $1 billion annually, and the residual fungicides on plants lead to health concerns for consumers. Gray mold caused by *B. cinerea* causes significant losses in both indoor and outdoor production systems and decreases *Cannabis* yield by up to 32%. With the rapid expansion of the cultivation of *Cannabis*, especially in North America, there is a need to focus on pathogen attacks in this crop plant. Plant growth-promoting rhizobacteria have a potential role in sustainable food production, particularly in the presence of biotic and abiotic stresses, including those associated with global climate change, to feed our growing global population. Plant-beneficial microbes provide an alternative and can be suitable tools for *Botrytis* control and enhance overall crop productivity in an environmentally sustainable way. The current study focuses on the biocontrol activity of bacteria against *Botrytis cinerea* of the cannabis plant. Morphological analysis and scanning electron microscopy helped us determine the interaction between biocontrol (microbes) and *Botrytis.* Microbiological studies performed to characterize the selected beneficial bacteria for their ability to produce lytic enzymes involved in plant pathogenic inhibition and plant growth stimulation revealed cellulase, protease, lipase, amylase, ACC-deaminase and phosphatase activity. The study allowed the detection of several enzymatic mechanisms involved in plant growth and protection and revealed the potential of members of phytomicrobiomes as a biocontrol and biostimulant in cannabis plants. The current project aims to reduce fungal pathogen infection (*Botrytis cinerea*) in *Cannabis* plants using plant-beneficial microbes which will help the producers and sellers in reducing the limitations of *Cannabis* production and limit the use of synthetic fungicides that are harmful to human health and increase greenhouse gas emission.

[O74] GENETIC CONTROL OF FLOWERING IN *CANNABIS SATIVA*. Soheil S. Mahmoud.
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We employed RNA-Seq and differential transcript expression analysis to identify genes that control flower initiation and development in *Cannabis sativa*. They study led to the identification of several differentially expressed MADS-box type transcription factor genes, homologous to those that control flower initiation and organ identity in *Arabidopsis thaliana*. In this presentation I will review the cloning and *in planta* functional analysis of some of these genes. Inn summary, we constitutively expressed TF genes in *A. thaliana* plants, and evaluated the effects on flower initiation, flower morphology, and monoterpene metabolism in flowers. Our results demonstrated that ectopic expression of *SVP* can severely affect flower organ identity. However, overexpression of *SEP* and *AGL* orthologs does affects floral morphology, although plant growth and development, and timing of flowering could be impacted in transformed plants. These TFs do not appear to affect monoterpene production in transformed plants.
Keywords: Cannabis sativa, Arabidopsis thaliana, flower timing, organ identity, transcription factors

[O75] HOW TO DETERMINE THE OPTIMAL FLOWERING-STAGE PHOTOPERIOD FOR CANNABIS PRODUCTION. Youbin Zheng. School of Environmental Sciences, University of Guelph, 50 Stone Road East, Guelph, Ontario, N1G 2W1, Canada
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Cannabis sativa (cannabis) is a short-day plant. High-THC ((–)-Delta-9-trans-tetrahydrocannabinol) cannabis has been increasingly cultivated in controlled environments for medical and recreational usages. To promote flowering and produce high-yield inflorescence, and to ensure the inflorescences contain the highest cannabinoids and terpenoids, cultivators predominantly employ a 12-hour (h)

uninterrupted dark period (i.e., 12h photoperiod) in a 24h day during the flowering stage in controlled environment (CE) cannabis production. Recent research has demonstrated that certain cannabis cultivars exhibit the capacity to flower under photoperiods exceeding 12h; and our previous study demonstrate a positive linear correlation between the photosynthetic photon flux density (ranging from approximately 200 to 1800 µmol/m^2/s) and the yields in some high-THC cannabis cultivars. The aforementioned knowledge led us to believe that there is an optimal flowering-stage photoperiod, not necessarily 12h, for a given high-THC cannabis cultivar. But how can we cost effectively and reliably determine the optimal photoperiod? This presentation will answer these questions based on our own research results and the existing literature.

***[O76] OPTIMIZATION OF SOLVENT-BASED EXTRACTION USING A CENTRIFUGE ON THE BASIS OF PARTICLE SIZE AND THE AGITATION TIME.** Ritul Jyani[1], Philip Wiredu Addo[1], Sarah MacPherson[1], Nichole Taylor[2], Michelle Shearer[2], Fredrick Gallant[3], Maxime Paris[3], Valerie Orsat[1], and Mark Lefsrud[1]. [1]McGill University, Macdonald Campus, 21111 Lakeshore, Sainte-Anne-de-Bellevue, QC, H9X 3V9; [2]BloomLabs Cannabis Solutions, 173 Dr Bernie MacDonald Dr, Bible Hill, NS B6L 2H5; and [3]EXKA Inc., 7625 Rte Arthur Sauvé, Mirabel, QC J7N 2R6
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Legalization of cannabis has spurred research aimed towards improving cannabinoid extraction efficiency, with solvent-based extraction still being a prominent method in the industry. The objective of this study was to optimize a centrifugal extraction system for better yield and improved solvent recovery. The centrifuge used for extraction consists of two cycles: agitation, to mix the biomass with the solvent and spin cycle, to recover the ethanol absorbed in the biomass after drainage.

The solvent recovery during the spin cycle for two different rotation speeds (1000rpm and 1200rpm) for 5 minutes was compared. Pre- and post- spin cycle samples were diluted in an MCT (Medium Chain Triglycerides) oil to dissolve ethanol and were run through Gas Chromatography/Mass Spectroscopy for analysis. A t-test on the results yielded a p-value of 0.42, indicating that the 1200 rpm does not significantly differ from the 1000rpm in recovering more ethanol.

The optimization focused on two parameters: particle size and agitation time for cold ethanol (-40°C) extraction of cannabinoids. Specifically, three particle sizes – fine, medium and coarse, separated with meshes with openings of 582 µm and 1184 µm, were analysed for three agitation durations (5, 13 and 21 minutes) and varying spin cycle from 1000 to 1200rpm. A central composite face-centred design was used to ascertain the optimal value of parameters targeting maximum cannabinoid yield. Quantification of yield was performed by analysing the cannabinoid content pre- and post- extraction using High-Performance Liquid Chromatography. The finer particles with more agitation time are hypothesised to yield more cannabinoids because of the more surface area exposed to the solvent.

Overall findings will offer insight into the potential for more efficient extraction of cannabinoids on an industrial scale.

****[O77] EFFECT OF ENHANCED EFFICIENCY NITROGEN FERTILIZERS AND ANVOL™ ON SPRING WHEAT PRODUCTION AND SOIL HEALTH.*** *Harsh Bagria[1], Tarlok Singh Sahota[2], and Brian McLaren[3]. [1]Natural Resource Department, Lakehead University, 955 Oliver Rd, Thunder Bay, ON, Canada, P7B 5E1; and [2]Lakehead University Agriculture Research Station, 5790 Little Norway Rd, Thunder Bay, ON, Canada, P7J 1G1*
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Nitrogen (N) is an essential macronutrient that plays a critical role in the cultivation of spring wheat, affecting several physiological and developmental processes. The widespread use of N fertilizers can result in environmental contamination, as approximately half of the N applied as fertilizers is lost through various pathways. Urea treated with N stabilizers such as urease inhibitors and nitrification inhibitors could be an effective way to reduce N losses. The application of enhanced efficiency N fertilizers such as polymer-coated urea and urea supplemented with inhibitors of urease and nitrification is expected to improve the growth, yield, and quality of spring wheat, outperforming the traditional application of untreated urea. This study tracked the effects of different N sources at two different application rates (80

kg ha^{-1} N and 120 kg ha^{-1} N) on plant growth attributes, field productivity, soil health metrics, and soil chemical and biological parameters. Nitrogen source had minimal effect on soil health, including only slight changes in microbial composition and nutrient levels. The use of either traditional urea or enhanced efficiency N fertilizers corresponded to the development of beneficial microbial communities. Plant phenotypic traits, grain characteristics, soil nitrate levels, and disease occurrence were not significantly influenced by the choice of N source, an outcome that can be attributed to a limited rainfall during the growing season of the experiment. Overall, N management strategies, which are adaptable to prevailing environmental conditions, that prioritize optimal nutrient absorption, improve soil structure, and promote sustainable agricultural practices are recommended.

***[O78] CAN STARTER POTASH APPLICATIONS IMPROVE THE YIELD AND CROP HEALTH OF CHICKPEA, MUSTARD, AND DURUM WHEAT IN THE BROWN SOIL ZONE OF SASKATCHEWAN?**

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Potash (KCl; 0-0-60) fertilizer is the most economical and widely used source for K and Cl agronomically, however, the link between potash fertilization and crop yield and disease incidence has not been investigated with chickpea, mustard, and durum wheat on the prairies. To address this gap, a field study near Central Butte, SK was completed as well as a controlled environment study using three soils taken from across the Brown soil zone of Saskatchewan. For the field study, starter potash was banded at 40 kg KCl / ha at two slope positions: a dry knoll and a moist depression. In both years of the field study, there were no significant increases in crop yield or a large reduction in disease found to result from the additional starter potash application. This outcome aligned with the soil test values of high exchangeable potassium and K supply rate found in the soil and the limited moisture available during both growing seasons. In the depressional site, greater crop yield and nutrient removal was observed due to the higher inherent soil fertility and additional moisture available. Crop and straw tissue analysis further showed no significant increases in K or Cl content from the KCl application and that most of the K and Cl uptake was contained in the straw portion rather than the grain. The controlled environment studies examined the effect of starter KCl, monoammonium phosphate (MAP), and copper sulfate ($CuSO_4$) alone and in combination on early crop growth and root and shoot disease incidence. Even though there were high extractable concentrations and supply rates of K and P and sufficient Cu levels in all three soils, significant early season growth responses to fertilization were sometimes observed, varying by soil and crop type. Increases in early season biomass were found in the mustard grown in the Chaplin association soil as well as the durum wheat and chickpea grown in the Sutherland association soil. In cases where benefits were observed from fertilization, the greatest increases were seen when the three fertilizers were used in combination. Generally, the plant tissue P, Cu, and Cl concentrations responded more to fertilization than K, possibly due to inherently large K supplies in the soils. Chickpea biomass values were influenced by the presence of the Chickpea Health Issue in the growth chamber, and there was no observed treatment effect on the severity of the Chickpea Health Issue or other diseases present.

***[O79] THE EFFECT OF VARYING FERTILITY MANAGEMENT REGIMES N THE YIELD AND QUALITY OF VARIOUS FORAGE SPECIS/MIX.**

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Soil fertility is a crucial for achieving desired crop yields; however, less attention is typically given to forage fertility than other annual cash crops. There are anecdotal reports of producers applying 100 lbs/acre of a 19-19-19 (N-P-K) fertilizer annually to their forages and it is unclear whether this is beneficial. In addition, despite the introduction of new forage plant varieties, including grasses such as Festulolium species (a cross between a ryegrass and a fescue), forage fertility recommendations in Ontario have not been updated since the 1980's. The objective of this trial was to determine the effect of fertility on the yield and quality of 19 different forage mixtures available in Ontario market over a three-year period. These treatments ranged from pure grasses to pure legumes and included common hay and

pasture mixes available on the market. The three fertility treatments to be tested include: 1) zero fertility control, 2) a one-time spring application/year of 19-19-19 NPK fertilizer, or 3) fertilize as needed according to OMAFRA guidelines based on soil testing. Forage yield was analysed for three years and forage quality analysis in the first year. Overall, our results have shown that the treatment fertilized according to OMAFRA recommendations yielded the most in each year and over the three years. The differences in yield between this treatment and the other two treatments grew with time, suggesting nutrient deficiencies were becoming more severe. By year 3, applying 100 lbs of 19-19-19 does not seem to increase the yield relative to the no fertilizer control. Grass-legume mixtures provided greater yields than those of solely grass-based mixtures and also do not require nitrogen applications, making them highly profitable. If planting a pure grass forage, over a 3-year period, grass mixtures yielded better than single grass species. The red clover-based mixture yielded more in the first year, whereas after that the alfalfa-based mixtures yielded more, ultimately being more productive across all three years of the study. Tissue potassium concentrations were lower compared to tissue phosphorus in the 19-19-19 NPK and the no fertility treatments. Hence, low soil extractable potassium concentrations may impact forage yield more than low soil test phosphorus concentrations; thus, potassium should not be underestimated when applying fertility to forages. However, the transferability of our study to other sites will vary depending on starting soil fertility levels, thus it is recommended to soil test your forage fields regularly to know your starting point.

*__[O80] EFFECT OF ENHANCED EFFICIENCY NITROGEN FERTILIZERS ON AGRONOMIC AND ENVIRONMENTAL PERFORMANCE IN GRAIN CORN.__ Baillie Lynds[1] and Yunfei Jiang[1]. [1]Department of Plant, Food and Environmental Sciences, Faculty of Agriculture, Dalhousie University, Truro, NS, Canada, B2N 5E3
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Enhanced-efficiency nitrogen fertilizers (EENFs) have the potential to improve crop yield and nitrogen (N) use efficiency while reducing N loss and protecting the environment. There are different types of EENFs, including slow-release, control-release, and stabilized N fertilizers. Previous research showed that the impact of EENFs on greenhouse gas (GHG) emissions and grain yield is inconsistent, as the efficacy of EENFs is variable depending on the soil type, temperature, humidity, microbial activity, availability of water, and crop species. The efficacy of EENFs in cereals in Maritime Canada has not been well-documented. The objective of this project is to evaluate the effects of different types, rates, and split applications of EENFs on environmental and agronomic performance in grain corn at two sites in Maritime Canada over two years. Our preliminary results from the 2023 field trial conducted in Truro, Nova Scotia showed that (1) fertilizer treatments increased grain yield compared to no fertilizer control; (2) EENF reduced environmental impact without yield penalty; (3) reduced N rate did not impact grain yield; and (4) single application at planting did not affect grain yield and residual soil nitrate concentrations immediately after harvest compared to split applications. Our findings will provide recommendations to growers regarding the best type, and the optimum rate and N split application timings of EENFs in grain corn and help improve food security and the overall sustainability of the agricultural industry.

***[O81] MECHANISMS OF DEMETHYLATION INHIBITOR RESISTANCE IN *CLARIREEDIA JACKSONII*.** E. McNab and T. Hsiang. School of Environmental Sciences, University of Guelph, 50 Stone Road East, Guelph, ON N1G 2W1, Canada.
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Dollar spot (caused by *Clarireedia* species) is one the most prevalent and costly diseases affecting turfgrasses in the North American Great Lakes region. With the high aesthetic standards for turfgrass appearance by turf managers and users, fungicides are heavily and frequently used which can lead to issues of resistance. Demethylation inhibitors (DMIs) are a commonly used class of fungicides to manage these diseases. The mode of action is the inhibition of biosynthesis of ergosterol, which is an essential component of fungal cell membranes. Since the first report of DMI resistance in 1981, reports have become increasingly common in many plant pathogens. There is ample literature investigating the mechanisms of DMI resistance (i.e., mutations affecting the CYP51 proteins, xenobiotic detoxification, and the expression of efflux transporters) in a wide range of fungi, but research into characterizing the mechanisms in the *Clarireedia* is still ongoing with only a few documented genetic elements associated

with resistance found, which only partially account for the observed resistance, to date. To investigate the resistance mechanisms further, we have sequenced the genomes of 18 *Clarireedia* isolates (including *C. jacksonii* and *C. monteithiana*) with a range of sensitivities to DMIs, including isolates obtained before DMI registration in Canada. The genomes have been investigated for previously documented mechanisms of DMI resistance and searched for any novel mutations associated with resistant isolates. Multiple insertions and point mutations have been observed in the *CYP51A* promoter of two resistant isolates as well as multiple point mutations in the coding sequence of the AtrB drug efflux transporter and the MfsM2 transcription factor in six and seven resistant isolates (out of 10 resistant isolates), respectively. We are currently conducting genome wide association studies to characterize identify potential sources of resistance and select targets for gene expression analysis. Further characterization of the DMI resistance mechanisms in these species may provide valuable insights into how DMI resistance occurs in *C. jacksonii*, and potentially lead to the development of improved resistance management and remediation strategies.

***[O82] FUNCTION OF THE CONCANAMYCIN PHYTOTOXINS IN THE POTATO COMMON SCAB PATHOGEN STREPTOMYCES SCABIEI.** Corrie V. Vincent and Dawn R. D. Bignell**.** Department of Biology, Memorial University of Newfoundland, 45 Arctic Ave, St. John's, NL, Canada, A1C 5S7
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Potato common scab (CS) is an economically important plant disease that occurs worldwide, including in potato growing regions in Canada. The disease is characterized by the development of superficial, raised, or pitted lesions on the potato tuber surface. The presence of CS lesions on potato tubers reduces the quality and market value of the crop, leading to significant financial losses for growers. The soil-dwelling bacterium *Streptomyces scabiei* (syn. *S. scabies*) is distributed worldwide and is the best-characterized causative agent of CS. *S. scabiei* produces several phytotoxic specialized metabolites that are known or predicted to contribute to CS disease development and severity. The principal pathogenicity factor produced by *S. scabiei* is the diketopiperazine thaxtomin A, which functions as an inhibitor of cellulose biosynthesis. *S. scabiei* also biosynthesizes polyketide compounds belonging to the concanamycin family, which function as inhibitors of vacuolar-type ATPases. Concanamycins are known to have phytotoxic activity, though their exact role in the pathogenicity of *S. scabiei* has not been established. It has been suggested that concanamycins may influence the CS lesion type and severity, and may have synergistic effects on toxicity with thaxtomin A. The purpose of this research is to investigate the function of the concanamycins in CS disease development. Mutant strains of *S. scabiei* that are altered in the production of concanamycins and/or thaxtomin A have been constructed, including gene deletion mutants that are unable to biosynthesize concanamycins and/or thaxtomin A, and overexpression strains that produce elevated levels of concanamycins along with normal or abolished thaxtomin A production. The mutants along with wild-type *S. scabiei* have been used in radish seedling and potato tuber slice bioassays to assess the virulence phenotypes of each. In the radish seedling assay, relative to the wild type, the concanamycin mutant and concanamycin overexpression strains showed a slight decrease and increase in virulence, respectively. The thaxtomin/concanamycin double mutant was significantly reduced in virulence relative to the thaxtomin mutant, while the thaxtomin mutant overproducing concanamycins was significantly increased in virulence. In the potato slice assay, the concanamycin mutant showed reduced pitting relative to wild-type, while concanamycin overproduction along with normal or abolished thaxtomin A production showed more severe pitting. Overall, these results demonstrate that production of concanamycins enhances the virulence of *S. scabiei* and may contribute to the development of more deep-pitted scab lesions on potato tubers.

***[O83] TRANSGENIC EXPRESSION OF PROTEIN-BASED INHIBITOR AGAINST TURNIP YELLOW MOSAIC VIRUS IN ARABIDOPSIS THALIANA.** J K Anuradha De Silva[1], Kihun Kim[1], Jacky Chung[2], John Weiland[3], Jihyun Hwang[1], Melvin Bolton[3], Mohammed Mira[4], Claudio Stasolla[4], Sachdev Sidhu[2], and Brian Mark[1]. [1]Department of Microbiology, Faculty of Science, University of Manitoba; [2]Faculty of Pharmacy, University of Waterloo; [3]Sugarbeet and Potato Research Unit, USDA Agricultural Research Services, ND, USA; and [4]Department of Plant Science, Faculty of Agriculture, University of Manitoba
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TYMV is a single-stranded RNA virus that mainly infects crops from the *Brassicaceae* family, and its infection can be severe due to its viral protease (TYMV PRO). TYMV PRO is essential for virus replication as it processes the viral polyprotein. Additionally, it acts as a deubiquitinase (DUB) that may interrupt the antiviral mechanisms in plants that are mediated by ubiquitin. A promising strategy for combating TYMV is to use a highly selective protein-based inhibitor called ubiquitin variant (UbV), which blocks the activity of TYMV PRO. Using phage display, we identified UbVs that selectively bind to the DUB domain of TYMV PRO. TYMV PRO and UbVs were expressed and purified to assess their binding abilities; UbV3 was the tightest binding inhibitor against TYMV PRO, with an IC50 of 19±2.7nM and EC50 of 0.3nM. To ensure the specificity, UbVs were tested against a panel of *A. thaliana* plant DUBs representing four prominent families. None of the UbVs are significantly bound with the plant DUBs. To confirm the ability of UbV3 to block the TYMV replication, transgenic *A. thaliana* expressing UbV3 was generated using the *Agrobacterium tumefaciens*-based transformation. The PCR, Western blot, ELISA, and subcellular colour localization analysis were assessed to determine the successful transformation and expression of UbV3 in *A. thaliana*. The seed germination percentage, plant height, the days at bolting and the dry weight of both wild type *A. thaliana* Col-0 and transgenic *A. thaliana* were tested using the One-way ANOVA and confirmed no significant change in plant growth and flowering. Based on the Pearson correlation coefficient between the amount of UbV3 and TYMV detection after the infection trial, the transgenic plants (r=-0.8) were identified to continue viral infection studies to determine if UbV3 expression protects the plant against TYMV infection.
Keywords: TYMV, protein inhibitors, viral protease, Arabidopsis thaliana, infection studies

***[O84] DECIPHERING *TETRANYCHUS URTICAE* - *ARABIDOPSIS THALIANA* INTERACTIONS: UNVEILING DETOXIFICATION MECHANISMS AND PLANT RESISTANCE STRATEGIES.** [1]Michele Antonacci, [1]Jorden Maglov, [1]Julia Pastor Fernandez, [1]Chetan Sharma, [1]Vladimir Zhurov, [2]Brendan Abiskaroon, [2]Maksymilian Chruszcz, and [1]Vojislava Grbic. [1]The University of Western Ontario, Department of Biology, 1151 Richmond Street, London, ON, Canada, N6A 5B7; and [2]Michigan State University, Department of Biochemistry & Molecular Biology, 288 Farm Lane, East Lansing, MI, USA, 48824
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The co-evolutionary dynamics between herbivorous pests and their plant hosts represent a complex interplay of biochemical and molecular mechanisms. This study elucidates the interaction between *Tetranychus urticae*, a detrimental herbivore worldwide, and *Arabidopsis thaliana*, an extensively used model plant. *T. urticae*, also known as the two-spotted spider mites (TSSM), is able to overcome a wide array of plant defences and to rapidly adapt to new host plants. The key mechanism enabling TSSM's adaptation to new host environments is its ability to modify its enzymatic detoxification system and develop metabolic resistance in just 25 generations after a host shift. Upon feeding on Arabidopsis leaves, TSSM encounters the accumulation of complex bland of defensive compounds including indole glucosinolates. Indole glucosinolates are secondary metabolites specific to Arabidopsis' botanic family (Brassicaceae) — which provide a chemical barrier against TSSM herbivory through their breakdown products. In the comprehensive study of Arabidopsis and TSSM interaction, the primary objective is to determine which indole glucosinolate derivatives (IGDs) in Arabidopsis provide resistance to TSSM herbivory and to investigate which detoxification patterns are adopted in TSSM to ward off these plant barriers. The analysis involves the use of Arabidopsis mutants with altered endogenous levels of IGDs to pinpoint candidate defensive metabolites. To demonstrate the toxicity of individual IGD candidates, they are orally delivered to mites. Once the Arabidopsis defences are established, the metabolomic analysis of mite extracts upon the application of an IGD is used to determine the pattern of compound modification in mite gut and to elucidate which detoxification gene family(ies) contributes to TSSM resistance. The function of putative detoxification enzymes in TSSM is further investigated by the utilization of environmental RNAi interference to knock down the candidate's gene expression. In conclusion, the overall investigation of plant-pest interactions aims to identify plant defensive compounds and mechanisms used by the TSSM to overcome their toxicity. This will not only enrich the understanding of ecological dynamics in plant-pest interaction but will also translate into tangible benefits for agriculture, including the development of resilient crop varieties and innovative pest management.

***[O85] PROTEOMIC ANALYSIS REVEALS NEW INSIGHTS RELATED TO THE INTERACTION BETWEEN *XANTHOMONAS PHASEOLI PV PHASEOLI* AND *PHASEOLUS VULGARIS* L.** Mylene Corzo-Lopez[1], Jason McAlister[2], Boyan Liu[2], Jennifer Geddes-McAlister[2], and K. Peter Pauls[1]. [1]Plant Agriculture Department, University of Guelph, Guelph, ON, Canada N1G 2W1; and [2]Molecular and Cellular Biology Department, University of Guelph, Guelph, ON, Canada N1G 2W1
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Xanthomonas phaseoli pv *phaseoli* (*Xpp*) is one of the causal agents of common bacterial blight (CBB) disease in *Phaseolus vulgaris* L (common bean). As a strategy to invade the host, this pathogen injects proteins into the plant cell that allow it to survive and multiply within the plant tissue and colonize the host. The plant response to the invading organism depends on which plant-microorganism recognition and immunity pathway is triggered, such as the Pathogen-Associated Molecular Pattern-Triggered Immunity (PAMP-PTI) or the Effector-Triggered Immunity (ETI). PAMP-PTI pathways activate the expression of genes associated with defense through Mitogen-Activated Protein Kinase (MAPK) cascades activated by the production of reactive oxygen species. In addition, ETI occurs in plants that carry resistant proteins that recognize the pathogen's virulence effector proteins. To understand the molecular mechanisms during the earliest stages of the plant pathogen interactions, a comparative proteomics analysis was conducted of the infection of common bean genotypes with *Xpp* strains. Our research employed a bottom-up proteomics approach to assess and characterize the interactions between two common bean recombinant inbred lines (RIL), one CBB resistant and another CBB susceptible, with a pathogenic strain and a non-pathogenic strain of bacteria. In this study, the *Xpp* differentially abundant proteins (DAPs) associated with pathogen virulence included the outer membrane protein and the polyphosphate-selective porin with higher abundance in the incompatible interaction at 48 hours post inoculation (hpi). The CBB resistant RIL-DAPs after challenging with the pathogenic strain, were mainly involved in the biosynthesis in secondary metabolites, such as isoflavones. Additionally, some DAPs were related to plant-pathogen interactions, such as ubiquitin-mediated proteolysis, and glyoxylate and dicarboxylate metabolism, demonstrating higher accumulation at 48 hpi. In contrast, the DAPs at 48 hpi after challenge with the non-pathogenic strain were mainly related to oxidative phosphorylation, photosynthetic processes, and pentose phosphate pathways. Interestingly, the CBB susceptible RIL showed no discernible differences in protein expression after being challenged with the two bacterial strains at 48 hpi. However, proteins involved in starch and sucrose metabolism, linoleic acid metabolism, lipid metabolism, vitamin metabolism, RNA degradation and glycolysis/glucogenesis pathways were induced faster in the compatible interaction than in the incompatible interaction at 72 hpi. Overall, this study provides valuable insights into the molecular mechanisms incompatible and incompatible interactions between *Xpp* and *P. vulgaris*. These findings will contribute to the development effective strategies for managing the common bacterial blight disease in common bean crop.

***[O86] INSIGHTS FROM NEXT GENERATION SEQUENCING: NOVEL VIRUSES AND VARIANTS IN HIGHBUSH BLUEBERRIES OF BRITISH COLUMBIA.** Sachithrani Kannangara[1], Juan Rodriguez[1], Adam Gilewski[1], Gerda de Villiers[2], Megan Ellis[2], Peter Ellis[2], Eric Erbrandt[3], and Jim Mattsson[1]. [1]Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada; [2]Phyto Diagnostics Company Ltd., 9381, Ardmore Drive, North Saanich, BC V8L 5G4, Canada; and [3]BC Blueberry Council, 275 32160 South Fraser Way, Abbotsford, BC V2T 1W5, Canada
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Highbush Blueberry (*Vaccinium corymbosum* L.) is an important fruit crop in British Columbia. Viral diseases are known to reduce the production of blueberries and are challenging to control. New viruses have been identified in many crops with the development of Next-generation sequencing (NGS) without relying on visual symptoms. This gives the advantage of detecting putative pathogens ahead of time and developing detection methods. The main objective of this research is to gain an unbiased overview of viruses in blueberry plants with virus-like symptoms using RNA-seq and develop more reliable diagnostic methods for the precise detection of disease. RNA-seq libraries were made from rRNA-depleted RNA extracts of 107 blueberry leaf samples with Scorch/Shock-like symptoms and 10 healthy samples. We screened *de-novo* assembled sequences against the NCBI database to find assemblies with viral origin. Results showed the presence of novel blueberry Scorch virus (BlScV) variants, two novel blueberry Luteoviruses, and a Tombusvirus-like associated RNA (tlaRNA). Phylogenetic analysis of coat protein (CP) divided BlScV variants into two main clusters. Further, we observed that the 5' end of the BlScV

genome is highly conserved and suitable for variant-insensitive detection by PCR. The blueberry Luteovirus genome sequences are ~5 kbp long and contain four potential open reading frames (ORF) for RNA-dependent RNA polymerase (RdRP) P1, P2 proteins, CP, and CP read-through protein. The two Luteoviruses, N and M2, have 84 % sequence similarity to each other. The sequence similarity between blueberry virus M (GenBank ID OR051501.1) and M2 indicated that M2 is a variant of the blueberry virus M. We confirmed the blueberry virus N and M2 assemblies by nanopore sequencing. We found that either of the Luteoviruses were widely present in two populations of diseased plants (91% and 93%) and present in healthy plants in fields as well as in nurseries. The blueberry tlaRNA assemblies are ~3 kbp long and lack a CP but contain an ORF to encode RdRP. While we have no evidence that the Luteoviruses cause disease, preliminary NGS results indicate that blueberry Luteovirus together with tlaRNA is overrepresented in diseased plants that lack the usual suspects Scorch and Shoch virus. Thus, we hypothesized that Luteovirus may act as a 'helper virus' for associated tlaRNAs to generate a hitherto unknown complex cause of symptoms in diseased blueberry plants. We are testing this hypothesis by single and mixed infections to observe symptom development and virus accumulation.

***[O87] A CLUBROOT PATHOGEN EFFECTOR DISRUPT AUXIN HOMEOSTASIS TO PROMOTE COLONIZATION.** Melaine González García[1], Marina Silvestre Vano[1], Soham Mukhopadhyay[1], Ian Major[2], and Edel Pérez López[1]. [1]Department of Plant Sciences, Faculté des Sciences de l'Agriculture et de l'Alimentation (FSAA), Université Laval, Quebec City, QC G1V 0A6, Canada; and [2]Laurentian Forestry Centre, 1055 Du PEPS Street, Quebec City, QC G1V 4C7, Canada
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Clubroot is a devastating disease caused by the obligate biotrophic protist *Plasmodiophora brassicae*. This disease is characterized by root swelling, which is related to alterations in host hormone metabolism, primarily involving auxins and cytokinins. In this study, we examined the role of an auxin-responsive Gretchen Hagen 3 effector from *Plasmodiophora brassicae* (*Pb*GH3). The Gretchen Hagen 3 family, widely distributed across the plant kingdom, conjugates various amino acids to plant hormones. Previously, it was reported that *Pb*GH3 conjugates auxins and jasmonic acid with proteinogenic amino acids *in vitro*; however, the role of this protein during clubroot infection remains unknown. We generated *Arabidopsis thaliana* lines overexpressing *Pb*GH3 to study their phenotype and response to clubroot infection. Initially, we examined morphological changes throughout the plant growth and development across the entire plant life cycle. Our findings revealed that *Pb*GH3 lines have shorter stems compared to the Col-0 wild type ecotype, while their main roots are longer. Additionally, these lines exhibit longer lateral roots and a higher density of root hairs in the maturation zone. We analyzed the auxin profile in the roots of *Pb*GH3 lines and Col-0 to identify any differences in plant hormone metabolism induced by the expression of *Pb*GH3. Furthermore, after germination, both Col-0 and PbGH3 lines were transplanted into different concentrations of indole-3-acetic acid (IAA) to investigate their tolerance to the exogenous application of the hormone. Both showed a decrease in root length; however, the effect was more pronounced in Col-0. We also monitored the expression of *Pb*GH3 during clubroot infection in Col-0 at several time points, noting very early expression at 2 days post-inoculation. Considering this, we quantified *Pb* in Col-0 and transgenic lines during early infection. Altogether, our results suggest that *Pb*GH3 induces an auxin-mediated increase in main root length and lateral root number, favoring infection during early colonization of the susceptible host.

***[O88] RNASEQ STUDY OF PARTIALLY RESISTANT AND SUSCEPTIBLE PEA GENOTYPES UPON *FUSARIUM AVENACEUM* INFECTION.** Sijan Pandit[1,2], Eoin O'Hara[2], Robert Gruninger[2], and Syama Chatterton[2]. [1]University of Lethbridge, 4401 University Drive, Lethbridge, AB, T1K 3M4, Canada; and [2]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403–1 Avenue South Lethbridge, AB, T1J 4B1, Canada
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Fusarium root rot, as part of the pea root rot complex (PRRC), is caused by a number of *Fusarium* species and is among the most devastating soil-borne diseases of field pea, causing complete yield loss in severe conditions. The generalist pathogen *Fusarium avenaceum* was identified as the predominant pathogen in the PRRC in Alberta. It can be difficult to manage because of its generalist lifestyle including multiple hosts in over 80 genera of plant communities. This study aimed to understand plant responses conferring partial resistance to *F. avenaceum* observed in some pea breeding lines. We evaluated

changes in gene expression by performing RNAseq in partially resistant and susceptible pea lines inoculated with *F. avenaceum* isolate 1306.08. Four pea genotypes including three partially resistant (PR) genotypes, K-2, 5001, and Carman and one susceptible (S) genotype, CDC Meadow were grown in standard greenhouse conditions. After 14 days of growth, the plants were inoculated with macroconidia of *F. avenaceum,* and the controls were treated with sterile water. The root tissue was sampled at 2 hours post-inoculation, followed by 3, 6, and 9 days post-inoculation and samples were subjected to RNA extraction and RNAseq analysis. The roots were rated for disease severity at 21 days post-inoculation. Of the five genotypes, K-2 had significantly lower disease severity compared to CDC Meadow. RNAseq of samples from four genotypes revealed a total of more than 18,000 differentially expressed genes among inoculated and un-inoculated roots of all the genotypes at all time points. Those differentially expressed genes were related to pathways such as plant-pathogen interactions, biosynthesis of secondary metabolites and photosynthesis. Detailed results for each genotype and time points will be discussed.

***[O89] METABARCODING REVEALS BACTERIAL ENDOPHYTES FROM BARLEY GRAINS ARE SIGNIFICANTLY ASSOCIATED WITH FUSARIUM HEAD BLIGHT, BARLEY GENOTYPE, AND TIME OF SAMPLING.** Vinuri Weerasinghe[1,2,3], Matthew Bakker[4], James Tucker[5], Dilantha Fernando[1], Ana Badea[1,5], and Champa Wijekoon[1,2,3]. [1]Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB, Canada, R3T 2N2; [2]Morden Research and Development Centre, Agriculture and Agri-Food Canada, Route 100, Unit 100-101, Morden, MB, Canada, R6M 1Y5; [3]Canadian Centre for Agri-Food Research in Health and Medicine, 351 Taché Avenue, Winnipeg, MB, Canada, R2H 2A6; [4]Department of Microbiology, University of Manitoba, 213 Buller Building, Winnipeg, Manitoba, R3T 2N2; and [5]Brandon Research and Development Centre, Agriculture and Agri-Food Canada, 2701 Grand Valley Road, P.O. Box 1000A, Brandon, MB, Canada, R7A 5Y3
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Barley (*Hordeum vulgare* L.) is the fourth most cultivated cereal crop in the world, and Canada is among the top ten barley producers. Fusarium head blight (FHB) is a destructive fungal disease in barley, affecting several industries including livestock feed and malting, leading to significant economic losses. The main pathogen, *Fusarium graminearum*, infects barley spikes and degrades grain quality. Changes in the plant microbiome, in particular the endophytes, may indicate changes in plant physiology, anatomy, and resistance to abiotic and biotic stress conditions. Interactions of endophytes with hosts and other microbes play a role in maintaining a plant's health. In fact, certain endophytes may be involved in defense against phytopathogens and plant growth improvement. Despite this, studies on endophytes of barley genotypes grown in Canada are limited. In this study, we investigated the endophytic microbiome of barley genotypes grown in Canada, with a focus on bacteria. Surface sterilized barley grains collected from 2021 and 2022 at the mid-dough stage and harvest stage were targeted for bacterial 16S rRNA amplicon sequencing using Illumina platform. Following a quality check, the sequence reads were trimmed, merged, dereplicated, and taxonomically ranked with reference to Silva database (v138.1). A taxonomic filtering was performed to remove amplicon sequence variants (ASVs) from non-bacterial, chloroplast and mitochondrial origin. Thereafter, a statistical analysis was performed on the metabarcoding data using phyloseq (v1.42.0) and MaAsLin 2 (v1.12.0) packages in R software (v4.2.3). The analysis indicated that Proteobacteria, Actinobacteriota and Firmicutes were predominant in the barley grain endosphere. Significant associations of bacterial ASVs with FHB, barley genotype, plant developmental stage and the growing season were demonstrated which may be used as indicators of FHB-resistance, for instance. In addition, the vertical transmission of bacterial endophytes via barley grains was investigated which may be applied for future breeding programs. Altogether, the findings of this study will benefit the breeders, growers, industries, and consumers of barley and barley-related products.

***[O90] COMMERCIAL FORMULATIONS CONTAINING *BACILLUS* SPECIES REDUCE THE DEVELOPMENT AND SURVIVAL OF *FUSARIUM OXYSPORUM* IN SOIL-LESS GROWTH MEDIA.** Denna N. Dalrymple[1] and Zamir K. Punja[1]. [1]Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada
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The genus *Bacillus* is a widely used bacterial group in research on the biological control of pests and pathogens. They are free-living beneficial microbes, many of which are plant growth-promoting

rhizobacteria (PGPR) which are beneficial to plants. The commercial product Tarantula® (Advanced Nutrients, Abbotsford, BC), primarily consists of *Bacillus* species, including *B. coagulans, B. mucilaginous, B. pumilus, B. subtilis, and Paenibacillus polymyxa.* This product was used to examine the effect of these PGPR against *Fusarium oxysporum* and populations of other microbes in coco coir growing medium. Previous in vitro experiments successfully demonstrated the antagonism between *Bacillus* spp. from the Tarantula® product against *F. oxysporum* on potato dextrose agar (PDA) medium. In vivo experiments with *Cannabis sativa L.* (cannabis) plants also showed the efficacy of the biocontrol agents to significantly suppress *F. oxysporum* symptoms in rooted plants. To investigate the effect of Tarantula® when added to growing substrates typically used in cannabis cultivation, experiments were carried out using two brands of coco coir, Forteco® and Truecoirs LLC. These were subjected to 4 treatments: sterile distilled water, Tarantula®, *F. oxysporum*, and a combination of Tarantula® and *F. oxysporum*. The coco media (3g) was placed into 4 dishes to which 3 mL of each treatment was added and sealed. The Tarantula® treatment was added 1 week prior to inoculation with *F. oxysporum* for the combination treatment. The dishes were shaken daily for better distribution of the treatment. Seven days post-treatment, 10-fold serial dilutions were done and aliquots of the 10^{-3} dilution of each treatment were spread-plated onto PDA plates with streptomycin (200 mg/mL). After 5 days of incubation, the colonies developing were counted. The colonies on untreated plates consisted of white, yellow, and pink yeast-like colonies, *Aspergillus* sp*.,* and *Penicillium* sp*.,* while plates inoculated with *F. oxysporum* yielded a lesser variety of these colonies and mostly *F. oxysporum* colonies. The colony forming units (CFU's) from each type of coco coir varied in numbers across all treatments. The overall number of colonies of *F. oxysporum* and other microbes were significantly reduced in the Tarantula® plus *F. oxysporum* treatment for both brands. These findings suggest a broad-spectrum inhibition against all microbes present in coco media. More studies are ongoing to further investigate the efficacy of *Bacillus* in growing substrates and the endophytic colonization of *Bacillus* spp. in stem tissues of cannabis*.*

***[O91] GENETIC MAPPING OF RESISTANCE TO FUSARIUM HEAD BLIGHT AND DON ACCUMULATION IN WATKINS LANDRACE WAT.1190580.** Sharandeep Dhaliwal[1], Maria Antonia Henriquez[2], Curt McCartney[2], Samuel Holden[1], and Gurcharn Singh Brar[3]. [1]Faculty of Land and Food Systems, The University of British Columbia, 2357 Main Mall, Vancouver, BC, Canada, V6T 1Z4; [2]Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB, R6M 1Y5; and [3]Agriculture/Forestry Centre, University of Alberta, 9011 116 St NW, Edmonton, AB, Canada, T6G 2P5
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Fusarium head blight (FHB) is an important fungal disease affecting the yield and quality of wheat. Deploying genetic resistance in wheat is an essential component of an integrated strategy for reducing the adverse effects of the disease. Most previous studies have mapped FHB resistance from Chinese or Brazilian germplasm. In a preliminary research 12 Watkins wheat landraces with MR/R resistance to FHB severity and deoxynivalenol (DON) toxin accumulation were identified. In the present study, we are utilizing one of the 12 Watkins landraces i.e., Wat.1190580 (origin: Iran) to identify gene(s)/QTL for FHB and DON resistance. Wat.1190580 has a resistant reaction to FHB and DON accumulation and used as a male/resistance donor parent to develop recombinant inbred lines (RIL) population: Paragon X Wat.1190580 (F8, n=75). Paragon is a European cultivar susceptible to FHB. The mapping population was screened at Morden (2021, 2022, 2023) and Carman (2021, 2022) for FHB infection (Incidence, severity, Fusarium damaged kernels, and DON) and phenological traits (plant height, days to anthesis). At first, Paragon X Wat.1190580 was genotyped using a wheat high-density 90K SNP array. Our results from 90K genotyping resulted in genetic maps with large genetic indicating allelic diversity in landraces not represented by the 90K SNP array. As 90K is identified as unsuitable for genotyping RILs derived from Watkins landraces, we genotyped the population using a skim-sequencing approach at 0.1x coverage and generating genome assembly of Wat.1190580. QTL regions associated with INC (2B, 5A), SEV (2B, 3B, 5B), DON (5A), FDKs (5A) resistance, and PHT (3A, 5A), and DTA (5A) were successfully mapped using the phenotypic data (field trials) and skim-sequencing data of Paragon X Wat.1190580.

***[O92] THE EVOLUTIONARY DYNAMICS OF AZOLE RESISTANCE IN *FUSARIUM GRAMINEARUM*.**
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Fusarium graminearum is a fungal pathogen that significantly threatens wheat and barley crops in temperate regions, causing annual global agricultural losses exceeding $1 billion. Although azoles are generally effective fungicides, recent data suggests that resistance towards azoles may be increasing in *F. graminearum* populations. To investigate the rate that *F. graminearum* can acquire resistance following prolonged exposure to common azoles, we conducted a series of *in vitro* evolution experiments. Strain DAOM233423, a well-characterized strain isolated in the 1980s before environmental azoles, was exposed to 1% DMSO for 6 weeks to acclimate the strain to the solvent exposure. Four replicate lineages were evolved to increasing concentrations of prothioconazole, tebuconazole, and a combination of both in equal concentration until extinction. The prothioconazole and combined treatment lineages reached a terminal MIC that exceeded the ancestor by a factor of 4, while lineages exposed to tebuconazole exceeded the ancestral MIC by a factor of 5. Whole genome sequencing will soon be conducted to identify putative genomic variations linked with fungicide resistance. Additionally, we are currently assessing phenotypic changes in evolved lineages, including colony morphology, cross-resistance to other azoles, virulence, and sexual/asexual reproduction. We hypothesize that the mutational basis of resistance will differ between azole treatments and to find varying levels of cross-resistance to other agricultural and clinical azoles. This research will improve our understanding of the genomic basis of azole resistance in *F. graminearum* and determine how different fungicide exposures influence the development of cross-resistance.

***[O93] THE ROLE OF HYD5 PROTEIN IN *FUSARIUM*-BARLEY INTERACTIONS.**
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Fusarium graminearum, a significant fungal pathogen, poses a threat to barley crops worldwide. Hydrophobin proteins, such as Hyd5, are known to play roles in the interactions of fungi with their environment, particularly in the colonization of hydrophobic surfaces. While the specific involvement of Hyd5 in *Fusarium*-barley interactions remains poorly understood, hydrophobins have been implicated in the excessive gushing of beer made from infected barley. In this study, a beer gushing experiment was conducted using malt that was infected with *F. graminearum* wild type 233423 or a Δhyd5 knockout strain produced via CRISPR-Cas9 gene editing. Heterologous expression of Hyd5 in *E. coli* was performed, followed by purification of the hydrophobin for beer gushing experiments. Additionally, hyd5 gene expression was examined using RT-qPCR during *in planta* infection (including during heading, at flowering, and eight days post-flowering) and in malted barley infected with *F. graminearum*. RNA extraction was carried out using TRIzol reagent, followed by cDNA synthesis and quantification of hyd5 transcripts, whose abundance was expressed relative to a housekeeping gene, as a unitless ratio. Although not statistically significant, a trend for reduced beer gushing in malt infected with the knockout strain suggested that Hyd5 may indeed play a role in beer gushing. This involvement was confirmed by a dramatic increase in beer gushing with the addition of heterologous Hyd5 (22 times more gushing compared to the control; T-test, $P = 2.14 \times 10^{-5}$). In the wildtype strain, there was a significant increase in hyd5 gene expression between the malt stages of steeping (0.002) and germination (0.035). However, no significant differences in hyd5 expression were found *in planta*. Our results support the role of Hyd5 in gushing, but this protein may not be heavily involved in the colonization of the plant in the field.

[O94] PREVALENCE OF *VERTICILLIUM* SPP. AND *PRATYLENCHUS* SPP. IN COMMERCIAL POTATO FIELDS IN EASTERN CANADA. Dahu Chen[1], Ryan Barrett[2], Benjamin Mimee[3], Tanya Arseneault[3], Louis-Pierre Comeau[1], Kamrun Nahar[1], Sebastian Ibarra Jimenez[4], and Bernie J. Zebarth[1]. [1]Fredericton Research and Development Centre, Agriculture and Agri-food Canada, 850, Lincoln Rd, Fredericton, NB E3B 4Z7; [2]Prince Edward Island Potato Board, 90 Hillstrom Ave, Charlottetown, PE C1E 2C6; [3]Saint-Jean-sur-Richelieu Research and Development Centre, Agriculture and Agri-food Canada, Saint-Jean-sur-Richelieu, QC J3B 3E6; and [4]Prince Edward Island Department of Agriculture, PO Box 2000, Charlottetown, PE C1A 7N8
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A survey of New Brunswick (NB) and Prince Edward Island (PEI) potato fields in crop rotation phase prior to potato production was conducted in fall (October and November) between 2017 and 2021. A total of 114 and 122 fields for NB and PEI, respectively, were surveyed with 20 to 35 fields each year tested in each province. Root lesion nematodes (RLN, *Pratylenchus* spp.) were detected in 99 and 98% of the fields for NB and PEI, respectively, and two root lesion nematode species, *P. crenatus* and *P. penetrans*, were identified in both provinces from 2017 to 2021. Based on 2019 and 2020 results, *P. crenatus* was detected in 100% of surveyed fields in both NB and PEI, while *P. penetrans* was detected in 29% of the fields in NB and 43% of the fields in PEI. *P. crenatus* accounted for 92 and 89% of the populations for NB and PEI, respectively, while *P. penetrans* accounted for 8 and 11%, respectively. *Verticillium dahliae* was detected in 94 and 95% potato fields in NB and PEI, respectively. All isolates obtained from potato cv. Russet Burbank in a baiting trial were *V. dahliae,* belonging to two lineages. *V. albo-atrum* was detected in a few fields at very low level, except two fields in NB where the *V. albo-atrum* was predominating over the *V. dahliae*. Previous crops did not affect *V. dahliae* population densities for NB and PEI, and did not affect RLN population in NB, but significantly affected RLN in PEI. Fall cover crop did not affect the populations of RLN and *V. dahliae* in PEI. The present study revealed that the potato pathogenic root lesion nematode *P. penetrans* was present in less than 50% of surveyed fields and accounted for around 10% of root lesion nematode population in NB and PEI, and *V. dahliae* was the dominant species and present in greater than 90% of surveyed fields in both provinces.

[O95] IMPACT OF CROP ROTATION ON THE MICROBIOMES OF SUDDEN DEATH SYNDROME (SDS) AND SOYBEAN CYST NEMATODE (SCN) SUPPRESSIVE SOILS OF SOYBEANS IN SOUTHERN ONTARIO, CANADA. R. Malla[1], L.A. Phillips[2], K.E. Dunfield[1], B.Seuradge[2], A. Wragg[2], and O.S. Wally[2]. [1]School of Environmental Sciences, OAC, University of Guelph, 50 Stone Rd E, Guelph, ON N1G 2W1, Canada; and [2]Harrow Research and Development Centre, Agriculture and Agri-Food Canada, 2585 County Road 20, Harrow, ON N0R 1G0, Canada
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Sudden Death Syndrome (SDS), caused by *Fusarium virguliforme*, and Soybean Cyst Nematode (SCN), *Heterodera glycines*, pose significant threats to North American soybean production, with annual losses exceeding $1.3 billion USD. This study compares a long-term soybean monoculture in Essex, Ontario, which exhibits low levels of SDS and SCN, with a traditionally rotated field in Chatham, Ontario, where similar disease suppression is not observed. Analysis up to 2023 indicates that rotational practices in fields prone to SDS can reduce disease severity by 45% and increase yields by 48% over six years. Soybeans in maturity group 1 (MG1) experience yield reductions in rotated plots, while yields for maturity group 2 (MG2) remain stable, suggesting that disease suppressiveness can be rapidly induced, potentially within five years. Reintroducing rotation in the Essex site led to minor yield changes and a slight increase in disease levels, but these remained lower than in previous years, suggesting the medium-term durability of soil suppressiveness. Our methods include growth room bioassays and bacterial and fungal taxonomic amplicon sequencing of soil and cyst samples collected in both spring and fall of all study years, to analyze soil microbiome dynamics and the relationship between SCN presence and SDS severity. Sequencing data was processed using a customized dada2 pipeline to identify amplicon sequence variants. Results indicate that soybean monoculture promotes greater species richness and diversity in suppressive soils compared to rotated crops. Overall microbial community composition was evaluated using ordination techniques and PERMANOVAs. Our ongoing molecular and microbiological studies are focused on elucidating the mechanisms behind soil-mediated disease suppression in soybeans, with a particular emphasis on the interaction between SCN and SDS. This

research underscores the critical role of specific microbial communities in developing soil conditions that suppress both SDS and SCN effectively. The identification of these key microbial agents has the potential to lead to the development of biocontrol strategies, offering new, sustainable (both economically and environmentally) recommendations for growers to minimize the impact of these pests. This approach not only aims to enhance yield and reduce losses but also contributes to the broader goal of sustainable agriculture.

[O96] PREVALANCE STUDY AND EVALUATION OF COMMERCIAL CULTIVARS AS AN IMMEDIATE MEASURE TO FIND VERTICILLIUM MANAGEMENT OPTIONS ON CANOLA. Venkat Chapara[1], Anitha Chirumamilla[1], Amanda Arens[1], and Larissa Jennings[1]. [1]North Dakota State University/Langdon Research Extension Center
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The disease verticillium stripe on canola caused by a soil-borne pathogen, Verticillium longisporum, was found recently in North Dakota (ND). An extensive survey was conducted in major canola-growing counties of ND to determine the prevalence of the disease verticillium stripe. After swathing or harvesting in the fall, the survey was done by inspecting canola stubbles for disease infections with Verticillium stripe. Twelve canola-growing counties in ND were targeted, with a minimum of four to five fields scouted in each County. However, thirty fields were scouted in Cavalier County, the central canola-growing County in North Dakota. The survey group walked in a "W" pattern, stopping at five spots and uprooting twenty stem stubbles from the ground at every spot after swathing or straight-cut to harvest. Each sampling point was separated by 328 feet. In all, the roots of a hundred canola stubbles with likely infection of verticillium were collected, bagged, and labeled with the field location. All the symptomatic stems with roots were evaluated for incidence by cross-section clipping of canola stems just half an inch below ground level. For the cultivar screening study, eleven commercial canola cultivars with unknown resistance to verticillium stripe were planted to monitor the resistance level against the pathogen V. longisporum under field conditions. The trial was planted in a randomized complete block design (RCBD) with four replications. The amount of verticillium stripe infection obtained in the research plots was from artificial inoculum. Statistical analysis was done using Agrobase Generation II software. Fisher's least significant difference (LSD) was used to compare means at p ($\alpha = 0.05$). The percentage of incidence and severity of verticillium stripe in cultivar evaluation was done using the prevalence study procedure. The survey results indicated that the presence of verticillium stripe was found in low amounts in eleven out of twelve counties surveyed. None of the cultivars showed resistance to verticillium stripe and were statistically non-significant from each other, with a mean incidence and severity of 35% and 9%, respectively. This study's results will create awareness of the presence of verticillium stripes in canola-growing counties and the lack of cultivar resistance in the commercially growing cultivars of canola in ND.

[O97] GINSENOSIDE MOBILITY IN GINSENG GARDEN SOIL. Andrew Rabas and Mark A. Bernards[1]. [1]Western University, 1151 Richmond Street, London, ON, Canada, N6A 3K7
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American ginseng (*Panax quinquefolius*) is a perennial herbaceous plant that matures over several years. It is primarily cultivated for its high value in Traditional Chinese medicine in Asia. However, ginseng growers face the significant challenge of ginseng replant disease (GRD), which refers to the enduring negative effects of ginseng cropping on subsequent plantings, regardless of intervals, extending beyond normal pathogen carryover. Alongside pathogens, it is speculated that ginsenosides, secondary metabolites produced by ginseng, may contribute to GRD as they possess phytotoxic properties that inhibit ginseng seed germination. Ginsenosides can be further categorized as protopanaxadiols (PPD) and protopanaxatriols (PPT), as they differ in hydroxylation and glycosylation patterns. While it is known that ginsenosides are released by ginseng into their surrounding soil, little is known about their fate once in the soil. My project aimed to explore the behaviour of ginsenosides in ginseng garden soil, focusing on the capacity for soil particles to bind them and their movement through the soil matrix. Five different concentrations of ginsenosides were applied to columns filled with soil collected from a ginseng garden, and water was used to promote their movement. Ginsenosides in the initial flowthrough (i.e. unbound ginsenosides) and subsequent washings were processed using LCMS. After 10 weeks, each soil column was segmented, and the distribution of ginsenosides within the soil column was established through extraction and LCMS analysis. Analysis of the initial flowthrough and subsequent washings revealed a

higher proportion of PPT passed through the soil than PPD, with the majority of ginsenosides eluted within the first four weeks. At lower concentrations of applied ginsenosides, PPD bound more readily to the upper portion of the soil column, whereas at higher concentrations, PPD was found throughout the entire column. In summary, PPD exhibits stronger binding to soil than PPT, while PPT showed greater mobility in ginseng garden soil. These findings provide insight into ginsenoside dynamics in soil and allow a better understanding of their potential role in ginseng garden soils and their contribution to GRD.

[O98] INTERACTIONS BETWEEN *APHANOMYCES EUTEICHES* AND *FUSARIUM AVENACEUM* AND *GRAMINEARUM*. Michelle Hubbard[1], Olivia Zajac[1], Anas Eranthodi[2], Syama Chatterton[2], David Overy[3], and Nora Foroud[2]. [1]Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, 1 Airport Rd, Swift Current, SK, Canada, S9H 3X2; [2]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1st Ave S, Lethbridge, AB, Canada, T1K 6M5; and [3]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6
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Root rot can severely limit pea and lentil production. This disease is caused by a complex of pathogens, including *Aphanomyces euteiches* (Ae), *Fusarium avenaceum* (Fa) and *F. graminearum*, (Fg) as well as other *Fusarium* species, *Pythium* species and *Rhizoctonia solani*. Root rot tends to be more severe when Ae and *F. redolens* or *F. solani* are present, relative to any of the three alone. However, co-infection with Ae and Fa has not been shown to increase root rot severity and the impact of Fg on Ae root rot has not been explored. Both Fa and Fg produce various mycotoxins (secondary metabolites) that include the enniatins from Fa and deoxynivalenol (DON) from Fg. We aimed to explore the impacts of co-occurrence of Fa and Fg and their fore mentioned mycotoxins on the growth of Ae *in vitro* and on root rot of peas. Mutant strains of Fa that overexpress (OX) or are deficient (KO) for enniatin production (FaOX and FaKO, respectively), and a mutant strain of Fg that is deficient in DON production (Fgtri5-) and wildtype (WT) strains of both organisms (FaWT and FgWT) were used. From *in vitro* experiments using Petri plate cultures where Ae was placed in the centre of the plate, and four agar plugs of the *Fusarium* isolate in question were placed equidistant from Ae, FaWT and FaOX reduced Ae radial growth, while the FaKO (loss of enniatin production) did not. *In vitro* assays involving commercially available enniatins reduced Ae radial growth and oospore production. The FgWT strain also reduced Ae growth; surprisingly, the FgTri5- mutant (deficient in DON production) had an even stronger impact, suggesting that other factors likely also contribute to the Fg/Ae interaction. However, when culture filtrate from FgTri5- was added to solid media on which Ae was grown, Ae growth was not inhibited. The reverse was true of culture filtrate from FgWT. In vermiculite, but not in soil, Ae+FgWT and Ae+Fgtri5- both reduced root rot severity relative to Ae inoculation alone. Thus, it appears that interactions between Ae and Fa and Fg are complex, and largely, but not entirely, dependant on secondary metabolites.

[O99] PRESCREENING AND MONITORING EVALUATION USING SEQUENCING TECHNOLOGIES FOR *PHYTOPHTHORA* AND OOMYCETES. Guillaume J. Bilodeau[1] and Hervé Van der Heyden[2]. [1]Canadian Food Inspection Agency, Ottawa Laboratory Fallowfield, Ottawa plant laboratory, Ottawa, On, Canada, K2H 8P9; and [2]Agriculture and Agrifood Canada, Saint-Jean-sur-Richelieu Research and Development Centre, 430 Gouin Blvd, Saint-Jean-sur-Richelieu, Qc, Canada, J3B 3E6
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Metagenomics can provide insightful information on species diversity and improve surveillance of introduced species. While isolation and bating could underestimate species diversity, high throughput sequencing can be used as a new tool for early detection of oomycetes, including *Phytophthora* species, endemic or regulated and invasive alien species, that can cause major diseases in agricultural and forest ecosystems. High throughput sequencing (HTS) technologies allow us to investigate different sample types, process large numbers of samples, and produce even greater volumes of genomic data. Metabarcoding tools on different genetic regions and combining Ion Torrent or Oxford Nanopore sequencing and custom bioinformatics pipelines can be used to evaluate potential sampling schemes for pathogens in forestry and agriculture and help identify dispersal and spreading pathways. Sampling methods exploiting eDNA isolated from air, soil, and tissues revealed sources of oomycetes likely to

cause problems. Few monitoring activities for *Phytophthora* and other organisms were evaluated to understand the limitations of the technology in biosurveillance. Hence, we aim to provide a framework combining sampling tools with HTS-based methods, appropriate bioinformatic pipelines, and qPCR assays for the early detection of emerging and invasive alien species and determination of sample type of samples that can be used for prescreening of pathogens' presence and prevalence. Evaluation of such methods will help improve early warning, promote public awareness, and support our regulatory activities.

***[O100] PROFILING ENVIRONMENTAL AND SEASONAL VARIATIONS IN CONDENSED TANNINS AND METABOLITES OF BIRDSFOOT TREFOIL (*LOTUS CORNICULATUS* L.) CULTIVARS.** Solihu Kayode Sakariyahu[1,2], Tim McDowell[1], Justin Renaud[1], Yousef Papadopoulos[3], Kathleen Glover[3], Rebecca Brown[4], Mike Peel[5], Heathcliffe Riday[6], Susanne Kohalmi[2], and Abdelali Hannoufa[1,2]. [1]London Research and Development Center, Agriculture and Agri-Food Canada, London, ON; [2]Department of Biology, Western University, London, ON; [3]Kenville Research and Development Centre, Agriculture and Agri-Food Canada, Kentville, NS; [4]Univ. Rhode Island, Kingston, RI, [5]USDA-ARS, Logan; UT; and [6]USDA-ARS, Madison, WI
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Lotus corniculatus L., also known as birdsfoot trefoil (BFT), is a perennial non-bloating temperate forage widely grown due to its accumulation of high levels of condensed tannins (CT) in foliage. BFT has also shown the ability to limit the burden of parasitic nematodes in ruminants. While numerous ruminant health benefits have been associated with the consumption of BFT, the high variations in condensed tannins in this plant species present a significant challenge for its use in cattle feeding due to antinutritional attributes that can occur when CT levels are elevated. Several studies have examined the effects of environmental conditions on CT accumulation in BFT under controlled conditions; however, the variations in CT levels and other plant metabolites in BFT cultivars in response to environmental and seasonal factors under field conditions remain largely unexplored. Here, we combine conventional CT quantification and metabolome profiling with high-resolution liquid chromatography mass spectrometry (LCMS) to understand the environmental and genetic factors that impact both CT and metabolite profiles. Eight BFT cultivars grown in Kentville, Canada, Rhode Island, and Utah in the United States were investigated, revealing significant variations in soluble CT content and as well as metabolite composition. We observed pronounced fluctuations in CT levels among the cultivars, and geographic location, with those grown in Kentville having the highest CT levels. Geographic location was found to be the most influential factor in the CT levels. Our LCMS metabolomic analyses identified a suite of metabolites including isoflavonoids and lipid subclasses. Targeted metabolomic analysis revealed the presence of (-)-epicatechin monomer, dimeric procyanidin B2, and trimeric procyanidin C1 in the BFT samples. Similar to the CT levels, geographical location was the determinant factor in the metabolome profile however, specific metabolites that are building blocks of CTs were only moderately correlated with CT levels across all locations. An integrated transcriptomic and metabolomics study is underway to identify the molecular basis of the observed genotype-specific variations and environmental effects on CT and other metabolites in BFT cultivars. These results and further molecular genetic analysis will provide valuable insights into the plasticity of CT production in response to environmental cues, offering opportunities for targeted breeding and management strategies to enhance the nutritional quality and resilience of birdsfoot trefoil for improved animal health and reduced methane emission in animals.

[O101] METABOLIC ENGINEERING-INDUCED TRANSCRIPTOME REPROGRAMMING ENHANCES OIL COMPOSITION IN OAT (*AVENA SATIVA* L.). Zhou Zhou[1], Rajvinder Kaur[2], Thomas Donoso[1], Jae-Bom Ohm[3], Rajeev Gupta[3], Mark Lefsrud[2], and Jaswinder Singh[1]. [1]Department of Plant Science, McGill University, Ste Anne de Bellevue, QC, H9X 3V9, Canada; [2]Department of Bioresource Engineering, McGill University, Ste Anne de Bellevue, QC, H9X 3V9, Canada; and [3]Cereal Crops Research Unit, Edward T. Schafer Agricultural Research Center, USDA ARS, Fargo, North Dakota, 58102, USA
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The endeavor to elevate the nutritional value of oat (*Avena sativa*) by altering the oil composition and content position it as an optimal crop for fostering human health and animal feed. However, optimization of oil traits on oat through conventional breeding is challenging due to its quantitative nature and complexity of the oat genome. We introduced two constructs containing three key genes integral to lipid

biosynthesis and/or regulatory pathways from Arabidopsis (*AtWRI1* and *AtDGAT1*) and Sesame (*SiOLEOSIN*) into the oat cultivar 'Park' to modify the fatty acid composition. Four homozygous transgenic lines were generated with a transformation frequency of 7%. The expression of these introduced genes initiated a comprehensive transcriptional reprogramming in oat grains and leaves. Notably, endogenous *DGAT*, *WRI1*, and *OLEOSIN* genes experienced upregulation, while genes associated with fatty acid biosynthesis, such as *KASII*, *SACPD*, and *FAD2*, displayed antagonistic expression patterns between oat grains and leaves. Transcriptomic analyses highlighted significant differential gene expression, particularly enriched in lipid metabolism. Comparing the transgenic oat plants with the wild type, we observed a remarkable increase of up to 34% in oleic acid content in oat grains. Furthermore, there were marked improvements in the total oil content in oat leaves, as well as primary metabolites changes in both oat grains and leaves, while maintaining homeostasis in the transgenic oat plants. These findings underscore the effectiveness of genetic engineering in manipulating oat oil composition and content, offering promising implications for human consumption and animal feeding through oat crop improvement programs.

***[O102] THE RELATIONSHIPS AMONG PHYTOHORMONES AND BENZYLISOQUINOLINE ALKALOIDS DURING EARLY DEVELOPMENT OF *PAPAVER RHOEAS* L.** Zeynab Azimychetabi[1], Anna B. Kisiala[1], Scott C. Farrow[1], and R. J. Neil Emery[1]. Biology Department, Trent University, Peterborough, ON, Canada, K9L 0G2
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Benzylisoquinoline alkaloids (BIAs) are widely distributed in the plant kingdom, playing essential roles in defense against pathogens and herbivores. These compounds are of great interest for both ecological and pharmaceutical research. The biosynthetic pathways of several BIAs in opium poppy (*Papaver somniferum*) have been well-characterized, however, how individual genes within these pathways are regulated remains largely unknown. Phytohormones are a class of naturally occurring, small organic molecules that coordinate a comprehensive suite of physiological processes in plants at very low concentrations. Because phytohormones may alter production of secondary metabolite defense compounds, we hypothesize that phytohormones regulate BIA metabolism. To date, phytohormones and BIA profiles have not been investigated simultaneously during ontogenesis in any member of the Papaveraceae family. Therefore, we investigated phytohormone and BIA profiles of Field poppy (*Papaver rhoeas* L.) during the first 5-days of in vitro culture. Our data clearly showed that the production of BIAs depends on the developmental stage and starts between days three and four at shoot emergence. Phytohormone profiles changed during this time simultaneously, and directly correlated with changes observed in BIA levels. In addition, for the functional investigation of phytohormones that control the BIA pathway, silencing their biosynthesis, degradation, and response factor genes will help confirm their function. To knock down the genes related to phytohormones and BIA biosynthesis and/or regulation, we used virus-induced gene silencing (VIGS). The results from the VIGS experiment demonstrated that modifying the expression of genes associated with a class of phytohormones, Cytokinins, leads to variations in the production of compounds across various branches of the BIA pathway.

[O103] PROANTHOCYANIDINS IN POPLAR ROOTS: EFFECTS ON MYCORRHIZAL COLONIZATION AND NITROGEN UPTAKE. Daisuke Yamakawa, C. Peter Constabel, and Barbara J. Hawkins. Centre for Forest Biology & Department of Biology, University of Victoria, PO Box 3020 STN CSC, Victoria, BC, Canada, V8W 2Y2
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Proanthocyanidins (PAs), also known as condensed tannins, are plant secondary metabolites commonly found in trees. PAs are known for their roles in plant defense, soil nutrient cycling, and applications in human medicine and diet. Although much research has focused on the roles of PAs in plant shoots, few studies address the functions of PAs in roots. Evidence from *in vitro* studies suggests that PAs act as anti-microbial and anti-fungal compounds. In roots, anti-fungal properties of PAs could negatively affect colonization by mutualistic mycorrhizal fungi. We aimed to evaluate the effects of PAs on mycorrhizal colonization in poplar roots, as well as on N uptake by colonized roots.

Poplar (*Populus tremula* × *Populus tremuloides*) was chosen as our study species because poplars produce a wide range of phenolic compounds and abundant PAs, including in roots. We utilized previously generated transgenic poplar lines with contrasting root PA concentrations, created by overexpression of MYB transcription factors that activate or repress the PA pathway. Wild type, and high- and low-PA lines were inoculated with the ectomycorrhizal fungus *Laccaria bicolor* or the arbuscular mycorrhizal fungus *Rhizophagus irregularis*. A non-inoculated control treatment was included. Plants were grown in a sandwich culture system that allows co-culture of the mycorrhizal fungi and roots, or inoculated with the fungi in soil in a greenhouse experiment. Uptake rates of ammonium and nitrate by control and inoculated roots were measured using a microelectrode ion flux measurement system (MIFE™), a non-invasive method that measures net flux of specific nutrient ions at precise root locations, and by ^{15}N-labelling.

The poplar line with low levels of PAs and other flavonoids in shoots also had relatively low root PA concentrations. This line was less colonized by ectomycorrhizae in sandwich and soil culture. No colonization by arbuscular mycorrhizae was evident for any poplar line. Plants from all lines inoculated with *Laccaria* had lower survival and root PA concentrations than controls and plants inoculated with *Rhizophagus*. Ammonium and nitrate net fluxes were low in sandwich culture roots, except in roots inoculated with arbuscular mycorrhizae, which showed significant ammonium efflux. To confirm these trends, measurements of ^{15}N uptake by sandwich culture roots, and of ammonium and nitrate fluxes in soil-grown roots are in progress. Understanding the effects of the interaction of root PAs and mycorrhizal fungi on mycorrhizal colonization and N uptake will contribute to our knowledge of ecological and physiological impacts of PAs in the rhizosphere.

***[O104] A PROMOTER FOR THE METABOLIC ENGINEERING OF GLANDULAR TRICHOMES IN LAVENDER.** Reza Sajaditabar[1] and Soheil Mahmoud[1]. [1]Department of Biology, The University of British Columbia: Okanagan Campus, 3333 University Way, Kelowna, BC, Canada, V1V 1V7
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Lavenders produce abundant, high-quality, terpene-rich essential oils (EO) in glandular trichomes (GT) present on the surfaces of the above-ground plant parts. In these glands, terpene synthases (TPS), the enzymes responsible for terpenes synthesis, are specifically and strongly expressed. Lavenders represent excellent candidates as bioreactors for metabolic engineering to produce high-value terpenes. However, the common approach of overexpressing genes under the control of constitutive promoters such as the CaMV35s promoter has been problematic as it often adversely affects plant health, presumably due to the cytotoxic effects of metabolites produced in non-GT plant cells. To address this, GT-specific promoters offer an alternative, enhancing transgene expression exclusively in GT. This study aims to engineer terpene metabolism in GT of *Lavandula latifolia* using GT-specific promoters including those corresponding to the linalool synthase (LINS) and 1,8 cineol synthase (CINS) genes, which are strongly and specifically expressed in lavender GTs. *Lavandula latifolia* leaves were transformed with *Agrobacterium tumefaciens* strains containing different fragments of LINS and CINS promoters fused to the *gusA* reporter gene, which encodes β-glucuronidase (GUS) enzyme. Plants in which GUS expression is driven by the CaMV35s promoter serve as positive control. Transformed plants are being evaluated for GUS expression. Preliminary results indicate that several promoters can drive gene expression in *L. latifolia* in GTs.

***[O105] SOYBEAN CYTOCHROME P450S AND THE MAKING OF ALIPHATIC SUBERIN MONOMERS.** Lorena S. Yeung[1], Delicia Wong[1], Sangeeta Dhaubhadel[1,2], and Mark A. Bernards[1]. [1]Department of Biology, Western University, London, ON, N6A 5B7, Canada; and [2]London Research and Development Centre, Agriculture and Agri-Food Canada, 1391 Sandford St, London, Ontario, N5V 4T3, Canada
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Suberin is a phenolic-lipophilic biopolymer that functions as a physical barrier to protect plants from desiccation and pathogen infection. Soybean (Glycine max [L.] Merr) cultivars with varying amounts of root suberin show differential resistance to root pathogens (more suberin = stronger partial resistance), making suberin a potential focus for the production of enhanced crops. 18-hydroxyoleic acid and 18-dicarboxylic acid are two of the most prominent aliphatic suberin monomers in soybean. Production of

hydroxy-fatty acids requires terminal hydroxylation of fatty acid substrates, while production of dicarboxylic acids requires sequential oxidation of fatty acid substrates through hydroxy- and oxo-fatty acids. Whether one or two enzymes are involved is unknown. Previous study demonstrated a positive correlation between expression levels of CYP86A37 and CYP86A38 and the deposition of 18-hydroxyoleic acid in soybean hairy roots. However, definitive proof for substrate specificities of the respective enzymes is lacking. Additionally, the enzyme(s) responsible for catalysis of 18-dicarboxylic acid in soybean remains unknown. My research focuses on employing biochemical techniques and genome editing to characterize the molecular and functional roles of CYP86A37 and CYP86A38 in aliphatic suberin biosynthesis in soybean. Screening recombinant protein using in vitro enzyme assays, I surveyed the substrate specificity of CYP86A37 and CYP86A38. Among the two recombinant enzymes, CYP86A38 was non-functional for all the substrates used in the study, while recombinant CYP86A37 hydroxylated 16:0, 18:0, 18:1, 20:0, 22:0 and 24:0 fatty acids, oleic acid (18:1) was the preferred substrate. In planta, both 18-hydroxy oleic acid and 1,18-dicarboxylic oleic acid were reduced in cyp86a37/cyp86a38 CRISPR soybean lines. These results are novel as they confirm the role of CYP86A37 as a functional fatty acid ω-hydroxylase responsible for the production of soybean aliphatic suberin monomers 18-hydroxyoleic acid directly and 1,18-dicarboxylic oleic acid indirectly. Further understanding of key enzymes involved in aliphatic suberin biosynthesis is important as it establishes the foundational research towards the protection and improvement of one of Canada's most important crops.

***[O106] BUILDING OF SUBERIN - THE IMPORTANCE OF TIMING AND A STRONG FOUNDATION.**
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Suberin is a cell wall-associated biopolymer that has both poly(phenolic) and poly(aliphatic) elements assembled into chemically and spatially distinct domains. Domain-specific monomers are formed via a branched pathway between phenolic and aliphatic metabolisms. I previously conducted stable isotope labeling experiments in which [^{13}C]-glucose was administered to wound-healing potato tuber (*Solanum tuberosum*) discs at different times post-wounding. This revealed highly coordinated, temporal changes in the regulation of the phenolic and aliphatic metabolic 'branches'. Notably, during early stages of wound-healing, carbon from glucose was rapidly incorporated into phenolic-destined metabolites, while at later stages it was shared between phenolic- and aliphatic-destined metabolites. This data supported previously published transcript accumulation data (RNAseq). But, what is the importance of these dynamic changes in suberin monomer biosynthesis, and more specifically how does the preferential synthesis of phenolics affect suberin assembly and ultrastructure? To assess this, RNAi-mediated silencing of an uncharacterized St*HCT* (hydroxycinnamoyl transferase) was employed to disrupt phenolic biosynthesis upstream of ferulic acid (a key component of the phenolic domain and esterified phenolics of the aliphatic domain). This work is premised on the idea that the phenolic domain acts as an anchor within the primary cell wall to facilitate attachment of the aliphatic domain and the corollary that a disrupted phenolic domain will compromise suberin function. Here I present chemical analyses to assess composition, permeability measurements to assess the functionality, and electron microscopy to evaluate the ultrastructure of suberin collected from St*HCT-RNAi* tubers. Suberin is an attractive target for crop enhancement as it acts an innate physical barrier that confers resistance to drought, pathogens, and desiccation during crop storage. Better understanding of its temporal regulation and ultrastructure can help inform strategies for crop enhancement through genetic engineering and/or marker-assisted breeding.

***[O107] SUBERIN PRODUCTION IN SOYBEAN IS MICROBIOME-RESPONSIVE.**
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Plant stress response mechanisms allow crop species to be resilient and productive in the face of environmental stress. Plant-associated microorganisms (i.e., the microbiome) contribute to this stress tolerance, including outcompeting pathogens. To further tolerate stress, plants naturally reinforce the cell

walls of some tissues with suberin, a hydrophobic polymer regulated by the stress phytohormone abscisic acid (ABA). Root suberin can limit root pathogen colonization in crops like soybean (*Glycine max*). Soybean is a globally important oilseed crop that is susceptible to drought and salt stress. Current literature has shown that the soybean microbiome can support abiotic stress tolerance, while root suberin provides biotic stress tolerance The primary objective of this research was to determine root suberin-microbiome relationship in early soybean development and if that relationship is phytohormone-dependent.

Three soybean cultivars with varying degrees of pathogen tolerance (low = OX20-8, moderate = Amsoy 71, high = Conrad) were grown in micropropagation containers with and without microbiome treatment. The total suberin content was measured for each cultivar at three time points in early vegetative development (emerged cotyledons, unifoliate leaves, first trifoliate leaves). Root and rhizosphere microbiomes were subject to metagenomic sequencing to identify suberin-associated microbiota across these soybean cultivars. To test whether the role of phytohormones in these plant-microbe interactions, we replicated the microbiome experiment for the Conrad cultivar with the addition of fluridone, an ABA biosynthesis inhibitor.

Current results indicate that only the Conrad cultivar, with high pathogen tolerance, increases suberization in response to microbiome treatment early in plant development. This increase in suberin content did not occur in Conrad plants treated with fluridone, suggesting ABA biosynthesis is required for microbiome-responsive suberization. The microbiome results also demonstrate typical plant-associated microbiota that are strongly associated with sample type (e.g., root vs rhizosphere).

Continued research on plant-microbe interactions contributes to efforts in sustainable agriculture to feed a growing global population. Increased suberin content in response to the microbiome may contribute to further stress tolerance in soybeans, and understanding this relationship may lead to the development of stress resistant cultivars.

[O108] GONE WITH THE WIND: CUTICULAR WAXES AS PRECURSORS OF VOLATILE ORGANIC COMPOUNDS. Jeff Y. Chen[1,2], Aswini Kuruparan[1,2], Mahbobeh Zamani-Babgohari[1,2], and Eliana Gonzales-Vigil[1,2]. [1]Department of Biological Sciences, University of Toronto - Scarborough, Scarborough, ON, Canada, M1C A14; and [2]Department of Cell and Systems Biology, University of Toronto, Toronto, ON, Canada, M5S 3G
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Plant surfaces are sealed by a lipidic layer known as the cuticle, which provides the first line of defence against the environment. However, it is traditionally considered a physical barrier that provides passive protection from biotic and abiotic stress. In *Populus trichocarpa* (poplar, black cottonwood tree), the cuticle accumulates *cis*-9 alkenes (hydrocarbons with one double bond) on the abaxial side of expanded leaves. Unlike other cuticle components in *P. trichocarpa*, alkenes show a peculiar accumulation pattern: they increase as leaves expand and then decrease in more mature leaves, which led us to investigate the fate of the alkenes in older leaves. A thorough examination of the lipid profiles of older leaves revealed an increase in shorter aldehydes accompanied the decrease in alkenes. Moreover, we found that the distribution of carbon length of the aldehydes mirrored the distribution of carbon length of the alkenes, indicating that they were biosynthetically related. Through a series of experiments, we determined that oxidation of *cis*-9 alkenes leads to two aldehydes, one of them being nonanal, an important insect pheromone. The breakdown is a spontaneous reaction that occurs upon exposure to air and light. Furthermore, the oxidation was also observed in other plant systems that produce alkenes, including wheat spikes and maize silks. These results change the current paradigm that cuticular waxes are a non-reactive barrier and bring them to the forefront as precursors of volatile molecules, notably molecules with well-established roles in insect communication.

***[O109] IDENTIFICATION OF QUANTITATIVE TRAIT LOCI (QTL) FOR ERUCIC ACID CONTENT IN *BRASSICA NAPUS* L.** Yong Liu[1], Genyi Li[1], Harmeet S. Chawla[1], Robert W. Duncan[1], and Curt McCartney[1]. [1]Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB, R3T 2N2
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Brassica napus L., commonly known as canola or rapeseed, is an economically significant crop due to its high oil content and quality. Erucic acid (C22:1 ω-9) is a long-chain monounsaturated fatty acid, which is a major component of *B. napus* oil and plays a crucial role in determining its nutritional and industrial properties. Erucic acid is used in a wide range of industrial applications, often as a highly effective industrial lubricant, and is in high demand as a raw material in modern manufacturing. The objective of this research was to identify and analyze the quantitative trait loci (QTL) responsible for high levels of erucic acid in *B. napus*. Two doubled haploid (DH) populations were generated from parental genotypes with contrasting erucic acid content. The two DH populations (CBER1 and CBER2) consisted of 183 and 182 individuals, respectively. The populations were compared in randomized complete block designs (RCBD) in two locations in 2020, 2021 and 2022 and fatty acid analyses were conducted using gas chromatography. DNA samples were extracted from the leaf tissues of the population individuals, and genotyping was performed using genotyping by sequencing (GBS). Genetic maps were produced from the detected SNPs and InDels. An inclusive composite interval QTL mapping (ICIM) approach was employed to detect significant QTL with high statistical confidence. Multiple QTL associated with erucic acid content were detected across multiple site-years. These QTL were distributed across different chromosomes, indicating the polygenic nature of erucic acid regulation. In this study, 7 and 5 QTL were found in CBER2 and CBLD2 populations, respectively. Among them, the QTL found on the A04 chromosome of the CBLD2 population reached a maximum variation of 27%. Minor QTL were also shown on chromosomes A07, C01, C05 and C02. The identified QTL provide valuable insight into the genetic basis of erucic acid high quantity trait in *B. napus*. These findings can facilitate marker-assisted selection (MAS) programs aimed at developing *B. napus* genotypes with increased erucic acid content. Furthermore, the identified QTL can serve as targets for future functional studies, enabling a deeper understanding of the molecular mechanisms involved in erucic acid biosynthesis and metabolism.

***[O110] TOC159 RECEPTORS: THE ROLE OF PLASTID MEMBRANE GALACTOLIPIDS IN TARGETING TO THE CHLOROPLAST OUTER ENVELOPE.** Michael Fish[1], George Saudan[2], Simon Chuong[3], Masoud Jelokhani-Niaraki[2], and Matthew Smith[1]. [1]Department of Biology, Wilfrid Laurier University, 75 University Avenue West, Waterloo, ON, Canada, N2L 3C5; [2]Department of Chemistry & Biochemistry, Wilfrid Laurier University, 75 University Avenue West, Waterloo, ON, Canada, N2L 3C5; and [3]Department of Biology, University of Waterloo, 200 University Avenue West, Waterloo, ON, Canada, N2L 3G1
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Plastids are a dynamic group of organelles in plant cells that facilitate a variety of functions in different tissues. They can also transition between types in response to different developmental and environmental cues. The most well-studied plastids are the chloroplasts, which house the machinery for photosynthesis. Chloroplast biogenesis and function rely on the targeting of chloroplast preproteins, where N-terminal chloroplast transit peptides direct preproteins to the translocon at the outer membrane of the chloroplast (TOC complex), where they are recognized and imported. Chloroplast preprotein targeting, recognition and translocation through the chloroplast outer envelope by the TOC complex are well characterized processes. However, the same processes for many outer envelope proteins remain poorly understood. TOC159 receptors, key components of the TOC complex, represent one such example. We have shown previously that TOC159 receptors use a novel targeting signal, composed of a highly conserved bi-partite sequence at the C-terminus, containing β-signal-like and transit peptide-like motifs. Structural predictions of the TOC159 receptor membrane domain using AlphaFold2, with far-UV circular dichroism (CD) spectroscopy of the membrane domain expressed in *Escherichia coli* and purified from inclusion bodies suggest a β-barrel membrane anchor in detergent and when reconstituted in liposomes. Green fluorescent protein targeting experiments in plant cells of *Arabidopsis thaliana* and *Allium cepa* using confocal fluorescence microscopy, cell fractionation and immunoblotting demonstrate that the β-signal-

like motif is necessary for targeting, where the transit peptide-like motif significantly improves targeting fidelity. Additionally, the transit peptide-like motif exhibits a preferential interaction toward galactolipids unique to the plastid membrane as shown by Langmuir-Blodgett trough experiments using galactolipid monolayers and CD spectroscopy experiments using liposomes containing galactolipids. Together, these experiments demonstrate higher maximum insertion pressures of the transit peptide-like motif in the presence of galactolipid monolayers compared to monolayers composed of phosphatidylcholine (PC). The transit peptide-like motif is unstructured in buffer and in the presence of PC liposomes, but form α-helical structures in the presence of liposomes containing galactolipids. This implies a role for lipid composition in targeting. A better understanding of TOC159 receptor biogenesis is critical in describing how TOC complexes are assembled and function in the chloroplast outer envelope, responsible for regulating chloroplast biogenesis and plastid morphogenesis in plant cells.

[O111] THE REGULATORY FUNCTION OF PLASTID CHAPERONE HSP90C C-TERMINAL EXTENSION. Bona Mu[1,2], Adheip Monakan Nair[1,2], and Rongmin Zhao[1,2]. [1]Departments of Biological Sciences, University of Toronto Scarborough; and [2]Cell & Systems Biology, University of Toronto, Toronto, Canada
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HSP90Cs are essential molecular chaperones localized in the plastid stroma that maintain protein homeostasis and assist the import and thylakoid transport of chloroplast proteins. While HSP90C contains all conserved domains as an HSP90 family protein, it also possesses a unique feature in its variable C-terminal extension (CTE) region. This study elucidated the specific function of this HSP90C CTE region. Our phylogenetic analyses revealed that this intrinsically disordered region contains a highly conserved DPW motif in the green lineages. With biochemical assays, we showed that the CTE is required for the chaperone to effectively interact with client proteins PsbO1 and LHCB2 to regulate ATP-independent chaperone activity and to effectuate its ATP hydrolysis. While the CTE truncation mutants could support plant growth and development indistinguishably from the wild-type protein under normal conditions, higher HSP90C expression was observed to correlate with a stronger response to specific photosystem II inhibitor DCMU, and CTE truncations dampened the response. Additionally, when treated with lincomycin to inhibit chloroplast protein translation, CTE truncation mutants showed a delayed response to PsbO1 expression repression, suggesting its role in chloroplast retrograde signalling. Our study therefore provides insights into the mechanism of HSP90C in client protein binding and in the regulation of green chloroplast maturation and function, especially under stress conditions.

***[O112] IDENTIFICATION AND CHARACTERIZATION OF OEP6 MOTIFS AND THEIR ROLE IN TARGETING TO THE CHLOROPLAST OUTER MEMBRANE.** Holly Ferguson[1], Matthew Smith[1], and Simon Chuong[2]. [1]Wilfrid Laurier University, 75 University Ave W, Waterloo, ON, Canada, N2L 3C5; and [2]University of Waterloo, 200 University Ave W, Waterloo, ON, Canada, N2L 3G1
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The chloroplast is a type of membrane-bound plastid commonly known for its role in photosynthesis. Chloroplasts evolved from a cyanobacterium that was engulfed by a eukaryotic cell and through this endosymbiotic process, the majority of the cyanobacterial genes were lost to the host nucleus. Therefore, the vast majority of chloroplast proteins necessary for its biogenesis and function are encoded in the host nucleus, translated in the cytoplasm, and then transported from the cytosol back to the chloroplast. Proteins that are targeted to different compartments of the chloroplast require targeting signals to facilitate their delivery and import. The import of these stromal peptides is facilitated by the activity of protein complexes at the outer and inner envelope membranes, TOC and TIC, respectively. To date, chloroplast outer envelope proteins (OEPs) have been reported to utilize one of five different targeting mechanisms: (1) an N-terminal transit peptide; (2) a transmembrane domain located at either the N-terminus (signal-anchored proteins) or (3) the C-terminus (tail-anchored proteins); (4) a signal included within a β-barrel structure that forms a channel; and (5) a reverse transit peptide-like signal at the C-terminus (Fish *et al.* 2022). My research focuses on OEP6, which is predicted to be a tail-anchored protein, but whose targeting mechanism is not yet well-characterized. My study aims to identify and characterize features

such as the predicted α-helical transmembrane domain and positively charged flanking regions that play a role in the targeting of OEP6 to the chloroplast outer membrane. Fusion OEP6 constructs tagged with green fluorescent protein (GFP) will be transformed into onion epidermal cells using biolistic bombardment and introduced into *Arabidopsis* mesophyll cell protoplasts using polyethylene glycol-mediated protocols where their intracellular localization will be determined using epifluorescence and confocal microscopy. To test the importance of secondary structures of OEP6 in its targeting, the localization of fusion constructs containing mutations or deletions of these predicted secondary structures in plant cells will be examined. The findings generated from this study will contribute to the overall understanding of intracellular protein trafficking, specifically the role of protein secondary structures or motifs with defined properties. Specific to the chloroplast, understanding the targeting and import of proteins will have applications to both the agricultural and biotechnological industries.

***[O113] PLASTID MOLECULAR CHAPERONE HSP90C INTERACTS WITH THE SECA1 SUBUNIT OF SEC TRANSLOCASE FOR THYLAKOID PROTEIN TRANSPORT.** Adheip Monikantan Nair, Tim Jiang, Bona Mu, and Rongmin Zhao. Department of Biological Sciences, University of Toronto Scarborough, Toronto, ON; Department of Cell & Systems Biology, University of Toronto, Toronto, ON
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The plastid stroma-localized chaperone HSP90C plays a crucial role in maintaining optimal proteostasis within chloroplasts and participates in protein translocation processes. While existing studies have revealed HSP90C's direct interaction with the Sec translocase-dependent client pre-protein PsbO1 and the SecY1 subunit of the thylakoid membrane-bound Sec1 translocase channel system, its direct involvement with the extrinsic homodimeric Sec translocase subunit, SecA1, remains elusive. Employing bimolecular fluorescence complementation (BiFC) assay and other in vitro analyses, we unravelled potential interactions between HSP90C and SecA1. Our investigation revealed dynamic interactions between HSP90C and SecA1 at the thylakoid membrane and stroma. The thylakoid membrane localization of this interaction was contingent upon active HSP90C ATPase activity, whereas their stromal interaction was associated with active SecA1 ATPase activity. Furthermore, we observed a direct interaction between these two proteins by analyzing their ATP hydrolysis activities, and their interaction likely impacts their respective functional cycles. Additionally, using PsbO1, a model Sec translocase client pre-protein, we studied the intricacies of HSP90C's possible involvement in pre-protein translocation via the Sec1 system in chloroplasts. The results suggest a complex nature of the HSP90C-SecA1 interaction, possibly mediated by the Sec client protein. Our studies shed light on the nuanced aspects of HSP90C's engagement in orchestrating pre-protein translocation, and we propose a potential collaborative role of HSP90C with SecA1 in actively facilitating pre-protein transport across the thylakoid membrane.

[O114] ADVANCING CANOLA PROTECTION: QPCR SCREENING AND MARKER DEVELOPMENT FOR VERTICILLIUM STRIPE DISEASE RESISTANCE. Mohamed Samir Youssef[1], W. G. Dilantha Fernando[1], Robert Duncan[1], Sally Vail[2], Isobel A. P. Parkin[2], and Harmeet Singh Chawla[1]. [1]Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB, Canada, R3T2N2; and [2]Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, Saskatoon, SK, Canada
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Verticillium longisporum (VL), a soil-borne vascular fungal pathogen, poses a significant threat to cruciferous crops including canola (oilseed rape), and can cause up to 80% yield loss in severe cases. VL gains access to plants through the roots and colonizes the vascular system, resulting in verticillium stripe (VS) disease. This disease is an emerging threat to canola production in Canada, and its severity is anticipated to increase with rising temperatures due to climate change and increasing inoculum load in the fields with VL infestations. Thus, developing canola cultivars resistant to VS is critical to protect Western Canadian producers from substantial yield losses. A unique characteristic of this pathogen is its systemic, non-homogenous, and delayed colonization of the plant xylem, leading to an extended symptomless latency period. Consequently, the severity of infection in the field is challenging to assess, as symptoms become apparent only at crop maturity, and are often confused with natural senescence. Traditional methods for assessing Verticillium disease severity in canola, such as visual scoring of microsclerotia on harvested stubble, unsatisfactorily reflect genotypic resistance as they are heavily

influenced by the plant's ripening stage. To address these limitations, we aim to enhance the phenotyping process by developing a quantitative PCR (qPCR) method that accurately differentiates levels of quantitative resistance to *V. longisporum* in canola genotypes under field conditions. In this study, we are screening a diverse collection of 260 *B. napus* genotypes for resistance to VS using qPCR. Genome-wide association studies (GWAS) will be employed to identify QTL associated with VS resistance. The GWAS panel includes commercial canola cultivars, re-synthesized *B. napus* genotypes, and other genetically diverse germplasm. Upon identifying the most relevant polymorphisms, such as SNPs and Indels in the VS resistance QTL, we will develop KASP or simple PCR-based markers. These markers will be pivotal in introducing newly identified VS resistance alleles into elite Western Canadian breeding materials and cultivars. Our research aims to provide a robust tool for improving canola resistance to verticillium stripe, enhancing yield stability and sustainability for canola producers in Western Canada.

***[O115] IDENTIFICATION OF MICROORGANISMS WITH CLUBROOT BIOCONTROL POTENTIAL AND INVESTIGATION OF MECHANISMS OF THEIR ACTION.** Ananya Sarkar[1], Anna Kisiala[2], Vedanti Ghatwala[2], Neil Emery[2], Habibur Rahman[1], and Nat N.V. Kav[1]. [1]Department of Agricultural, Food & Nutritional Science, University of Alberta, Edmonton, AB, Canada; and [2]Biology Department, Trent University, Peterborough, ON, Canada
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Clubroot disease, caused by *Plasmodiophora brassicae*, results in substantial crop losses in crucifers in Canada and worldwide. The disease forms club-shaped galls in susceptible Brassica hosts that reduce yield and productivity. Microbial biocontrol agents can antagonize plant pathogens through their wide range of mechanisms, including induction of broad-spectrum resistance. In our study, we observed improvement in plant parameters when susceptible *Brassica napus* roots were treated with selected *Bacillus*, *Pseudomonas* and *Trichoderma* strains in presence of *P. brassicae* pathotypes 2B, 3H, 3D and 5X-LG1. Application of a cocktail formulation comprising of *Bacillus atrophaeus* (DSM 7264), *Pseudomonas parafulva* (DSM 17004) and *Trichoderma virens* (DSM 1963) resulted in up to 35% reduction of clubroot severity, as well as improvement in plant parameters such as root length, length of inflorescence and number of silique against pathotype 3H. Levels of endogenous phytohormones (e.g. auxin, jasmonic acid, cytokinin (CK) ribosides and glucosides) as well as secondary metabolites (e.g. coniferin, syringin) and glucosinolates (e.g, gluconasturtiin, glucobrassicin) were altered in the roots of treated plants across 1-, 4-, and 7 days post-inoculation (DPI), along with modulation of gene expression related to these biological metabolites and their pathways. Additionally, analysis of CKs secreted by the individual microbial strains revealed striking differences in CK forms (e.g. free-bases, ribosides, glucosides) and types (e.g. cZ and iP) in both those released to the culture supernatant and retained in the cellular pellet fractions. These differences may represent important underlying factors to account for the beneficial effects observed on treated plants. Taken together, our results suggest that the three microbial strains identified may be used for biocontrol of clubroot disease in canola and have provided insights into their possible modes of action, which will be useful for research that develops new agents of biocontrol.

[O116] MODULATION OF PLASTIDIAL PROTEIN TURNOVER BY *PB*PAE, A *PLASMODIOPHORA BRASSICAE* PLASTID-ASSOCIATED EFFECTOR THAT FACILITATES CLUBROOT DISEASE PROGRESSION IN ARABIDOPSIS. Musharaf Hossain, Christopher D. Todd, Yangdou Wei, and Peta C. Bonham-Smith. Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK, Canada, S7N 5E2
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Clubroot disease, caused by the soilborne protist *Plasmodiophora brassicae*, is a major threat to Canada's ~$30 billion annual canola industry. A typical disease symptom is the formation of root galls, through induced hyperplasia and hypertrophy of infected tissues, establishing in a nutrient sink to sustain intracellular pathogen development. As an intracellular obligate biotroph, *Plasmodiophora brassicae* secretes an array of effectors while colonizing host plant root tissues, resulting in clubroot disease. During *P. brassicae* pathogenesis amyloplast (containing starch grains) abundance increases and they become tightly associated with secondary plasmodial structures prior to their dynamic turnover during late secondary stage clubroot progression. To date, *P. brassicae* effectors required for the manipulation of source-sink carbon allocation, together with the identity of host metabolite transporters seconded to the

translocation process during *P. brassicae* infection, have yet to be identified. Here, we report the identification of a *P. brassicae* plastid-associated effector (PAE), *Pb*PAE, and propose a functional role(s) during clubroot development. Transient expression of *Pb*PAE-GFP, in the leaves of *Nicotiana benthamiana,* shows chloroplast association and results in chlorosis. Through mutational analysis of the effector the essential sequences for chloroplast association, leading to chlorosis, have been identified. Overexpression of *Pb*PAE-GFP in Arabidopsis supports its association with chloroplasts (and subsequent chlorosis) but more importantly its association with amyloplasts in root tissues. Live cell imaging shows *Pb*PAE-GFP associated with amyloplasts in plant cells hosting *P. brassicae* secondary plasmodia. Transgenic leaf chlorosis suggests that *Pb*PAE is involved in promoting plastidial degenerative processes. *Pb*PAE interaction with the substrate recognizing adaptor protein (*At*ClpS1) of the Clp-protease complex supports a role for *Pb*PAE in modulating plastidial proteostasis and facilitating carbon flow from host tissues to sustain pathogen development in infected plant roots. Furthermore, we have subsequently identified a second *P. brassicae* plastid-associating effector, highlighting the importance of amyloplast association with the plasmodial structure for the establishment of a nutrient sink and carbon flow from host to the developing pathogen during disease progression.

***[O117] CLUBROOT RESISTANCE OF *BRASSICA NAPUS* INTROGRESSED FROM *BRASSICA OLERACEA*.** Sonia Navvuru[1], Nat N.V. Kav[1], and Habibur Rahman[1]. [1]Department of Agricultural, Food and Nutritional Science, 4-10 Agriculture/Forestry Centre, University of Alberta, Edmonton, AB T6G 2P5, Canada
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Brassica napus canola is affected by several biotic and abiotic stresses, including clubroot disease, caused by *Plasmodiophora brassicae*, which can result in a yield loss of 29-90%. To date, the major clubroot resistance (CR) genes of the *Brassica* A genome has been used in breeding clubroot resistant cultivars; however, this type of resistance has been reported to become ineffective after cultivation for a few years. Conversely, the C genome of *B. oleracea* carries resistance to a broad spectrum of pathotypes but its potential in breeding clubroot resistant canola has not yet been exploited. We have developed several *B. napus* lines (F_{10}) carrying CR genes from *B. oleracea*. The objectives of this research were to develop a genetically stable clubroot-resistant line and to understand the genetic control of the C genome resistance. In order to accomplish this, 252 F_{10} plants descendent from 14 resistant and 5 partially resistant F_9 families were grown and inoculated with *P. brassicae* pathotype 3H, and the plants were evaluated for fertility and CR at harvest. All plants were also self-pollinated to obtain F_{11} seeds and crossed to a susceptible canola to obtain F_1 seeds. Disease Severity Index (DSI) of the 14 resistant families ranged from 0 to 100% with a mean of 39±6.20%, while the DSI for the partially resistant families varied from 0 to 88.89% with a mean of 55.81±10.63%. In fact, three of the 14 resistant F_{10} families were observed to be non-segregating, i.e. showed stability for resistance. Silique set under self-pollination (0-9 scale, where 9=good and 0=poor) and number seeds/siliques produced on crossing of the plants of the 14 resistant families ranged from 0 to 9 with a mean of 5.18±0.20, and 0 to 20 with a mean of 5.27±0.42, respectively. For the partially resistant families, it varied from 0 to 9 with a mean of 5.34±0.29, and 0.00 to17.60 with a mean of 4.76±0.52, respectively. Most importantly, silique set of the three non-segregating resistant families varied from 4 to 8 with a mean of 6.37±0.31, and seed set ranged from 0.00 to 16.75 with a mean of 7.46±1.20. Based on this, 28 F_1s were selected and were grown along with their parents to confirm their resistance. Different segregating populations including recombinant inbred lines (RILs) will be developed to understand the genetic control of the CR and mapping of this resistance. Our research is expected to facilitate the use of the C genome resistance in breeding and pyramiding with the A genome resistance for durable CR in this crop.

[O118] MULTI-OMICS ANALYSIS OF MECHANISMS BEHIND THE "GAME OF HIDE AND SEEK" IN THE *BRASSICA NAPUS - LEPTOSPHAERIA MACULANS* PATHOSYSTEM. Shuanglong Huang[1], Peng Gao[2], Dilantha Fernando[1], and Gary Peng[2]. [1]Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada; and [2]Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, Saskatoon, SK S7N 0X2, Canada
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Blackleg is caused primarily by the hemibiotrophic fungus *Leptosphaeria maculans (Desmaz.) Ces. & De Not.*, is one of the most economically significant diseases in many canola/oilseed rape (*Brassica napus L.*) growing regions in the world, often causing significant yield losses. Genetic resistance has been proven effective in mitigating blackleg infection and impact. Seedling resistance generally follows the gene-for-gene theory. For example, the recognition of avirulence genes *AvrLm3* and *AvrLm9* by the respective resistance genes *Rlm3* and *Rlm9* will result in a resistant reaction. However, this recognition can be masked by the presence of *AvrLm4-7* in the *L. maculans* isolate known as the 'game of hide and seek'. Recent evidence has shown that there is no direct interaction between *AvrLm4-7* and *AvrLm3* or *AvrLm9*, or between *Rlm9* and *AvrLm9* or *AvrLm4-7*, suggesting *AvrLm4-7* may conform to the guard or decoy models and interact with unknown targets in the host that represses the recognition of *AvrLm3* or *AvrLm9* by the corresponding resistance gene. To reveal the mechanisms underlying this masking effect, we conducted RNA sequencing (NovaSeq 6000 System, Illumina) and proteomic (TMT-based technology) studies on *B. napus* '02-22-2-1' (*Rlm3* carrier) and 'Goéland' (*Rlm9* carrier) seedlings at 3- and 7-days post inoculation (dpi) with *L. maculans* isolates carrying *avrLm4-7-AvrLm3-AvrLm9* (typical resistant reactions) and *AvrLm4-7-AvrLm3-AvrLm9* (resistant reactions masked), respectively. A total of 2.33 billion pair-end reads were generated from 36 cDNA libraries (18 for each of resistant and masked *AvrLm3-Rlm3* and *AvrLm9-Rlm9* interactions). On average, 72.58% of these reads were aligned to the coding region of the reference genome of *B. napus* oilseed rape variety 'Darmor-bzh' (AST_PRJEB5043_v1). In the resistant *Rlm3-AvrLm3* interactions, we detected 434 and 6611 upregulated differentially expressed genes (DEGs; $P < 0.05$) compared to masked interactions at 3 dpi and 7 dpi, respectively, of which 24 upregulated DEGs were commonly found at both post-inoculation stages. A smaller number of upregulated DEGs were found in the resistant *Rlm9-AvrLm9* interaction, with 16 upregulated DEGs at three dpi and 147 at seven dpi compared to masked interactions. The GO enrichment analysis based on the common DEGs between resistant and masked *AvrLm3-Rlm3* and *AvrLm9-Rlm9* interactions indicated that biological processes, including endoplasmic reticulum to Golgi vesicle-mediated transport, response to stress, response to endoplasmic reticulum stress, Golgi organization, intra-Golgi vesicle-mediated transport, negative regulation of cell death, xenobiotic transport, retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum, as well as defense response were actively involved in the 'game of hide and seek'. Integration of RNA-sequencing and proteome data from resistant and masked *AvrLm3-Rlm3* and *AvrLm9-Rlm9* interactions at 3 dpi and 7 dpi also identified the genes that are highly correlated between RNA-sequencing and proteome data, some of which are possibly associated with the 'game of hide and seek'. This multi-omics study help identify key players in the 'game of hide and seek' for this pathosystem and provide a tool to illuminate similar interactions in other pathosystems.

[O119] DECIPHERING THE MOLECULAR EVENTS BEHIND SYSTEMIN-INDUCED RESISTANCE AGAINST *BOTRYTIS CINEREA* IN TOMATO PLANTS. Julia Pastor-Fernández[1], Neus Sanmartín[1], Maria Manresa[1], Cédric Cassan[2,3], Pierre Pétriacq[2,3], Yves Gibon[2,3], Jordi Gamir[1], Beatriz Romero Rodriguez[4], Araceli G. Castillo[4], Miguel Cerezo[1], Victor Flors[1], and Paloma Sánchez-Bel[1]. [1]Metabolic Integration and Cell Signaling Laboratory, Biochemistry and Molecular Biology Section. Department of Biology, Biochemistry and Natural Sciences, Universitat Jaume I. Avd Vicente Sos Baynat s/n 12071 Castellón, Spain; [2]Univ. Bordeaux, INRAE, UMR1332 BFP, 33882 Villenave d'Ornon, France; [3]Bordeaux Metabolome, MetaboHUB, PHENOME-EMPHASIS, 33140 Villenave d'Ornon, France; and [4]Instituto de Hortofruticultura Subtropical y Mediterránea "La Mayora" (IHSM "La Mayora"), Universidad de Málaga-Consejo Superior de Investigaciones Cientificas (UMA-CSIC), Campus Teatinos, 29010 Málaga, Spain. Correspondence to: jpastorf@uwo.ca

Plant defense peptides are paramount endogenous danger signals secreted after a challenge intensifying the plant immune response. The peptidic hormone Systemin (Sys) has been shown to participate in resistance in several plant-pathosystems, although the mechanisms behind Sys- Induced Resistance (IR) when exogenously applied remain elusive. We performed proteomic, metabolomic and enzymatic studies to decipher the Sys-induced changes in tomato plants either in the absence or the presence of *Botrytis cinerea* infection. Sys treatments triggered direct proteomic rearrangement mostly involved in carbon metabolism and photosynthesis. However, the final induction of defense proteins required concurrent challenge, triggering priming of pathogen-targeted proteins. Conversely, at the metabolomic level, Sys-treated plants showed an alternative behaviour following a general priming profile. Out of the primed metabolites, the flavonoids rutin and isorhamnetin and two alkaloids correlated with the proteins 4-

coumarate-CoA-ligase and chalcone-flavanone-isomerase triggered by Sys treatment. In addition, the proteomic and enzymatic analyses revealed that Sys conditioned the primary metabolism towards the production of available sugars that could be fuelling the priming of callose deposition in Sys-treated plants; furthermore, PR1 appeared as a key element in Sys-IR. Collectively, the direct induction of proteins and priming of specific secondary metabolites in Sys-treated plants indicated that posttranslational protein regulation is an additional component of priming against necrotrophic fungi.

[O120] BLACKLEG PREVENTION IN POTATO BY PATHOGEN AND BACTERIOPHAGE IDENTIFICATION. Binod Pageni, Michele Konschuh, Jonathan Neilson, Melanie Kalischuk, and Lawrence Kawchuk. Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 – 1 Avenue South, Lethbridge, AB, Canada, T1J 4B1; Department of Biological Sciences, 4401 University Drive, University of Lethbridge, Lethbridge, AB, Canada, T1K 3M4; and Department of Plant Agriculture, 601 Gordon Street, University of Guelph, Guelph, ON, Canada, N1G 1Y2
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Pectobacterium and Dickeya species are Gram-negative pectolytic pathogens that may cause blackleg and soft rot in potato. Blackleg is a seed-borne disease distributed largely by movement of certified potato seed within and between potato growing areas. Analysis of diseased potato samples from western Canada between 2021 and 2024 by multi-locus sequence typing (MLST) revealed an increase in the Pectobacterium species diversity and confirmed the absence of the relatively aggressive Dickeya species. Previous studies reported that blackleg and soft rot in Canada were caused mostly by Pectobacterium atrosepticum and Pectobacterium carotovorum. Recovery of additional Pectobacterium species, including Pectobacterium polaris, Pectobacterium parmentieri, and most recently Pectobacterium brasiliense, was observed in the present study. Pectobacterium brasiliense is considered one of the most pathogenic species among the Pectobacteriaceae and has a broad host range among horticultural crops. An expanding industry increases disease pressure by seed movement between regions and environmental conditions associated with climate change, appear to be contributing to blackleg incidence, diversity, and impact. Although low temperatures and high moisture levels at sprouting usually increase the incidence of blackleg, the occurrence of highly pathogenic Pectobacterium species results in blackleg even under relatively dry warm conditions. Identifying closely related blackleg pathogens through the development of in-field isothermal diagnostics provides easy and rapid confirmation of bacterial species associated with disease. Isolation and genomic sequencing of blackleg pathogen endemic lytic bacteriophage from field samples, identified members of the Podoviridae, Myoviridae, and Siphoviridae. Most phage show a high specificity, only infecting one pathogen from specific farms or regions, but broad host range phage were occasionally isolated. Identification of specific sequences such as clustered regularly interspaced short palindromic repeats (CRISPR) Cas 4 RecB-like nuclease in some phage suggests an ability to defeat the pathogen's defensive capabilities. Laboratory and field trials confirmed that the phage reduced disease incidence and severity and increased yields by 100%, providing an environmentally friendly biocontrol treatment to enhance potato production for an expanding market.

***[O121] SOIL MICROBIOME AND SOIL PROPERTIES ASSOCIATED WITH THE RISK OF CAVITY SPOT ON CARROTS IN HIGH ORGANIC MATTER SOILS.** Umbrin Ilyas[1], Lindsey J. du Toit[2], M. Kalischuk[1], and Mary Ruth McDonald[1]. [1]Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada, N1G 2W1; and [2]Department of Plant Pathology, Washington State University, Mount Vernon, WA, USA, 98273
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Cavity spot is an economically important disease of carrot that is caused by several soilborne species of *Pythium* and *Globisporangium*. The disease appears as superficial dark lesions on carrot roots impacting quality. Currently, disease management is limited to pre-seeding fungicide application, and avoidance of fields with a history of cavity spot. Diagnostic tools are unavailable to identify fields with high-risk for cavity spot. It is hypothesized that the soil microbiome and soil properties, in addition to soilborne inoculum, influence disease development. Bulk muck soil (organic matter 40–80%) was collected from six fields in 2021, twelve fields in 2022, and twelve fields in 2023 in the Holland Marsh, Ontario. These samples were collected soon after seeding for microbiome and soil nutrient analysis. The fields were grouped as low or high-risk based on cavity spot severity assessed in previous years by the local integrated pest

management program. Non-metric multi-dimensional Scaling and PERMANOVA of metagenomic data from 2021-22 showed distinct microbial communities in low vs. high-risk soils. The relative abundance of the following taxa was significantly greater in low-risk soils compared to high-risk soils in both years; fungi in Aspergillaceae, Helotiales, Hypocreales, and Mortierellaceae; bacteria in Burkholderiales, Chitinophagaceae, and Rhizobiales; and the oomycetes *Albugo*, *Saprolegnia*, and *Phytopythium.* The abundance of *Globisporangium* was greater in high-risk soils. Analysis of metagenomic data from samples collected in 2023 is in progress. Soil nutrient analysis for 2021–23 soils showed low-risk soils had significantly less organic matter (~59%) and higher pH (~7) and calcium content (~83%) compared to high-risk soils (70% organic matter, pH ~6, and 70% calcium content). Envfit analysis showed that the composition of microbial communities in both low and high-risk soils was influenced by soil properties, with bacterial communities having the greatest influence. This information will help to identify fields with greater risk of cavity spot, enabling growers to avoid high risk fields.

[O122] PERFORMANCE OF SWEET POTATO UNDER HIGH-TUNNEL PRODUCTION SYSTEM IN SASKATCHEWAN. Jazeem Wahab[1], Reynald Lemke[1], Raju Soolanayakanahally[1], Champa Wijekoon[2], Edmund Mupondwa[1], Erl Svendsen[1], Dale Tomasiewicz[1], and Evan Derdall[1]. [1]Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK, S7N 0X2; and [2]Canadian Centre for Agri-Food Research in Health and Medicine, 351 Tache Ave, Winnipeg, MB, R2H 2A6
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Sweet potato (*Ipomea batatas* L) is the sixth most important food crop in the world, after rice, wheat, potato, maize, and cassava. Sweet potato is predominantly grown in African and Asian countries, and it is becoming increasingly popular in the Western World including Canada. Sweet potato production is increasing steadily in Canada. For example in 2022, Canada grew approximately 1200 ha of sweet potato, produced 17,000 tonnes valued at $ 15 million. This is a corresponding increase of 57%, 31%, and 24% respectively from 2018. Sweet potato is a warm season crop and requires minimal inputs (water, fertilizer etc.) Presently, the Canadian sweet potato production is centered in Ontario and Quebec. The present project explores the feasibility of producing sweet potatoes on the prairies taking advantage of climate change induced relatively warmer temperatures and longer growing seasons. Results of a 2023 study conducted under high-tunnel production system (i.e. simulated climate change environment) at the Canada-Saskatchewan Irrigation Diversification Centre, Outlook, SK, is presented in this paper. Treatments included three sweet potato cultivars (Radiance, L105, and Orleans), two planting methods (Bare-ground and Black plastic soil mulch), and two irrigation regimes (Partial -and Full-irrigation, using drip system). The crop was planted on June 6, 2023 and harvested on September 11, 2023: i.e. (121 DAP). The harvested roots were graded based on root diameter: 'Petite' (35-60 mm), 'USA No. 1 (45-90 mm) and 'Jumbo' (>90 mm). On average, the crop yielded 23 t/ha Petite roots, 37 t/ha USA No.1 roots, and 7 t/ha Jumbo roots. All three cultivars produced similar Petite and Jumbo yields. However, L105 produced the highest USA No.1 yield (43 t/ha), Radiance the second highest yield (37 t/ha) and Orleans the lowest yield (31 t/ha). Soil plastic mulch produced 31% higher Petite yield, 18% higher USA No.1 yield, and three-fold Jumbo yield relative to bare-soil planting. Both Full and Partial irrigation produced similar yields. Root yield and grade size distribution in response to cultivar, irrigation and planting methods will be discussed.

[O123] CULTURAL PRACTICES INFLUENCE WEED COMMUNITY AND SEEDBANK DYNAMICS IN THE LIVING LABS ATLANTIC. McKenzie-Gopsill A[1], Nyiraneza J[1], and Fillmore S[2]. [1]Agriculture and Agri-Food Canada Charlottetown Research and Development Centre; and [2]Agriculture and Agri-Food Canada Kentville Research and Development Centre
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Stagnant yields and declining soil health are common characteristics of high-intensity, low-residue cropping systems, such as potato, particularly in northeastern North America. Incorporating cultural practices including cover cropping and manure application is a way to combat declines in agroecosystem health and potato productivity. However, manure application and the use of cover crops may exacerbate weed issues through seedbank additions. As part of the Living Labs Atlantic this study investigated how the cultural practices of cover cropping and manure application and their associated management activities can alter weed community dynamics and weed seedbank composition. In year one manure plots

had greater weed seedbank density and species richness; however, this did not result in greater in-season weed biomass. Manure application resulted in a gradual decline in weed seedbank density over time regardless of cover crop treatment. Further, manure application increased the in-season competitive ability of cover crops, resulting in greater weed suppression per unit of cover crop biomass. In contrast, in the absence of manure, weed seedbank density remained largely unchanged through time regardless of cover crop treatment. We found that management practices associated with annual and perennial cover crops had distinct ecological filtering effects throughout the rotation on the weed community and prevented the dominance of any particular species. Together, our results demonstrate that combining the cultural practices of annual or perennial cover cropping and manure application contributes to weed suppression and should be considered an important component of sustainable potato production.

[O124] GLOBAL REGULATION OF PLANT PATHOGENICITY IN THE COMMON SCAB PATHOGEN *STREPTOMYCES SCABIEI*. Wanyue Li, Aaron Rees, and Dawn R. D. Bignell. Department of Biology, Memorial University of Newfoundland, 45 Arctic Avenue, St. John's, NL, Canada, A1C 5S7
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Common scab (CS) is a plant disease caused by soilborne bacteria belonging to the genus *Streptomyces.* The disease affects the quality and market value of root and tuber crops such as potato, beet, carrot and radish. At least a dozen or so *Streptomyces* species are responsible for CS worldwide, of which *Streptomyces scabiei* is the best characterized. This organism produces several phytotoxic specialized metabolites as well as secreted proteins and phytohormones that are known or suspected to contribute to plant host colonization and disease development. While there has been much effort in understanding how these known or potential virulence factors contribute to CS disease, there is less known regarding the genetic factors that control the onset of pathogenicity in *S. scabiei*.

Most studies on virulence gene regulation in *S. scabiei* have focused on the thaxtomin A (ThxA) phytotoxin, which is a critical for the development of CS. ThxA biosynthesis is stimulated by plant-derived molecules such as cello-oligosaccharides and suberin and is controlled at the molecular level by the transcriptional activator TxtR and the cellulose utilization repressor CebR. In addition, several members of the *bld* (bald) gene family of global regulators, as well as a member of the leucine-responsive regulatory protein family, have been shown to modulate ThxA production and virulence in *S. scabiei*. Given that there are more than 800 predicted regulatory genes in the *S. scabiei* genome, it is likely there are additional regulators that control the production of ThxA and other virulence factors in *S. scabiei.*

This study focuses on *afsR,* which is highly conserved in *Streptomyces* species and is a known global regulator of specialized metabolite production in non-pathogenic species. Given that deletion of *afsR* in the acid scab pathogen *Streptomyces acidiscabies* resulted in reduced ThxA production, we predict that ThxA production in *S. scabiei* is also under control of *afsR*, and that *afsR* may additionally be required for production of other virulence factors in this organism. To address this, *S. scabiei* strains that overexpress or carry a deletion of the *afsR* gene were constructed, and the strains were assessed for the production of ThxA and other phytotoxic specialized metabolites. In addition, plant bioassays were conducted to investigate the impact of *afsR* gene deletion and overexpression on the virulence phenotype of *S. scabiei.* Overall, this work advances our understanding of the genetic factors that control virulence factor production and CS disease development by *S. scabiei.*

[O125] DROUGHT-RESILIENT DIPLOID POTATOES FOR SHORT AND LONG GROWING SEASON AGROCLIMATES AS DEPICTED THROUGH GENOME-WIDE ASSOCIATION STUDIES. Bourlaye Fofana[1], David Main[1], Moshin Zaidi[1], and Benoit Bizimungu[2]. [1]Charlottetown Research and Development Centre, Agriculture and Agri-Food Canada, 440 University Avenue, Charlottetown, Prince Edward Island, C1A 4N6, Canada; and [2]Fredericton Research and Development Centre, Agriculture and Agri-Food Canada, 95 Innovation Road, PO Box 20280, Fredericton, NB E3B 4Z7
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In the context of climate change, crops production has become a challenge in most agrosystems due to drought. Using a panel of 384 diploid potato clones, we recently conducted a genome-wide association study on maturity and drought tolerance traits. A wide phenotypic diversity was observed in the collection, and drought-tolerant potato clones that are early or late maturing were detected. Using genotype-to-

phenotype genome-wide association studies, the genetic architecture for each trait was uncovered, and the associated genes and single nucleotide polymorphic (SNP) markers identified. The reported data suggest that the identified potato clones can be used as climate adaptation solutions for short and long growing season agrosystems and the SNP markers used for breeding maturity and drought tolerance traits in potatoes.

[O126] GENOMIC DISSECTION OF ISLAND SYNGAMEONS: ARBORESCENT ASTERACEAE FROM ST HELENA (SOUTH ATLANTIC OCEAN). Quentin Cronk[1], Andreas Kolter[2], and Mikko Paajanen[1]. [1]Department of Botany and Beaty Biodiversity Museum, University of British Columbia, Vancouver, BC, Canada V6T 1Z4; and [2]Centre for Biodiversity Genomics, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1
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The genera *Commidendrum* (4 spp.) and *Melanodendron* (1 sp.) from St Helena (South Atlantic Ocean) form a single clade whose ancestor reached the island in the early Pliocene. All species have highly divergent morphologies linked to ecology. *Commidendrum* and *Melanodendron* are known to form an intergeneric hybrid and *Commidendrum* is known to form interspecific hybrids. Plant genomics can untangle complex histories of hybridization on islands. Genomic evidence is presented that hybridization has occurred in the *Commidendrum*/*Melanodendron* clade due to recent conservation efforts due to planting species in proximity. Furthermore, there is genomic evidence that hybridization events may be ancient, with the species forming a syngameon, so raising the genetic effective population sizes (Ne) of species. A syngameon is here defined as: “a group of otherwise distinct species interconnected by limited gene exchange, i.e. the most inclusive interbreeding evolutionary unit” (Suarez-Gonzalez et al., "Adaptive introgression: a plant perspective" Biology Letters 2017). Such hybridization events are postulated to be a continual source of background ‘evolutionary rescue’ of species from any small population size impacts over geological time, a phenomenon of particular importance and impact on islands. Genomic studies are an essential tool for the study of plant evolution on islands, and for endemic plant conservation.

[O127] NUTRIENT LIMITATION IN SUBARCTIC TERRESTRIAL PLANT COMMUNITIES. John Markham and Emily Klapprat. Department of Biological Sciences, University of Manitoba, Winnipeg, MB, Canada, R3T 2N2
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Nutrient limitation is increasingly being recognized as a determinant of community structure of terrestrial communities in the subarctic. We use fox dens as natural experiments to look at the effect of nutrient enrichment on plant communities at the subarctic treeline. Our work shows that many tundra plants show an increase in nutrient content and specific leaf area on fox dens, but there is also a shift in plant composition, with dens having species that are less reliant on mycorrhizae that can access organic nitrogen in the soil. We also show that trees at the northern treeline have very poor seed production and viability, both increasing in trees growing fox dens. This suggests that nutrient-enriched sites could be hot spots of tree reproduction, treeline expansion and squirrel feeding. While increased soil nutrient availability can drive changes in plant traits and composition, soil properties are partially driven by plant properties and species composition. We test this by comparing the fertility of soil under *Empetrum nigrum*, *Salix planifolia* and *Vaccinium uliginosum* growing in undisturbed woodland and an area that experienced a severe fire 28 years ago and where vegetation had developed into monospecific patches. As expected, soil from *Salix* patches was more fertile, with test plants (*Elymus molis*) having twice the growth rate in this soil type. Soil from *Salix* patches also had twice the concentration of inorganic N and in the burn site, a higher pH, but there was no difference in the depth of the organic layer, rate of soil respiration, or the soil water holding capacity. These results suggest that in the subarctic climate plant species can have an effect on soil fertility.

[O128] TESTING ECOWOOL PELLET APPLICATION AS AN ENVIRONMENTALLY FRIENDLY AMENDMENT IN GREENHOUSES. Liette Vasseur[1], Avalon Halgreen[2], Natasha Hearn[1], Reem Mahamoud[2], and Vaughn Mangal[2]. [1]Department of Biological Sciences and [2]Department of Chemistry, Brock University,1812 Sir Isaac Brock Way, St Catharines, On L2S 3A1
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Because of growing concerns about environmental degradation and health risks caused by chemical contamination in soil and crops, farmers are interested in finding strategies to reduce the use of chemical fertilizers and pesticides while improving the overall ecosystem health. This is the same for greenhouse operators where there is a growing interest for new technologies and environmentally friendly amendments. With the need to find strategies to avoid the use of agrochemicals while improving the health of soils, testing of new products in controlled conditions is essential. Nurseries and greenhouses can grow crops in soil, especially if they sell liv plants to the public. In this study, we tested the use of Ecowool product (wool pellet) as a soil amendment with five different crops (marigold, green pepper, yellow bean, spinach, and basil) to determine its capacity to improve soil health and fertility and therefore crop performance. The experiment was carried out in the Brock's greenhouse in two experimental runs where plants were exposed to 1) 5%, 2) 10% and 3) 20% Ecowool, 4) synthetic commercial fertilizer, and 5) water only (control). Each experimental run had four replicates for each species and treatment and the experiments last 55 days (one plant per pot). At the end of the experiment, fresh and dry shoot, and root weights were recorded and soil and leachate water from the pots chemical contents were analyzed. The results showed few significant differences among treatments for the five species biomass with a trend of heavier plants in the 5% Ecowool and the lowest weight being in the 20% Ecowool. Chemical analyses showed an increase in nitrogen, potassium, and organic carbon to soils with increase concentrations of Ecowool but levels of salts at 20 % (wt/wt) Ecowool applications were toxic. Zinc levels in soil were also higher than in control with water. Concentrations of nitrogen, potassium, zinc and cupper in marigold's shoot increased with the application of Ecowool compared to the fertilizer and water treatments. This was not the case for the four other species. The study suggests that Ecowool at low concentrations may be an effective alternative as an amendment to crops but, applications should be limited to avoid increasing salts and some heavy metals in soil and plants over time.

[O129a] DESIGNING AND IMPLEMENTING A USER-FRIENDLY PLANT COMMUNITY SURVEY PROTOCOL TO HELP CONSERVATION ORGANIZATIONS SELECT REINTRODUCTION SITES FOR AN ENDANGERED PRAIRIE BUTTERFLY IN MANITOBA. Katherine Dearborn[1] and Richard Westwood[1,2]. [1]Department of Environmental Studies and Sciences, University of Winnipeg, 515 Portage Ave., Winnipeg, MB, R3B 2E9; AND [2]Department of Biology, University of Winnipeg, 515 Portage Ave., Winnipeg, MB, R3B 2E9
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Over 99% of the original extent of tall-grass prairie habitat in Manitoba has been eliminated by agricultural development. As a result, approximately one third of all endangered species in Canada are prairie species. One such species is the Poweshiek skipperling butterfly. Poweshiek populations in Canada have been in decline for several decades, and are currently confined to a handful of isolated patches of tall-grass prairie habitat that are owned and managed by various Manitoba-based conservation organizations. To prevent extirpation, these organizations have been harvesting eggs from female skipperlings in the summer, raising the caterpillars at the Assiniboine Park Zoo over the winter to reduce overwinter mortality, and then returning mature pupae to the same sites they collected eggs from in the spring. Their efforts seem to have increased local abundances of Poweshiek skipperling over the past few years, but given the high degree of isolation among remaining populations, the species is unlikely to recover on its own without simultaneous reintroductions into formerly-occupied habitat.

Selecting reintroduction sites and ensuring they contain enough suitable habitat to support a reintroduced population can be very challenging. Plant community composition is often an important indicator of habitat suitability, particularly for Lepidopterans (butterflies and moths). However, plant species identification can be a barrier for conservation practitioners tasked with planning reintroductions. We aimed to design a field-based vegetation survey protocol that would provide the necessary data to inform the selection of reintroduction sites for Poweshiek skipperling, while remaining broadly accessible to staff with minimal training in botany. We used our protocol to collect plant community data from numerous conservation-

owned candidate sites in 2021 and 2022, and then incorporated our data into a spreadsheet-based decision tool we built to rank sites for Poweshiek skipperling reintroductions. Our efforts culminated in the selection of an initial release site in the spring of 2023. We are hopeful our methods will be useful to other conservation practitioners faced with similar decisions in the future.

***[O129b] CHARACTERIZING DEFENSE MECHANISMS IN *ARABIDOPSIS THALIANA* AGAINST *TETRANYCHUS URTICAE* HERBIVORY.** Jorden Maglov[1], Julia Pastor-Fernandez[1], Michele Antonacci[1], Alexander Harrison[1], Emilie Widemann[1], Vladimir Zhurov[1], and Vojislava Grbic[1]. [1]Department of Biology, Western University, London, Ontario, Canada
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Tetranychus urticae (two-spotted spider mite) is an extreme generalist herbivore with the ability to feed on over 1100 plant species, including 150 of agricultural importance. The two-spotted spider mite's polyphagous nature is driven by rapid adaptation to plant defenses. However, the specific plant defense compounds mites must overcome to achieve a host-adapted state are largely unknown. *Arabidopsis thaliana* is a challenging and non-preferred host for *T. urticae,* making it an excellent model to study mite-host adaptation. It has previously been shown that a class of tryptophan-derived compounds specific to the Brassicaceae family, indole glucosinolates, contribute partially to the *A. thaliana* defense response. The remaining phytochemicals that protect the plant against mite herbivory are unknown. We used combined metabolomic and transcriptomic approaches to identify classes of plant compounds that are induced upon mite feeding. HPLC-MS and RNA-seq revealed that both phenylpropanoids and flavonoids increase in abundance *in planta* upon mite feeding. Next, we measured mite fecundity on mutant *A. thaliana* plants defective in overall phenylpropanoid and flavonoid biosynthesis to assess mite performance. We found that mite fecundity significantly increases on phenylpropanoid and flavonoid mutants relative to wild-type plants, suggesting that compounds within these pathways are toxic to spider mites. We next fed mites with these plant compounds and screened for resulting mite mortality levels to confirm the toxicity of these compounds *in vivo.* This study identified phenylpropanoids and flavonoids as novel defense compounds protecting *A. thaliana* against spider mite herbivory. Because many phenylpropanoids and flavonoids are ubiquitous among plants, this study may shed light on mite adaptation mechanisms to not only *A. thaliana*, but economically important plants as well. Additionally, these findings may enable the development of novel pest control strategies through the identification of toxic phytochemicals.

[O129c] BRAWLING WEEDS AND THE FIGHT FOR CROP SURVIVAL. Clarence Swanton, Sasan Amirsadeghi, Nicole Berardi, William Kramer, and Andrew McKenzie-Gopsill. University of Guelph
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Direct competition for light, water, and nutrient resources is traditionally considered the driving variable of plant competition. Recent research, however, has suggested that resource competition is not the primary mechanism by which weeds induce crop yield loss. Crop-weed competition begins with plant communication, the ability of the crop seedling to detect the presence of neighboring weed seedlings. Once the crop seedling interprets this incoming communication, significant molecular and physiological changes occur. Such changes include a rapid increase in cellular singlet oxygen, a decline in photosynthesis, a loss in the crop plants' ability to defend against insect and disease damage, and a loss in the crop seedlings' ability to assimilate nitrogen. These four novel competition mechanisms alter the growth trajectory of the crop seedling contributing to a rapid decline in crop yield potential.

[O130] DECIPHERING THE ROLE OF ER-LOCALIZED HSP90 FAMILY HEAT SHOCK PROTEIN IN PLANT DEVELOPMENT AND STRESS RESPONSES. Rongmin Zhao, Jenan Noureddine, and Morvenley Mamenta**.** Department of Biological Sciences, University of Toronto Scarborough, and Department of Cell & Systems Biology, University of Toronto, Toronto, Canada
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Endoplasmic reticulum (ER) is the organelle for lipids biosynthesis and the entry point of numerous proteins that are sorted through the cellular secretory pathway, therefore playing an important role in many cellular processes. Proteins that get into the ER membrane or lumen must be properly folded and a cohort of highly conserved molecular chaperones reside in ER to aid in the folding and subsequent

secretion process. Different from the other classes of molecular chaperones within ER, the HSP90 family heat short proteins are present, but only in higher multicellular organisms suggesting a critical role of ER-localized HSP90 family protein in cell differentiation and cell-to-cell communications. In our lab, we are interested in the structure and function of the specific ER-localized HSP90.7 from *Arabidopsis thaliana*. We identified that the protein contains unique structural elements that regulate the protein's chaperone activity and play critical roles in ER-specific stress resistance. We also aimed to understand whether the plant ER-localized HSP90.7 has a different mechanism of action from its animal orthologs. Additionally, we screened and identified an HSP90.7 knockout mutant line that showed a seedling lethality phenotype together with defective trichomes development, improper chloroplast functionality, and impaired apical meristem maintenance and differentiation. Comparative transcriptome and proteome analyses revealed roles of the protein in a multitude of cellular processes. Particularly, we measured a much-reduced auxin content in both root and shoot tissues and then investigated how the cellular auxin biosynthesis and transport systems are impacted when the HSP90.7 protein is missing. This study therefore not only fulfilled a gap in understanding the essential role of HSP90 paralogs in eukaryotes, but also provided a mechanistic insight on the ER localized chaperone in regulating plant growth and development via modulating cellular auxin homeostasis.

[O131] ARABIDOPSIS ICK/KRP CYCLIN-DEPENDENT KINASE INHIBITORS ARE INTRINSICALLY DISORDERED PROTEINS AND REGULATED BY BOTH UBIQUITIN-DEPENDENT AND UBIQUITIN-INDEPENDENT MECHANISMS. Shengjian Ye[1,2], Sheng Wang[1], Ron Chan[1], Ling Cao[1], and Hong Wang[1]. [1]Dept. of Biochemistry, Microbiology & Immunology, University of Saskatchewan, Saskatoon SK, S7N 5E5, Canada; and [2]Present address: Aquatic and Crop Resource Development, National Research Council of Canada, Saskatoon, SK, S7N 0W9, Canada
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Plants have a family of cyclin-dependent kinase (CDK) inhibitors called ICKs (interactors/inhibitors of CDK) (or KRPs, Kip-related proteins). ICK proteins have important functions in cell proliferation, endoreduplication, plant growth and reproductive development. Since the functions of ICKs depend on the protein levels, it is crucial to understand how ICK protein levels are regulated. It has been shown previously that the ubiquitin (Ub) proteasome system (UPS) has a major role in the degradation of ICKs. However, little is known regarding the specific signal sequences that confer instability to ICKs. Using various computational tools including AlphaFold2, we have shown that ICK proteins are mostly disordered and unstructured except for the conserved C-terminal region. Experimentally, we observed consistently that all ICK proteins ran slower than their expected molecular sizes in gel electrophoresis, which is a feature observed on intrinsically disordered proteins (IDPs). These results suggest that ICKs are IDPs. To identify sequence signals responsible for ICK instability and degradation, we fused various Arabidopsis ICK sequences to the green fluorescent protein (GFP), and determined their effects on the fusion proteins in plants, yeast and *E. coli*. The N-terminal regions of ICKs drastically reduced GFP fusion protein levels in Arabidopsis plants. A number of short sequences of 10 – 20 residues were found to decrease GFP fusion protein levels, when fused at the N-terminus or C-terminus. Three of the four short sequences from ICK3 showed a similar function in yeast. Intriguingly, three short sequences from ICK1 and ICK3 caused the degradation of the fusion proteins in *E. coli*. We thus have identified a number of short protein-destabilizing sequences. In addition to the established Ub-dependent protein degradation, the finding that some of the short sequences still show the protein-destabilizing property in *E. coli* suggests that they function through a Ub-independent mechanism since *E. coli* does not have the major components of the eukaryotic UPS system. The present results provide new insight regarding how ICKs are regulated. Importantly, since an estimated 25-30% of the eukaryotic proteomes contain long intrinsically disordered regions, the present results may provide useful leads for studying many other unstable proteins containing intrinsically disordered regions.

***[O132] EXPLORING SPECIFICITY OF PLANT RLCK-VII SIGNALLING.** Eleanor Khochaba[1] and Thomas A. DeFalco[1]. [1]Department of Biology, Western University, 1151 Richmond St, London, ON, Canada N6A3K7
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Receptor kinases (RKs) are receptors at the cell membrane that perceive exogenous or endogenous ligands to initiate essential signalling cascades vital for various aspects of plant growth, development, and immunity. Though many RKs have been identified, the molecular mechanisms downstream of receptor activation are not fully understood. Receptor-like cytoplasmic kinases (RLCKs) are key components of downstream RK signalling. RLCKs associate with receptor complexes to execute downstream signal transduction via substrate phosphorylation. Despite apparently similar mechanisms of activation and substrate interaction, individual RLCKs can exhibit distinct functionalities and involvement in specific RK pathways, sometimes even exerting opposing effects. For instance, within the RLCK-VII family of kinases, both BIK1 and PBL13 interact with RBOHD, an NADPH oxidase, to regulate immune responses; however, their phosphorylation either promotes or inhibits RBOHD function, respectively. Other RLCK-VIIs, such as PBL34 and PBL15, have also been found to function in RK pathways regulating specific aspects of development. Our research focuses on understanding the specificity within RLCK-mediated signalling, using both genetic and biochemical approaches. By generating chimeric RLCK constructs, wherein the N-terminus, kinase domain, and C-terminus are interchanged, we aim to decipher the roles of individual protein domains in dictating RLCK signalling specificity. The results of this project will contribute to our understanding of the signalling mechanisms governing diverse aspects of plant biology, as well as how kinases target their protein substrates.

***[O133a] DOWNSTREAM SIGNALING RESULTING FROM DAMAGED RIBOSOMAL RNA BY POKEWEED ANTIVIRAL PROTEIN (PAP).** Tanya Prashar[1] and Katalin A. Hudak[1]. [1]Department of Biology, York University, 4700 Keele St, Toronto, ON, Canada, M3J 1P3
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In addition to their role in translation, ribosomes serve as a central hub for detecting mRNA damage, which could cause ribosome stalling, collisions, or slowed translation elongation. Ribosome surveillance pathways, such as the integrated stress response (ISR) leading to GCN2-dependent eIF2α phosphorylation, or ribosome quality control (RQC) causing E3 ubiquitin ligase Hel2-dependent ubiquitination of 40S ribosomal subunit, are triggered depending on the extent and nature of mRNA damage. However, the mechanisms of sensing and signaling ribosomal RNA (rRNA) damage are not fully understood. We investigated downstream signaling pathways triggered by depurinated 25S rRNA caused by pokeweed antiviral protein (PAP) expression in *Saccharomyces cerevisiae*. PAP is a ribosome-inactivating protein (RIP) found in *Phytolacca americana*, a native North American plant. PAP's antiviral activity arises from its inhibition of protein translation resulting from the removal of an adenine residue from the sarcin-ricin loop (SRL) in 25S rRNA. Depurinated rRNA prevents the binding of elongation factors, thus limiting both viral and cellular protein production. In this study, our findings demonstrate that the expression of PAP in yeast leads to depurination of 25S rRNA causing inhibited cell growth and reduced viability. Additionally, our results reveal a low-level increase in GCN2-dependent GCN4 translation levels indicating minimal ISR activation upon PAP expression. Furthermore, we examined whether PAP expression activates RQC and observed a Hel2-dependent increase in ubiquitination levels, suggesting potential ubiquitination of 60S or 40S ribosomal subunits. These findings offer initial evidence supporting the idea that ribosomes with depurinated rRNA might be subject to proteasomal degradation. Our future work involves studying whether depurinated ribosomes are engaged in active translation and quantifying their elongation rate, which may indicate when cells detect damage to rRNA. The sarcin-ricin loop is a critical component of the ribosomal GTPase center required for translation elongation, and our research will link effects of its depurination to activation of stress response pathways to understand how cells detect and manage damage to rRNA.

[O133b] *ASCOPHYLLUM NODOSUM*-DERIVED FUCOIDAN INDUCES FLOWERING BY REGULATING THE *MIR156*-MEDIATED AGE PATHWAY IN ARABIDOPSIS. Ramin Bahmani[1], Pramod Rathor[1], and Balakrishnan Prithiviraj[1]. [1]Marine Bio-Products Research Laboratory, Department of Plant, Food and Environmental Sciences, Faculty of Agriculture, Dalhousie University, Nova Scotia, B2N5E3, Canada
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Flowering, the change from vegetative development to the reproductive phase, represents a crucial and intricate stage in the life cycle of plants, which is tightly controlled by both internal and external influences. In this study, we investigated the effect of *Ascophyllum nodosum* extract (ANE) on the flowering time of Arabidopsis. We found that a 0.1% concentration of ANE induced flowering in Arabidopsis, accompanied by the upregulation of key flowering time genes: *FT* (*FLOWERING LOCUS T*), *SOC1* (*SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1*), and *LFY* (*LEAFY*). Further investigation showed that ANE specifically promotes flowering through the *MIR156*-mediated age pathway. ANE treatment resulted in the repression of negative regulator genes, *MIR156*, while simultaneously enhancing the expression of positive regulator genes, including *SPL*s and *MIR172*. This, in turn, led to the downregulation of AP2-like genes, which are known floral repressors. It is worth noting that ANE did not alleviate the late flowering phenotype of *MIR156*-overexpressing plants and *spl* mutants. Furthermore, ANE-derived fucoidan mimics the function of sugars in regulating *MIR156*, closely mirroring the effects induced by ANE treatments. It suppresses the transcript levels of *MIR156* and AP2-like genes while inducing those of *SPL*s and *MIR172*, thereby reinforcing the involvement of fucoidan in the control of flowering by ANE. In summary, our results demonstrate that ANE induces flowering by modulating the *MIR156-SPL* module within the age pathway, and this effect is mediated by fucoidan.

***[O134] THE IDENTIFICATION AND FUNCTIONAL ASSESSMENT OF *PLASMODIOPHORA BRASSICAE* EFFECTORS.** Emilee Storfie[1], Leonardo Galindo-González[2], Sheau-Fang. Hwang[1], and Stephen Strelkov. [1]Department of Agricultural, Food and Nutritional Science, University of Alberta, 116 St & 85 Ave, Edmonton, AB T6G 2R3, Canada; and [2]Canadian Food Inspection Agency, 1400 Merivale Rd, Ottawa, ON K1A 0Y9, Canada
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Plasmodiophora brassicae is an obligate biotrophic pathogen that causes clubroot disease on canola (*Brassica napus*). To facilitate infection, the pathogen secretes effectors to manipulate the defence response and other important biological pathways of the host. This study seeks to identify and characterize selected effectors secreted by *P. brassicae* pathotype 3A to facilitate its infection of *B. napus*. RNA sequencing was conducted at 7-, 14-, and 21-days post-inoculation of resistant and susceptible rutabaga (*B. napus* ssp. *rapifera*) cultivars. Predicted effectors with non-redundant transcripts and low covariance were identified and analyzed across time points and cultivars. Gene expression validation was performed using NanoString technology. Two highly expressed putative effectors, SPR01261.1 and SPQ99289.1, were selected for further investigation. The functionality of each effector's signal peptide, which enables their secretion, was confirmed using a yeast signal sequence trap assay. Each effector localized to the nucleus and cytoplasm *in planta* when monitored via fluorescent protein tagging in *Nicotiana benthamiana*. As the pathogen cannot be cultured *in vitro*, functional studies of *P. brassicae* effectors are often labour-intensive and time-consuming. Additionally, many *in silico* tools provide limited information. Bacterial and yeast heterologous protein expression systems were evaluated and compared to determine their suitability for *P. brassicae* protein isolation. For the bacterial systems, the open reading frames of SPR01261.1 and SPQ99289.1 were cloned separately into pDEST17 (T7 promoter and N-terminal 6xhistidine tag), pDEST15 (T7 promoter and N-terminal glutathione S-transferase tag), and pMAL-c6T (tac promoter and N-terminal 6xhistidine tagged *malE* gene) vectors. These constructs were then transformed into different expression strains of *Escherichia coli* and *Vibrio natriegens*. For the yeast system, each open reading frame was cloned separately into pPICZα (AOX1 promoter, α-factor SP, and C-terminal 6xhistidine tag) and pPICZ (AOX1 promoter and C-terminal 6xhistidine tag) vectors and then transformed into *Pichia pastoris*. After inducing protein expression, the expression level and solubility of each protein were confirmed by Western blotting. Once expressed and purified, the functions of SPR01261.1 and SPQ99289.1, predicted to encode a serine carboxypeptidase and an unknown protein with a kinase domain, respectively, were evaluated using enzyme assays.

Identifying and characterizing effectors secreted by *P. brassicae* will enhance our understanding of its infection mechanisms to help guide future management practices.

***[O135] GENOMIC ANALYSIS OF THE *PUCCINIA STRIIFORMIS* F.SP *TRITICI* POPULATIONS CAUSING STRIPE RUST IN CANADA.** Bohan Wei[1,2], Ryan Gourlie[1], Rodrigo Ortega Polo[1], Nathaniel Zhin-Loong Lim[1], Rhodesia Celoy[1], Stephen Strelkov[2], and Reem Aboukhaddour[1]. [1]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1 Ave S, Lethbridge, AB, Canada, T1J 4B1; and [2]Department of Agriculture, Food and Nutritional Science, University of Alberta, 116 St & 85 Ave, Edmonton, AB, Canada T6G 2R3
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Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici* (*Pst*), significantly impacts global wheat production. Other forms of this pathogen can infect barley and other grasses, contributing to the complexity of stripe rust management. Despite its global importance, the genomic evolution of *Pst* in Canada remains underexplored. This study aims to fill this gap by analyzing temporal genomic changes in *Pst* populations from Canada, focusing on their evolution and adaptation mechanisms. We conducted whole-genome Illumina short-read sequencing (NovaSeq, Génome Québec) and de novo assembly (MaSuRCA) of 27 *P. striiformis* isolates collected between 1984 and 2023 from wheat, barley, and foxtail barley across Alberta, Quebec, and PEI. Assemblies were annotated with the FunGAP or Funnanotate pipelines utilizing RNA reads from *Pst* CYR34 urediniospores. Four previously published isolates from the UK and USA were also included in downstream analysis. To explore genetic diversity and relatedness reads we conducted variant calling. Reads were quality-checked with FASTQC, and SAMtools was used to sort and align reads to the reference genome PST-130. Variant calling was performed with HaplotypeCaller and GenotypeGVCF from Genome Analysis Toolkit. SNPs were filtered for quality and depth, converted to phylip format, and a maximum-likelihood tree was generated using RAxML and visualized with IToL. The phylogenetic tree revealed four major branches encompassing all isolates, with Canadian isolates distinct from those in the UK and USA. Significant genomic differences were observed between pre-2000 and post-2010 collections, and between samples from 2022-2023. Our next steps involve using Pangloss to create a pangenome and analyze core and accessory genes between pre-2000 and post-2010 groups to uncover evolutionary patterns and adaptation mechanisms in the Canadian *Pst* population. Preliminary results will be presented. We will also investigate genes related to host specificity, focusing on wheat, barley, and foxtail barley. Tracing gene changes from 1984 to 2023 will enhance our understanding of core gene involvement in stripe rust virulence in Canada, providing insights into future disease management strategies. Our data reveals new insights into the evolution of diverse *Pst* phenotypes over different periods, highlighting pathogen adaptation dynamics and informing predictive models for disease management.

***[O136] DEVELOPMENT OF A KASP ASSAY FOR DETECTION OF SUCCINATE DEHYDROGENASE MUTATIONS ASSOCIATED WITH SDHI RESISTANCE IN *STEMPHYLIUM VESICARIUM*.** Julia Scicluna[1], Emily McFaul[1], Afsaneh Sedaghatkish[1], Bruce D. Gossen[2], and Mary Ruth McDonald[1]. [1]Department of Plant Agriculture, University of Guelph, 50 Stone Rd E, Guelph, ON, Canada, N1G 2W1; and [2]Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK, Canada, S7N 0X2
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Stemphylium leaf blight (SLB) caused by *Stemphylium vesicarium* is the most common foliar disease of onion in Ontario. SLB management relies on repeated fungicide applications each year and most fungicides contain succinate dehydrogenase inhibitor (SDHI) active ingredients. Resistance to the SDHI active ingredients fluxapyroxad and penflufen has increased since 2012 in Ontario and SDHIs have poor efficacy in the field. Isolates of *S. vesicarium* from New York State classified as highly resistant to SDHI fungicides frequently had one of three mutations (G79R, H134R and C135R) in the gene encoding succinate dehydrogenase subunit C (*sdhC*). In the current study, a Kompetitive Allele Specific PCR (KASP) assay was designed to detect the single nucleotide polymorphisms (SNPs) of G79R, H134R and C135R in *sdhC*. The assay was tested on 70 *S. vesicarium* isolates collected in Ontario from 2012-2023 that were classified as either sensitive or resistant to fluxapyroxad and penflufen based on mycelial growth assays. The C135R and G79R mutations were identified in 4% and 11% of isolates resistant to

either active ingredient, while the H134R mutation was identified in 43% of isolates. The H134R mutation increased in frequency from 20% in 2021 to 55% in 2023, while the C135R mutation remained consistent overtime. The G79R mutation was only detected in isolates from 2023. The G79R, H134R and C135R mutations were not identified in the remaining resistant isolates (42%), which indicates that other mutations may be contributing to SDHI resistance. The H134R mutation appears to be responsible for most of the SDHI resistance in Ontario. This KASP assay can be used to evaluate *S. vesicarium* populations for *sdhC* mutations early in the growing season. This would allow growers to avoid some or all SDHI fungicides that would not be effective for management of SLB. The KASP assay is fast and labour efficient compared to many other approaches to determine fungicide resistance in plant pathogens.

***[O137] GENOME-WIDE ASSOCATION STUDY (GWAS) OF STEM RUST RESISTANCE IN WESTERN CANADIAN WINTER WHEAT.** Kaitlyn A. Pidherny[1], Jim G. Menzies[2], Colin W. Hiebert[1,2], Harwinder S. Sidhu[3], and Curt A. McCartney[1]. [1]Department of Plant Science, University of Manitoba, 222 Agriculture Building, Winnipeg, MB, Canada R3T 2N2; [2]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB, Canada, R6M 1Y5; [3]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1st Ave S., Lethbridge, AB, Canada, T1J 4B1
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Puccinia graminis f. sp*. tritici* (*Pgt*), a fungal pathogen, is the causative agent of stem rust on wheat (*Triticum aestivum*). *Pgt* is an economically important disease of wheat, having the potential to cause significant losses to wheat production in Canada. As a result, stem rust is a Priority 1 disease in the western Canadian variety registration system. Due to the development of resistant varieties and through the eradication of barberry, no stem rust epidemics have occurred in western Canada since the 1950s. The genetic basis for stem rust resistance in most Canadian wheat cultivars is not fully understood. The objective of this study is to identify resistance genes present in a winter wheat population, consisting of approximately 300 hard red winter wheats from western Canada, and 100 hard red winter wheats from other regions (United States, eastern Canada, and Europe). The population has been phenotyped for stem rust resistance in field trials and indoor seedling inoculations. The population has been genotyped with single nucleotide polymorphism (SNP) markers from the Wheat Barley 40K Infinium SNP array and the TraitGenetics wheat 25K Infinium SNP array, which span the wheat genome. Field stem rust nurseries were grown at two locations, Winnipeg and Carman, Manitoba in 2023. These trials were randomized as alpha lattice designs with two replicates per trial. Plots were single 1m long rows and were inoculated with a mixture of *Pgt* races. Nurseries were mist irrigated to promote disease development. Data were collected on plant height, stand, heading date, and stem rust field severity and infection response. Field trials will be repeated in 2024. Infection type data was recorded from indoor seedling inoculations with individual races. Statistical analyses will identify quantitative trait loci (QTL). Preliminary results from genome-wide association study (GWAS) analysis suggest there are QTL of interest for resistance to stem rust located on chromosomes 1B, 2A, 2B, 2D, 3D, and 7B.

***[O138] GENETIC ANALYSIS AND GENOMIC SELECTION MODELS FOR LEAF RUST RESISTANCE IN CANADA WESTERN RED WINTER WHEAT.** Anirup Sengupta[1], Brent D. McCallum[1,2], Colin W. Hiebert[1,2], Harwinder S. Sidhu[3], and Curt A. McCartney[1]. [1]Department of Plant Science, University of Manitoba, Room 222 Agriculture Building, 66 Dafoe Road, Winnipeg, MB, Canada, R3T 2N2; [2]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB, Canada, R6M 1Y5; and [3]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1st Avenue South, Lethbridge, AB, Canada, T1J 4B1
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Leaf rust, caused by the fungus *Puccinia triticina*, is a common disease of wheat that affects both yield and quality. It is considered a Priority 1 disease by the Prairie Recommending Committee for Wheat, Rye, and Triticale (PRCWRT). Therefore, leaf rust resistance is an important trait that is evaluated in the registration of wheat varieties in western Canada. Host resistance is also an effective strategy for sustainable disease management. However, the genetic basis of leaf rust resistance remains unknown in Canada Western Red Winter (CWRW) wheat. The objectives of this research were to identify the quantitative trait loci (QTL) controlling leaf rust resistance using genome-wide association study (GWAS)

and develop genomic selection (GS) models for improving leaf rust resistance in winter wheat. The study involved a GWAS panel comprising around 300 western Canadian winter wheat breeding lines and cultivars, and 100 winter wheat breeding lines and cultivars from the USA, eastern Canada, and Europe. The GWAS panel was assessed for leaf rust resistance in seedling tests, with multiple *P. triticina* races. In addition, this panel was tested for resistance in inoculated field trials in Winnipeg and Morden, Manitoba, following randomized alpha lattice designs, with two replicates per field trial during the 2022-23 and 2023-24 growing seasons. The genotyping was done using the Illumina Infinium Wheat Barley 40K SNP array and the 25K wheat Infinium array. The DNA marker and leaf rust datasets were used for GWAS. Here, individual markers were tested for association with leaf rust reactions (field and seedlings). Significant QTLs associated with leaf rust resistance have been identified from the GWAS analyses, indicating the presence of *Lr* genes in the GWAS panel. However, the specific identity of these genes has yet to be determined. The leaf rust and SNP marker data were also used to develop genomic selection (GS) models for estimating leaf rust resistance in CWRW breeding germplasm. The accuracy of these genomic selection (GS) models for predicting the leaf rust resistance of wheat germplasm was evaluated through cross-validation. Improved understanding of the resistance genes in Canadian winter wheat and DNA markers for selecting these genes will improve the efficiency of wheat breeding programs. Improvements in breeding efficiency will accelerate genetic gain in wheat breeding programs and result in the development of new improved varieties for cultivation in Canada.

***[O139] UNVEILING A DNA VIRUS SECRETS: *DE NOVO* METHYLATION PROFILING OF GRAPEVINE RED BLOTCH VIRUS VIA LONG-READ SEQUENCING.** Vahid J Javaran[1,2], Pierre Lemoyne[1], Dong Xu[1], Dave T Ste-Croix[1], Peter Moffett[2], and Mamadou L Fall[1]. [1]Saint-Jean-sur-Richelieu Research and Development Centre, Agriculture and Agri-Food Canada, 430 Boulevard Gouin, Saint-Jean-sur-Richelieu, QC J3B 3E6, Canada; and [2]Centre SÈVE, Département de Biologie, Université de Sherbrooke, 2500 Boulevard de l'Université, Sherbrooke, QC J1K 2R1, Canada
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Geminiviruses are a diverse group of single-stranded DNA (ssDNA) viruses known for their significant impact on agricultural crops globally, including the grapevine industry. Grapevine red blotch virus (GRBV), a member of the *Geminiviridae* family specifically classified under the genus *Grablovirus*, is the causal agent of Grapevine Red Blotch Disease (GRBD). GRBV causes severe economic losses in the grape and wine production sectors by affecting the quality and quantity of grape fruits. GRBV has a monopartite circular ssDNA genome and is transmitted by the three-cornered alfalfa hopper. There have been no successful reports on the enrichment and isolation of viral particles from GRBV-infected plants, which hinders the development of rapid and field-deployable serological tests that rely on the virion. Consequently, we hypothesized that the coat protein (CP) region of the GRBV genome is highly methylated, resulting in compromised translation and synthesis of the CP and the formation of the virion. Therefore, we used a novel methodology for *de novo* methylation profiling of GRBV, leveraging the capabilities of Nanopore sequencing to analyze the virus in its native circular form. Our comprehensive approach involved the extraction of DNA from three distinct GRBV-infected grapevine samples that display red blotch symptoms, and a PCR product of GRBV as a negative control. The protocol entailed several enzymatic treatments to linearize the unwanted circular dsDNA, followed by exonuclease treatment to remove all linear DNAs. A subsequent sequencing step, combined with the super accurate Dorado's modified base calling model, enabled the identification of 5mC and 6mA methylations on GRBV genome and in different coding regions. Our findings revealed a remarkable methylation pattern within the GRBV genome, particularly within the CP coding region which exhibited significantly elevated levels of 5mC methylation compared to other viral genes. This unexpected hypermethylation suggests a pivotal role of the CP gene in the GRBV-grapevine interaction during the infection lifecycle and could provide insights into the mechanisms of viral gene regulation and virion stability. Our research provides a valuable foundation for future electron microscopy-based investigations into the role of 5mC methylation in the viral CP gene and its impact on virion formation and integrity, offering novel insights into virus-host interactions and the epigenetic mechanisms influencing viral pathogenicity.

***[O140] PURPOSE-GROWN BIOMASS CROPS IN NOVA SCOTIA: STATISTICAL PREDICTIVE YIELD MODELLING AND REAL-WORLD VERIFICATION**. Emily G. Mantin[1], Laura K. Weir[1], Yousef A. Papadopoulos[2], and J. Kevin Vessey[1]. [1]Department of Biology, Saint Mary's University, 923 Robie Street, Halifax, NS, Canada, B3H 3C3; and [2]Agriculture & Agri-Food Canada, 58 Sipu Awti, Truro, NS, Canada, B2N 4H5
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The bioeconomy of Nova Scotia could be stimulated by the increased production of purpose-grown biomass crops grown on marginal agricultural lands. Biomass yields of four crops of interest (switchgrass, miscanthus (*Miscanthus* × *giganteus* L.), coppiced hybrid-poplar and willow) were predicted using linear mixed-effects models created from published data in areas with similar climates to Nova Scotia. These models were validated and refined using yields from five field sites established across the province. Two locally sourced, low-cost soil amendments (pulp and paper mill effluent residue and liquid anaerobic digestate) and one plant biostimulant (*Ascophyllum nodosum* extract) were applied to the crops during the establishment year to evaluate effects on crop establishment and early yield. This research focuses on two of the five aforementioned local field sites, Bible Hill and Nappan. The grasses were harvested annually, while the trees were harvested after one 3-year growth cycle post-coppicing. Mean miscanthus biomass yield three years post-establishment (Year 4) across two sites was 7,200 kg ha^{-1} $year^{-1}$, while switchgrass yield was 1,800 kg ha^{-1} $year^{-1}$. The mean predicted yields across field sites, based on the developed models, were 6,700 kg ha^{-1} $year^{-1}$ and 4,000 kg ha^{-1} $year^{-1}$ for miscanthus and switchgrass, respectively. Mean hybrid-poplar and willow biomass yields across sites after one growth cycle were 1,200 kg ha^{-1} $year^{-1}$ and 1,700 kg ha^{-1} $year^{-1}$, respectively, while yield models predicted biomass yields of hybrid-poplar (3,300 kg ha^{-1} $year^{-1}$) and willow (4,900 kg ha^{-1} $year^{-1}$) across Bible Hill and Nappan field sites. Biomass yields reported in the field are likely lower than predicted due to the infancy of the field trials; these crops have likely not reached their maximum yield potential yet. Minimal differences were reported between amendment treatments and management factors during establishment have also been identified as important influences on early yields of these crops.

***[O141] A SEED TREATMENT FOR THE MANAGEMENT OF SOYBEAN CYST NEAMTODE ON DRY BEANS.** Emma McIlveen[1], Chris Gillard[1], and Owen Wally[2]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada, N1G 2W1; and [2]Harrow Research and Development Centre, Agriculture and Agri-Food Canada, 2585 Essex County Rd 20, Harrow, ON, Canada, N0R1G0
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The soybean cyst nematode (*Heterodera glycines*, SCN) is the principal soil-borne pest threatening soybean production in North America, inflicting annual losses exceeding $50 million in Ontario alone. Its ability to infect dry beans (*Phaseolus vulgaris* L.) has heightened concerns in regions like Southern Ontario, where dry bean and soybean cultivation areas significantly overlap. In dry beans, SCN can induce similar detrimental phenotypic effects as in soybeans, including stunted growth, decreased pod numbers, and reduced seed size. Notably, much of the yield reduction in soybeans occurs without overt phenotypic symptoms, a phenomenon not yet fully explored in dry beans. Despite extensive research into SCN management strategies in soybeans, such as seed treatments, crop rotation, and genetic resistance, similar studies in dry beans remain sparse. This discrepancy underscores the urgent need for focused research on effective management approaches, including seed treatment efficacy and genetic resistance in dry beans. This study evaluates the effectiveness of novel and commercial seed treatments for controlling SCN in dry beans. We tested an experimental compound from Syngenta Canada Ltd. at various concentrations on black beans (cv. Blacktails) and kidney beans (cv. Dynasty), and compared these to established treatments, pydiflumetofen (Saltro® (Syngenta)) and fluopyram (Ilevo® (BASF)). Field trials conducted in 2023 provided early-season data on SCN control by examining cyst counts in root samples. Notably, roots treated with fluopyram exhibited a significant reduction in cyst density compared to the control group. Specifically, the black beans treated with fluopyram in one field exhibited a significant reduction in cysts per root and cysts per gram root compared to the control group. Soil samples were also analyzed to determine the nematode's reproductive factor, and crop yields were measured. Initial results indicated that the seed treatments did not significantly influence full-season SCN control. To verify these findings and expand on them, the field trials will be repeated in 2024, with

additional trials planned in a controlled environment. This research has the potential to introduce seed treatments as a novel and effective strategy for managing SCN in dry beans, contributing to sustainable agricultural practices in affected regions. Our findings not only address a significant gap in the current research but also offer practical implications for enhancing crop protection in a niche agricultural sector in Ontario.

[O142] EFFECT OF HUMIC-BASED SOIL AMENDMENT ON PLANT GROWTH, YIELD AND SYMBIOTIC NITROGEN FIXATION OF FIELD PEA (*Pisum sativum* L.) Pramod Rathor[1], Thomas D. Warkentin[2], and Malinda S. Thilakarathna[1]. [1]Department of Agricultural, Food and Nutritional Science, University of Alberta, 9011- 116 St, NW, Edmonton, AB, Canada, T6G 2P5; and [2]Crop Development Centre, University of Saskatchewan, College of Agriculture and Bioresources, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8
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The use of biostimulants, including humic-based soil amendments, in crop production has garnered considerable attention in recent years due to their organic origin and their ability to improve soil health, plant growth, yield, and nutritional quality. Humalite, a naturally occurring organic soil amendment rich in humic acid and deposited in large amounts in southern Alberta, was investigated in this study for its impact on plant growth, yield, and nitrogen fixation of field pea. Field pea plants inoculated with *Rhizobium leguminosarum* bv. *viciae* (3841) were grown in pots under greenhouse conditions using nitrogen deficit soil media prepared by mixing soil with sand at a ratio of 1:2 (v/v) and supplemented with five different humalite rates (0, 200, 400, 800 and 1600 kg ha^{-1}). Symbiotic nitrogen fixation capacity was assessed using the ^{15}N isotope dilution method. Results showed that plants treated with humalite displayed augmented root traits [root length (21-50%), root surface area (24-51%), volume (26-53%), average nodule weight (11-91%)], plant biomass [shoots (13-29%) and roots (29-54%)], shoot nitrogen concentration (12-33%), shoot total nitrogen content (38-53%), nitrogen derived from the atmosphere (8-14%), and total shoot nitrogen fixed (48-80%) per plant compared to the control plants at the flowering stage (BBCH:65). Furthermore, at seed maturity stage (BBCH: 89), plants treated with humalite at 400 and 1600 kg ha^{-1} exhibited a significant increase in plant biomass (4-14%), number of seeds (8-16%), seed weight (3-11%), seed nitrogen content (8-20%), and total seed nitrogen fixed (7-22%) per plant. These findings demonstrate that humalite can effectively serve as a humic-based organic soil amendment to enhance plant growth, root nodulation, symbiotic nitrogen fixation, and yield of field peas, thereby supporting sustainable agricultural practices.

***[O143] ON-FARM ASSESSMENT OF YIELD RESPONSE OF GRAIN CROPS TO SOIL PH AND LIMING IN CENTRAL ALBERTA.** Chirchir Jedida[1], Dyck Miles[2], Enesi Rebecca[1], Gorim Linda[1]. [1]Department of Agricultural, Food, and Nutritional Science, University of Alberta, Edmonton, AB, Canada; and [2]Department of Renewable Resources, University of Alberta, Edmonton, AB, Canada
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Soil pH, a measure of acidity and alkalinity, influences nutrient availability and crop yields. Millions of acres in Alberta are believed to have pH <5.5, resulting in decreased yields. Soil pH variability within fields has not been fully assessed, and agronomic lime research in the prairies is dated. One strategy to address low soil pH is lime application. Agricultural lime is commonly used, but the effectiveness of other liming materials, such as Cement Kiln Dust (CKD), is worth investigating. CKD is a by-product of cement manufacturing, and it has the potential to ameliorate soil acidity. The aim of this study was to (i) evaluate soil pH variations within whole fields and their effects on crop grain yield in a two-year rotation, and (ii) understand the effects of a single lime (CKD) application on crop yields within this rotation. A study was conducted in two fields, in 2022 and 2023, in Central Alberta, using CKD. One field had a canola-wheat rotation and another oat-wheat rotation. Topsoil estimation of soil pH and organic matter (SOM) was conducted using soil Optix. Geo-statistical techniques were used to link soil pH and crop yield maps in each field. A Before-After Control-Impact (BACI) design with at least three replications per field was used to assess the effects of liming on crop yields. Two treatments, CKD lime, and no-lime control, were evaluated in strips within the fields. Soil pH variability results from the generated maps indicated that within the canola-wheat rotation, canola and wheat yields increased by 50 % and 18.8 %, respectively, as soil pH increased to higher levels ranging from 5.5 to 7.5. In the oat-wheat rotation, oats, and wheat

yields decreased by 42.8 % and 35.7 %, respectively, with a pH increase ranging from 5.5 to 7.5. In the strips with the canola-wheat rotation, lime increased canola yields by 2.6 %; however, it did not affect wheat. Oat and wheat yields were reduced by 5.6 % and 2.8 % after liming in strips with the oat-wheat rotation. Crop yields showed a strong to moderate relationship (R^2 =0.42 to 0.67) with pH and SOM. This research indicates that pH and SOM play a significant role in improving crop productivity and, hence, should be monitored in crop fields to develop better site-specific recommendations.
Keywords: Liming, soil pH, crop yield, crop sequences, spatial variability

***[O144] THE EFFECT OF INTEGRATED CROP MANAGEMENT PRACTICES ON WEED GROWTH AND PERSISTENCE TRAITS.** Uthpala Ekanayake[1], Rob Gulden[1], Chris Willenborg[2], Jonathan Rosset[1], and Dilshan Benaragama[1]. [1]Department of Plant Science, Faculty of Agricultural and Food Sciences, University of Manitoba,66 Dafoe Road, Winnipeg, MB, R3T 2N2, Canada; and [2]Department of Plant Science, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, SK, S7N 5A8, Canada
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The potential of Integrated Crop Management (ICM) via combining fertilizer management and cultural weed management has been understudied, yet understanding the impact of ICM on weed growth and persistence is crucial for managing herbicide resistance. In 2023, a four-way factorial field experiment was established as split-block design with four replicates at the Carman research field, Manitoba to evaluate the impact of ICM on weed growth and weed seed germination traits in a spring wheat (*Triticum aestivum* L.). The treatments were; fertilizer application timing (spring, fall), placement (broadcast, banding), rate (50%, 100%), and weed management (IWM, standard). Integrated Weed Management included narrow row spacing (6"), high crop density (400 plants m^{-2}), and early seeding while the standard weed management was 12" row spacing, 200 plants m^{-2} crop density, and late seeding. Weed emergence and growth were monitored within designated quadrants in each plot. Weed seeds collected in two cohorts (populations with similar emergence timing) were subjected to germination tests. Crop and weed management practices interactively influenced crop growth, thus increasing competition on weeds. The combination of half-rate with standard weed management had 23% greater crop biomass than half-rate and IWM. Weed density was significantly affected by the interaction of fertilizer timing and weed management where the combination of fall application and IWM had a 75% lower density compared to spring with standard weed management. Wild oat (*Avena fatua* L.) heights at maturity were influenced by fertilizer rate and weed management interaction, with a 39% increase observed in the half-rate with standard compared to full-rate with IWM. Similarly, the interaction of fertilizer rate, timing, and weed management significantly impacted redroot pigweed (*Amaranthus retroflexus*L.) heights, showing a 41% increase under banding, full-rate, and standard compared to broadcasting, full, and IWM. Weed biomass was 89% lower in the combination of fall application with IWM, than spring with standard. The germination of wild oats from the first emerged cohort was significantly influenced by all treatments. Fall application increased germination by 6% compared to spring-banding by 5% compared to broadcasting, half rate by 10% compared to full; and IWM by 9% over standard. The second cohort also showed significant responses, with banding and half-rate leading to 5% and 8% higher germination rates, respectively. Redroot pigweed responded positively to the half-rate, showing an 8% increase in germination. These preliminary findings suggest a complex interplay between fertilizer and weed management on crop-weed growth and weed seed persistence.

[O145] THE EFFECT OF BORON ON CLUBROOT SEVERITY AND DEFENSE MECHANISMS IN *BRASSICA NAPUS*. A. Sedaghatkish[1], S. Chesney[1], B. D. Gossen[2], and M. R. McDonald[1]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1, Canada; and [2]Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, Saskatoon, SK, S7N 0X2 Canada
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Clubroot, caused by *Plasmodiophora brassicae* Wor., is an important disease of canola (*Brassica napus* L.) and other Brassica crops worldwide. This soil-borne Chromist pathogen causes the formation of 'clubbed' roots that disrupt nutrient uptake and result in severe yield loss. Resting spores of the pathogen are long-lived and the rapid emergence of resistance-breaking pathotypes make sustainable management strategies crucial. Application of boron (B) to the soil has been shown to reduce clubroot

severity in both controlled environment and field trials, but the optimal application rates and mechanism(s) of pathogen suppression require further investigation. One hypothesis was that application of boron increased cell wall thickness, making plants less susceptible to pathogen colonization and development. In the current study, the effect of boron on clubroot severity and plant defense was examined in four lines of *B. napus* in growth room studies and gene expression analysis. Controlled environment studies demonstrated that an application equivalent to 16 kg B ha^{-1} provided a modest but consistent reduction in clubroot severity. The putative boron-tolerant line Mytnickij had lower clubroot severity than Westar, ACS-N39 and another putative boron-tolerant line, Prota. Further studies were done on plants that received boron at a rate of 8 kg B $ha^{-1,}$ as there was concern about phytotoxicity at higher rates. The application of 8 kg B ha^{-1} had little or no effect on cell wall properties in stained root cross-sections of young plants that were analysed using ASSESS image analysis software. Substantial changes associated with application of 8 kg B ha^{-1} were observed in genes involved in cell wall synthesis, pathogen defense, and abiotic stress tolerance. Several genes in the phenylpropanoid pathway, responsible for synthesizing a wide variety of secondary metabolites crucial in plant defense, including flavonoids and lignin, were differentially regulated with the addition of boron. Also, genes associated with ethylene biosynthesis (involved in hormonal defence signaling) and boron transporters were upregulated in response to boron treatment in combination with *P. brassica* infection. This highlights the role of even moderate rates of boron in enhancing resistance to *P.* brassicae. The results suggest that boron can be important for plant defense. These results support previous reports that application of boron reduced clubroot severity, possibly by improving the crop's defense response during colonization by *P. brassicae*.

[O146] BACTERIAL LEAF STREAK SURGE ON THE CANADIAN PRAIRIES: INSIGHTS AND MANAGEMENT STRATEGIES. Shaheen Bibi[1], Malini Jayawardana[1], and Dilantha Fernando[1].
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Bacterial Leaf Streak (BLS) poses an increasing challenge for wheat and barley growers in the Canadian Prairies. This emerging disease is caused by *Xanthomonas translucens* pv. *undulosa* and *Xanthomonas translucens* pv. *translucens*. Over the recent years, the spread of this disease has intensified, resulting in notable crop losses, occasionally reaching levels as high as 40% yield loss. To tackle this growing issue, we aim to understand the mechanisms behind BLS transmission and develop effective management strategies. In pursuit of our objective, we have collected disease samples from diverse regions across Canada including Alberta and Manitoba. Bacteria were isolated from symptomatic lesions on plant leaves and spikelets using semi-selective media. The identification of bacteria to pathovar levels was conducted through multiplex PCR, utilizing primers cbsA-1, cbsA-2, cbsA-3, and cbsA-4 to amplify the cbsA gene while S8.pep amplified the Xtu unique peptidase gene. In our initial screening, we observed that the majority of the disease is attributed to *Xanthomonas translucens* pv. *undulosa*. In addition to these diagnostic initiatives, we are also exploring novel approaches to manage BLS. This involves assessing the efficacy of well-characterized biocontrol agents, *Pseudomonas brassicacearum* strain DF41 and *Pseudomonas chlororaphis* strain PA23, against the pathogen. Our preliminary findings are encouraging, indicating that these agents hold potential as a sustainable approach to mitigating BLS. Furthermore, our initial screening of Canadian wheat varieties aims to uncover any resistance to BLS. Our early findings suggest that the disease affects most Canadian wheat varieties. In addition, Multilocus sequence analysis (MLSA) of four housekeeping genes (*rpod, dnaK, fyuA* and *gyrB*) will be used to evaluate the genetic diversity of the Canadian isolates from wheat and barley. This underscores the immediate necessity for comprehensive research to determine the most effective and timely management practices for controlling BLS.

[O147] A SURVEY FROM 2006-2023 TO STUDY THE STATE AND PREVALENCE OF FUSARIUM HEAD BLIGHT DISEASE ON WHEAT IN ALBERTA. Monika Dayarathne[1], Michael Harding[2], and Dilantha Fernando[1]. [1]Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada, R3T2N2; [2]Crop Diversification Centre South, Alberta Agriculture and Irrigation, 301 Horticulture Station Road East, Brooks, AB, Canada T1R 1E6
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Fusarium head blight (FHB) is a severe fungal disease affecting wheat, barley, oats, other small grain cereals, grasses, and corn. Although FHB has been a common and damaging disease in Manitoba for nearly three decades, it is a relatively 'new' disease in Alberta. Thus, a field survey from 2006 to 2023 was carried out to study the FHB status and prevalence in Alberta fields. Fusarium-like species were isolated, identified, and counted from samples from wheat heads randomly collected from selected fields in every wheat-producing county in Alberta from the Peace River region in the north through to the most southern regions in Alberta. A relatively low level (0.54%) of FHB prevalence in 2006, increased up to 70% by 2021 demonstrating significant change in FHB prevalence during this period, and the considerably high risk of future FHB infection in wheat in Alberta. Similarly, FHB incidence also increased steadily since 2006. In contrast, a very low FHB severity was found in Alberta fields across time, except for 2015 and 2016, which had favorable environmental conditions that promoted the development of FHB. The most frequently recovered species were *F. graminearum, F. avenaceum*, and *F. culmorum* followed by *F. poae* up to 2015. In 2006, *F. graminearum* accounted for 7.57% of all species; however, by 2021, that percentage had dropped to 3.5%, making *F. graminearum* an uncommon species in Alberta fields. The distribution of *F. graminearum* showed that it is no longer concentrated in southern Alberta. Interestingly *F. poae* showed a rapid increase in prevalence when compared to other Fusarium species and became the dominant species in 2021. *Fusarium graminearum* isolates comprising 3ADON genotype were more common over 15ADON isolates, supporting a shift from 15ADON to 3ADON in Alberta over this period. Changes in the environmental conditions and other agronomical practices may play a role in species composition dynamics and the shift towards 3ADON in Alberta. Since the prevalence and incidence of FHB is increasing in Alberta fields, it is important to conduct further annual surveys to monitor the status of FHB in this province. This survey was continued up to 2023 and the data analysis for 2022 and 2023 is underway.

[O148] ARE NEMATODES INVOLVED IN THE EMERGING CHICKPEA HEALTH ISSUE IN SASKATCHEWAN? Fernanda Gouvea Pereira[1], Mario Tenuta[1], Michelle Hubbard[2], and Sarah Anderson[3]. [1]Department of Soil Science, University of Manitoba, Winnipeg, Manitoba, Canada; [2]Agriculture and Agri-Food Canada, Swift Current, Saskatchewan, Canada; and [3]Saskatchewan Pulse Growers, Saskatoon, Saskatchewan, Canada
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Chickpea crops in southern Saskatchewan have been facing health problems characterized by symptoms such as chlorosis, wilting, and plant die-off. First noticed in 2019, this issue has affected a wide area, including the main chickpea-growing region in the province. Crop specialists conducted field soil surveys in symptomatic and asymptomatic locations; the University of Manitoba analyzed the resulting 143 soil samples for the presence of plant parasitic nematodes. The pin nematode (*Paratylenchus ssp.*) was recovered at unusually high densities and fairly frequently from samples. To investigate if *Paratylenchus* were feeding on chickpea, we conducted a growth chamber study utilizing soil samples with high *Paratylenchus* density collected from the 2022 survey. Three treatment groups were used: infested soil with chickpea plants present (CDC-Corrine, 17 reps), infested soil without plants (4 reps), and non-infested soil with chickpea (3 reps). Infested chickpea soil had an initial *Paratylenchus* population of 502 $100g^{-1}$ dry soil. After 16 weeks, nematodes from soil and roots were extracted by Cobb sugar-flotation. *Paratylenchus* and other prominent nematodes were identified to the genus by morphological features and to species by molecular means (sequencing of the partial 18S, 28S (D2-D3), and ITS (ITS 1 & ITS2) regions of the rDNA gene). Sequencing showed the species of *Paratylenchus* to be *P. projectus*. At the end of the experiment, chickpea soil and roots in infested pots had a mean of 5,518 *Paratylenchus* per $100g^{-1}$ dry soil (±1180 s.e.), with a reproduction factor of 10.9 (±2.35 s.e.), highlighting chickpeas as an excellent host. Without the chickpea host, pin nematode population declined by 96%. However, the plants did not exhibit any disease symptoms. This study confirms that *Paratylenchus projectus*, recovered from Saskatchewan, is a parasite of the tested chickpea variety. Future greenhouse and microplot experiments are necessary to investigate the effects of *Paratylenchus* on chickpea health, if other crops are hosts, and to understand its impact on the chickpea health issue in Saskatchewan.

[O149] ADVANCEMENT OF B2-BASED DSRNA EXTRACTION METHOD: COST-EFFECTIVENESS COMPARISON OF HTS-BASED VIRUS DETECTION METHODS. Mamadou L. Fall, Dong Xu, and Pierre Lemoyne. Saint-Jean-sur-Richelieu Research and Development Centre, Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu, Quebec, Canada J3B 3E6
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Viral diseases pose a significant threat to global food production. Unlike bacterial or fungal infections, treating virus-infected plants is impractical. Therefore, minimizing the impact of viruses on crop production depends on our ability to monitor and anticipate outbreaks. Early detection is crucial for implementing effective mitigation strategies. Virion-associated nucleic acid (VANA) and metagenomic sequencing are commonly used to analyze the virome. VANA sequencing tends to favor DNA and enveloped RNA viruses, while metagenomic sequencing is influenced by large-genome organisms and their prevalence. We have developed a new method using dsRNA-binding proteins (B2-based) and compared its cost-effectiveness with four existing methods using the Illumina MiSeq platform. The results indicate that dsRNA sequencing surpasses metagenomics in terms of cost-effectiveness for detecting grapevine viruses and for characterizing their genomes, regardless of genome type, size, or heterogeneity. Among the tested methods, the DRB4-based dsRNA method (commercial kit) showed the highest accuracy, followed by the cellulose-based method, and the B2-based dsRNA method. However, our B2-based dsRNA method stood out as the most affordable and rapid option. In the broader context of One Health, which involves monitoring both known and unknown viruses across various environments such as plants, animals, insects, and soil, dsRNA sequencing offers a unique opportunity to enhance our ability to monitor and predict viral outbreaks.

***[O150] PECTIN DYNAMICS DICTATES ANISOTROPIC CELL GROWTH DURING MESOPHYLL MORPHOGENESIS.** Diksha Bhola and Anja Geitmann**.** Department of Plant Science, Faculty of Agricultural and Environmental Sciences, McGill University, Montreal, Canada
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Plants exhibit complex structure-function relationships showcased most eminently by the leaves. They are the major sites for fundamental biophysical processes such as photosynthesis and respiration. The efficiency of these processes is governed by the overall architecture of leaves, wherein each tissue layer contributes in an additive manner.

Of critical importance for photosynthetic efficiency is the 3D arrangement of mesophyll cells and intercellular spaces as it determines the diffusion of gases through the inner leaf tissue. Structural traits such as mesophyll cell shape, area and volume, intercellular connectivity of air spaces between mesophyll cells, mesophyll cell walls facing intercellular spaces, and porosity of the mesophyll tissue affect mesophyll conductance and net photosynthetic capacity. Mesophyll morphogenesis is controlled by cell wall polysaccharides that dictate non-uniform and anisotropic growth process and control cell detachment resulting in a complex aerenchymatic tissue. The aim is to understand how mesophyll cells develop their 3D shapes from the dense embryonic tissue and how the network of interconnected air spaces is formed. Here we use *Arabidopsis thaliana* wildtype and mutants with altered pectin methyl esterification to elucidate how cell wall polysaccharide composition correlates with tissue morphogenesis and how altered cell wall properties affect leaf anatomy. Two complementary microscopic techniques are employed to characterize mesophyll cell morphogenesis. Confocal laser scanning microscopy in combination with immunohistochemistry is used to map various cell wall polysaccharides during mesophyll development. Synchrotron-based X-ray microcomputed tomography (micro-CT) is used to obtain cellular and tissue level information in non-destructive manner. Image analysis and processing is done by MorphoGraphX and ImageJ software. We found that lowly esterified pectin are enriched in cell wall segments that maintain continued cell-cell contact even during air space formation in the tissue. Genetically modified enhanced levels of highly methyl esterified pectin causes higher degree of cell wall expansion and bigger cells. Clearly, changes in pectin chemistry plays an important role in influencing the growth of individual cells, their morphogenesis and cell-cell connectivity thereby affecting mesophyll tissue porosity.

***[O151] SNAKE CHARMMING: UNDERSTANDING COBRA THROUGH BIOINFORMATICS AND MUTATIONAL ANALYSIS.** Kamryn Diehl[1] and Geoffrey Wasteneys[1]. [1]Department of Botany, University of British Columbia
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Cellulose, the most abundant biopolymer on the planet, is the main component of plant cell walls and plays a pivotal role in plant development and adaptation to their dynamic environments. Despite its importance, the precise mechanisms facilitating cellulose biosynthesis and its regulation remain disjointed. COBRA, a glycosylphosphatidylinositol (GPI)-anchored protein on the outer leaflet of the plasma membrane, has emerged as a critical player in cellulose biosynthesis with the potential to bridge some of our knowledge gaps related to the deposition of cellulose in the cell wall. The null mutant, *cob-4*, is unable to produce sufficient cellulose and is seedling lethal, cementing COBRA's critical role in plant survival. The *cob-1* allele, caused by a point mutation, has a conditional phenotype resulting in reduced cellulose production and root-tip swelling when seedlings are grown on high-sucrose media. It is unclear why *cob-1* misregulates cellulose production, specifically when supplied with high sucrose. Theoretically, there should be an ample supply of UDP-glucose for building cellulose polymers.

My research aims to utilize molecular dynamic simulations such as CHARMM to dissect COBRA's functional domains and post-translational modifications in combination with the analysis of unexplained mutant phenotypes. COBRA contains an N-terminal cellulose binding domain (CBD), a central cysteine-rich domain, a C-terminal GPI anchor, and is N-glycosylated at 9 locations. Prediction software on protein structure suggests the CBD is distal to the plasma membrane, with three highly conserved aromatic residues. Substitution of these amino acids result in seedling lethality, consistent with COBRA's function requiring interaction with cellulose. Furthermore, the *cob-1* and *hulk-1* conditional mutants have point mutations between the cysteine-rich domain and the CBD. These mutations alter the mutants' surface electrostatic charge, potentially affecting cellulose binding.

To further understand why cellulose loss is triggered in *cob-1* by high levels of exogenous sucrose, mutants were plated on defined media with varying amounts of sucrose. Whereas radial swelling of root tips was induced on Hoagland's medium with 4.5% sucrose, swelling could be also be induced on ½ Murashige-Skoog (MS) medium with just 1% sucrose. The presence of ammonium in the MS formulation could account for the enhanced phenotype, potentially by inhibiting uptake of potassium, which along with nitrate, is known to alleviate ammonium toxicity partially through the expression of cellulose synthase genes. This finding opens up new avenues to explore the complex relationship between COBRA, cellulose biosynthesis, and plant adaptation to environmental stress.

[O152] FROM SINGLE CELLS TO COMPLEX TISSUES - THE MOLECULAR DECODING OF PLANT SEXUAL REPRODUCTION AT SINGLE CELL RESOLUTION. Katharina Bräutigam[1,2]. [1]Cell and Systems Biology, University of Toronto, Toronto, ON, Canada; and [2]Department of Biology, University of Toronto Mississauga, Mississauga, ON, Canada
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Plant organs are complex structures that are composed of a variety of cell types. At the molecular level, organ formation reflects precisely coordinated cell differentiation programs and an integrated network for gene regulation. Here, molecular complexity can be informative. For example, epigenetic factors such as chromatin organization into accessible or inaccessible regions or DNA methylation patterns set the stage for the regulation of gene expression.

In our work, we chart for the first time, the epigenome and transcriptome landscape of reproductive organs in *Populus* at single cell resolution. We created cell type inventories and characterize molecular cell differentiation paths. We further detect waves of chromatin re-organization that precede changes in the transcriptome, and we characterize early divergent meristem identities that mark early stages in sex determination. This wealth of data allows us now to integrate the different types of information to create models for the separate male and female reproductive development.
We selected sexual reproduction for our study as it represents one of the most central processes in life. The focus on the dioecious *Populus* allowed us to study reproductive development in flowers with

relatively simple, reduced morphology. Trees in the genus *Populus* further separate the production of male and female organs onto different individuals. This mode of reproduction differs from the mixed anatomy of bisexual flowers that is observed in plants such as *Arabidopsis* and allows to tease apart sex-specific pathways.

Our work provides mechanistic insights into the regulatory mechanisms of sex determination and sex expression, and it provides valuable information to ensure reproductively healthy forests.

[O153] FORMATION OF A STABLE TUBULAR ER NETWORK REQUIRES A LOCALIZED PHOSPHATIDYLCHOLINE SYNTHESIS IN ARABIDOPSIS. Weina Wang. McGill University
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Phosphatidylcholine (PC) is a major component of phospholipid to constitute bilayers of the endoplasmic reticulum (ER) membrane. Membrane fusion of different ER tubules driven by RHD3 in Arabidopsis functions to form and maintain the interconnected ER network, whilst synthesis and rearrangement of membrane lipid is required to form and remodel the ER during continuous membrane fusion. However, it is still unclear how the role of PC affects the ER formation and remodeling, especially in the process of membrane fusion mediated by RHD3. Through forward genetics, a genetic enhancer of rhd3-1 named ren10 was identified. In this study, the REN10 gene was cloned by map-based cloning, which encodes phosphorylcholine cytidylyltransferase (CCT1) which is the rate-limiting enzyme in the biosynthesis of PC. The deletion or mutation of CCT1 leads to short root hairs and aggregated ER network. And CCT1 is partially localized in the ER and is involved in the regulation of ER formation. The membrane targeting of CCT1 in ER is reduced in the absence of RHD3 although there is no physical interaction between CCT1 and RHD3. The localized PC synthesis in the ER is reduced in ren10 mutant. We conclude that the localized PC synthesis is required to form and maintain a tubular ER network.

[O154] TESTING THREE ALTERNATIVE TECHNOLOGIES AGAINST POWDERY AND DOWNY MILDEWS ON WINE GRAPE, GREENHOUSE CUCUMBER, FIELD ZUCCHINI AND STRAWBERRY. Andrew C. Wylie[1], Irina Perez-Valdes[1], and Rose Buitenhuis[1]. [1]Vineland Research and Innovation Centre, 4890 Victoria Avenue North, Box 4000, Vineland Station, ON, Canada, L0R 2E0
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Powdery and downy mildews are perennial diseases that cause economically significant damage across horticulture. These diseases, caused by a variety of pathogens, are managed with a combination of strategies including fungicides, to which these organisms develop resistance. Effective and safe strategies that also manage fungicide resistance continue to be sought. Alternatives to conventional treatments for mildews need to be carefully tested for efficacy, phytotoxicity, practicality and other considerations. We were interested in performing field and greenhouse trials to investigate three alternative controls for mildews: a photodynamic inactivation application (SUN-D-06, Suncor AgroScience), a hydroxyl radical treatment (Clean Works), and an air purification/enzymatic degradation reactor process (Clean Air Zone Ag). The photodynamic inactivator treatment was tested in naturally inoculated field trials on powdery mildew of zucchini (*Podosphaera xanthii*) where it demonstrated efficacy. The hydroxyl radical treatment was tested on hoophouse strawberry inoculated with *Podosphaera aphanis*. Infections were eliminated but preliminary results were inconclusive. This treatment was tested at pilot scale on hoophouse-grown grapes inoculated with *Erysiphe necator*, demonstrating suppression of powdery mildew, and at commercial scale with natural *Erysiphe necator* and *Plasmopara viticola* infection showing suppression of powdery mildew as well as reduction of downy mildew. The air capture and enzymatic degradation reactor was tested in greenhouse cucumber inoculated with *Podosphaera xanthii* where it reduced powdery mildew disease severity. With efficacy demonstrated for these three technologies, future efforts are considered including further validation of these results, calibration of the treatments and engineering applications. The three alternative methods for suppression of mildews tested show promise for disease suppression and fungicide resistance management, adding potential management strategies to reduce crop damage from these pests.

[O155] DEVELOPING 'STONY HARD' PEACH TO MITIGATE CLIMATE CHANGE EFFECTS AND LONGER SHELF LIFE. Jayasankar Subramanian[1] and Naincy Sharma[1]. [1]University of Guelph, Vineland Station, ON
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The *stony hard* gene in peach is not new but has not been looked up favorably so far. Only few varieties with stony hard gene exist in the world and none of them seem to be suitable for Ontario based on our observations at Vineland. We intend to develop peaches with stony hard genes that will be suitable for the changing climate, by selecting cultivars from crosses involving stony hard parent. Due to their prolonged shelf life and thus improving the chances of being consumed, these peaches, will reduce the wastage and thus carbon footprint, contributing to mitigate climate change. Further the stony hard peaches tend to hang longer in the trees and store better thus providing the growers huge advantage. This will also reduce the post harvest spoilage thus reducing the greenhouse gas emissions. Finally, such firmer fruits, which will contain all other traits of peach, are preferred by the younger generation over the juicy fruits that tend to drip and considered messy by younger generation. Since the conventional selection process will take multiple years, we are characterizing the gene PpYUC11 that confers stony hard trait so that we can develop molecular markers for this gene. Using the molecular markers, we can select them in the seedling stage in the greenhouse itself so only those expressing the gene will be forwarded for further selection. This saves time, money and space and thus helps environment as well.

[O156] CRANBERRY RESPONSES TO IN-FIELD EXPERIMENTAL WARMING. Lauren A E Erland[1]. [1]Agriculture, University of the Fraser Valley, 33844 King Rd., Abbotsford, BC, V2S 7M8
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Cranberries (*Vaccinium macrocarpon* Ait.) are a speciality fruit crop which represent a $184M farm gate value in 2022. British Columbia (B.C.) is one of the major cranberry producing regions in Canada, which is second only to the United States for worldwide supply. Our recent work has shown that cranberry growing regions will be differentially impacted under future climate scenarios with both temperature and precipitation leading to potential challenges for producers. Producers in B.C. already use unique and adapted mechanisms for cranberry production as approaches such as flooding, freezing and sanding fields is not viable in the existing climate. Building on existing ongoing varietal evaluation studies at the BC Cranberry Research Farm in Delta, BC, our objective was to examine the impacts of future climate scenarios on cranberry growth and productivity through the application of passive in field warming experiments. We have constructed passive warming chambers in three varieties of cranberries: Haines, Mullica Queen and RS9811 in 2022. These represent an established variety (Mullica Queen), a newer variety with delayed phenological development (Haines) and an unreleased variety with delayed colouring (RS9811). These warming domes were found to increase temperatures by 3-5 °C which is representative of future climate scenarios. Cranberries in warmed and control plots are monitored throughout the year and data including phenology, growth patterns, bud set, fruit characteristics, quality and yield have been monitored. While most effects on fruit yield are anticipated to be observed in year 2, we present year 1 data which has identified, as anticipated, an advance in phenological development, modification of upright to runner development, reduced yield and phytochemical changes through an untargeted metabolomics study.

[O157] EPIDEMEOLOGY OF *NEOPESTALOTIOPSIS* SPP. IN STRAWBERRY. Justin McNally[1], Adam Dale[2], Erica Pate[3], and Melanie Kalischuk[1,2]. [1]Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada, N1G 2W1; [2]Ontario Crop Research Centre, University of Guelph, Simcoe, Ontario, Canada, N3Y 4K3; and [3]Ontario Ministry of Agriculture, Food and Rural Affairs, Simcoe, Ontario, Canada, N3Y 4K3
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Strawberry (*Fragaria* x *ananassa* Dutch.) is a popular fruit grown commercially for fresh market and processing in Ontario with a farm gate value of $40 million. *Neopestalotiopsis* sp. is a new and emerging pathogen that causes devastating root and crown rot disease in field and greenhouse strawberry. Currently, chemical control methods and resistant germplasm are unavailable. To determine the incidence of the pathogen in Ontario, a three-year monitoring project was initiated from 2020-2022. Fungi were isolated from symptomatic strawberry tissues and characterized. Molecular techniques were used

to identify the fungi using the β-tubulin 2 (Tub2), internal transcribed spacer (ITS) of the nuclear ribosomal sequence and the eukaryotic translation elongation factor 1-α (eEF1α) genomic region. Of the 45 symptomatic samples collected, incidence of the aggressive species *Neopestalotiopsis* sp. was 29%. Symptoms of Neopestalotiopsis disease include leaf spot, crown rot, root rot and dieback. In leaves, leaf spots of *Neopestalotiopsis* sp. can be confused with leaf scorch (*Diplocarpon earlianum*), leaf spot (*Mycosphaerella fragariae*) or phomosis blight (*Phomopsis obscurans*). In fruits, *Neopestalotiopsis* sp. symptoms can resemble anthracnose (*Colletotrichum* spp.). In crowns and foliage, symptoms of *Neopestalotiopsis* sp. are similar to those of *Phytophthora* sp. or *Colletotrichum* spp. Since visual observations of Neopestalotiopsis disease are unreliable, a sensitive and specific derived cleaved amplified polymorphic sequence (dCAP) was identified, and a marker developed to differentiate between the aggressive and less aggressive species of *Neopestalotiopsis* using a multi-locus sequence typing (MLST) strategy. To identify resistance to the aggressive species of *Neopestalotiopsis,* F1 hybrid germplasm from the University of Guelph strawberry breeding program was screened. Detached leaf and whole plant infection assays identified a line with a high level of resistance to *Neopestalotiopsis* sp. with an average lesion diameter significantly smaller than susceptible day neutral 'Albion' and moderately susceptible June-bearing 'Jewel'. Future efforts will examine the stability of this resistance and application of the germplasm in an integrated pest management strategy.

***[O158] THE DIVERSITY OF BIOACTIVE COMPOUND PROFILES IN CANADIAN PRAIRIE SMALL FRUITS AND THEIR ANTIOXIDANT AND ANTI-HYPERTENSIVE POTENTIAL AS FUNCTIONAL FOODS.** Chamali Kodikara[1,2,3], Sura Srinivas[1], Nandika Bandara[3,4], Thomas Netticadan[1,2], Sijo Joseph[1,4], and Champa Wijekoon[1,2,3]. [1]Agriculture and Agri-Food Canada, Morden Research and Development Centre, Morden, Manitoba, Canada, R6M 1Y5. [2]Canadian Centre for Agri-Food Research in Health and Medicine, Winnipeg, MB R3C 1B2, Canada. [3]Department of Food & Human Nutritional Sciences, University of Manitoba, Winnipeg, MB R3T 2N2, Canada; and [4]Richardson Centre for Food Technology and Research (RCFTR), University of Manitoba, 196 Innovation Drive, Winnipeg, Manitoba, R3T 2N2, Canada
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Background: Prairie berries are cold hardy fruits consumed by Canadians for their perceived health benefits. Phenolic compounds and fatty acids are important groups of bioactive molecules in berries. Assessment of the antioxidant and anti-hypertensive properties of the berries enables us to identify them as a potential functional food for human health.
Research objective or question(s): To examine the contents of phenolic compounds, fatty acid composition, antioxidant activities and anti-hypertensive capacities of fifteen different berries grown in prairies.
Methods: The UHPLC-HRMS method was developed and used for the comprehensive and simultaneous analysis of 66 phenolic compounds in 14 different types of Canadian wild berries. GC-MS was used to analyze the fatty acids in the aforementioned berries. Total phenolic content (TPC), DPPH free radical scavenging assay, ferric reducing antioxidant power assay (FRAP), ACE inhibitory activity assay and the assessment of total flavonoid content were conducted to check the antioxidant and antihypertensive potential of all the selected wild berry types.
Results: Wild grapes were rich in phenolic compounds such as resveratrol (4.2±0.02 µg/g), while gooseberries were rich in isoquercetin (84.8±0.08 µg/g) and paracoumaric acid. Moreover, saskatoon berries were rich in chlorogenic acid and quercetin. Rutin and chlorogenic acid were the most abundant phenolic compounds in chokecherry. Essential fatty acids such as linoleic and linolenic acids were found in wild grapes, seabuckthorn and Saskatoon berries. The highest TPC was found in nanny berries whereas the highest FRAP was found in chokeberries. Snowberries showed the highest DPPH activity and chokecherries had the highest ACE inhibitory activity followed by haskap berries.
Discussion: Recent findings have shown that diets that are rich in antioxidants can protect humans against degenerative diseases such as diabetes, neurogenerative and cardiovascular diseases. A novel UHPLC-HRMS method and GC-MS analysis of fatty acids proved that the underutilized wild berries consist of unique and beneficial phenolic compounds and essential fatty acids. In addition, they may act as potential antioxidants as well as antihypertensive agents. The information from this study may help in

finding applications for underutilized prairie berries as potential sources of functional food in the pharmaceutical and nutraceutical industries.
Keywords: Bioactive compounds, UHPLC-HRMS, GC-MS, Canadian small fruits, antioxidants

***[O159] EXOGENOUS APPLICATIONS OF DOUBLE-STRANDED RNA TO INDUCE RNA INTERFERENCE FOR THE CONTROL OF THE NOVEL FUNGAL PATHOGEN *NEOPESTALOTIOPSIS* SP. AFFECTING STRAWBERRY.** Sarah Koeppe[1] and Melanie Kalischuk[1]. [1]Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON N1G 2W1, Canada
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Neopestalotiopsis sp. is an aggressive novel fungal pathogen of strawberries that currently lacks a recommended control method. RNA interference (RNAi) is a mechanism triggered by double-stranded RNA (dsRNA) that has the potential to be a highly effective and specific crop protection strategy, however, its potential has yet to be explored for this pathogen. The RNA-induced silencing complex (RISC) is a versatile, sequence-specific innate immunity protein complex involved in the RNAi pathway. Exogenous application of dsRNA complementary to an integral gene of pathogen or pest can provide systemic, RNAi-based resistance for the host crop in the form of spray-induced gene silencing (SIGS). Two genes of interest that play integral roles in the functioning of this pathogen are beta-tubulin and cytochrome P450 subfamily 51 (CYP51), both of which are targets for several fungicides. Beta-tubulin plays an integral role in the formation of tubulin fibres during chromosome separation in cell division. CYP51 has two paralogues in *Neopestalotiopsis* sp., and both encode for an enzyme that is necessary for the production of ergosterol, a fungi-specific sterol needed to maintain cell membrane integrity. To assess the efficacy of these genes as a target, they were first characterized to identify the locations of introns, exons, splicing sites, and motifs. From this information, several dsRNA constructs were built, four at the lengths of 200 base pairs (bp), 400bp, 600bp, and 800bp for beta-tubulin, and four for CYP51, 400bp and 800bp for each paralogue. An in vitro assay was developed to assess the efficacy of each construct with their respective pathogen. Beta-tubulin showed no efficacy as an RNAi target for control of *Neopestalotiopsis* sp., regardless of the construct used, potentially due to a resistance mechanism in the pathogen. The CYP51 paralogues show some potential in controlling the pathogen but have yet to be fully assessed. Based on the current research and these results, SIGS, and RNAi as a whole, appears to be a potential environmentally friendly option for crop protection against fungal pathogens, and further research in the field will allow for the development of alternative controls to conventional chemical fungicides.

[O160] LEAFY GREEN VEGETABLE PRODUCTION IN SASKATCEWAN. Jazeem Wahab, Janitha Wanasundara, Edmund Mupondwa, Erl Svendsen, Raju Soolanayakanahally, and Evan Derdall. Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2
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Vegetable production is a leading sector of the Canadian Horticulture industry. In 2022, Canada grew approximately 109,000 ha ‘Field’ vegetables with a Farm gate value of $ 1.6 billion. However, Saskatchewan accounted for only about 0.5% of production area and 0.5% of Farm gate value. The relatively short and cooler growing season is a major constraint for growing high-value warm-season vegetables in Saskatchewan. Climate change mediated warmer temperatures and longer growing seasons could be effectively capitalized to grow vegetables in Saskatchewan. Irrigation is essential for sustainable vegetable production. Government of Saskatchewan’s recent 10-year - $ 4 billion - 202,000 ha irrigation expansion project expects vegetable production to play a key role. Many cool-season crops, including Leafy-Greens’ have gained prominence as ‘Super Food’ or ‘Super Green’. Research is being carried out at the Canada-Saskatchewan Irrigation Diversification Centre, Outlook, Saskatchewan, to identify superior cultivars and develop Best Management Practices for popular ‘Greens’. Results from the 2022 growing season Bok Choy and kale studies are presented in this paper. Bok Choy cvs. Asian Delight, Li Ren Choi, Mei Qing Choi, Win Win Choi, Bopak, and Joi Choi; and kale cvs. Starbor, White Russian, Winterbor, Redbor, and Black Magic were evaluated at two sequential plantings under open-field and high-tunnel production systems. The second planting was done about one week after harvesting the first crop. The ‘Regular-type’ Bok Choy’ cv. Joi Choi produced the highest marketable yield under both

field (115 t/ha) and high-tunnel (81 t/ha) production systems. The 'Baby Bok Choy' cv. Mei-Qin Choi produced the highest marketable yield under both field (61 t/ha) and high-tunnel (52 t/ha) production systems. 'Early' planted Bok Choy produced higher marketable yields, larger, and more attractive heads compared to the 'Late' planted crop under both production systems. Kale cv. White Russian produced the highest marketable leaf yield under both field (27 t/ha) and high-tunnel (37 t/ha) production. Under field-production, late planting adversely (about 50% lower) affected leaf yield relative to early planting. However under high-tunnel, planting date had no effect on leaf yield. The effects production system and planting dates on the performance attributes of Bock Choy and kale will be discussed in detail.

***[O161] OPTIMIZATION OF LIGHT INTENSITY FOR GROWTH OF MINT (*MENTHA* SPP.) IN CONTROLLED ENVIRONMENTS.** Andrew Burns, Mike Dixon, Mike Stasiak, and Youbin Zheng.
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Controlled environment agriculture (CEA) is a versatile technology that has the potential to reduce the environmental impact of commercial farming while simultaneously enhancing crop yield and quality. This technology is particularly promising for medicinal plants, as it offers opportunities to increase the content of valuable compounds. Innately antimicrobial, medicinally active, and valued for its desirable flavor and aroma, mint (*Mentha* species) is a historically and economically significant herb of the Lamiaceae family. The essential oil, which is mainly found in glandular trichomes on leaf and stem surfaces, is the most economically important component of the plant for its use in food, cosmetics, and hygienic products. Challenges presented by traditional field farming of mint, namely diseases such as verticillium wilt and increasingly unpredictable weather extremes, may be addressed in CEA. This research was conducted to optimize environmental parameters such as light intensity, photoperiod, and carbon dioxide concentration for mint growth and production of high-quality essential oil. The capital (e.g., fixtures) and energy costs associated with crop lighting are substantial crop inputs for all CEA production systems. Therefore, to optimize lighting inputs, it is necessary to determine how the quantity of photosynthetically active radiation (PAR) affects mint growth and essential oil production in CEA. A gradient design was employed in which a mint crop was grown in a heterogeneous lighting environment where individual plants were exposed to unique and well-characterized light levels. Key growth and yield parameters were collected and related to individual plants' light levels using regression-style analyses. A subset of plants representative of the various light level acclimations were subjected to whole-plant net carbon exchange rate (NCER) measurements to assess the reliability of extrapolating short-term NCER measurements to model longer term mint growth and yield dynamics.

***[O162] HARNESSING CONTROLLED ENVIRONMENT SYSTEMS FOR ENHANCED PRODUCTION OF MEDICINAL PLANTS.** Ajwal Dsouza[1], Mike Dixon[1], Mukund Shukla[2], and Thomas Graham[1]. [1]
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Medicinal plants (MPs) are valued for their contributions to human health. However, the growing demand for MPs and the concerns regarding their quality and sustainability have prompted the reassessment of conventional production practices. Controlled environment cropping systems, such as vertical farms, offer a transformative approach to MP production. By enabling precise control over environment factors, such as light, carbon dioxide, temperature, humidity, nutrients, and airflow, controlled environments can improve the consistency, concentration, and yield of bioactive phytochemicals in MPs. This presentation explores the potential of controlled environment systems for enhancing MP production. First, I will describe how controlled environments can overcome the limitations of conventional production in improving the quality of MP. Next, I will propose strategies based on plant physiology to manipulate environment conditions for enhancing the levels of bioactive compounds in plants. These strategies include improving photosynthetic carbon assimilation, light spectrum signalling, purposeful stress elicitation, and chronoculture. I will describe the underlying mechanisms and practical applications of these strategies. Finally, I will highlight the major knowledge gaps and challenges that limit the application of controlled environments, and discuss future research directions.

[O165a] TEMPERATURE IMPACT ON PLANT GROWTH AND DEVELOPMENT OF SELECTED VEGETABLES. Peter A. Ofori, Raphael Ofoe, Efoo B. Nutsukpo, and Lord Abbey. Department of Plant, Food, and Environmental Sciences, Faculty of Agriculture, Dalhousie University, 50 Pictou Road, Bible Hill, NS B2N 5E3, Canada
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Temperature stress impacts the growth, development, and productivity of crops, and this continue to be important due to sustained global climate change. A study was performed to determine the effects of different temperatures (10°, 22°, and 35°C) on the morpho- physiological and biochemical responses of mint, lettuce, and tomato in a controlled environment. The results revealed that plant height and SPAD value of mint were not significantly ($p > 0.05$) affected by 35°C and 22°C, but reduced by *ca*. 51% and 38% respectively, compared to 22°C. The 10°C and 35°C significantly ($p < 0.001$) reduced plant height by 55% and 28%; and stem girth by *ca*. 60% and 49% of lettuce, respectively compared to 22°C. The height and stem girth of tomato were not significantly ($p > 0.05$) altered under both 22°C and 35°C, but were reduced considerably by *ca*. up to 62% and 66% respectively under 10°C compared to 22°C. The SPAD value was significantly ($p < 0.001$) increased by *ca*. 42.3% under 10°C compared to 22°C and 35°C. Total protein, sugar, carotenoids, flavonoids and phenolics contents were significantly ($p < 0.001$) affected by the interaction between crop species and growth temperature. The findings can contribute to the development of strategies for improving the tolerance of these crops to temperature extremes and ensuring food security in the face of climate change. Further studies should be conducted to evaluate the effect of these temperature regimes on the metabolite profile of these selected vegetables.
Keywords: climate change, abiotic stress, cold stress, heat stress, stress tolerance

***[O165b] EXPLORING THE IMPACT OF FAR-RED AND BLUE LED LIGHT RATIOS ON *BOTRYTIS CINEREA*'S MORPHOGENESIS.** Abheet Aulakh[1], William Jordan[1], and Valerie Gravel[1]. [1]Department of Plant Science, McGill University – Macdonald Campus, 21111 Lakeshore Road, Sainte-Anne-de-Bellevue, QC H9X3V9
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Botrytis cinerea is the most important necrotrophic fungal pathogen infecting about 200 species of crops. Along with field crops, its devastating effect in control environment cropping system is of major concern. Being a fragile fruit, strawberries are greatly affected by grey mold caused by *Botrytis cinerea*. Current management strategies, primarily fungicides, face challenges due to the pathogen's genetic variability and widespread fungicide resistance. While considering the pathogen's response to light for inducing adaptive response, this study explores an innovative approach using light manipulation to inhibit the morphogenesis of *B. cinerea* and enhance plant resistance. The adaptability, energy efficiency, and customizable spectrum of light-emitting diodes (LEDs) offer promising tools for this purpose. Recent research has demonstrated that specific wavelengths of light, particularly red, far-red, and blue, can significantly affect plant-pathogen interactions by altering the pathogen development and increasing host resistance. Based on these findings, our study aimed to evaluate the effects of different light ratios of far-red to blue light (5:1, 1:5, and 1:1) on strawberry resistance to *B. cinerea*, with a particular focus on changes in the pathogen morphogenesis. Three experimental assays were conducted to assess the effect of light treatments in comparison to control treatments (ambient and dark) on mycelial growth, sporulation, and spore germination. Results showed an interesting observation with unaffected mycelial growth under light treatments but a significant effect on sporulation among the treatments, as 5:1 and 1:5 completely inhibited the spore production and there was less sporulation in 1:1 as compared to dark and ambient light controls. Considering the spore germination after 7 hours post inoculation, blue and far-red dominant light ratios (1:5 and 5:1) have lower germination percentage than other treatments. These observations indicate that manipulating light spectra through LEDs can potentially disrupt the life cycle of *B. cinerea*, thereby reducing its virulence.

[O166] COMPARING PHENOTYPIC SELECTION WITH GENOMIC SELECTION WHEN BREEDING FOR NEW VARIETIES OF COMMON BEAN (PHASEOLUS VULGARIS): AN EMPIRICAL STUDY.
Robert McGee[1], Isabella Chiaravalotti[1], Marysia Zaleski-Cox[1], Evan Wright[2], Karen Cichy[3], Diego Jarquin D[4], and Valerio Hoyos-Villegas[1]. [1]McGill University, Department of Plant Science, Raymond Building, 21111 Lakeshore Road, Ste. Anne de Bellevue, Quebec, H9X 3V9, Canada; [2]Michigan State University (MSU), Department of Plant, Soil and Microbial Sciences, 1066 Bogue Street, East Lansing, 48824, Michigan, USA; [3]USDA-ARS, 1066 Bogue Street, Michigan State University (MSU), East Lansing, 48824, Michigan, USA; and [4]University of Florida (UF/IFAS), Agronomy Department, 2089 McCarty Hall B, Gainesville, Florida, USA.
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Since the 1900s, yield of common bean (*Phaseolus vulgaris*) has only increased by 1 % per year (i.e. genetic gain), far below the ~3 % genetic gain required to feed the growing world population. To address this challenge, new approaches are needed to rapidly develop new high yielding common bean varieties. Breeding for yield is however challenging because it is a complex quantitative trait controlled by multiple genes each with minor allelic effects, unlike simple traits that are controlled by small set of genes. Genomic selection (GS) seeks to overcome this challenge by capturing the minor allelic effects of multiple genes across the whole genome simultaneously, thereby enabling more accurate selection for quantitative traits. Whether GS is superior to the conventional approach of selecting the highest yield lines (phenotypic selection: PS) in common bean is unknown because no known empirical studies have directly compared the breeding outcomes of GS and PS.

In this project, to directly compare GS and PS, two breeding pipelines were initiated in parallel from the same pool of 38 advanced cranberry bean breeding lines. To initiate the PS pipeline, five parents were selected solely on their phenotype (highest yielding) for 10 bi-parental crosses. The resulting F_2 plants will undergo PS in the field starting in summer 2024. In contrast, in the GS pipeline, five parents were selected with the highest genomic estimated breeding values (GEBVs) calculated from a GS model (rrBLUP) trained using phenotypic (seed yield) and genomic data (8,757 SNPs) from a 2021 training population consisting of 119 advance lines (286 genotypes) from a mix of common bean market classes. Hybridity of the resulting 212 F_1 seeds from the GS pipeline was determined using newly developed Kompetitive Allele Specific PCR (KASP) markers, revealing how the % of true hybrids differed wildly between different parental combinations. F_2 seeds from these true hybrids were advanced in the greenhouse via single seed descent (SSD) to the F4 generation in 2023-2024. The resulting F_5 seeds will be bulked in the field in summer 2024. In summer 2026, once both pipelines, PS and GS, have reached PYTs, genetic gain, selection accuracy, and cycle time will be directly compared to determine if GS does or does not outperform PS in common bean. The findings from this project will help inform common bean breeding programs of the merits and challenges of implementing GS within their existing breeding programs.

[O167] A MULTISPECIES AMPLISEQ APPROACH TO ASSESS INTRA- AND INTER-SPECIFIC DIVERSITY OF *SPHAGNUM* AND ASSIST RESTORATION EFFORTS.
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Peatlands cover about 2% of the total land area of New Brunswick, and the province is the leading producer of peat in Canada. Peatlands primarily consist of mosses from the genus *Sphagnum*, which includes 160 species worldwide that are challenging to identify in the field or without substantial expertise. After peat extraction, peatlands can be restored, and their ecosystem functions (including carbon accumulation) can be reinstated within 10-20 years. Although *Sphagnum* has the ability to recover from residual fragments and spread by spores over long distances, success of recolonization varies among species due to hydrological changes, loss of original soil characteristics, and the unique niches each species inhabits. Reintroduction of target *Sphagnum* species may be crucial to restore *Sphagnum* diversity and to accelerate the re-establishment of a natural vegetation. In this study, we used a bioinformatic approach to identify 526 regions from distinct single-copy genes exhibiting higher interspecific diversity. We then developed an amplicon sequencing approach to quickly characterize these regions in 700+ individuals collected from natural and restored peatlands in New Brunswick, which

had been visually assigned to seven different species groups: *S. angustifolium* and *S. fallax* (section Cuspidata), *S. flavicomans*, *S. fuscum* and *S. rubellum* (section Acutifolia), and *S. magellanicum* (*sensu lato*) and *S. papillosum* (section Sphagnum). We conducted structure and phylogenetic analyses to clarify the identities of these individuals and used intra- and inter-specific variability to assess differences between natural and restored peatlands. Individuals within the *S. magellanicum* complex were easily classified as *S. diabolicum*, *S. divinum* or *S. medium*. Additionally, 55% of individuals visually identified as *S. fuscum* were found to be genetically distinct, and demonstrated to belong to *S. beothuk*, previously unreported in Atlantic Canada (outside of Newfoundland). Population analyses showed no significant differences between natural and restored peatlands, which is promising for future restoration efforts. The tools presented in this study offer a cost-effective method for multispecies genetic diversity assessments in peatland-inhabiting *Sphagnum* and provide a solid foundation for further improvements and adaptations.

***[O168] GENOME-WIDE ASSOCIATION ANALYSIS OF LODGING-RELATED CULM TRAITS IN DIVERSE SPRING WHEAT (*TRITICUM AESTIVUM* L.) POPULATION.** Ginelle Grenier[1], Muhammad Iqbal[2], Curt McCartney[1], Gavin D. Humphreys[3], Dean Spaner[2], and Belay T. Ayele[1]. [1]Department of Plant Science, University of Manitoba, Winnipeg, Manitoba, Canada; [2]Department of Agricultural, Food and Nutritional Sciences, Edmonton, Alberta, Canada; and [3]Ottawa Research and Development Center, Agriculture and Agri-Food Canada, Ottawa, Ontario, Canada
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Lodging is a common constraint to spring wheat (*Triticum aestivum* L.) production as it lowers harvest efficiency and causes significant yield and end-use quality losses. It is a quantitative trait regulated by many genes and environmental factors including agronomic practices. The traditional approach of reducing lodging risks in wheat through introducing semi-dwarfing genes may limit the yield potential of modern cultivars, prompting the need to identify alternate genetic components that can improve lodging resistance. To this end, this study conducted a genome-wide association study (GWAS) in multiple environments using a diverse mapping panel. The mapping panel was phenotyped for various lodging-related culm traits at Feekes growth stage 11.1 including the breaking strength (N), bending moment (g cm), and lodging index (g cm N^{-1}) of the second basal internode. The same panel was genotyped using the 90K iSelect BeadChip Array, and a set of 18611 resultant single nucleotide polymorphism (SNP) markers were used for GWAS analysis to determine their association with lodging-related traits examined. Our analysis identified a total of 61 SNP markers and 23 putative QTL regions displaying significant associations with the internode breaking strength, bending moment, and lodging index traits across all trial environments. Furthermore, we identified a QTL on chromosome 1B that is associated with both internode bending moment and lodging index, and another QTL on chromosome 2A that is consistently associated with internode breaking strength in all individual trial environments. The results of this study may have potential use in marker-assisted selection for lodging resistance in spring wheat.

[O169] PAN-GENOME AND LONG-READ STRUCTURAL VARIANT LANDSCAPE OF 51 BRASSICA NAPUS GENOMES UNVEIL CANOLA'S HIDDEN GENETIC DIVERSITY FOR CROP IMPROVEMENT. Sampath Perumal[1], Kevin Koh[1], Raju Chaudhary[1], Peng Gao[2], Isobel Parkin[2], and Andrew Sharpe[1].
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Background:
Canola (Brassica napus), also known as rapeseed, is a globally important crop widely cultivated for its oil and protein-rich seeds, with applications in the food, biofuel, and animal feed industries. However, its genetic improvement is challenging due to its narrow genetic base.To overcome the challenges in improving canola genetics, constructing a comprehensive pan-genome that captures the genetic diversity of the entire population is essential. The pan-genome is a collection of all genes and genetic variations including structural variations (SVs) present in a species, including rare and novel variations that are not captured in traditional reference genomes.
Nanopore sequencing technology was used to sequence 50 canola spring type parents. Long-read assembly was developed for the 50 NAM parents and a pan-genome was constructed. Structural variants

were characterized using nanopore reads, and panSV was developed. In addition, short-read DNA was used for SNP analysis, and RNA sequence data was used for gene-annotation and expression analysis.

Results:
A pan-genome for 50 spring type canola parents was constructed using nanopore-based genome assembly. This approach accurately assembled complex genomic regions and enhanced the quality of the pan-genome. Structural variants were characterized using long-reads, and >230K SV were identified across the 50 NAM parents, with almost 50% of them being present in close proximity to 5Kb gene regions. Interestingly, 1% of the SV are expected to have evolved from transposable elements (especially by active retro-transposons). This resource provides a valuable tool for understanding the genetic architecture of a population and identifying genes and genetic variations associated with desirable traits. This study reports the successful construction of a pan-genome for 50 spring NAM canola parents using long-read based genome assembly and structural variant annotation. The pan-genome provides a comprehensive representation of the genetic diversity present in the spring type canola population, including rare and novel genomic variations not captured in traditional reference genomes. The resulting pan genome resources will be a valuable resource for genetic studies and breeding efforts in canola, ultimately leading to improved crop yield and quality.

***[O170] GENOME-WIDE ASSOCIATION AND GENOMIC SELECTION FOR OIL AND FATTY ACID PROFILE IN RAPESEED (*BRASSICA NAPUS* L.).** Jared Bento[1], Jia Sun[1], Sakaria Liban[1], Curt McCartney[1], Harmeet Chawla[1], and Robert Duncan[1]. [1]Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB, Canada, R3T2N2
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The overarching goals of rapeseed (*Brassica napus* L.) breeding efforts include the improvement of yield- and seed-quality-related traits to meet the evolving demands of a growing population. Genome-wide association studies (GWAS) and genomic selection (GS) are important biotechnological methods that provide the potential to improve selection efficiency and shorten crop breeding cycles. These biotechnologies facilitate more rapid responses to agronomic and quality challenges, as well as enhance the sustainability of plant breeding programs by reducing the crop inputs, carbon emissions, and other procedures associated with long-term programs.

This study has three main objectives: 1) GWAS to identify quantitative trait loci (QTL) for five seed quality traits (overall oil content, erucic, oleic, linoleic, and linolenic acids), 2) evaluating GS accuracy in predicting rapeseed hybrid fatty acid profile components, and 3) evaluating the "GS + de novo GWAS" method proposed to improve GS prediction accuracy.
We analyzed 454 *Brassica napus* genotypes (92 parents, 362 hybrids) grown over 48 site-years. All genotypes were genotyped via *Brassica* 60K Illumina SNP array.

Across 24 unique GWAS analyses, 161 QTL were identified, including 22 QTL for erucic acid. Several QTL coincide with candidate genes identified in literature. Novel QTL have also been identified for all five traits, warranting further candidate gene investigation.

Prediction accuracies for each seed quality trait were compared across 135 unique analyses, evaluating responses to GS models (nine regression models), population (five model training/validation population designs), and marker density (three marker sets containing low, intermediate, and high densities). Prediction accuracies (represented by correlation between predicted and actual phenotypes) range from 0.023 (overall oil content) to 0.897% (linoleic acid content). Prediction accuracies exhibited negative correlation to trait complexity, positive correlation to degree of training/validation population relatedness, and no significant differences among marker densities or parametric models. Machine learning models performed either equivalent or worse than common parametric models. Overall oil content, the most complex trait analyzed, showed accuracy improvements as high as 0.745 when varying the aforementioned factors.

By incorporating significant markers from GWAS, the accuracies of “GS + de novo GWAS” methods were compared to conventional GS models. Prediction accuracy response appears trait-dependent: two traits

exhibited marginal increases (erucic, oleic), one exhibited marginal decreases (linolenic), and two exhibited no differences relative to conventional GS (linoleic, overall oil content).
The promising accuracy of GS observed in this study supports its potential utility in future *Brassica* breeding programs.

[O171] CROSS-SPECIES COMPARATIVE SEQUENCE-BASED GENE EXPRESSION MODELLING IN LEGUMES. Nicolas Raymond[1], Sheikh Jubair[1], Jordan Ubbens[2], Xi Zhang[2], Fatima Davelouis[1], Ruchika Verma[1], David Staszak[1], Dustin Cram[2], Halim Song[2], Yongguo Cao[2], Christine Sidebottom[2], Yasmina Bekkaoui[2], Morgan Kirzinger[2], Deborah Akaniru[1], and David Konkin[2]. [1]Alberta Machine Intelligence Institute, Edmonton, Canada; and [2]Aquatic and Crop Resource Development, National Research Council of Canada, Saskatoon, Canada
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Advances in genomics, machine learning and gene editing present an opportunity to accelerate trait discovery and breeding by incorporating base-level functional interpretation into breeding and research strategies. Natural genetic diversity represents an extremely rich resource for modelling gene expression but comes with the challenges associated with non-independence of variation due to evolutionary processes. In order to build neural network-based gene expression models that predict transcription and transcript stability directly from DNA sequence, we are leveraging cross-species differences in gene expression from matched RNA-seq and PRO-seq datasets for reference lineages of a variety of cool season legumes including, field pea (*Pisum sativum*), grass pea (*Lathyrus sativus*), faba bean (*Vicia faba*), and barrel medic (*Medicago truncatula*). Here, we detail our progress on these models, and highlight potential applications for variant interpretation and transcript association studies.

[O173] HUMIC PRODUCTS: TO USE OR NOT TO USE IN YOUR FIELD. Linda Y. Gorim[1]. [1]Department of Agricultural, Food and Nutritional Science Room 410 Agriculture/Forestry Centre, University of Alberta, Edmonton, Alberta, Canada T6G 2P5
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Humic products are widely sold to Canadian producers as either soil amendments or biostimulants. Several humic products are available in solid and liquid forms. In Alberta, huge deposits of humalite have been applied by producers but questions on appropriate humalite application rates for specific crops, its impact of crop yield and soil health; and its interaction with nitrogen rates are unknown. Most trials on humic products have been conducted indoors. Information from prairie-specific field trials to aid producers' decision making are lacking. Therefore, a study was initiated in 2021 at three sites representing three soil zones with the objective to (i) identify humalite application rates for different soil zones, and (ii) assess the effects of humalite in the presence of reduced urea on crop yield. We further conducted an incubation experiment using soil from different soil zones to assess the interaction of soil pH, humalite and soil nutrients. Results indicate that field application of humalite at 200 and 400 lbs/ac produced high crop yields depending on urea rates. Soil with high SOM did not respond to humalite application especially in a wet year. There are indications that humalite effects maybe moisture and crop specific: More effects in wheat than canola and in dry years. Leaf applied humic product are not effective – should be soil applied. Humic products differ and decision to use them should be economics based. A strong interaction between humalite, soil zone and pH was observed in the incubation experiment.

[O174] GROWTH-PROMOTING RHIZOBACTERIA MITIGATES SALT STRESS IN RICE THROUGH THE ENHANCEMENT OF ANTIOXIDANT DEFENSE, ION HOMEOSTASIS, AND PHOTOSYNTHETIC PARAMETERS. Ayesha Siddika[1], Alfi Anjum Rashid[2], Shakila Nargis Khan[2], Amena Khatun[3], Muhammad Manjurul Karim[2], PV Vara Prasad[4], and Mirza Hasanuzzaman[1]. [1]Department of Agronomy, Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh; [2]Department of Microbiology, University of Dhaka, Dhaka 1000, Bangladesh; [3]Noakhali Science and Technology University, Noakhali-3814, Bangladesh; and [4]Department of Agronomy, Kansas State University, Manhattan, KS, United States
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The ongoing expansion of global salt-affected land is a significant factor limiting crop growth and yield, particularly for rice. This experiment explores the mitigation of salt-induced damage on rice (*Oryza sativa* L. cv BRRI dhan100) by applying plant growth-promoting rhizobacteria (PGPR) cultures. Rice seedlings, five- and six-weeks post-transplanting, were subjected to salt stress via two treatments with 50 and 100 mM NaCl at seven-day intervals. Bacterial cultures, comprising endophytic PGPR strains (*Bacillus subtilis* and *B. aryabhattai*) and an epiphytic PGPR strain (*B. aryabhattai*), were administered at three critical stages: during transplantation of 42-day-old seedlings, five weeks later at the vegetative stage at 35 days after transplanting (DAT), and seven weeks later at 49 DAT during panicle initiation stage. Salt stress prompted osmotic, ionic, and oxidative stress, in rice plants, causing a dose-dependent decrease in relative water content, chlorophyll content, stomatal conductance, chlorophyll fluorescence, IAA concentrations, and various growth parameters. Furthermore, osmotic stress escalated the hydrogen peroxide content and proline accumulation, while ionic stress disrupted ion balance by increasing Na^+ and reducing K^+ content. Both types of stress generated reactive oxygen species, impairing the antioxidant defense system and causing oxidative damage, as well as methylglyoxal (MG) toxicity, which was visible in heightened malondialdehyde levels, electrolyte leakage, and Glyoxalase I (Gly I) and Glyoxalase II (Gly II) activities. PGPR treatment alleviated these negative effects by enhancing osmotic and ionic balance, demonstrated by improved water balance and reduced Na^+ content and Na^+/K^+ ratio. Additionally, PGPR fortified the antioxidative defense system and MG detoxification in salt-exposed rice plants by increasing ascorbate and glutathione levels, antioxidant enzymes (ascorbate peroxidase, dehydroascorbate reductase, monodehydroascorbate reductase, glutathione reductase, catalase, peroxidase, superoxide dismutase, lipoxygenases, glutathione peroxidase, glutathione *S*-transferase), and glyoxalase enzymes (Gly I and Gly II). The introduction of PGPR led to enhancements in yield attributes (including effective tillers per hill, panicle length, rachis per panicle, filled grains per panicle, and 1000-grain weight), consequently boosting the grain yield per hill. In conclusion, this research highlights the potential of PGPR to bolster physiological and biochemical functionality in rice, serving as an effective buffer against salt stress-induced damage.

[O175] EFFECTS OF DEFOLIATION ON ROOT TRAITS, NITROGEN FIXATION, SOIL NITROGEN AVAILABILITY, SOIL ENZYME ACTIVITIES AND SOIL BACTERIAL COMMUNITIES OF FORAGE LEGUMES. Malinda Thilakarathna[1], Danielito Dollete[1], Rhea Amor Lumactud[2], Cameron Carlyle[1], and Krzysztof Szczyglowski[3]. [1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada, T6G 2P5; [2]Department of Plant, Food, and Environmental Sciences, Dalhousie University, Truro, Nova Scotia, Canada, B2N 5E3; and [3]Agriculture and Agri-Food Canada, London Research and Development Centre, London, Ontario, Canada, N5V 4T3
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Forage legumes fix atmospheric nitrogen through a mutualistic relationship with rhizobia bacteria. However, frequent defoliation stress from grazing and mowing can alter the source-sink relationship between above-ground and below-ground tissues, potentially impacting their nitrogen-fixing ability. In this study, we evaluated the effects of defoliation intensities on nodulation, root phenotypic traits, plant biomass, symbiotic nitrogen fixation, soil available nitrogen, soil enzyme activities, and soil microbial community structure of alfalfa (*Medicago sativa* L.) and red clover (*Trifolium pretense* L.). Two defoliation intensities were applied at flowering: mild (removing half of above-ground biomass) and severe (leaving only 2 cm stubble), along with non-defoliated controls. Mild defoliation positively affected final shoot biomass in both legumes but had negative effects on nodulation and non-symbiotic root traits, including root biomass. The symbiotic nitrogen fixation capacity was reduced in red clover under severe defoliation stress, whereas it was unaffected in alfalfa. The available nitrogen content in red clover was greater following severe defoliation than in mild and non-defoliation, but no changes were observed in alfalfa following defoliation. Severe defoliation significantly increased soil enzyme activities of β-1, 4-glucosidase, β-D-cellobiosidase, and phosphatase enzymes in both legumes. Defoliation had no significant effect on shifting soil bacterial diversity or taxonomic composition. Overall results suggest that defoliation intensity had a deleterious effect on root traits, a positive influence on C and P extracellular enzyme activities, but varied influence on the shoot growth, symbiotic nitrogen fixation, and soil available nitrogen based on the forage legume.

[O176a] EFFECT OF ROW SPACINGS/GEOMETRY AND RATES OF S APPLICATION ON ALFALFA YIELD AND QUALITY IN NORTHERN ONTARIO. Tarlok Singh Sahota[1], Harmeet Singh[1], Mikala Parr[2], David Thompson[2], and Kim Jo Bliss[3]. [1]LUARS, 5790 Little Norway Road, Thunder Bay, ON, P7J 1G1; [2]Level Six, 99 Foster Dr, Sault Ste. Marie, ON P6A 5X6; and [3]EARS, Chapple, ON P0W 1E0
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A field experiment with combinations of three row spacings/geometries (regular seedings at 6-7" row spacings, missing an alternate row and missing one row after every two rows by keeping the seed rate constant in the three cases) and four rates of S application (0, 24, 36 and 48 kg S ha^{-1} all at seeding or early spring and 48 kg S ha^{-1} applied in two splits; half at seeding/early spring and half after the first cut) replicated four times in RCBD was conducted during 2020-'23 at Thunder Bay, and during 2020-'22 at Algoma and Emo. In two out of three years at Thunder Bay, missing one row after every two rows produced the highest dry matter yield (DMY) of alfalfa. However, averaged over three years, row spacings recorded the similar DMY (6.05 to 6.29 Mg ha^{-1}). Pre seeding soil test for S was 6 ppm at Thunder Bay and 8 ppm at Algoma. Averaged over three years, DMY increased linearly with the application of S up to 36 kg S ha^{-1} (from 5.82 Mg^{-1} to 6.59 Mg^{-1}) and exhibited a Law of Diminishing Returns thereafter. At Algoma, DMY of alfalfa increased with the application of 24 kg S ha^{-1}. Rates higher than 24 kg S ha^{-1} didn't improve the DMY further. Row spacings or application of S didn't influence DMY of alfalfa at Emo. Feed quality was tested only at Thunder Bay, where averaged over three years, protein content (19.1%-19.5%) or RFV (127-128) in the first cut didn't vary much with the row spacings. Same was true for the second cut (21.3-21.5% protein and 126-129 RFV). Highest first cut protein content was obtained with 24 kg S ha^{-1} (20%) and the highest RFV with the 48 kg S ha^{-1} applied in two splits (131). In the second cut, highest protein content was recorded with 36 kg S ha^{-1} (21.7%) and the highest RFV (131) with 24 kg S ha^{-1}. Application of S @ 36 kg S ha^{-1} could be recommended at Thunder Bay, and @ 24 kg S ha^{-1} at Algoma.

[O176b] CLIMATE CONDITIONS IN THE NEAR-TERM, MID-TERM AND DISTANT FUTURE FOR GROWING SOYBEANS IN CANADA. Budong Qian[1], Ward Smith[1], Qi Jing[1], Yong Min Kim[2], Guillaume Jégo[3], Brian Grant[1], Scott Duguid[4], Ken Hester[5], and Alison Nelson[6]. [1]Ottawa Research and Development Centre, Science and Technology Branch, Agriculture and Agri-Food Canada, Ottawa, ON K1A 0C6; [2]Brandon Research and Development Centre, Science and Technology Branch, Agriculture and Agri-Food Canada, Brandon, MB R7A 5Y3; [3]Québec Research and Development Centre, Science and Technology Branch, Agriculture and Agri-Food Canada, Québec, QC G1V 2J3; [4]Morden Research and Development Centre, Science and Technology Branch, Agriculture and Agri-Food Canada, Morden, MB R6M 1Y5; [5]Oilseeds, Pulses, Special Crops and Industrial Bioproducts, Market and Industry Services Branch, Agriculture and Agri-Food Canada, Ottawa, ON K1A 0C5; and [6]Director's Office RDT Manitoba, Science and Technology Branch, Agriculture and Agri-Food Canada, Winnipeg, MB R3C 3G7
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The soybean industry in Canada aimed to extensively expand soybean production to benefit from new early-maturing varieties and the warming climate. However, setbacks in the soybean industry since 2017 demonstrated the impacts of climate risk and global market uncertainty. Therefore, a better understanding of future climate conditions that will impact soybean growth in Canada is needed for decision-making in the sector, such as prioritizing regions for expansion and developing climate change adaptation strategies through either agronomic management practices or breeding new cultivars. Based on climate projections from a set of global climate models, we analyzed climate conditions for growing soybeans including growing season start, crop heat units, precipitation, precipitation deficits, and climate extremes, in the near-term (2030s), the mid-term (2050s) and the distant future (2070s). We found that a future warmer climate with an increase of 1.6, 2.8 and 4.1°C in the growing season (May – September) mean temperature averaged over Canada's land area in the near-term, mid-term and distant future under SSP3-7.0, would favour the expansion of soybean production further north and west. However, an increase of approximately 200 mm in precipitation deficits on the semiarid Canadian Prairies in the mid term would constrain soybean production unless irrigation could be introduced. Heat- and drought-tolerant cultivars should be developed to adapt soybean production to a changing climate, in addition to the adoption of late-maturing cultivars that would benefit from the lengthened growing season and increased crop heat units.

[O177] *DE NOVO* WHOLE-GENOME ASSEMBLIES AND A COMPARATIVE PANGENOME ANALYSIS OF THE SOILBORNE PLANT PATHOGEN *PLASMODIOPHORA BRASSICAE*. Sandra M. Velasco-Cuervo[1], Yoann Aigu[1], Leonardo Galindo-González[1-2], Sheau-Fang Hwang[1] and Stephen E. Strelkov[1]. [1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada; and [2]Ottawa Plant Laboratory (Fallowfield), Science Branch, Canadian Food Inspection Agency, Ottawa, ON, Canada
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Plasmodiophora brassicae causes clubroot, a soilborne disease of canola (*Brassica napus*) and other crucifers. Pathogen isolates are classified into pathotypes based on their virulence on the hosts of the Canadian Clubroot Differential (CCD) set. Genomic resources for *P. brassicae*, especially for Canadian pathotypes, are currently limited. The main objective of this project is to identify differences between pathotypes of *P. brassicae*, facilitating molecular identification and enhancing understanding of the diversity and relationships between them. High Fidelity (HiFi) sequencing was utilized to generate long-reads and construct *de novo* whole-genome assemblies for single-spore isolates of *P. brassicae*, representing seven important pathotypes. The assemblies currently have an average completeness of 80.84% based on BUSCO analysis, and an average genome size of 24.55 Mb. The first annotation round for each assembly resulted in an average of 30.05% of the genome annotated as repetitive regions. A pangenome was constructed using the seven *P. brassicae* assemblies, revealing a core genome that accounted for 66.7% of the total genome length and an accessory genome comprising 33.92%. Nine-hundred eighty-one structural variants (897 bi-allelic and 84 multi-allelic) were identified, with an average of 60,000 SNPs observed between the assemblies. A comprehensive genome annotation is underway. Selected SNPs and structural variants will be tested through Sanger sequencing to validate the results from the bioinformatic analyses. This approach will enable the identification of polymorphic regions and development of a metabarcoding assay for *P. brassicae* pathotype detection. These findings can also be integrated into studies of the pathogen's evolution and genomic architecture.

[O178] GENOMIC INVESTIGATION OF WESTERN CANADIAN APHANOMYCES EUTEICHES ISOLATES FROM MULTIPLE HOST LEGUME CROPS. Zelalem Taye[1], Jamuna Paudel[1], Lou Kun[1], Cormier Trista[1], Ethan Done[1], Jennifer Town[1], Syama Chatterton[2], Michelle Hubbard[3], Hossein Borhan[1] and Nicholas Larkan[1]. [1]Saskatoon RDC, Agriculture & Agri-Food Canada, Saskatoon, Saskatchewan, Canada; [2]Lethbridge RDC, Agriculture & Agri-Food Canada, Lethbridge, Alberta, Canada; and [3]Swift Current RDC, Agriculture & Agri-Food Canada, Swift Current, Saskatchewan, Canada
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Aphanomyces root rot (ARR) is a significant challenge to pea cultivation in Western Canada. Its impact is also progressively extending to other crops like lentils and dry beans. Recent advances in pathology testing involving *Aphanomyces euteiches* isolates from diverse host crops have revealed intriguing nuances suggesting the existence of varying degrees of host specificity within distinct populations of *A. euteiches*. In addition, metagenomic investigations have also unveiled a higher level of genetic diversity within field populations than previously expected. These insights into the complex nature of ARR underscore the need for comprehensive research to help inform management strategies in the region. In the pursuit of identifying resistance possibilities and other management options in different host crops and environments, and advancing molecular diagnostic techniques for pathogen monitoring, it is crucial to gain insights into the population dynamics of *A. euteiches* and any potential host-specific relationships linked to pathogen genotype. In this presentation, diversity of *A. euteiches* in the region, genomes of isolates from pea and lentil, and lesson learned from pathology of the pathogen and future work aimed at characterizing *A. euteiches* populations across Western Canada will be presented.

[O179] SINGLE-CELL DNA SEQUENCING OF *PLASMODIOPHORA BRASSICAE* REVEALS CLONAL CHARACTERISTICS. A. Sedaghatkish[1], B. D. Gossen[2], and M. R. McDonald[1]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1, Canada; and [2]Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, Saskatoon, SK S7N 0X2, Canada
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This study explored the genomic variation in *Plasmodiophora brassicae* Wor., an obligate Chromist pathogen responsible for clubroot disease in canola (*Brassica napus* L.) and other brassica crops. The

genetic diversity of individual resting spores from a single clubbed canola root of a collection from Normandin, Quebec, pathotype 5X, was assessed. The 'x' designation indicates that the pathotype can overcome first generation clubroot resistance in canola. An enzymatic method was developed to remove cell walls from resting spores to produce protoplasts. The ~4,000 individual protoplasts were barcoded and DNA of each cell was sequenced. Elbow plot analysis indicated the presence of at least two clonal groups. Complementing this, silhouette clustering, which evaluates the proximity of points within clusters to those in neighboring clusters, confirmed the presence of at least two clones. Hierarchical clustering identified five distinct clones, consisting of 829 cells (Clade 1), 1120 cells (Clade 2), 1140 cells (Clade 3), 183 cells (Clade 4), and 445 cells (Clade 5). Principal component analysis supported the presence of five clones. Heat maps were generated to visualize the genetic diversity across these clones and to compare the single-cell data with bulk sequences from five field collections, including the original Normandin 5X. Clade 3, which had the highest number of cells, showed a high similarity to the original field collection. The identification of 2 to 5 clades among 4,000 resting spores demonstrates that the *P. brassicae* population in a single club is genetically diverse. Large differences among the clones supported our hypothesis from a previous study that entire genotypes are retained over time in the population of *P. brassicae*. The genetic diversity this represents has important implications for breeding for resistance, as no single-gene source of resistance is likely to be durable. Furthermore, the dissimilarity among genotypes suggests they are not siblings from sexual reproduction, indicating that pathogen increase within an infected host plant is predominantly or exclusively clonal.

[O180] METAGENOMICS-BASED MICROBIAL COMMUNITY PROFILING IN THE QUEST FOR POTATO WART BIOLOGICAL CONTROL AGENTS. Ishraq Akbar[1,2], Yichao Shi[1], Bart. T. L. H. van de Vossenberg[3], Theo A. J. van der Lee[3], Sean Li[4], Linda Jewell[5], Hai D.T. Nguyen[1], and Wen Chen[1,2].
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Potato wart is a soil-borne disease characterized by cauliflower-like growths on potatoes, caused by the obligate biotrophic chytrid fungus *Synchytrium endobioticum*. Recent outbreaks of this quarantine pathogen in Prince Edward Island severely impacted local agricultural economy. The current containment strategy involves strict phytosanitary measures combined with the use of potato varieties resistant to specific pathotypes, of which there are 40 in total. However, these measures require taking land out of production, and the resistant varieties are not universally effective. To aid in developing an alternative and sustainable, long-term solution for managing this disease, our research investigates soil fungistasis, leveraging native soil and endophytic microbial communities. We hypothesize that introducing *S. endobioticum* inocula disrupts the ecological equilibrium of the phytomicrobiome, prompting potato plants' defense systems to recruit and enrich specific beneficial microorganisms from the soil and rhizosphere to combat the pathogen. To test this hypothesis, we employed Nanopore sequencing to profile and compare the bacterial communities in healthy and diseased soil and/or potato tuber samples from three locations endemic with potato wart disease. We used whole genome amplification (WGA) to increase DNA quantities for sequencing—a technique regularly employed for *S. endobioticum* inoculum detection. Microbiomes were recovered by metabarcoding the full length of the bacterial 16S rRNA gene region and performing shotgun metagenomic sequencing. The preliminary results confirmed the effectiveness of our Nanopore sequencing protocols by reliably identifying nearly all species in mock communities. High sequencing depth provided comprehensive representation of community diversity. Nevertheless, significant shifts were observed in the community compositional structure between original and WGA-treated samples. Comparative network analysis further indicated that WGA led to reduced connectivity, modularity, and feed-forward loop motifs, emphasizing the necessity for careful interpretation of microbial interplay patterns in the search for *S. endobioticum* antagonists. Insights into the microbial dynamics in soils used for potato production, particularly those affected by potato wart infestation, will enable us to identify and isolate potential biocontrol agents for this pathogen and develop strategies to manage and mitigate the impact of the disease.

[O182] ALLELIC DIVERSITY AND EVOLUTIONARY PATTERNS OF *TOXB* GENE IN *PYRENOPHORA TRITICI-REPENTIS* AND RELATED SPECIES: A GLOBAL PERSPECTIVE. Mohamed Hafez[1], Ryan Gourlie[1], Megan McDonald[2]; Melissa Telfer[1], Marcelo A. Carmona[3], Francisco J. Sautua[3], Caroline S. Moffat[4], Paula M. Moolhuijzen[4], Pao Theen See[4], and Reem Aboukhaddour[1]. [1]Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre, Lethbridge, AB, Canada; [2]School of Biosciences, University of Birmingham, Institute of Microbiology and Infection, Edgbaston, Birmingham, UK; [3]Cátedra de Fitopatología, Facultad de Agronomía, Universidad de Buenos Aires, Buenos Aires, Argentina; and [4]Centre for Crop and Disease Management, School of Molecular and Life Sciences, Curtin University, Australia
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Pyrenophora tritici-repentis, known for causing tan spot, exerts significant damage as a foliar pathogen on wheat globally. It produces several necrotrophic effectors, among which ToxB is the chlorosis-inducing effector predominant in the fertile crescent and surrounding regions. So far, research on ToxB has been sporadic. In this study, we investigated the allelic diversity and evolutionary patterns of *ToxB* gene in *P. tritici-repentis* in a global collection representing different races and geographic regions. To gain a comprehensive insights into *ToxB* evolution, we examined their presence and variability in *P. tritici-repentis* and other related fungal species. *ToxB* was found to be geographically limited to specific regions in North Africa and the Fertile Crescent. The presence of the *toxb* gene (the *ToxB* homolog) was exclusive to isolates of races 3 and 4, primarily identified in Canada and Syria. Notably, the presence of *toxb* was also observed for the first time in the barley net blotch pathogen *Pyrenophora teres*. Evolutionary analysis of *ToxB*/*toxb* genes indicated selection pressure characterized by functional loss, duplication events, and diverse mutations. A notable finding was the discovery of a ~5.6-kb Copia-like retrotransposon, referred to as Copia-1_Ptr, inserted into the *toxb* gene of a race 3 isolate. This insertion led to the impairment of ToxB's function, marking a unique case of effector gene disruption caused by a transposable element in *P. tritici-repentis*. Exploration of ToxB-like protein distribution in other ascomycetes revealed their presence in 19 additional species, including the Leotiomycetes class, marking the first report of ToxB-like proteins in this class. The presence/absence pattern of ToxB-like proteins challenged species relatedness as indicated by a phylogenetic analysis, suggesting a past horizontal gene transfer event during the evolution of the *ToxB* gene. The correlation between selection pressure, fitness, and the isoform of secreted effectors underscores the significance of studying allelic variations in effector-encoding genes on a global scale.

[O183] ENDOGENOUS RUST PEPTIDES FROM PUTATIVE SHORT OPEN READING FRAMES IDENTIFIED USING PEPTIDOMICS AND DE NOVO SEQUENCING STRATEGIES. Christof Rampitsch[1], Slavica Djuric-Ciganovic[1], Zhen Yao[1], and Mark Lubberts[2]. [1]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101, Rte 100, Morden MB, Canada R6M 1Y5; and [2]Summerland Research and Development Centre, Agriculture and Agri-Food Canada, Hwy 97, Summerland BC, Canada V0H 1Z0
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Puccinia triticina (Pt) is an obligate fungal parasite that causes leaf rust on wheat. This disease occurs annually and potentially results in large yield losses. Host-pathogen communication at the protein level has been well-studied in this and similar pathosystems, but the potential roles of peptides (smaller than 10 kDa) has not been examined. Small peptides, transcribed from short open reading frames, have been reported from model fungal species. This research investigates the role(s) of such peptides in the wheat-rust interaction, using top-down LC-MS analyses to detect novel peptides. For the LC-MS approach we evaluated several approaches, including N-terminal enrichment and C4 RP-HPLC, before settling on SEC-HPLC. Enriched peptides were left intact or digested with trypsin and then analyzed by LC-MS in a high-resolution Orbitrap mass spectrometer. Automated de novo sequencing, which does not require any databases, was used to obtain candidate peptide sequences and these were queried against wheat and rust genomic sequences to eliminate fragments resulting from protein turnover or breakdown. To find potential short open reading frames, peptides were mapped back on to the genomic sequence of Pt, while accounting for both codon redundancy, all reading frames and potential de novo sequencing errors (e.g. AB to BA reversals). We have found several candidate peptides with no significant homology to the

Pt nor to the Triticum aestivum genomes, but which match short open reading frames on the Pt genome. The most recent research progress will be presented.

***[O185] CHANGES IN SENSITIVITY OF *CLARIREEDIA JACKSONII* TO THE DEMETHYLATION INHIBITOR FUNGICIDE PROPICONAZOLE AFTER 30 YEARS OF USE.** Andrea Rether[1], Mikaela Ryan[1], Nava Brimble[1], Alexa Nguyen[1], and Tom Hsiang[1]. [1]School of Environmental Sciences, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1
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Dollar spot is the most prevalent turfgrass disease in the Great Lakes Region, and repeat fungicide use is required to prevent aesthetic damage caused by symptoms. Repeat fungicide applications of the same chemical family select for fungicide-resistant biotypes in fungal populations. There are reports of decreased sensitivity to propiconazole, a demethylation inhibiting (DMI) fungicide, in populations of *Clarireedia jacksonii*, the causal agent of dollar spot. In 1993, a baseline study was conducted where eight populations of *C. jacksonii* in Ontario were sampled and tested for sensitivity to propiconazole. This study was repeated 10 and 20 years later where six of the original eight populations were sampled. In 2023, twelve populations of *C. jacksonii* in Ontario were sampled and tested for sensitivity to propiconazole. EC_{50} values (effective concentration for 50% inhibition of growth) were generated for all 981 isolates collected. Isolates collected in this study were less sensitive (mean EC_{50} = 0.079 µg/ml) than those collected in 2013 (mean EC_{50} = 0.054 µg/ml), 2003 (mean EC_{50} = 0.026 µg/ml), and the baseline study (mean EC_{50} = 0.008 µg/ml). Future work assessing the relationship between mean EC_{50} values and the number of DMI applications made on the sampled dollar spot populations will increase our understanding of field resistance risk in Ontario.

***[O186] IMPROVING BACTERIAL LEAF STREAK MANAGEMENT IN WHEAT: DEVELOPMENT OF A RAPID LOOP-MEDIATED AMPLIFIATION (LAMP) PROTOCOL FOR SEED TESTING.** Valentina Anastasini[1], Heting Fu[2], Jie Feng[2], T. Kelly Turkington[3], Michael Harding[4], Constanza Fleitas[1], and Randy Kutcher[1]. [1]Cereal and Flax Pathology Group, Department of Plant Sciences, University of Saskatchewan, College of Agriculture and Bioresources, 51 Campus Drive, Saskatoon, Saskatchewan, S7N 5A8; [2]Alberta Plant Health Lab, Crop Diversification Centre North, 17507 Fort Road NW, Edmonton, Alberta, T5Y 6H3; [3]Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, 6000 C&E Trail, Lacombe, Alberta, T4L 1W1; and [4]Alberta Agriculture and Irrigation, 301 Horticultural Stn Rd E, Brooks, Alberta, T1R 1E6
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Over the past decade, there has been a notable rise in outbreaks of bacterial leaf streak (BLS) in cereals grown in many regions in Canada and the United States. This can be attributed to various factors, including changes in agronomic practices, favourable weather conditions, and the absence of resistant cereal cultivars. As a result, BLS, once considered to occur sporadically, has now become a prevalent and damaging foliar disease in affected areas. Addressing the root causes of these outbreaks is necessary to effectively manage the spread of BLS and mitigate its impact on cereal crop yield and quality. Seed infection is the primary source of BLS inoculum; therefore, this project aims to detect the bacterium on wheat kernels. We developed a Loop- mediated Amplification protocol (LAMP) to detect the pathogen on seed as part of an integrated disease management strategy. The assay includes the design of specific primers targeting a gene encoding a hypothetical protein specific to *X. translucens* pv. *undulosa*, the pathovar that has the greatest effect on wheat. The LAMP assay amplifies the target DNA rapidly under isothermal conditions, enabling simple and rapid visual detection and differentiation, without sophisticated or specialized equipment. Specificity and sensitivity were tested using DNA of *Xanthomonas* spp. and non-*Xanthomonas* spp. Of five specific primer sets, the most sensitive was selected for the seed testing protocol. This protocol seeks to enhance our capacity to monitor BLS on wheat samples, contributing to more effective disease control measures.

***[O187] EVALUATING THE INFLUENCE OF NITROGEN ON ROOT ARCHITECTURE AND CLUBROOT RESPONSE IN *BRASSICA* GENOTYPES.** Danna Rotariu, Yoann Aigu, Rudolph Fredua-Agyeman, Sheau-Fang Hwang, and Stephen Strelkov. Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada
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Studies have shown that high nitrogen availability can increase the severity of infection by obligate plant parasites. In clubroot disease, caused by the obligate soilborne parasite *Plasmodiophora brassicae*, nitrogen has been reported to affect the resistance of *Brassica napus*, but only for specific cultivar/isolate interactions. In addition, nitrogen is also an essential element for plant growth, including root architecture and development. The aim of this project is to determine if changes in *Brassica* root system development associated with nitrogen application affect clubroot response. In the first phase of this study, variable levels of nitrate were assessed for impact on root architecture in four *Brassica* genotypes grown hydroponically, which helped to identify three nitrogen concentrations ideal for characterizing genotype and nitrogen effects on roots. Three software packages for conducting root analyses were compared to identify the best program for the evaluation of complex root systems. A potting system was then developed to evaluate clubroot resistance under variable levels of nitrogen without artificially modifying the early stages of root development. Fifty *Brassica* genotypes, selected for their root architecture diversity, were screened against the resistance-breaking pathotype 3A of *P. brassicae*. The genotypes with the highest modulation of resistance level by nitrogen fertilization was selected with the future objective of testing the effect of root architecture modification on clubroot response, independently of the nitrogen effect on plant defense. This study will help to identify and quantify the potential impact of root architecture on clubroot resistance.

***[O188] EFFECTS OF FREEZE AND THAW TEMPERATURE CYCLES ON THE SURVIVAL OF PLASMODIOPHORA BRASSICAE RESTING SPORES.** K. Holy[1], B. D. Gossen[2], and M. R. Mcdonald[1]. [1]Department of Plant Agriculture, University of Guelph, 50 Stone Rd. E, Guelph, ON N1G 2W1, Canada; and [2]Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada
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Clubroot disease, caused by *Plasmodiophora brassicae* (Woronin), can cause substantial yield loss in several economically important Brassica crops. After host maturity, the 'clubbed' roots remain in the soil and release resting spores back into the surrounding soil. The spores can remain viable in the soil for many years. Repeated freeze-thaw cycles under controlled conditions reduced spore viability by up to 85%, but natural cycles in the field have not been examined. A field trial was conducted at the Ontario Crops Research Centre – Bradford during the winter of 2022–2023. Clubs were buried at 10–15 cm depth, which would be the typical depth for clubbed roots, or placed on the soil surface to assess the effect of natural freeze-thaw cycles. A control treatment was maintained in a freezer at -20°C. Plastic mesh bags were used to closely mimic natural conditions, allowing the clubbed material to interact with the soil. Temperature sensors were placed in bags from each treatment. The number of freeze-thaw cycles was vastly different between the buried treatment (2 cycles) and the soil surface treatment (32 cycles) during the winter season. Spore viability was assessed using an Evans Blue vital stain and confirmed in a bioassay on susceptible canola (*Brassica napus* line ACS N39). Evans Blue staining showed that the frozen control and buried club treatments maintained 94% spore viability in the spring of 2023, whereas the soil-surface clubs had only 54% spore viability. In the bioassay, inoculation with spores from clubs from the soil surface produced clubroot severity of 79% compared to clubs that were buried (91%) or maintained in a freezer (94%). These results strongly suggest that freeze-thaw cycles reduced both resting spore viability and subsequent infection success. The study was repeated in 2023–2024 and results are being assessed.

***[O189] UNRAVEL TO BUILD: PTEROCARPAN BIOSYNTHESIS FROM LEGUMES TO HETEROLOGOUS HOSTS**. Audrey Cote[1], Brandon Saltzman[1], and Mehran Dastmalchi[1]. [1]Department of Plant Science, McGill University, 21111 Lakeshore Road, Ste-Anne-de-Bellevue, QC, Canada, H9X3V9
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Pterocarpans are specialized metabolites, characteristic of legume species (Fabaceae), associated with plant defence response. Pterocarpans are classified as phytoalexins, as they are often biosynthesized in response to abiotic or pathogenic stresses. Therefore, they have potential as antimicrobial or protective

compounds, which could be leveraged for agricultural or medicinal applications. The challenge is to identify unique compounds and their corresponding bioactivity by producing them at scale. Pterocarpan biosynthesis is tightly regulated and requires elicitation in narrow lineages and tissues. To this end, we are attempting to unravel pterocarpan biosynthesis by drawing on several legumes for “parts” (genes) and reassembling the pathway in *Nicotiana benthamiana*. We have introduced enzymes to transform flavanone substrates, first to an isoflavone scaffold and further downstream, culminating in the formation of a pterocarpan, (+/-)-medicarpin. The final steps in pterocarpan biosynthesis are catalyzed by a unique class of enzymes named dirigent proteins (DPs). Our results indicate novel subcellular localization of uncharacterized DPs in two subclasses: isoflav-3-ene synthase (I3S) and pterocarpan synthase (PTS). We conducted *Agrobacterium*-mediated transient expression in *N. benthamiana*, expressing legume DP orthologs fused translationally at both the N and C-terminus with yellow fluorescent tags (YFP). Further, co-infiltration was performed with organelle markers tagged with a cyan fluorescent protein (CFP) to confirm accurate localization. The appropriate targeting of enzymes in such a multi-protein complex could ultimately dictate the titers and output in an engineered bioproduction platform. In addition, our heterologous pterocarpan pathway will serve as a synthetic biology tool to characterize other unknown features and find optimal isoforms across the legume world. This bioproduction system can enable a larger-scale yield of pterocarpans for rigorous testing of the suggested agricultural (e.g., pesticides) and biomedical activities (e.g., antimicrobial, phytoestrogenic, and anticancer drugs).

***[O190] CHARACTERIZATION OF A CYSTEINE PROTEASE FROM PHYTOLACCA AMERICANA AND ITS ASSOCIATION WITH POKEWEED ANTIVIRAL PROTEIN.** Annabelle Audet[1] and Katalin A. Hudak[1]. [1]Department of Biology, York University, 4700 Keele Street, Toronto, ON, Canada, M3J 1P3
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The plant apoplast is an essential extracellular space that harbors a diverse array of proteins crucial for plant defense. Papain-like cysteine proteases (PLCPs) and ribosome inactivating proteins (RIPs) are prominent constituents of the Phytolacca americana (American pokeweed) apoplast; however, their functions remain largely unexplored. We recently identified that the RIP Pokeweed Antiviral Protein (PAP) binds a putative cysteine protease in pokeweed that we refer to as Phytolacca americana cysteine protease 1 (PaCP1) and this interaction may be involved in the plant stress response. We hypothesize that binding inhibits either protein’s activity or that PaCP1 may proteolytically process PAP. Through bioinformatic predictions, PaCP1 was identified as a papain-like cysteine protease exhibiting conserved structural features specific to these proteins. Enzymatic activity assays confirmed PaCP1's functionality and its classification as a cysteine protease. Furthermore, yeast-two hybrid assays validated the PAP-PaCP1 interaction, while localization studies indicated their extracellular co-localization in the apoplast. Subsequent enzymatic assays demonstrated that PaCP1proteolytically cleaves PAP, suggesting a potential role for the distinct degradation products. Future investigations will focus on elucidating the biological significance of the PAP-PaCP1 interaction under various stress conditions. Differential expression studies under drought, salicylic acid treatment, and bacterial infection will shed light on the adaptive responses of PAP and PaCP1. Moreover, analysis of PAP cleavage products during these stresses will provide insights into their potential role in the plant’s stress response. Since plants are constantly being challenged by a multitude of abiotic and biotic stresses, this work will contribute to identifying how different components of the plant’s defense system may work together in the extracellular space. This ultimately improves our understanding of plant defense strategies, emphasizing the role of the extracellular space as the plant's primary line of defense.

[O191] GLUTAMINE ACTIVATION OF TOR REGULATES PROTEIN SYNTHESIS IN DEVELOPING PEAS. Brendan O`Leary, Vinti Kumari, and Christoph Rampitsch
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TOR kinase is the hub of an important signalling network in eukaryotes that integrates both nutritional and hormonal signals to regulate cellular activities. Most studies on upstream regulation of TOR in plants have been conducted on Arabidopsis seedlings, particularly meristems, where TOR is most strongly responsive to light and sucrose, and little information is available on TOR function in other plant tissues. Here we observe clear differences in the nutritional regulation of TOR in different tissues, highlighted by Gln being the sole observable nutrient activator of TOR in developing pea seeds. In mature Arabidopsis leaves, Gln

is also the strongest nutrient activator of TOR, although many amino acids and sugars also have the ability to activate TOR to a lesser degree. By contrast, in both the roots and shoots of Arabidopsis seedlings exogenous Gln does not appreciably activate TOR under non-stressed conditions. Furthermore, in developing pea seeds Gln activation of TOR is independent of light, whereas in mature leaves and seedlings TOR signalling is strongly dependent on light. The effect of TOR regulation on certain aspects of leaf metabolism is also light dependent. Using specific inhibitors we observe that, besides Gln, TOR activation in developing pea seeds is completely dependent on auxin signalling and respiratory ATP generation. Therefore, as in other tissues and organisms, TOR activity in developing seeds serves to integrate information from multiple signals in order to direct seed growth and metabolic processes. Phosphoproteomic analysis of TOR signalling in developing pea seeds identified established and novel downstream TOR phosphorylation substrates and revealed a clear categorical enrichment of proteins involved translation regulation among the differentially phosphorylated targets. Subsequent experiments demonstrated that bulk protein accumulation in developing pea cotyledons is dependent on TOR signalling. Therefore, Gln fed to developing seeds via the phloem promotes protein synthesis both as a substrate and as a signal via TOR. Manipulation of Gln-TOR signalling in seeds, once better understood, could be used to maximize seed yield and quality traits, like protein content.

***[O192] EXPLORING THE ALKENE BIOSYNTHETIC PATHWAY IN *POPULUS TRICHOCARPA*.**
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Plants use Very-Long-Chain Fatty Acids (VLCFAs, more than 18-carbons long), for a myriad of purposes, including building membranes, storing energy and sealing surfaces. VLCFAs are elongated two carbons at a time from long-chain fatty acids at the ER surface by the Fatty Acid Elongation (FAE) complex. The first enzyme of the complex, 3-ketoacyl-CoA Synthase (KCS), catalyzes the rate-limiting step and selects the substrate that are elongated in each cycle of the complex. In *Populus trichocarpa*, *PtKCS1* has been shown to be the gene responsible for alkene biosynthesis in leaves, elongating *cis-ω9* VLCFAs that subsequently get modified into alkenes deposited on the cuticle. The adjacent gene *PtKCS2,* which is 73% similar at the protein level, shows preference towards saturated VLCFAs. Surprisingly, rationally engineered chimeric proteins combining domains of the two genes show promiscuous and high activity with larger accumulation of VLCFAs products than PtKCS1 and PtKCS2, even when supplemented with exogenous substrates that are not present in native yeast such as polyunsaturated and odd-chain fatty acids. We further explored the elongation of *cis-ω9* and *cis-ω7* substrates and observed possible product competition among the two unsaturated VLCFAs series. These results serve as a starting point to extend our knowledge on the alkene biosynthetic pathway in poplar and provide potential candidates for engineering specific unsaturated VLCFAs in plants at higher levels.

[O193] POPLAR LEAF BUD RESIN BIOCHEMISTRY: SEASONAL PATTERNS AND ENZYMES FOR RESIN SYNTHESIS IN BLACK COTTONWOOD (*POPULUS TRICHOCARPA*).
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The synthesis and copious accumulation of resin is a mechanism by which temperate trees protect dormant leaf buds against frost, herbivory, and other stresses. Such resins contain a diverse array of secondary metabolites including terpenoids, benzenoids, and phenolics. *Populus trichocarpa* and *P. balsamifera* leaf bud resin is distinguished from resin of other poplars by a high *O*-methylated dihydrochalcone content. The biosynthesis of leaf bud resin is poorly understood, and to date no enzymes involved in leaf bud resin synthesis have been characterized. We used transcriptomics and differential gene expression analysis to identify a gene encoding a dihydrochalcone-specific *O*-methyltransferase, which we named PtDOMT1. This enzyme is a highly selective and regiospecific *O*-methyltransferase which methylates only the 4- and 4'-positions of dihydrochalcones. Similar to other plant *O*-methyltransferases, it uses S-adenosyl-*L*-methionine as a methyl donor. PtDOMT1 was not active with any other flavonoid or phenolic substrate tested, and thus represents a unique molecular tool for investigating resin-associated gene expression. A seasonal time series in *P. trichocarpa* indicated that in lateral leaf buds, resin biosynthesis and accumulation occurs primarily in late summer synchronous with

bud development, with only minor changes observed in the dormant period. The expression of PtDOMT1 is coordinate with bud developmental and expansion. To our knowledge, this work represents the first molecular analysis of leaf bud resin biosynthesis in plants.

[O194] REGIOSELECTIVE *O*-METHYLATION OF STILBENES IN SACCHARINAE GRASSES. Nan Lin[1], Andy CW Lui[1], Kah Chee Pow[2], Zhuming Fan[2], Chen Jing Khoo[2], Quan Hao[2], and Clive Lo[1]. [1]School of Biological Sciences and [2]School of Biomedical Sciences, The University of Hong Kong, Pokfulam Road, Hong Kong, China
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Stilbenes are plant specialized metabolites synthesized in response to abiotic or biotic challenges, offering protection against reactive oxygen species or pathogen infection. They are also promising candidates for nutraceutical and pharmacological applications due to a wide range of health beneficial properties. Interestingly, stilbenes are only sporadically distributed in several phylogenetically distinct lineages. In the grass family, sorghum (*Sorghum bicolor*) and sugarcane (*Saccharum officinarum*) were reported to accumulate resveratrol and piceatannol, respectively, which are stress-induced hydroxylated stilbenes. *Sorghum* and *Saccharum* are closely related genera belonging to subtribe Saccharinae.

In this study, we report the identification of *O*-methylated stilbenes, pinostilbene (3-*O*-methylated in A ring) and pterostilbene (3,5-bis-*O*-methylated in A ring) in infected sorghum seedlings, and isorhapontigenin (3'-*O*-methylated in B ring) in wounded wild sugarcane. Meanwhile, we have characterized a novel stilbene *O*-methyltransferase (SbSOMT) which is essential for pathogen-inducible pterostilbene biosynthesis in sorghum. SbSOMT and related homologs are restricted to *Sorghum* but not found in *Saccharum* or other Saccharinae genera. Phylogenetic analysis suggested that the genus-specific SOMT were recruited from canonical caffeic acid *O*-methyltransferases (COMTs) after divergence of *Sorghum* genus from other genera in Saccharinae. COMTs are widespread in the plant kingdom catalyzing *O*-methylation of a wide range of phenolic substrates.

Using piceatannol as a substrate in recombinant enzyme assays, SbSOMT catalyzed A-ring *O*-methylation to produce 3'hydroxypinostilbene and 3'-hydroxypterostilbene successively. On the other hand, SbCOMT catalyzed B-ring *O*-methylation of piceatannol to produce isorhapontigenin. Subsequently, crystal structures of SbSOMT-stilbene complexes were solved and the enzyme was depicted as a homodimer with an open conformation. SbSOMT shows strong global resemblance to sorghum COMT (SbCOMT), but close examination of the substrate binding pockets revealed subtle differences in their amino acid compositions. Molecular characterization demonstrated the requirement of two hydrophobic residues (Ile144 and Phe337) for substrate binding that leads to stilbene A-ring *O*-methylation. On the other hand, the equivalent residues (Asn128 and Asn323) in SbCOMT facilitate an opposite binding orientation that favors stilbene B-ring *O*-methylation. In this regard, a highly conserved COMT likely catalyzes the wounding-induced isorhapontigenin production in wild sugarcane. Overall, this work rationalized the regioselectivities of stilbene *O*-methylations by SOMT and COMT, facilitating future attempts for bioengineering of different *O*-methylated stilbenes.

***[O195] MODULATION OF CLOCK IN WHEAT VIA DIPLOID AND HAPLOID GENE EDITING.** Sandhya Gautam[1,2], Fengying Jiang[2], Chelsi Harvey[2], Andre Laroche[2], Guanqun Chen[1], and John Laurie[2]. [1]Department of Agricultural, Food and Nutritional Science, University of Alberta, 2-06 Agriculture-Forestry Center, Edmonton, AB, Canada, T6G 1C9; and [2]Lethbridge Research and Development Center, Agriculture and Agri-Food Canada, 5403 1 Avenue South, Lethbridge, AB, Canada, T1J 4B1
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Wheat (Triticum aestivum) is one of the major field crops of Canada with significant nutritional and economic value. Climate change has impacted Canada's overall wheat production in recent years. Therefore, the development of new wheat germplasm resilient to variable climatic conditions is essential. Genetic changes play a crucial role in crop improvement. Genetic modification in wheat; a complex polyploid crop (AABBDD), is challenging due to large genome and multiple gene copies. This study focuses on modulating circadian clock genes in wheat to enhance various plant characteristics. Core clock genes are a group of transcription factors that regulate a large number of downstream genes involved in various important biological pathways and therefore, play a vital role in plant growth and

development. Thus, modulating the clock could lead to significant improvements in crop performance. In this study, we employed two innovative gene editing methods- “Diploid editing” and “Haploid induction (HI)-edit” to edit two clock genes; Clock-1 and Clock-2. The diploid method involves gene editing via wheat transformation and produces transgenic edited lines, while HI-edit involves maize transformation and the subsequent use of transgenic maize lines to pollinate wheat plants and thus, produces transgene-free edited lines. We have successfully edited wheat plants using both methods and a comparison between the two approaches shows that diploid edit has higher editing efficiency (42-44%) than HI-edit (4.29%). While the HI-edit has lower efficiency, it has a shorter time to develop a fixed-edited line. Evaluation of these mutant lines for both genes is ongoing. Thus, this study offers valuable insights into wheat genome modification and serves as a significant resource for future wheat genome research.

***[O196] SPEED EDITING: HIGH THROUGHPUT GENE EDITING USING CRISPR/CAS9 SYSTEM IN *BRASSICA NAPUS*.** Rajbir Kaur[1,2], Mohamed Samir Youssef[1,2], Robert Duncan[1], and Harmeet Singh Chawla[1]. [1]Department of Plant Science, University of Manitoba, 66Dafoe Road, Winnipeg, MB, Canada, R3T2N2; [2]These authors contributed equally to this work
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Brassica napus is an allotetraploid crop species with 2n=4x=38 developed through interspecific hybridization between *B. rapa* and *B. oleracea* and following the events of chromosomal doubling and genomic rearrangements. Even though canola/rapeseed ranks as the second most significant source of vegetable oil globally, it still encounters gaps between achieved and potential yield due to various biotic and abiotic factors. Addressing these challenges necessitates precise and innovative approaches to plant breeding and genetics. Gene editing, particularly the CRISPR/Cas9 system, offers an innovative solution to these limitations by enabling targeted modifications at specific genomic locations. By leveraging CRISPR/Cas9 technology, it is possible to enhance the resilience of canola to abiotic and biotic stress. *Brassica napus* has a complex polyploid genome that often requires editing of multiple homoeologous genes, thereby complicating the process of gene editing for this species. For the concurrent editing of multiple genes with CRISPR/Cas9, separate promoters must be employed to drive the expression of Cas9 and each distinct single-guide RNA (sgRNA). This can result in overly large constructs, complicating the vector's delivery into the host plant. To streamline this process, the current study adopts a more efficient strategy where multiple sgRNAs are engineered into a single transcript, expressed under a single promoter. Moreover, addressing the laborious and low-efficiency tissue culturing typically associated with CRISPR/Cas9, this study proposes a direct spray-based transformation method that circumvents these traditional bottlenecks. By enhancing the transformation and regeneration processes, this approach aims to reduce soma clonal variation and accelerate the development of genetically edited *B. napus*. Shattering tolerance, which is extensively documented in the scientific literature, will serve as the initial trait to assess the efficacy of this approach. Using our high throughput CRISPR/Cas9 method, we targeted three genes *SHP*, *IND*, and *ALC,* described to confer shattering tolerance in oilseed rape. We have successfully generated Cas9-positive T1 plants and are in the process of phenotypic and genotypic characterization of the CRISPR mutants.

[O197] FUNCTIONAL VALIDATION OF A CANDIDATE GENE CONTROLLING SOYBEAN ROOT SYSTEM ARCHITECTURE BY CRISPR-CAS9 TECHNOLOGY. Benjamin Karikari[1,2], Waldiodio Seck[1,2], Davoud Torkamaneh[1,2], and François Belzile[1,2]. [1]Département de phytologie, Université Laval, Québec, QC, Canada, G1V 0A6; and [2]Institut de biologie intégrative et des systèmes (IBIS), Université Laval, Québec, QC, Canada, G1V 0A6
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Soybean (*Glycine max* (L) Merr.) is a vital crop, providing plant-based protein and oil globally. To meet increasing food security demands under unpredictable changes in the climate, enhancing soybean yield and quality is crucial. Root systems are central to plant survival and productivity, enabling access and uptake of nutrients and water. They are also key determinants of plants’ ability to withstand nutrient depletion and extreme weather conditions including drought, heat and flooding. Considering this, we employed a core set of 137 Canadian soybean lines with over 2 million high-quality single nucleotide polymorphism (SNP) markers to perform a genome-wide association study to identify major loci and candidate genes for root system architecture (RSA) traits. One locus explaining 21% of variation for the total length of the roots (*qTLR1*) was located on chromosome 1. Gene models within/around *qTLR1* were

examined using the SoyBase database (https://www.soybase.org/) and other bioinformatic tools. Within the linkage disequilibrium block containing the peak SNP, the *GmLAX1* gene was identified at 140.17 kb upstream of the peak SNP. From the transcriptome data available on SoyBase, this gene has the highest expression in the root compared to other tissues across developmental stages. To functionally validate the modulatory role of *GmLAX1* in RSA, two guide RNAs within exon 1 were selected for CRISPR/Cas targeted mutagenesis via *Agrobacterium rhizogenes*-mediated transformation. Preliminary results suggest that *GmLAX1* is a repressor of secondary roots in terms of their emergence and elongation in soybean. Thus, the knock-out of *GmLAX1* shows potential for enhancing total length and density of the root system, mainly via its effect on the number of secondary roots. Such root systems may increase the resilience of soybean cultivars to abiotic and biotic stressors in the face of changing climatic conditions. These insights may be used to guide breeding strategies aimed at developing soybean varieties with improved RSA.

[O198] GENE EDITING-ASSISTED FUNCTIONAL GENOMICS STUDIES IN WHEAT (TRITICUM AESTIVUM L.). Andriy Bilichak, Louie Lopos, Emanpreet Kaur, and Natalia Bykova. Morden Research and Development Center, Agriculture and Agri-Food Canada, 101 Rte 100 #100, Morden, MB R6M 1Y5, Canada
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Improvement in agronomic traits in crops through gene editing (GE) relies on efficient transformation protocols for delivering the CRISPR/Cas9-coded transgenes. Recently, a few embryogenesis-related genes have been described, the co-delivery of which significantly increases the transformation efficiency. This study aimed to examine factors affecting Agrobacterium-mediated transformation and gene editing in wheat (Triticum aestivum L.) to optimize high-throughput gene editing for functional genomics studies. Here, we characterized the transgenic and GE events in wheat (cv. Fielder) when transformed with GROWTH-REGULATING FACTOR 4 (GRF4) and its cofactor GRF-INTERACTING FACTOR 1 (GIF1) chimeric gene. We used the Agrobacterium-mediated transformation method and immature wheat embryos as ex-plants. The T-DNA integrity and transgenes copy number were measured using PCR and digital droplet PCR. The GE rate was quantified with qPCR and verified with Sanger sequencing. Eventually, the gRNA activity for 10 different gRNAs targeting 30 loci was correlated with epigenetic profile (DNA methylation, histone posttranslational modifications, ChIP RNA polymerase, and ATAC-seq) at the target regions.

Transformation efficiency in our experiments ranged from 22% to 68%, and the editing events were faithfully propagated into the following generation. Both low- and high-copy-number integration events were recovered in the T0 population with various levels of integrity of the left and right T-DNA borders. We also generated a population of wheat plants with 10 different gRNAs targeting 30 loci in the genome. A comparison of the epigenetic profiles at the target sites and editing efficiency revealed a significant positive correlation between chromatin accessibility and mutagenesis rate. Overall, the preliminary screening of transgene quality and GE events in the T0 population of plants regenerated through the co-delivery of GRF–GIF can allow for the propagation of the best candidates for further phenotypic analysis.

[O199] CRISPR/CAS9 BASED LOSS-OF-FUNCTION GENE EDITING CONFERS BROAD-SPECTRUM CLUBROOT TOLERANCE IN CANOLA. L. Wang[1,3], R. Wen[2], B. Luo[1], K. Yang[1], X. Liu[2], T. Dumonceaux[2], G. Peng[2], and W. Xiao[1]. [1]Department of Biochemistry, Microbiology and Immunology, University of Saskatchewan, Saskatoon, SK, Canada S7N 5E5; [2]Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, Saskatoon, SK S7N 0X2; and [3]Department of Plant Sciences/Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8
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Canola (*Brassica napus* L.) is the number one cash crop in Canada and contributes $29.9 billion dollars to the Canadian economy annually. Nevertheless, the canola industry faces an ongoing threat from clubroot disease, with an increased number of infested fields each year, especially in Alberta. The causal agent of clubroot is a protist, *Plasmodiophora brassicae* Woronin, causing large, disorganized growths (clubs/galls) on infected roots that disrupt water and nutrient uptake and result in wilting, stunting and premature ripening of canola. Each large gall contains millions of resting spores persistent in the soil for

up to 20 years, making the disease difficult to control. The current disease management strategy is to grow clubroot-resistant (CR) cultivars in rotations. However, the existing CR varieties carry race-specific, dominant resistant (R) genes that can be broken down with a shift in the pathogen population and continuous cropping. In this study, we screened Arabidopsis mutant collection and identified a gene that when modified confers robust tolerance to clubroot and tentatively named it *CRT1*; loss of function in *CRT1* resulted in tolerance or even immunity against the clubroot disease. Furthermore, the Arabidopsis *CRT1* mutant showed enhanced resistance to multiple clubroot pathotypes, indicating that the tolerance is race/pathotype-independent. Two orthologous *CRT1* genes were identified in *B. napus* and both were targeted through the CRISPR/Cas9 gene editing. In total, 203 independent transformation lines were obtained and 50 T0 plants were genotyped to determine editing status. Thus far, we have identified one line exhibiting homozygous mutations in both genes, another line with heterozygous mutations in both genes, and several additional lines with mutations in only a single gene. Clubroot disease test on the homozygous double mutant plants has demonstrated promising results of tolerance. Considering the broad-spectrum tolerance conferred by this gene and its potential for resilience against tolerance breakdown, incorporating it into elite or commercial canola varieties could have significant potential for developing durable tolerant cultivars by the canola industry.

Abstracts for Poster Presentations

[P1] FIRST REPORT OF *FUSARIUM SPOROTRICHIOIDES* AND *FUSARIUM CEREALIS* CAUSING ROOT ROT OF SOYBEAN IN CANADA, WITH POTENTIAL IMPLICATIONS FOR CROP ROTATION STRATEGIES. Ahmed Abdelmagid[1], Mohamed Hafez[2,3], and Fouad Daayf[4]. [1]Morden research and development center, 101 Rte 100 #100, Morden, MB R6M 1Y5; [2]Agriculture and Agri-Food Canada, Lethbridge Research and Development Center, Lethbridge, Alberta T1J 4B1, Canada; [3]Department of Botany and Microbiology, Faculty of Science, Suez University, Suez 43518, Egypt; and [4]Department of Plant Science, University of Manitoba, Winnipeg, Manitoba R3T2N2, Canada
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Soybean plants exhibiting poor standing, stunting, and leaf chlorosis were collected from Manitoba fields in 2017. Symptoms included few nitrogen-fixing nodules, reddish brown-to-black lesions on tap and lateral roots, and cortical decay in roots and lower stems. Among 240 isolated strains, 5 were identified as *Fusarium sporotrichioides* Sherb., and 12 as *Fusarium cerealis* based on morphology. A PCR-based diagnostic test specifically targeted the trichothecene gene cluster in *F. sporotrichioides*, with primer SPO1 amplifying a 541 bp fragment in fungal isolates from commercial soybean crops and artificially infected roots. Trichothecene (TRI) gene expression was detected in infected soybean roots using RT-PCR with TRI gene-specific primers. *F. cerealis* isolates were confirmed via sequencing the translational elongation factor 1-alpha (TEF1) gene using universal primers EF1 and EF2. Under controlled conditions, all isolates caused typical root rot symptoms in soybean, significantly reducing shoot and root length. The pathogens were reisolated from infected plants and reidentified as *F. sporotrichioides* and *F.* cerealis as mentioned above. This represents the inaugural report of *F. sporotrichioides* and *F. cerealis* as causal agents of root rot in soybean within Canada. While these pathogens are commonly linked with Fusarium head blight in cereals, their newfound ability to cause root rot in soybean underscores the importance of understanding their broader impact. This finding may necessitate reconsideration of future crop rotation strategies.

[P2] THE OCCURRENCE AND SPREAD OF CLUBROOT IN ALBERTA (2005-2023). Y. Aigu, V.P. Manoli, S.F. Hwang, and S.E. Strelkov. Department of Agricultural, Food and Nutritional Science, 410 Agriculture/Forestry Center, University of Alberta, Edmonton, AB T6G 2P5, Canada
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Clubroot, caused by the obligate parasite *Plasmodiophora brassicae*, is a soilborne disease of canola (*Brassica napus*) and other cruciferous hosts. Infection by *P. brassicae* is associated with the formation of large galls on the roots of susceptible plants, leading to yield losses estimated at 10% to 15% globally. In Alberta, Canada, clubroot was first identified on canola in 2003 and targeted surveys have been conducted annually since 2005, generating a large data set. Since 2010, the disease has mainly been managed by the planting of clubroot-resistant cultivars. However, in 2013, resistance-breaking populations of *P. brassicae* were detected on canola in Alberta for the first time. The main objective of this study was to characterize the spread of the clubroot pathogen, including the patterns and rates of dissemination of non-resistance-breaking (NRB) and resistance-breaking (RB) populations of *P. brassicae*. In the context of a mosaic of resistant and susceptible host genotypes, epidemiological approaches were combined with geographical representation to enhance understanding of *P. brassicae* dissemination, evaluate the efficacy of efforts to limit clubroot spread, and predict its further progress. New cases of clubroot have been continuously detected every year. By 2023, clubroot had been identified in nearly 4000 fields across Alberta. Isolates of *P. brassicae* from over 600 of those fields were pathotyped using the Canadian Clubroot Differential set, with nearly 450 found to represent RB populations.

[P3] CHARACTERIZATION OF EFFECTOR *Pb*PE29: ITS POTENTIAL ROLE IN SUCCESSFUL *Plasmodiophora brassicae* COLONIZATION OF *Brassica napus* L. (CANOLA). Cresilda V. Alinapon, Chris D. Todd, and Peta C. Bonham-Smith. Department of Biology, 112 Science Place, University of Saskatchewan, Saskatoon, SK, Canada S7N 5E2
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Clubroot, a swollen gall or club-shaped root, is a devastating disease of Brassicas caused by *Plasmodiophora brassicae*, a soil-borne obligate biotrophic plant pathogen. Clubroot management programs have been developed throughout the world to try to mitigate this problem. Unfortunately, these strategies have been unsuccessful in limiting the spread of the disease. To successfully colonize plants, pathogens secrete a wide range of effectors that interact with host targets to manipulate the host physiology or deregulate host immune responses. *Pb*PE29 is an effector secreted by *P. brassicae* during the secondary stage (initiated between 5-7 days post inoculation (dpi) with resting spores) of pathogen infection of Arabidopsis roots. Transcript of *PbPE29* is expressed between 14-28 dpi – late secondary stage of infection and during the development of galls on the roots of infected plants. Transient expression of *Pb*PE29-GFP and $^{\Delta SP}$*Pb*PE29-GFP (minus signal peptide) in *N. benthamiana* leaves, show endoplasmic reticulum and nuclear localization, respectively. Neither *Pb*PE29-GFP nor $^{\Delta SP}$*Pb*PE29-GFP induce PCD when transiently expressed in *N. benthamiana* leaves. Uninfected transgenic Arabidopsis lines, over-expressing *Pb*PE29 and *Pb*PE29-FLAG, show WT phenotype, however, 21 dpi with *P. brassicae* resting spores, the roots of both transgenic lines appear to be more susceptible to infection and produce more galls when compared to WT roots. We are currently working on the molecular interaction, function and mechanism of *Pb*PE29, and its role in clubroot gall formation.

***[P4] EVALUATION OF WHEAT FOR RESISTANCE TO BACTERIAL LEAF STREAK UNDER CONTROLLED CONDITIONS.** Valentina Anastasini[1], T. Kelly Turkington[2], Constanza Fleitas[1], and Randy Kutcher[1]. [1]Cereal and Flax Pathology Group, Department of Plant Sciences, University of Saskatchewan, College of Agriculture and Bioresources, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8; and [2]Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, 6000 C and E Trail, Lacombe, Alberta, Canada
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Bacterial leaf streak (BLS) is a significant threat to cereal crops, particularly in the Prairies of Canada and the United States. This emerging foliar disease, caused by *Xanthomonas translucens*, has increased in the past decade, affecting numerous cultivated and non-cultivated cereal species. The pathogen is classified into pathovar (pv) based on adaptation to host species; pv. *undulosa* has the greatest effect on wheat. An effective disease management program is dependent on timely and correct identification of the causal agent. Control strategies for the management of BLS in cereals crops are limited. Development of BLS resistance wheat cultivars is a crucial strategy, but a long-term process. We have initiated a search for wheat germplasm with resistance to BLS. The main objective is to identify potentially resistant commercial varieties and promising sources of resistance in a diverse panel of wheat genotypes. Germplasm will be evaluated under both field and controlled conditions. At present, we have assessed 96 registered durum and bread wheat varieties.

[P5] EXPLORING THE DIVERSITY OF *STREPTOMYCES* BACTERIA CAUSING COMMON SCAB DISEASE IN NEWFOUNDLAND. Artho Baroi[1], Matthew Drodge[1], Gustavo A. Díaz Cruz[1,2], and Dawn R. D. Bignell[1]. [1]Department of Biology, Memorial University of Newfoundland, 45 Arctic Avenue, St. John's, NL, Canada, A1C 5S7; and [2]Phytopathology Department, Plant Protection Research Center (CIPROC), Agronomy School, Universidad de Costa Rica, San Jose, Costa Rica
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Common scab (CS) is a disease that has a negative impact on the quality and market value of seed, processing and table stock potatoes. The disease is characterized by the presence of necrotic scab-like lesions on the surface of affected tubers. Although potato is the most economically important host for the disease, other root crops such as beet, carrot, and parsnip can also be affected. CS is caused by several different species of soilborne bacteria belonging to the genus *Streptomyces,* of which *Streptomyces scabiei* is the first described and is the best characterized. *S. scabiei* and other CS pathogens produce a phytotoxic specialized metabolite called thaxtomin A, which functions as a plant cellulose biosynthesis inhibitor and is the principal pathogenicity determinant responsible for CS development. In addition, other phytotoxic specialized metabolites are thought to contribute to disease symptom development or severity by some *Streptomyces* species. A previous study conducted by our lab investigated the *Streptomyces* species responsible for potato CS on the island of Newfoundland, Canada. This study identified the thaxtomin-producing *Streptomyces europaeiscabiei* as a probable causative agent of CS in Newfoundland, and a novel plant pathogenic *Streptomyces* strain that does not produce thaxtomin A was

also isolated. However, other known CS pathogens such as *S. scabiei* were not detected, and this may be due to the small sample size that was used in the study. The goal of the current study is to provide new insights into the diversity of *Streptomyces* species responsible for CS in Newfoundland. Potato tubers and beets exhibiting superficial, raised and/or deep-pitted scab lesions were collected from different locations on the Avalon Peninsula and from central Newfoundland, and *Streptomyces* bacteria were isolated in pure culture from the lesions. The isolates were screened for pathogenicity using a radish seedling and potato tuber slice bioassay, and the strains were tested for production of thaxtomin A and other known *Streptomyces* phytotoxins. Additional strain isolations are currently in progress, and future work will include multi-locus sequence analysis for identification of the pathogenic isolates.

[P6] UNDERSTANDING THE INTERACTION BETWEEN BLACKLEG RESISTANCE AND VERTICILLIUM STRIPE DISEASE IN CANOLA. Carol. N. Bvindi[1], Aria Dolatabadian[2], and W. G. Dilantha Fernando[1]. [1]Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB, R3T2N2 Canada; and [2]The University of Western Australia, 35 Stirling Highway, 6009, Perth Australia.
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Blackleg caused by *Leptosphaeria maculans is a common disease of canola, found everywhere across canola growing areas except in China The most effective control of Blackleg is R gene-mediated resistance; to date, 19 R genes have been identified in Canola.* Recently, verticillium stripe caused by *Verticillium longisporum* has emerged as a threat to canola production in Canada. Host-specific resistance against *V. longisporum* in canola has not been reported, and none of the commercial varieties show resistance to verticillium stripe disease. *V. longisporum* and *L. maculans* can exist simultaneously in canola; In the quest for *V. longisporum* resistance in canola, it is imperative to understand if there is an interaction between the resistance already recorded in canola-blackleg interaction with *V. longisporum* and if this resistance can be used in managing Verticillium stripe disease. We studied the interaction between the blackleg gene for gene resistance and the three lineages of *V. longisporum* on blackleg and verticillium stripe symptoms. We hypothesized that resistance to blackleg in the canola genotype may reduce the induction of disease by both pathogens, while a breakdown of resistance due to virulence alleles of the blackleg pathogen would lead to the plant being weakened and allow the vascular disease caused by verticillium stripe pathogen to cause disease. Topas introgressed with a single R-gene in the Topas background, were inoculated with the three lineages (A1D1, A1D2, and A1D3) of *V. Longisporum* and then with the corresponding Avr/avr genotype of *L maculans*. At maturity, we evaluated blackleg and verticillium stripe severity. Our results show that in most Topas lines tested, the interaction between the R genes and Avr with the A1D1 lineage of *V. longisporum*. This interaction significantly affects blackleg symptoms but not Verticillium stripe symptoms. However, the interaction between R genes and avr with the A1D1 lineage of *V. Longisporum* does not significantly alter blackleg or verticillium stripe symptoms. Thus, the known R-gene resistance in blackleg-canola interaction may not effectively manage verticillium stripe.

***[P7] THE PHASED GENOME AND COLD RESPONSIVE TRANSCRIPTOME FOR ALLOTETRAPLOID POTATO WILD RELATIVE *SOLANUM ACAULE* BITTER.** Camargo-Tavares, J.C.[1], Achakkagari, S.[1], Praslickova, D.[1], Martini, C.[1], Bizimungu, B.[2], Anglin, N.L.[3,4], Manrique-Carpintero, N.[3*], Lindqvist-Kreuze, H.[3], Tai, H.H.[2], and Strömvik M.V.[1]. [1]Department of Plant Science, McGill University, Sainte-Anne-de-Bellevue, QC, Canada; [2]Agriculture and Agri-Food Canada Fredericton Research and Development Centre, Fredericton, NB, Canada; [3]International Potato Center (CIP), Lima, Peru; and [4]USDA ARS Small Grains and Potato Germplasm Research, Aberdeen, ID, USA
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Potato wild relatives within the *Solanum* section Petota are an important source of genetic diversity, contributing to the improvement of modern potato cultivars (*S. tuberosum*) to withstand various climate-related challenges. The allotetraploid species *Solanum acaule* Bitter has been particularly valuable in introducing cold tolerance traits into potato breeding programs. This study represents the first sequenced and phased subgenomes of an allopolyploid *Solanum* species. Our phylogenetic analysis shows that a Clade 4 species is the progenitor of subgenome 2 of *S. acaule*, while the progenitor of subgenome 1

remains unidentified and may be extinct (Clade 3). The genome assembly totals 1.34 Gb across 24 chromosomes with an N50 of 56.2 Mb, indicating a theoretical tetraploid genome size of 2.68 Gb over 48 chromosomes. Comparative transcriptomic analysis under cold stress between *S. acaule* and the autotetraploid *S. tuberosum* cv. Atlantic shows that *S. acaule* exhibits fewer differentially expressed genes. Analysis of the C-repeat binding factor (CBF) regulon, a transcription factor involved in regulating cold response, reveals multiple gene duplications and gene losses.

[P8] STRATIFIED EFFECTS OF TILLAGE AND CROP ROTATION ON SOIL MICROBES IN C AND N CYCLING AT TWO SOIL DEPTHS IN LONG-TERM CORN, SOYBEAN, AND WHEAT PRODUCTION.
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Understanding the soil bacterial communities involved in carbon (C) and nitrogen (N) cycling can inform beneficial tillage and crop rotation practices that address sustainability and crop production endpoints simultaneously. Herein we evaluated the bacterial diversity, compositional structure, and functions associated with C-N cycling for two soil depths (0-15 cm vs. 15-30 cm) under different long term soil tillage (conventional tillage [CT] vs. no-till [NT]) and crop rotation (monocultures of corn, soybean, and wheat vs. a corn-soybean-wheat rotation) production systems. Soil microbial communities were recovered and characterized through metabarcoding the 16S rRNA gene V4-V5 regions using Illumina MiSeq sequencing platform. The results showed that long-term NT farming reduced soil bacterial diversity at a depth of 15-30 cm compared to CT, while no significant difference was observed at 0-15 cm. The bacterial community differed significantly between the two soil depth under NT, but not under CT. Notably, over 70% of the tillage-responded KEGG orthologs (KOs) abundance associated with C fixation (primarily involved in reductive citric acid cycle) were higher under NT than under CT at both depths. NT also enhanced N fixation-related bacteria at 0-15 cm and denitrification-related bacteria at both soil depths. Crop type and rotation regimes had limited effects on bacterial diversity and compositional structure; however, specific carbon-nitrogen (C-N) cycling genes varied among crops. For instance, three KOs associated with the Calvin-Benson cycle for carbon fixation and four KOs related to various nitrogen cycling processes were more abundant in wheat compared to corn and soybean, across both soil depths. We conclude that for long-term corn, soybean, and wheat production systems, tillage practices had a greater influence than crop rotation on the soil bacterial community by affecting its diversity, compositional structure, and functionality, particularly regarding C and N cycling processes. Overall, this study highlights the importance of integrated management practices that account for the combined effects of tillage, crop rotation, and crop types on soil bacterial functional groups to enhance sustainable agriculture.

***[P9] EXPLORING FUSARIUM WILT RESISTANCE IN *BRASSICA* GENOTYPES LINKED TO ROOT ARCHITECTURAL TRAITS UNDER SEMI-HYDROPONIC CONDITIONS.**
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Fusarium oxysporum, a soilborne fungal pathogen, causes wilt in a wide range of hosts, including canola (oilseed rape; *Brassica napus*). The integration of genetic resistance with specific root system architectural traits that are less favorable for disease development holds potential for improved control of *F. oxysporum*. However, traditional methods for assessing host responses to this fungus in the soil require substantial space, labor, and time. In this study, 38 genotypes of *Brassica napus* (AACC), *Brassica rapa* (AA), and *Brassica oleracea* (CC) were evaluated for Fusarium wilt resistance. The evaluation was conducted at the seedling stage under semi-hydroponic conditions. One-week-old seedlings were inoculated using a root-dip method in a conidial suspension of a virulent *F. oxysporum* isolate collected in Alberta in 2020. After 21 days in the semi-hydroponic system, seven root traits were measured using an EPSON Perfection V800 scanner and analyzed with WinRHIZO™ software. Strong correlations were detected among the seven root traits measured. A significant, albeit relatively weak negative correlation (coefficient value from -0.3 to -0.2), was identified between the root traits and

Fusarium wilt disease severity. This finding suggested that genotypes with intricate and expansive root systems showed increased resistance to Fusarium wilt. The results not only identified potential root system architectural traits associated with Fusarium wilt resistance, but also underscored the effectiveness of semi-hydroponics as a reliable and straightforward approach for resistance screening under controlled conditions.

[P10] BIOLOGICAL CONTROL OF *FUSARIUM GRAMINEARUM* AND *VERTICILLIUM LONGISPORUM* CAUSING FHB AND VERTICILLIUM STRIPE IN CANOLA BY PHYLLOSPHERE AND RHIZOSPHERE BACTERIA FROM CANOLA AND SOYBEAN. Monika Dayarathne[1] and Dilantha Fernando[1]. [1]Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada, R3T2N2
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Verticillium stripe in canola is a soil borne disease caused by *Verticillium longisporum*. Currently, there is no identified resistance or registered fungicides available to effectively manage this disease. Fungicides are used to suppress Fusarium head blight (FHB) in wheat, which is caused by *Fusarium graminearum* species complex (FGSC). However, the pathogen's ability to evolve defense mechanisms to elude existing treatments makes the use of fungicides difficult to maintain. Therefore, it would be beneficial to look for biological agents that are effective in controlling these pathogens to lessen the impact of these diseases along with chemical control. *In vitro* and *in vivo* biocontrol assays were carried out to evaluate antifungal potential of well-characterized biocontrol agents, *Pseudomonas chlororaphis* (PA23, soybean rhizosphere), *P. brassicacearum* (DF41, canola rhizosphere), and *Bacillus amyloliquefaciens* (BS6, canola endophyte) against pathogens causing Verticillium stripe of canola and FHB of wheat. Dual culture assays with 2 isolates of *V. longisporum* and 12 *F. graminearum* isolates (3ADON and 15ADON chemotypes from Alberta, Manitoba, and Saskatchewan) were conducted and showed that all three biocontrol agents (BCAs) significantly ($p>0.05$) suppressed the growth of *V. longisporum* and *F. graminearum.* Greenhouse inoculations also confirmed that BS6 is an efficient biocontrol agent for wheat FHB and Verticillium stripe of canola. To elucidate the responsible antibiotics involved in PA23, PA23-63: phenazine-minus and PA23-8: pyrrolnitrin-minus mutant strains were tested against Fg and Vl. Phenazine and pyrrolnitrin compounds are key secondary metabolites contributing to the antagonistic and antifungal activity of PA23. However, in PA23, mutations in phenazine and pyrrolnitrin biosynthetic genes exhibited equal or more antifungal activity *in vitro* compared to the wild type, which means phenazine and pyrrolnitrin are not the major products directly contributing to *V. longisporum* and *F. graminearum* biocontrol. However, using a scanning electron microscope, crude extract of bacterial isolates will be assessed for its capacity to induce structural abnormalities in fungal mycelium for the precise determination of the biocontrol mechanisms. Further, RFP/GFP transformed isolates of BCA's and pathogens will be used to observe the pathogens and BCA's interactions within the host tissues. In addition, metabolomic data from both pathogen and BCAs will reveal mechanisms of action of BCAs during biotrophic, and necrotrophic phases of the pathogen.

[P11] EVALUATION OF DIFFERENT STRATEGIES TO CONTROL STRAWBERRY ANGULAR LEAF SPOT (*XANTHOMONAS FRAGARIAE*). Maxime Delisle-Houde[1], Valérie Tremblay[1], François Demers[2], Stéphanie Tellier[3], Gabrielle Labrie[1], Valérie Fournier[1], Nicholas Lefebvre[4], and Russell J. Tweddell[1]. [1]Département de phytologie, Université Laval, Québec, QC G1V 0A6, Canada; [2]Club les productions Écolo-Max, Lévis, QC G7A 2N7, Canada; [3]Ministère de l'Agriculture, des Pêcheries et de l'Alimentation du Québec, Direction régionale Capitale-Nationale et Chaudière-Appalaches, Québec, QC G1N 3Y7, Canada; and [4]Département des sols et de génie agroalimentaire, Université Laval, Québec, QC G1V 0A6, Canada
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In strawberry (*Fragaria* × *ananassa*), the management of angular leaf spot (ALS) caused by the bacterium *Xanthomonas fragariae* is difficult due to the lack of effective control methods. In this study, various strategies were tested for their efficacy to control ALS including leaf stripping, hot-steam treatment, and application of chemicals registered or not against ALS during a two-years field assay. The chemicals tested were a copper-based pesticide, sodium carbonate peroxyhydrate, citric acid + lactic acid, hydrogen peroxide and hydrogen peroxide + peracetic acid. The field assays were conducted in 2022 and 2023 with the cultivar ACC Lila and the cultivar Sonata, respectively. Hot-steam treatment using an airtight plastic pallet box as controlled-atmosphere chamber and copper-based pesticide (Cueva® Commercial)

foliar sprays significantly reduced the disease severity one year out of two. While foliar applications of sodium carbonate peroxyhydrate and citric acid + lactic acid did not significantly influence ALS severity for both years. Applications of hydrogen peroxide and hydrogen peroxide + peracetic acid also failed to control the disease. This study shows the potential of copper-based pesticide and hot-steam treatment to control ALS of strawberry. The effect of weather conditions on the development of the disease is also presented.

[P12] EFFECT OF VOLATILE COMPOUNDS PRODUCED BY BROWN MUSTARD ON DIFFERENT PLANT BENEFICIAL AND PHYTOPATHOGENIC MICROORGANISMS. Marwa Mejri, Maxime Delisle-Houde, Thi Thuy An Nguyen, Martine Dorais, and Russell J. Tweddell. Département de phytologie, Université Laval, Québec, QC G1V 0A6, Canada
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Several studies showed the efficacy of biofumigation to control weeds, pests, and pathogens affecting horticultural crops. Biofumigation is based on the release of toxic volatile compounds (isothiocyanates) during the degradation of glucosinolates-rich plants of the Brassicaceae family. This study aimed to evaluate, *in vitro*, the toxicity of volatile compounds produced by mashes of brown mustard [*Brassica juncea* (L.) Czern.] (cv. Terminator) on the phytopathogenic fungi *Rhizoctonia solani* and *Fusarium oxysporum* and the biocontrol agents *Bacillus subtilis* and *Trichoderma harzianum*. Petri dishes containing PDA (fungi) or TSA (*B. subtilis*) inoculated with a mycelial disc (4 mm) or a bacterial suspension (1×10^8 colony forming units mL^{-1}) were deposited in hermetic chambers (500 mL) containing different concentrations (0-120 mg mL^{-1}) of aqueous suspensions of brown mustard mash. The fungal/bacterial growth was evaluated every 24 h during an exposition period of 72 h (22.5°C) to determine the effect of volatile compounds produced by grinded brown mustard on the growth of the tested microorganisms. Results obtained in this study show that volatiles generated by grinded brown mustard (cv. Terminator) can inhibit the growth of plant pathogens as well as biocontrol agents.

[P13] ANTIFUNGAL ACTIVITY OF ESSENTIAL OILS FROM DIFFERENT NORDIC PLANT SPECIES AGAINST *BOTRYTIS CINEREA*. Antoine Roy-Lemieux, Maxime Delisle-Houde, and Russell J. Tweddell. Département de phytologie, Université Laval, Québec, QC G1V 0A6, Canada
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Grey mold, caused by the fungus *Botrytis cinerea* Pers., affects a wide range of horticultural plant species. Control of the disease relies mainly on the use of synthetic pesticides that cause numerous negative effects in agriculture, the environment, and human health. The objective of the study was to evaluate the antifungal and prophylactic properties of vapors of essential oils (EOs) from different Nordic plant species including Labrador tea (*Ledum groenlandicum*), black spruce (*Picea mariana*), and Jack pine (*Pinus banksiana*) against *B. cinerea*. The fungus was cultivated at 22.5°C on agar in a hermetic chamber in presence of vapors produced by different quantities (0-100 µL) of EOs from Labrador tea, black spruce, or Jack pine. After different incubation periods (0-96 hours), the mycelial growth was measured. In order to evaluate the prophylactic effect of EOs, tomatoes (cv. Micro-Tom) previously inoculated with a suspension of *B. cinerea* were incubated at 22.5°C in presence of vapors generated by either of EOs. After an incubation period of 96 hours, the severity of grey mold was evaluated. The results obtained highlight the antifungal activity of vapors of EOs from Labrador tea, black spruce, and Jack pine against *B. cinerea*. Moreover, EOs allowed to significantly ($p \leq 0.05$) reduce the severity of grey mold on tomatoes. Future work will be undertaken to evaluate the potential use of these EOs in a commercial context.

[P14] POTENTIAL OF FOREST PLANT EXTRACTS TO CONTROL ANGULAR LEAF SPOT OF CUCURBITS. Sabra Mimouni[1], Maxime Delisle-Houde[1], François Demers[2], Martin Filion[3], and Russell J. Tweddell[1]. [1]Département de phytologie, Université Laval, Québec, QC G1V 0A6, Canada; [2]Club les productions Écolo-Max, Lévis, QC G7A 2N7, Canada; and [3]Saint-Jean-sur-Richelieu Research and Development Center, Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu, QC J3B 3E6, Canada
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Angular leaf spot (*Pseudomonas syringae*) is a bacterial disease leading to significant yield losses in cucurbit crops. Control of the disease relies mainly on the use of copper-based pesticides that are often

not very effective. Moreover, repeated applications of copper can have negative impacts for the environment and human health. This study aimed to evaluate the antibacterial properties of ethanolic extracts from different forest species (sugar maple, silver maple, white spruce, Canada yew) against *P. syringae*. Minimum inhibitory concentrations (MICs) and minimum bactericidal concentrations (MBCs) of the extracts were first determined *in vitro*. Some extracts were afterwards tested for their efficacy as seed treatment against *P. syringae* in squash and cucumber. The results obtained showed bacteriostatic and bactericidal activities of the extracts (MICs = 0.39-3.13 mg mL^{-1}; MBCs = 12.5-50 mg mL^{-1}) and revealed the efficacy of sugar maple leaf extracts as seed treatment. Indeed, seed treatment with sugar maple leaf extracts significantly ($p \leq 0.05$) reduced the rate of *P. syringae* contaminated seeds as compared to the control. Future work will be undertaken to evaluate the potential of sugar maple leaf extracts to control the development of angular leaf spot on squash and cucumber plants cultivated in greenhouse.

***[P15] EFFICIENT *IN VITRO* DOUBLED HAPLOID PRODUCTION IN *BRASSICA NAPUS* FROM ISOLATED MICROSPORE CULTURE.** Xinlong Dong, Rudolph Fredua-Agyeman, Stephen E. Strelkov and Sheau-Fang Hwang. Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB T6G 2P5, Canada
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Canola (*Brassica napus*) is the second most important oilseed crop in the world. Doubled haploid (DH) technology enables the rapid generation of 100% homozygous lines within only two generations. In this study, five DH populations were developed from F_1 plants derived from crossing clubroot-resistant donors (♂) with the clubroot susceptible *B. napus* cv. 'Westar' (♀). To do this, 16 to 52 buds were surface-sterilized in 7% $Ca(ClO)_2$ and rinsed 3× in sterile water. The buds were ground with a mortar and pestle, filtered through six layers of cheesecloth, and centrifuged to recover the microspores. The isolated microspores were treated overnight with 50 mg/L colchicine in NLN13 medium to induce chromosome doubling, and then resuspended in NLN13 medium without colchicine for 28 days in the dark at 30°C. Embryos with cotyledons and hypocotyls were transferred to solid B5 agar plates containing 2% sucrose and 0.1mg/L GA3. After 1-2 months of incubation, the mature seedlings were transferred to a potting soil in the greenhouse. The number of embryos transferred to solid medium for the five populations ranged from 392 to 13,471. The plantlet (seedlings with large true leaves and good root development) regeneration rate ranged from 21% to 32%, with the highest being 47%. This DH production protocol was about 2-3× more efficient than other methods. The developed DH populations will be used to map genomic regions associated with clubroot resistance in five clubroot-resistant donors from the U of Alberta Pathology Lab Collection.
Keywords: Double haploid, Embryogenesis, Microspore, Brassica napus, Clubroot

***[P16] REAL-TIME NUTRIENT ASSESSMENT IN ONIONS USING PICKETA-LENS TECHNOLOGY.** Ifesinachi Nelson Ezeh[1], Xavier Hébert-Couturier[2], and Mary Ruth McDonald[1]. [1]Department of Plant Agriculture, University of Guelph, Crop Science Building, University of Guelph, 50 Stone Road E. Guelph, Ontario, Canada, N1G 2W1; and [2]Picketa Systems Inc., J. Herbert Smith Center, H-225, Head Hall, 17 Dineen Drive, P.O. Box 4400, Fredericton, NB, Canada, E3B 5A3
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The fertilizer recommendations for onions grown on high organic matter soils have not been updated for decades. Cultivars have changed over time as have some production practices, with more applications of micronutrients and foliar fertilizers. This study provided baseline tissue analysis data to train the new Picketa-Leaf Evaluated Nutrient System (LENS) technology for the real-time nutrient status of onions. In 2023, 235 onion samples were collected from the field, including a replicated trial with foliar manganese and additional foliar fertilizers. Each sample was first scanned using the LENS and then sent for tissue nutrient analysis at SGS Laboratories. In 2024, a controlled environment (CE) trial was conducted on onions to induce specific nutrient deficiencies. The 2023 field results showed that onions exceeded the optimum foliar nutrient concentration in almost all cases. The LENS trained on the data had the strongest associations for potassium, calcium, and nitrogen (N) with R^2 values of 0.74, 0.72, and 0.67, respectively. More samples are needed to train the system for these and other nutrients. The CE trial tested the effects of low (50% of recommended) nitrogen and low (50%) and high (150%) manganese (Mn) levels on

onion leaf tissue content, plant height, fresh weight, and dry weight at the 5- and 7-leaf growth stages. Nutrients were applied in modified Hoagland's solution and treatments were compared to standard (half-strength) Hoagland's solution. There were no differences in plant height at the 5-leaf stage. At the 7-leaf stage, the low N treatment had shorter plants (35.4 cm) compared to the low Mn treatment (40.9 cm). Similar results were found for dry weight, 2.9 g, and 3.7 g for low N and low Mn, respectively. However, these treatments were not different from the standard treatment. Although a reduction in Mn was intended stress to the plant, growth was sustained and there were no differences in tissue Mn (42 - 44.5 ppm). The CE findings demonstrated that it was possible to create a N deficiency, although lower rates of N should be tested. The tissue N was 3.7% for the standard treatment and lower, 3.5% for the low N, but both were within the recommended range of 2-3 %. Lower and higher rates of Mn will have to be evaluated to show a difference in growth. Real-time LENS technology could be an important tool for fertilizer use efficiency. Evaluations will continue in the field and CE.

[P17] PROTOCOL FOR DEVELOPING MUTAGENIZED WHEAT UNDER IN VITRO SELECTION PRESSURE FOR FUSARIUM HEAD BLIGHT RESISTANCE. Clinton Dovell, D Ryabova, Susan Stasiuk, Harpinder Randhawa, Harwinder Sidhu, and Nora A. Foroud. Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 -1st Avenue South, Lethbridge AB, Canada, T1J 4B1
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Fusarium head blight (FHB) is a devastating disease of wheat and related cereals cause by the fungus Fusarium graminearum, and related species. We have been developing microspore-derived doubled haploid wheat plants from F1 hybrids under selection pressure for FHB resistance. The selection pressure we employ utilizes Fusarium graminearum mycotoxins which are included with the microspores in the embryo induction medium. We have been adapting our protocol to develop a mutagenized wheat population under this in vitro selection pressure. We have compared ultraviolet (UV) and ethylmethanosulfonate (EMS) mutagenesis treatments of the microspores prior to application of the mycotoxins. For this protocol, we are utilizing fixed wheat lines rather than F1 hybrids, with the intention of developing a mutagenized population from which we can (a) identify novel genetics associated with FHB resistance, and (b) screen the efficacy of our in vitro selection method in selecting microspores with FHB resistance genetics. We are still in the process of developing doubled haploid plants which will be screened down the line for FHB resistance. Here, we will present our preliminary data on our protocol development.

[P18] FORECASTING FUSARIUM HEAD BLIGHT EPIDEMICS IN THE MARITIME PROVINCES OF CANADA. Emily Johnstone, Morteza Mesbah, Kristen Murchison, and Adam J. Foster. Charlottetown Research and Development Centre, Agriculture and Agri-Food Canada, 440 University Avenue, Charlottetown, PE, Canada, C1A 4N6
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In the Maritime provinces of Canada, Fusarium head blight (FHB) is an economically important disease of wheat and barley. *Fusarium graminearum* is the primary cause of FHB and results in contamination of grain with the mycotoxin deoxynivalenol (DON). Epidemic occurrences of this disease are related to field management practices and environmental conditions in the weeks surrounding anthesis. Management of FHB is difficult due to a short fungicide application window therefore, weather-based disease forecasting tools have been developed to assess in-season FHB risk and support fungicide decision making. Currently, no FHB risk assessment tool is available to cereal producers in the Maritimes. The objective of this study was to evaluate North American FHB forecasting models in the Maritimes to determine the most accurate method and environmental factors for predicting the occurrence of FHB epidemics when grain is contaminated with ≥ 0.9 ppm DON. The most accurate model from the evaluation was then used to guide fungicide applications. Using 12 years of historical cultivar recommendation data, 10 fungicide trials, and 37 sites years of regional FHB surveillance, found that a model using using 7-day pre-anthesis relative humidity and temperature performed best in the Maritimes for both wheat and barley. Building on these findings we designed and implemented a web-based tool for FHB forecasting for Maritime cereal growers. This tool, integrated into an RShiny application, uses Environment Canada weather data to provide daily FHB risk assessments on regional maps. The tool will be launched in the 2024 growing season hosted by the Atlantic Grain's Council.

[P19] QPCR METHODS TO DETECT AND QUANTIFY THE NOVEL *FUSARIUM GRAMINEARUM* ANX CHEMOTYPE VARIANT. Abbey Saunders, Emily Johnstone, and Adam J. Foster. Charlottetown Research and Development Centre, Agriculture and Agri-Food Canada, 440 University Avenue, Charlottetown, PE, Canada, C1A 4N6
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Fusarium head blight (FHB) is an economically important disease of cereal crops globally. FHB is caused by numerous species of pathogenic fungi in the genus *Fusarium*, however the greatest concern is *Fusarium graminearum* for its contamination of grain with secondary metabolites such as deoxynivalenol (DON). DON is classified as a trichothecene, a group of mycotoxins known to cause immunotoxic and neurotoxic effects when ingested. The trichothecene group also includes the novel toxin 7α-hydroxy, 15-deacetylcalonectrin (ANX), for which there are currently no rapid detection methods available. In this study, three quantitative polymerase chain reaction (qPCR) assays were developed for detection of the *Tri1* gene polymorphism responsible for ANX strains. Consensus alignment of a collection of *Tri1* gene sequences from ANX isolates and isolates of other chemotypes was conducted. At ANX-specific polymorphism sites, primers and probes were designed to specifically amplify ANX producing isolate target DNA. As the probe was designed on a single polymorphic region, a locked nucleic acid (LNA) was incorporated into the sequence to enhance target specificity. In total, 2 SYBR Green assays and an LNA HEX labelled probe assay specifically amplified ANX chemotype strains without amplification of other *F. graminearum* chemotypes or the 12 other *Fusarium spp.* tested. A four-fold standard curve was made from a series of dilutions of ANX isolate DNA to calculate qPCR efficiency and correlation coefficients. The assays were subsequently evaluated *in vivo* using the ANX standard curve to assess their efficacy in detecting and quantifying ANX DNA. This evaluation included target DNA extracted from wheat heads and seeds infected with ANX hyphae, and soil inoculated with macroconidia from a ANX producing strain. The results of the *in vivo* tests found the different SYBR Green assays had detectable limits of 198 DNA copies per reaction and 98 DNA copies per reaction, respectively. The LNA probe-based assay had a detectable limit of 198 DNA copies per reaction required for amplification. These assays are a new tool for rapid detection and quantification of ANX-producing isolates in plant tissue and soil, advancing research on the epidemiology and geographic distribution of this novel chemotype.

[P20] INFLUENCE OF COVER CROPS ON SOIL AND RESIDUE FUNGAL MICROBIOMES AND THEIR IMPACT ON FUSARIUM ROOT AND CROWN ROT. Harini S. Aiyer[1,2], Aaron Mills[3], Andrew Mckenzie-Gopsill[3], and Adam J. Foster[3]. [1]Agassiz Research and Development Centre, Agriculture and Agri-Food Canada, Agassiz, BC, Canada; [2]Faculty of Land and Food Systems, University of British Columbia, Vancouver, BC, Canada; and [3]Charlottetown Research and Development Centre, Agriculture and Agri-Food Canada, Charlottetown, PE, Canada
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Cover crops have many befits to agricultural crops including the ability to influence diseases such as Fusarium root and crown rot (FRCR) in crops grown in subsequent growing seasons. Eight cover crops including: alfalfa, crimson clover, buckwheat, phacelia, oilseed radish, brown mustard, sorghum-sudangrass, and annual ryegrass were evaluated in Prince Edward Island Canada for their effects on the soil microbiomes and residue microbiome and plant disease in barley and soybean crop in the following seasons. Additionally, three cover crop mixes were examined. Two field trials over two years utilized a randomized complete block design for cover crops and a split-plot design for subsequent barley and soybean planting. Internal transcribed spacer (ITS) amplicon sequencing characterized fungal community changes in the soil during the cover crop growing season and the subsequent year. Fungal alpha diversity increased over time and was significantly influenced by cover crop choice. Fungal pathotroph abundance was positively associated with oilseed radish, alfalfa, and phacelia, but negatively with sorghum-sudangrass. Beneficial symbiotrophic fungal groups were linked to sorghum-sudangrass and buckwheat. High *Fusarium* spp. abundance in soil and field residue samples correlated with the observations of FRCR incidence in barley and soybean roots. A greenhouse trial using soils from sorghum-sudangrass, buckwheat, brown mustard, alfalfa, phacelia, and no-crop plots, inoculated with Fusarium, confirmed the protective effect of disease suppressive soils from certain cover crops against FRCR. These findings suggest that specific cover crops can alter soil microbial communities, impacting plant health and disease levels in subsequent crops.

***[P21] EVALUATION OF THE HOST SPECIFICITY OF *VERTICILLIUM LONGISPORUM* IN WESTERN CANADA**. Lidan Gao[1], Haitian Yu[1], Godfrey Chongo[2], Stephen E. Strelkov[1], and Sheau-Fang Hwang[1]. [1]Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB, Canada, T6G 2P5; and [2]BASF Canada Inc., Saskatoon, SK, Canada, S7K 3J9
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Verticillium longisporum is a soilborne fungal pathogen that causes Verticillium stripe of canola (Brassica napus). This study evaluated the host specificity of *V. longisporum* on eight crops of economic significance in western Canada: canola, wheat, barley, pea, lentil, faba bean, soybean, and potato. Inoculations were conducted under greenhouse conditions, with each crop represented by 2 to 4 cultivars. Compared to the controls, inoculated treatments showed variable reductions in height and emergence across all crops. Soybean and lentil were the most severely affected, experiencing height reductions ranging from 83% to 94% for soybean, with emergence declining by 85% to 95% compared with the non-inoculated control. Principal component analysis indicated that wheat, barley, pea, and faba bean showed somewhat more tolerance to *V. longisporum* infection, experiencing smaller reductions in emergence and plant height. No signs or symptoms of disease were visible on barley or wheat. Nonetheless, the emergence of wheat, along with canola, lentil and faba bean, was significantly delayed compared to the non-inoculated controls. Symptoms of infection were most pronounced on canola, pea, and potato, although assessments of disease severity are still underway. Preliminary results suggest that several crop species may serve as hosts of *V. longisporum* in western Canada.

[P22] BALANCING SELECTION COMPLICATES MANAGEMENT OF CLUBROOT AND (POSSIBLY) OTHER PROBLEM DISEASES. Bruce D. Gossen[1], A. Sedaghatkish[2] and M. R. McDonald[2]. [1]Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, Saskatoon, SK, Canada; and [2]Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada
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Balancing selection occurs when multiple alleles are retained over time in a population, usually at very low frequency. Evidence is accumulating that *Plasmodiophora brassicae* Wor., the cause of clubroot in *Brassica* spp., retains many complete genotypes at low frequency. This likely occurs because the dominant genotype suppresses host resistance, facilitating host infection by other phenotypes. This retention of entire genotypes may explain the rapid breakdown of single-gene resistance to clubroot. Genotypes that can overcome the resistance may already be present in the pathogen population at low frequency. When a new host resistance gene is deployed, intense selection for virulent phenotypes would occur. The pathogen can produce billions of spores per infected plant, so clubroot can increase rapidly even from a low starting point. Stacked resistance genes or rotation of resistant cultivars in combination with crop rotation, which reduces spore populations by 90–99% over 2–3 years, could substantially reduce the risk of resistance breakdown. In addition, we suggest that the definition of balancing selection be expanded to include situations where one genotype / species ‘opens the door’ to less virulent genotypes, allowing them to infect a host. This may occur among AG groups of *Rhizoctonia solani* or among *Pythium / Globisporangium* spp. Isolation from rotting roots often yields many genotypes / species, only a few of which are aggressive on healthy roots. It appears likely that infection of a root by one genotype provides an opportunity for related pathogens to colonize the dying root and thus be maintained in the microbial population.

[P23] DO NEMATODES GET AROUND? A CASE OF SOYBEAN CYST NEMATODE IN A MANITOBA FIELD. Fernanda Gouvea Pereira[1], Nazanin Ghavami[1], Jason Voogt[2], and Mario Tenuta[1]. [1]Department of Soil Science, University of Manitoba, Winnipeg, Manitoba, Canada; and [2]Field to Field Agronomy Inc., Miami, Manitoba, Canada
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Soybean Cyst Nematode (SCN) is a devastating pathogen known for causing significant yield losses in soybean and certain dry bean varieties across North America. Although SCN was first identified in Manitoba in 2019 with low cyst populations, a subsequent investigation in July 2021 revealed an SCN symptomatic soybean field with cyst-laden roots in the Rural Municipality of Thompson. The affected area surrounded the field entranceway for machinery. Detailed soil sampling in the affected area was conducted in a grid patten (6 m x 10 m) covering 1,680 m^2. Molecular analysis confirmed the cysts to be

Heterodera glycines, establishing the presence of SCN in the field. The maximum egg density was 7,797 eggs 100 cm^{-3} soil, which is moderate to high for SCN levels, concentrated in the centre of the patch. Densities tapered to zero in visually healthy soybean growth areas. We were then curious if SCN had spread to other areas of the field and thus sampled the entire 93-acre field using a 1-acre grid pattern, yielding 91 soil samples. Four cores were taken at evenly spaced points within each grid, from 0 to 20 cm depth, and then composited for analysis. Soil samples were extracted for eggs, eggs stained, and counted to determine soil densities. Analysis of soil properties, pH, electrical conductivity (EC), total nitrogen (TN), soil organic carbon content (SOC), and the C:N ratio, were also done. Data analysis was conducted using SAS University, transformed to fit normality. Multiple Linear Regression was employed for modeling density relation to soil properties. No statistically significant correlations between soil properties and SCN egg counts were observed at the 5% significance level. The maximum observed egg count was 933 eggs 100 cm^{-3} soil, and the spatial distribution of SCN eggs reflected a nematode spread pattern based on translocation within the field. The highest egg density was at the affected field entrance, with spread in a north-south orientation attributed to direction of soil disturbance during seeding and tillage operations. Of note, the entrance area with SCN disease symptomology and highest egg densities did not reach complete reproductive maturity and consequently did not yield.

***[P24] SMOKE SIGNALING: VOLATILE TERPENES RELEASED IN BURNING *ARTEMISIA TRIDENTATA* NUTT. ARE ACCUMULATED IN GRAPEVINES.** Alisha Greene[1], Susan J Murch[1], and Robert O'Brien[2]. [1]Department of Chemistry, University of British Columbia, Syilx Okanagan Nation Territory, Kelowna, BC, Canada, V1V 1V7; and [2]Supra Research and Development, Kelowna, BC, V1X 6Y5
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Indigenous plants growing near vineyards emit volatile organic compounds (VOCs) that can influence grapevines and wine characteristics. Like humans, plants communicate with their relatives. Literature shows that *Artemisia tridentata*, commonly known as Big Sagebrush, communicates by releasing terpenes that trigger different physiological responses in related and kin plants With *A. tridentata* frequently found in the South Okanagan, where it often shares habitat with vineyards, understanding the impact of these terpenes on grapevines is essential to understanding wine terroir. We hypothesized that volatiles released in burning *Artemisia tridentata* accumulate in grapevines, potentially affecting wine production. Grapevines were subjected to cohabitation with *A. tridentata* and exposed to both atmospheric and collected smoke from the plant. Using a previously developed and validated GC-MS method, terpene accumulation in the grapevines was determined, An untargeted metabolomics experiment by high resolution mass spectrometry (OrbiTrap) approach was used to putatively identify the degradation metabolites of terpenes in the grapevines. *A.* tridentata-exposed vines were shown to have increased levels of camphor and its degradation products, as well as other terpenes present in the monoterpenoid biosynthesis pathway. Given that aromatic compounds play a crucial role in shaping the flavour and aroma profiles of wine varietals, understanding how grapevines respond to these environmental cues is important.
Keywords: Wine grapevines, Vitis vinifera, Artemisia tridentata, smoke chemistry, volatile organic compounds

[P25] RESISTANCE MECHANISMS TO FUSARIUM HEAD BLIGHT IN WINTER WHEAT IN RESPONSE TO *FUSARIUM* GRAMINEARUM. Maria A. Henriquez[1], Philip L. Walker[1], Mark F. Belmonte[2], Brent D. McCallum[1], Curt A. McCartney[3], and Harpinder S. Randhawa[4]. [1]Morden Research and Development Centre, Agriculture and Agri-Food Canada, Morden MB, Canada; [2]Department of Biological Sciences, University of Manitoba, 50 Sifton Road, Winnipeg, MB, R3T 2N2; [3]Department of Plant Sciences, University of Manitoba, 66 Dafoe Road, Winnipeg, MB, R3T 2N2; and [4]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada
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Fusarium head blight (FHB) is a devastating fungal disease responsible for significant yield losses in wheat and other cereal crops across the globe. FHB infection of wheat heads results in grain contamination with mycotoxins, ultimately reducing both grain quality and yield. Breeding strategies have resulted in the production of FHB-resistance, however, the underlying genetic mechanisms of resistance in the majority of these cultivars are still poorly understood. In this research, we provided insights into the

resistance mechanisms to FHB in AC Emerson and AC Morley winter wheat cultivars in response to *Fusarium graminearum*. In our RNA analysis we identified distinct defense responses within FHB-resistant cultivars including the enrichment of physical defense, and mycotoxin detoxification. Further, RNA analysis also revealed significant changes in gene expression in *F. graminearum* when infecting FHB-resistant cultivars compared to FHB-susceptible CDC Falcon. Together, these data provide insight into identifying new sources of FHB-resistance in winter wheat and improving our understanding of this important pathosystem.

***[P26] PATHOTYPES OF *PLASMODIOPHORA BRASSICAE* IN ONTARIO, 2023.** K. Holy[1], B. Gossen[2], and M.R. Mcdonald[1]. [1]Department of Plant Agriculture, University of Guelph, 50 Stone Rd E, Guelph, ON N1G 2W1, Canada; and [2]Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada
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Clubroot is a soilborne disease caused by *Plasmodiophora brassicae* (Woronin), which is a serious constraint to canola production in Canada. The pathogen exists as many pathotypes, which are genetically different strains of *P. brassicae* that can exhibit varying levels of virulence on differential Brassica hosts. The use of resistant varieties of canola is the most effective approach to disease management, but there are increasing reports of *P. brassicae* overcoming clubroot-resistant canola. The first clubroot resistant canola cultivar (*Brassica napus* cv. 45H29), was released in 2009. To measure the occurrence of virulent pathotypes that can overcome the resistance available in 45H29 (often referred to as first generation resistance), symptomatic 'clubbed' roots were collected from 12 fields in Ontario. The fields were primarily near Temiskaming, where much of the province's canola production occurs. The pathotype of each collection was determined based on the bioassay reaction of differential hosts lines from the Williams' and Canadian Clubroot differential sets. A disease severity index (DSI (0-100%)) was calculated, and a threshold of 50% disease was used to differentiate susceptible (DSI ≥ 50%) from resistant (DSI ≤ 49%) host lines. Overall, 11 of 12 collections were of virulent pathotypes that caused severe disease on a canola line with first generation resistance (*B. napus* cv. P607CL). All the collections contained pathotypes from the Williams' differential classes 2, 3, and 8, many of which did not fit into the current Canadian Clubroot differential set. This means they have not previously been described in Canada. To compliment the bioassays, a KASP (Kompetitive allele specific PCR) assay was used to screen samples for a single nucleotide polymorphism (SNP) in gene 9171 that was previously associated with high virulence in collections from China, Japan, Quebec, and Western Canada. None of the Ontario samples carried the SNP on gene 9171. This may indicate that the virulence in these Ontario collections came from a different genetic mechanism than those previously assessed. Sequencing of the Ontario collections to determine potential sites for virulence-specific SNPs is in progress.

***[P27] DOTHISTROMA NEEDLE BLIGHT DEVELOPMENT IN FAMILIES OF LODGEPOLE PINE: MECHANISMS OF RESISTANCE AND PRECIPITATION-RESISTANCE INTERACTIONS UNDER CLIMATE CHANGE.** Dana Hopfauf[1] and Jonathan Cale[1]. [1]University of Northern British Columbia, 3333 University Way, Prince George, BC V2N 4Z9
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Dothistroma needle blight (DNB) is a fungal disease that affects a broad range of pine trees globally. It is one of the most destructive foliar diseases of commercial timber trees in the world. Optimal conditions for infection and growth of the causal fungus, *Dothistroma septosporum*, consist of warm, wet weather during the growing season. These conditions are expected to become more prevalent in northern British Columbia (BC), Canada due to climate change. A promising management approach involves the establishment of resistant pine families through targeted breeding. This study will (1) determine how pine resistance/susceptibility interact with precipitation to affect DNB severity, and (2) investigate possible anatomical and phytochemical mechanisms underlying DNB resistance. The study will consist of two major components: a greenhouse experiment and analysis of phytochemical and anatomical traits. The greenhouse experiment will involve inoculating lodgepole pine seedlings with *D. septosporum* and subjecting them to standard and elevated, climate change-associated precipitation conditions. Developing seedlings will be evaluated for disease severity, and needles from resistant and susceptible pine families will be collected to characterize phytochemical and anatomical defense-related traits. Project findings will help identify climate change-tolerant DNB-resistant families for targeted breeding programs and provide

possible resistance biomarkers for rapid screening of additional breeding families—a necessary component of safeguarding Canada's forest sector.

[P28] FUNGICIDE INSENSITIVE IN *COLLETOTRICHUM LENTIS* ON LENTIL IN SASKATCHEWAN, 2020-2022. Michelle Hubbard[1], Zakir Hossain[1], Merek Wigness[2], and Bruce D. Gossen[2]. [1]Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, 1 Airport Rd, Swift Current, SK, Canada, S9H 3X2; and [2]Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK, Canada, S7N 0X2
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Anthracnose caused by *Colletotrichum lentis* is currently the most important foliar disease of lentil in Saskatchewan. Fungicides belonging to FRAC groups 11 (strobilurins), 7 (succinate dehydrogenase inhibitors) and 3 (demethylation inhibitors) are routinely used to manage this disease. Through field surveys in 2020, 2021 and 2022, we explored the insensitivity of *C. lentis* to fungicides in FRAC groups 11, 7 and 3 using radial growth and molecular methods. The distribution of anthracnose, its severity and group 11 insensitivity within fields as well as the impact of group 11 insensitivity on isolate growth and disease severity were investigated. Anthracnose symptoms were consistently more severe in low spots within fields relative to hilltops. Hot, dry conditions in 2021 suppressed anthracnose development such that only a few samples were available for assessment. Overall, insensitivity to strobilurins was widespread but there was little or no insensitivity to groups 3 and 7. The distribution of strobilurin insensitivity was often patchy and uneven within a single field. This patchy distribution likely occurs because *C. lentis* is transmitted primarily by rain-splash and lacks a air-borne phase to distribute spores across a region or even a single field. In these patches, insensitivity to strobilurins was correlated with lower anthracnose severity in 2020, but not in 2022. Strobilurin sensitivity status had no impact on isolate growth in the absence of a strobilurin, which is an indication that the mutation to insensitivity has not affected isolate fitness. Lentil growers in Saskatchewan should use fungicides with active ingredients other than, or in addition to, strobilurins for management of anthracnose.

***[P29] IDENTIFICATION OF PYTHIUM SPECIES ASSOCIATED WITH CAVITY SPOT LESIONS ON CARROTS IN THE HOLLAND MARSH, ONTARIO.** Umbrin Ilyas[1], Lindsey J. du Toit[2], and Mary Ruth McDonald[1]. [1]Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada, N1G 2W1; and [2]Department of Plant Pathology, Washington State University, Mount Vernon, WA, USA, 98273
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Cavity spot is caused by several species of soilborne *Pythium* categorized as slow (< 20 mm/day) or fast-growing (>20 mm/day) based on their growth rate on agar media. Some *Pythium* species are now classified as *Globisporangium* based on phylogenetic studies. However, for consistency, the term "*Pythium*" is used throughout this abstract. The objectives of this study were to (1) identify *Pythium* species associated with cavity spot lesions, and (2) determine if the diversity of *Pythium* isolates varies with lesion size, applications of the fungicide mefenoxam, or between fields with a history of low or high-risk of cavity spot. Lesions were cut from carrots sampled from eighteen commercial fields in the Holland Marsh, Ontario, Canada. Lesions were categorized as small (0.1 cm), medium (0.2–0.5 cm), large (0.6–1 cm), or very large (> 1 cm) based on the horizontal lesion length. Lesions were plated on a semi-selective agar medium to isolate *Pythium*. The isolates were identified using microscopy and Sanger sequencing of internal transcribed spacer on 18S r RNA gene, cytochrome c oxidase-I, and NADH dehydrogenase subunit 1 gene. In 2020–21, 220 medium-sized lesions from eight fields yielded 260 *Pythium* isolates, nearly all were *P. sulcatum*, except eight isolates that were *P. intermedium*. In 2022–23, 242 lesions of four different sizes were collected from ten carrot fields, including low and high-risk fields, and those with and without mefenoxam application. The 929 *Pythium* isolates belonged to seven species. Three were slow-growing: *P. sulcatum* (71% of all isolates), *P. violae* (18%), and *P. rostratifingens* (1%). Four were fast-growing: *P. intermedium* (5%), *P. sylvaticum* (3%), *P. irregulare* (1%), and *P. ultimum* (1%). There were no significant effects of mefenoxam or history of cavity spot risk on the diversity of *Pythium* isolates. The number of isolates of *P. violae* was 21% lower in fields in which mefenoxam had been applied vs no mefenoxam applications. There was a significant association of lesion size with the frequency of slow and fast-growing isolates based on chi-square test ($\chi^2 = 50$, $P = 0.0001$). Slow-growing species were isolated

from all lesion sizes whereas there were 63% more fast-growing species associated with large lesions as compared to medium-sized lesions. A maximum of three *Pythium* species were isolated from a single lesion, with these lesions exhibiting large to very large sizes. In conclusion, seven *Pythium* species associated with cavity spot lesions, with *P. sulcatum* being the most predominant.

***[P30] UNVEILING THE COMPLETE GENOME OF THE CLUBROOT PATHOGEN.** Muhammad Asim Javed[1-5], Soham Mukhopadhyay[1-5], Éric Normandeau[3], Anne-Sophie Brochu[1-5], and Edel Pérez-López[1-5]. [1]Départment de Phytologie, Université Laval, Québec (Québec), Canada, G1V 0A6; [2]Centre de recherche et d'innovation sur les végétaux (CRIV), Université Laval, Québec (Québec), Canada, G1V 0A6; [3]Institute de Biologie Intégrative et des Systèmes (IBIS), Université Laval, Québec (Québec), Canada, G1V 0A6; [4]L'Institute EDS, Université Laval, Québec (Québec), Canada, G1V 0A6; and [5]Centre SÈVE Université de Sherbrooke, Sherbrooke (Québec), Canada, J1K 2R1
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Plasmodiophora brassicae is the causal agent of clubroot disease of cruciferous plants and a major threat to the rapeseed (*Brassica napus*) and brassica vegetable industry worldwide. The clubroot pathogen has been reported in more than 80 countries, causing economic losses of hundreds of millions every year. In Canada, despite the identification and characterization of more than 40 clubroot pathotypes that pose a significant threat to the canola industry, high-quality assembled, and annotated genomes for Canadian isolates remain unavailable. Moreover, very little is known about the molecular strategies this pathogen employs to induce the characteristic clubs in the roots of susceptible hosts during infection or the mechanisms it uses to overcome genetic resistance. Therefore, complete, and high-quality genomes are essential to understand the evolution of plant pathogens and the strategies they use to overcome genetic resistance. In this presentation we introduce the first telomere-to-telomere genome assembly of *P. brassicae* (pathotype Pb3A), and the first complete genome for a member of the supergroup Rhizaria. We produced a 25.3 Mb assembly comprising 20 chromosomes, with an N50 of 1.37 Mb and significantly improved all genome assembly statistics. Using available transcriptomic data and protein evidence, we annotated the Pb3A genome, identifying 10,521 protein-coding gene models – the highest number in existing genomic resources for this pathogen. Furthermore, we have identified 200 additional candidate effector proteins beyond the lists generated from previously available genomes, potentially critical for pathogen virulence. By comparing the long-read genome assemblies of the European genome (e3) and Pb3A we identified structural variations between the two pathotypes. Finally, our results will enable more robust and cost-effective analyses in population and comparative genomics and help to uncover structural variations among genomes of different clubroot pathogen isolates or pathotypes that can be linked to pathogenicity or evolution.

[P31] SOYBEAN ROOT DISEASES IN MANITOBA: HISTORY, MONITORING, PREVALENCE, AND CROP ROTATION EFFECTS. Yong Min Kim[1], Ahmed Abdelmagid[2], Owen Wally[3], Ramona Mohr[1], and Debra McLaren[1] (ret'd). [1]Brandon Research and Development Centre, Agriculture and Agri-Food Canada, 2701 Grand Valley Rd, Brandon, MB, Canada, R7C 5Y3; [2]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB, Canada, R6M 1Y5; and [3]Harrow Research and Development Centre, Agriculture and Agri-Food Canada, 2585 Essex County Rd 20, Harrow, ON, Canada, N0R 1G0
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Soybeans were first cultivated in Manitoba at the Experimental Farm in Brandon in 1898 as a forage crop, following their initial introduction to Canada in 1893 and to the USA in 1851. The first documented occurrence of root rot in soybeans caused by *Fusarium* sp. in Manitoba was recorded in 1924. Although Phytophthora root rot was first observed in the USA in 1948, it was not until 2011 that Phytophthora root rot was first detected in Manitoba. The province's first soybean production statistics were recorded in 1942 with 2,510 acres cultivated, but significant commercial production of soybeans did not occur until the early 2000s in Manitoba. In 2012, Manitoba surpassed Quebec to become Canada's second-largest soybean producer after Ontario, reaching a peak of 2.3 million seeded acres in 2017. This increase was largely attributed to the development of early-maturing, high-yielding varieties. With the expansion of soybean cultivation in Manitoba, Agriculture and Agri-Food Canada initiated extensive root disease surveillance in 2012. The annual root disease survey aimed to assess the prevalence and distribution of soilborne pathogens affecting soybean root health and productivity across the province's major soybean-

growing regions, including Phytophthora root rot. In the 2023 growing season, 58 soybean fields were surveyed in Manitoba for root diseases, and Fusarium root rot was found to be the most prevalent root disease. *Phytophthora sojae* was detected in 84% of soil samples from the surveyed fields using molecular pathotyping. Additionally, charcoal rot, caused by *Macrophomina phaseolina*, was also identified in 2023 in Manitoba, where it was first reported in 2020. Furthermore, a long-term field study conducted near Brandon from 2014 to 2023 evaluated the effects of five crop rotations on soybean root diseases. The soybean-based rotation study comprises five crop rotations of soybean(S), canola(C) and wheat (W) with SC, SW, SWC, SCW and SSW, ranging in duration from two to three years in length. The results suggest that longer crop rotations with greater diversity tend to exhibit lower severity of soybean root rot disease in certain years, compared to shorter rotations or continuous soybean cropping. In summary, soybeans have become Manitoba's most important grain legume crop, and ongoing research continues to shed light on effective disease management strategies.

***[P32] PATHOTYPE SHIFTING OF SINGLE-SPORE ISOLATES OF *PLASMODIOPHORA BRASSICAE* OVER THREE MULTIPLICATION CYCLES.** B. Kirk, A. Botero-Ramirez, S.F. Hwang, and S.E. Strelkov. Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada
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The isolation of single-spores of the soilborne obligate parasite *Plasmodiophora brassicae* (clubroot of crucifers) is critical for generating genetically homogeneous pathogen collections. Multiplication of these isolates on various host genotypes can lead to shifts in their virulence, altering pathotype designations and affecting research outcomes, particularly in resistance labeling for new crop varieties. In this study, four single-spore isolates (SSIs) were used, two designated as pathotype 3H and two as pathotype 3A, based on their virulence on the Canadian clubroot differential set (CCD). These SSIs were obtained from a single gall previously classified as pathotype 3A that underwent three cycles of multiplication on the susceptible host ECD05 (*B. rapa* var. *pekinensis* cv. 'Granaat') prior to initial testing. Two additional multiplication cycles were conducted in ECD05 and a first-generation clubroot-resistant canola (*Brassica napus*) cv. '45H29'. After each multiplication cycle, changes in the virulence pattern of each isolate were assessed on a subset of CCD hosts, comprising ECD05, ECD06 (*B. napus* cv. 'Nevin'), ECD10 (*B. napus* var. *napobrassica* cv. 'Wilhelmsburger'), *B. napus* cv. 'Mendel', and '45H29'. After four multiplication cycles (three before the initial pathotyping and an additional round), three pathotypes retained their original designations. However, one pathotype showed decreased virulence on three hosts (ECD10, 'Mendel', and '45H29') following multiplication on ECD05, resulting in a shift in the pathotype designation from 3A to 3D. These results emphasize the importance of strategic stewardship of *P. brassicae* collections to maintain their stability and reliability, thereby enhancing the effectiveness of research and breeding activities.

***[P33] FUSARIUM HEAD BLIGHT AND RUST FUNGI IDENTIFICATION VIA MALDI-TOF MASS SPECTROMETRY.** Shimosh Kurera[1,2], Matthew Bakker[1], and Sean Walkowiak[2]. [1]Department of Microbiology, University of Manitoba, Winnipeg, MB, Canada R3T 2N2; and [2]Canadian Grain Commission, 196 Innovation Dr, Winnipeg, MB, Canada R3T 2N2
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Grain production contributes significantly to meeting human food and animal feed demands in Canada and in export markets. One of the key limitations to grain production is fungal disease. Identification of plant pathogenic fungi is important in effective disease management practices and can have implications for trade. In this study, we developed a rapid method to identify fungi responsible for Fusarium head blight (FHB) and rust cereal diseases using Matrix Assisted Laser Desorption/Ionization Time of Flight Mass Spectrometry (MALDI-TOF MS). MALDI-TOF MS generates unique peptide mass fingerprint (PMF) graphs from fungal proteins that can be used to distinguish one fungal species from another. To introduce fungal proteins into the mass spectrometer, different cell types (i.e., mycelia, conidiospores, urediniospores, or germinated urediniospore-mats) were used from *Fusarium* and *Puccinia* spp. To prepare the protein extract input, fungal cells were disrupted with formic acid followed by addition of acetonitrile to dissolve proteins. The protein extract is then ionized off of the target plate by the instrument laser. Proteins in the gas phase travel to a detector, and results are analyzed to generate a PMF graph for each fungal protein sample. The PMF profile is then compared to a reference library of known PMF

profiles for identification. In this work, a custom reference library was created for several *Fusarium* and *Puccinia* species, strains and races originating from across Canada. To create a single reference profile for each fungal species/strain/race, 20 PMF graphs were combined. After populating the reference library, we tested 710 unknown fungal samples isolated from *Fusarium* damaged kernels of wheat from 2021, 2022 and 2023 harvest years and were able to identify the *Fusarium* in these damaged kernels to the level of species. To confirm the identity of these fungi, high-throughput quantitative PCR (HT-qPCR) was performed using species specific DNA markers. MALDI-biotyping results agreed with the HT-qPCR results approximately 96% of the time. Similarly, 86 samples of rust spores that originated from different cereal hosts were identified to the species level with 100% accuracy using MALDI-biotyping. We also compared PMF profiles across tissue types, which revealed tissue specific differences in the PMF graphs. MALDI-biotyping of FHB pathogens to the species level is more accurate with PMF graphs derived from conidiospores compared to from mycelia. MALDI-TOF MS is a promising tool for rapid identification of both *Fusarium* and *Puccinia* spp. and can complement DNA-based testings that are currently used for fungal identification.

[P34] POWDERY MILDEW SPECIES ON MAPLE TREES IN CANADA. Miao Liu, Parivash Shoukouhi, Cameron Julie, and Sarah Hambleton. Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6
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Powdery mildew species that produce chasmothecia with hooked appendages on maple leaves were historically classified in the genus of *Uncinula* in Canada. In an internal Canadian Host-Pathogen Database, two species were reported, i.e. *U. bicornis* on *Acer macrophyllum* (bigleaf maple) from British Columbia and *U. circinata* on *A. rubrum* (red maple)*, A. saccharinum* (silver maple)*, A. saccharum* (sugar maple)*,* and *A. spicatum* (mountain maple) from several provinces. As early as 1914, Japanese mycologist Miyabe separated *Uncinula* spp. on maple trees into a new genus *Sawadaea* based on the observation that a portion of chasmothecial appendages of maple '*Uncinula'* were branched (either dichotomously or trichotomously), **differing from the unbranched appendages of the** grape powdery mildew *Uncinula necator* (current name: *Erysiphe necator*). In 1937, Homma accepted Miyabe's classification in his revision of Erysiphaceae in Japan, and recognized three *Sawadaea* spp. i.e *S. bicornis*, *S. tulasnei*, and *S. negundinis*. A phylogenetic study by Hirose and colleagues in 2005 proved *Sawadaea* is distantly related with '*Uninula* lineage' in *Erysiphe*. Up to date, ten species were accepted. *Sawadaea bicornis*, with its broad host and geographic range, was considered the only species present in North America until 2006 when Weiland and Stanosz reported the first incidence of *S. tulasnei*, an Old-world species, in North America. The identities of the Canadian maple powdery mildews need to be re-assessed under the up-to-date classification framework. Through phylogenetic analyses of rDNA ITS sequences and morphological examination of samples collected from Ottawa vicinity in recent years as well as historical specimens housed in Canadian National Mycological Herbarium (DAOM), we recovered two *Sawadaea* species on several maple species, i.e. *S. bicornis* on *Acer macrophyllum, A. negundo*, and *S. tulasnei* on *A. platanoides*. In addition, several specimens on *A. rubrum*, *A. saccharum*, and *A. spicatum* identified previously as *U. circinata* were confirmed belonging to the monotypic genus *Takamatsuella* (as *T. circinata*), erected by Braun and Shi (2012) based on its long genetic distance to *Sawadaea*. Through examining a large number of specimens, they observed that this species is often only present at teleomorph stage, which might reflect its unique biological characteristics.

[P35] DOWNCAST IS EFFECTIVE FOR FORECASTING ONION DOWNY MILDEW IN ONTARIO. Tyler Blauel, Kevin Vander Kooi, Julia Scicluna, Geoff Farintosh, and Mary Ruth McDonald. University of Guelph, Department of Plant Agriculture, Guelph
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Onion downy mildew, caused by the Oomycete *Peronospora destructor*, is a highly destructive foliar disease of onion. The disease does not occur every year in the Holland Marsh, Ontario. Symptoms develop 10 – 14 days after infection and downy mildew specific fungicides must be applied prior to infection to be effective. Disease forecasting is used to indicate when there is no risk of disease and no fungicides are needed and to properly time fungicide applications when there is disease risk. The integrated pest management program at the Ontario Crops Research Centre – Bradford is located in the Holland Marsh and provides disease management information to local growers. The program uses the

forecasting model DOWNCAST to predict the risk of sporulation and infection as sporulation infection periods (SIPs), based on daily air temperature, relative humidity, leaf wetness duration and temperature, plus temperature in the days following potential infection. Fungicide sprays are also recommended if downy mildew lesions are found on onions in the region, or if sporangia of *P. destructor* are found on spore traps. Rotorod spore traps are assessed three times a week throughout the growing season. From 2012 to 2023, the forecasting program was accurate in 10 of the 12 years. This included two years where DOWNCAST was accurate in predicting no disease risk and no downy mildew developed in the Holland Marsh. In 2022, DOWNCAST forecasted SIPs and airborne sporangia were later found, but the disease did not develop in grower fields, likely due to appropriately timed fungicide applications predicted by DOWNCAST. Weather conditions were very favourable for onion downy mildew development throughout the 2023 growing season. DOWNCAST predicted multiple SIPs and there were high numbers of sporangia found in spore traps. In a fungicide trial, a SIP was identified on 14 July and the first lesions found on 27 July. Disease was assessed on 1, 10 and 15 Aug as lesions per m^2 of plot. In the 15 Aug assessment, the treatment receiving the fungicide mefenoxam S (Ridomil) alternated with oxathiapiprolin plus mandipropamid (Orondis Gold) had 2 lesions, compared to 79 lesions m^2 in the nontreated check. In most years, onion downy mildew developed 14 – 17 days after sporangia were found. While the model alone is mostly effective, spore trapping can improve DOWNCAST to confirm disease risk. DOWNCAST continues to be a useful tool for onion growers in the Holland Marsh and other regions in Ontario.

[P36] GENETIC DIVERSITY IN VIRULENCE OF POPULATIONS OF *PUCCINIA CORONATA* VAR *AVENAE* F. SP. *AVENAE* COLLECTED USING EXTENSIVE SAMPLING TECHNIQUES COMPARED TO INTENSIVE SAMPLING TECHNIQUES. James Menzies[1], Sharon Deceuninck[1], and Henry Klein-Gebbinck[2]. [1]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, Manitoba, R6M 1Y5, Canada; and [2]Beaverlodge Research Farm, Agriculture and Agri-Food Canada, Beaverlodge, Alberta, T0H 0C0, Canada
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Puccinia coronata var *avenae* f. sp. *avenae* (*Pcaa*), the causal agent of crown rust, is a significant threat to oat production in Canada. The development and use of crown rust resistant oat varieties in Canada has helped mitigate the effects of this disease on oat yield and quality. A knowledge of the virulence characteristics of the pathogen population is essential to identify effective resistance genes to be incorporated into new oat varieties. This, in turn, requires the proper sampling of the pathogen population to determine its virulence characteristics and genetic diversity. Traditionally, collections have been made in Manitoba and eastern Saskatchewan by sampling one isolate of *Pcaa* per field from many fields over a large area, or by extensive sampling. Extensive sampling involves access to many fields in which there are *Pcaa* infected plants, as well as the physical and human resources to conduct the work, which are not always readily available. Alternatively, intensive sampling could be practiced in which many isolates of *Pcaa* are sampled from a few fields, reducing the number of fields in which access is required, and the resources necessary to conduct the work. The objective of this work was to compare extensive sampling and intensive sampling methods of natural populations of Pcaa in Manitoba in 2018, 2019 and 2020 to obtain genetically diverse collections, as determined using virulence. Difference between the two sampling methods were determined using the Shannon diversity index, followed by Hutcheson's t test. Extensive sampling collections of *Pcaa* were observed to be more genetically diverse than intensive sampling collections in 2018 and 2020, but there were no significant differences between the collections in 2019. A greater percentage of the races identified in the extensive sampling collections each year were represented by a single isolate as compared to the intensive sampling collections. Common or dominant races were observed as a greater proportion of the isolates collected in the intensive sampling collections as compared to the extensive sampling collections in 2018 and 2020. The extensive sampling method and the intensive sampling method achieved similar results in 2019, but considering the results obtained in 2018 and 2020, a more genetically diverse collection of isolates of *Pcaa* can be obtained using the extensive sampling method.

[P37] THE ROLE OF ASCOSPORE RELEASE OF *ANISOGRAMMA ANOMALA IN* THE MANAGEMENT OF EASTERN FILBERT BLIGHT IN ONTARIO, CANADA. Asifa Munawar[1], Cathy Bakker[1], Melanie Filotas[2], and Katerina Serlemitsos Jordan[1]. [1]Department of Plant Agriculture, Ontario Crop Research Centre, University of Guelph, Simcoe, Ontario, Canada, N3Y 4N5; and [2]Ontario Ministry of Agriculture, Food and Rural Affairs, Ontario Crop Research Centre, Canada, N3Y 4N5
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Although hazelnuts have been grown in Ontario for decades, their popularity in the province has increased considerably in the last ten years. One of the greatest threats to their production is the disease, eastern filbert blight (EFB), caused by the fungus *Anisogramma anomala.* The fungus releases ascospores that infect actively growing stem tissue in young shoots. Our current recommendations for spore release and fungicide application timing are based on research from Oregon, which has a different climate than Ontario. The goal of this project was to determine the ascospore release of *A. anomala* under Ontario weather conditions in order to target applications of preventative fungicides. GRIPST-2009 spore samplers were used to track airborne spores from March-October 2022-2023 at site 1 and site 2 in Norfolk County, Ontario. Sampling rods were collected 2-3 times per week at each site in 2022-2023 except the site 2 where daily data was collected from April-June 2023. The rods were stained in aniline blue solution and examined microscopically for fungal ascospores, and spore density (Particles/m^3) for each period was recorded. Meteorological data (temperature, rainfall) and phenology data on the cultivar, 'Jefferson' for both sites were also recorded. The first ascospore release at site 1 and site 2 coincided with bud-break (BB, April 18-22, 2022, and April 14-17, 2023, respectively). The highest release for site 1 (6 P/m^3 in 2022 and 275 P/m^3 in 2023) and site 2 (907 P/m3 in 2022 and 1343 P/m3 in 2023) was observed from the middle to end of May, close to the mature leaf stage (Growth stage 17-19). Site-1 had a low spore count in both years. Ascospore release was not observed before April and after June in either year. SAS multiple regression analysis indicated that total rainfall was significantly correlated with spore release in 2023 based on data from daily collection periods. Starting from BB spore release continued for 9 weeks in 2022 and 11 weeks in 2023. In Ontario, the standard spray program is 4 sprays at 2-week intervals starting at BB. Our data indicates the spores of EFB are present in Ontario orchards outside of the current recommended spray period. More years of data are needed to comprehend the aspects of changing weather conditions to accurately reflect spore release patterns. Our results merely provide a platform to build a future forecast model for Ontario growers to accurately time their management sprays.

[P38] PROFILING AVIRULENCE GENES OF *LEPTOSPHAERIA MACULANS* FOR RESISTANCE DEPLOYMENT IN CANADIAN PRAIRIE REGIONS. Chun Zhai and Gary Peng. Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada
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Genetic resistance is crucial for managing blackleg disease in canola. Additional R genes are being deployed in canola cultivars grown on in western Canada, but effective use of these R genes requires understanding the pathogen race structure and dynamics in different regions. In this multi-year study, thousands of blackleg samples were collected from commercial fields across various crop districts during canola disease surveys organized by the prairie provinces in 2022 and 2023. Isolates of *L. maculans* were analyzed for the presence/absence of 12 avirulence (*Avr*) genes using KASP markers (*AvrLm1, 2, 3, 4, 5, 6, 7, 9, 11, S/Lep2*) or host differentials (*AvrLm10,Lep1*).

Across the region, *AvrLm3, 5, 6, 7, 10*, and *11* were prevalent, each present in over 80% of the pathogen populations from the prairie provinces. This suggests that canola cultivars carrying any of the corresponding R genes, such as *Rlm5, Rlm6, Rlm7, Rlm10*, and *Rlm11*, will likely be highly resistant to blackleg. However, despite the common presence of *AvrLm3*, the corresponding R gene *Rlm3* may be ineffective due to the high frequency of *AvrLm7* in the pathogen population, which masks the effect of *AvrLm3*. Relatively, *AvrLm2* was more abundant in Saskatchewan, while *AvrLm4* was found at substantially lower frequencies in Alberta.

More than 60 races were identified within the pathogen population, indicating a high degree of diversity. Virulent races were present for most of the known R genes, except for *Rlm10*, highlighting the risk associated with deploying new R genes. Spatial and temporal deployment of R genes may be considered

for optimized uses of resistant canola cultivars, and this *Avr* profiling for each crop district will aid in regional recommendations for cultivars carrying effective R genes, as well as in the selection of new R genes for blackleg resistance breeding.

[P39] EFFECT OF DIFFERENT SOILLESS MIXES ON DEVELOPMENT OF CLUBROOT (*PLASMODIOPHORA BRASSICAE*). Komathy Prapagar[1], Shauna Chesney[1], Bruce D. Gossen[2], Merek Wigness[2], and Mary Ruth McDonald[1]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1, Canada; and [2]Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, Saskatoon, SK S7N 0X2, Canada
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Clubroot, caused by the soil-borne pathogen *Plasmodiophora brassicae*, can result in severe damage on canola (*Brassica napus*) and Brassica vegetables. Controlled environment studies are often part of research on the biology of *P. brassicae*. Occasionally no disease develops, even when viable inoculum is applied to a susceptible crop under optimum conditions for infection. A growth room study was conducted to assess the effect of two soilless mixtures on clubroot symptom development in canola. The growth room was set to 24°/21°C day/night cycle, 17-hour photoperiod and 50% humidity. The soilless mixes (Sunshine mix L4A from Sungro and BM6 HP from Berger) were assessed at three levels of inoculum concentration (0, $1x10^6$, $1x10^8$ spores/mL) and two levels of moisture (wet or dry mix), which had previously been shown to affect compaction of soilless mix. The experimental design was a three-way factorial in a complete block design with four replicates and 10 plants per experimental unit. The experiment was repeated. Seven and 12 days after seeding, the plants were inoculated with 5 mL of resting spores of pathotype 2. Roots were assessed for clubroot symptoms 6 weeks after inoculation and assigned to classes using a standard 0–3 scale where: 0 = no clubbing and 3 = clubs on > 2/3 of the root; a disease severity index was calculated. Fresh and dry weights of above-ground plant material were also assessed at 6 weeks. Severe clubroot developed in L4A mix at both inoculum concentrations, but there was little to no clubroot in BM6 and none in the non-inoculated control. Soil moisture at the time of compaction had no effect on any variable. Inoculation reduced plant fresh and dry weight; dry weight was lower on plants in LA4 soilless mix treatments than in the BM6, associated with higher clubroot severity. Sunshine LA4 mix is recommended for clubroot research. The reason for the variation in clubroot severity in the mixes is not known but could be related to characteristics of the peat moss or the surfactant component of the soilless mix.

***[P40] *BEAUVERIA BASSIANA*: A PROMISING FUNGAL ENDOPHYTE AGAINST CLUBROOT ON CABBAGE 2023.** Kelly Ruigrok[1], B. D. Gossen[2], and M. R. McDonald[1]. [1]Department of Plant Agriculture, University of Guelph, 50 Stone Road E, Guelph, ON; and [2]Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2 Canada
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Clubroot, caused by the soil-borne chromist *Plasmodiophora brassicae* Wor., is a constraint to production of brassica crops worldwide. Host resistance is generally not durable and management options are limited. The fungus *Beauveria bassiana* (Balsamo) Vuillemin is a well-known entomopathogen; several commercial formulations are available for management of insect pests. *Beauveria bassiana* is also reported to be endophytic, with beneficial effects on disease resistance and plant growth. A growth room study was conducted to assess its effect on cabbage transplants inoculated with *P. brassica*. The clubroot-susceptible cabbage (*Brassica* oleracea L.) cv. Bronco was seeded in plug trays. At the cotyledon stage, one *Beauveria* product (BioCeres @ 10 mL/L or Botanigard @ 8 mL/L) was applied as a foliar drench at 500 mL per tray. The hypothesis was that early application would maximize root colonization prior to inoculation of *P. brassicae,* mimicking cabbage seedlings being transplanted into an infested field. Plants were transplanted into pots 6 weeks after seeding and inoculated with 5 mL per seedling of resting spore suspension at 1 $x10^5$, 10^6 or 10^7 spores of *P. brassicae* per mL. The study was laid out in a randomized complete block design with four replicates; controls with no *B. bassiana* or no *P. brassicae* were included. Clubroot severity was assessed at 6 weeks after inoculation with *P. brassicae*. Severity in the absence of *B. bassiana* was 23, 58 and 87 DSI (disease severity index) for plants inoculated with 10^5, 10^6 and 10^7 spores of *P. brassicae*; application of Botanigard reduced DSI to 7, 14

and 48 DSI. Colonization of cabbage plants by *B. bassiana* was measured by plating 1-cm^2 sterilized leaf and root pieces on PDA. After 14 days at room temperature, conidia of *B. bassiana* were visible on infested plant tissue, but no significant interactions were observed. Average percent colonization for the leaf sections was 10% for Botanigard and 6% for Bioceres. It was not possible to assess colonization of the roots because of plate contamination. We conclude that inoculation of brassica transplants with *B. bassiana* to manage clubroot has promise and future research is warranted.

[P41] POTATO FIELD AND STORAGE SCOUTING FOR IDENTIFICATION OF POTATO FUNGAL DISEASES. M. Sayari[1], M. Elshetehy[1,2], P. Rehal[1], V. Bisht[3], C. Timoteo Assuntao[4], Nasem Badreldin[5], and F. Daayf[1]. [1]Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada; [2]Department of Botany, Faculty of Science, Tanta University, Tanta 31527, Egypt; [3]Manitoba Agriculture & Resource Development, 65 - 3rd Avenue NE, Carman, MB R0G 0J0, Canada; [4]Department of Agricultural Sciences, State university of Maringa, campus of Umuarama, Umuarama, Parana, 87502-970, Brazil; and [5]Department of Soil Science, University of Manitoba, Winnipeg, MB, R3T 2N2, Canada
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Disease scouting was done in 2023 in Manitoba potato fields and storage units. The aim of this project was to scout potato fields across various locations in Manitoba to assess the prevalence of diseases affecting potato crops. For this purpose, the objective was to identify and characterize potential causal agents responsible for these diseases in the collected samples. Fields were selected from different regions within the province of Manitoba to ensure representativity of potato-growing areas. Samples consisting of potato stems, roots and tubers exhibiting signs of disease, including discoloration, lesions, or any other visible symptoms were taken to the lab for analysis. Fungal pathogens were isolated using standard techniques, i.e., on Potato Dextrose Agar (PDA) media. Isolated pathogens were then subjected to microscopic examination for characterization up to the genus level. The plates were then incubated at 25°C. After 3 to 7 days, distinct fungal colonies were sub-cultured onto water agar medium. Following microscopic examination of the asexual spores, different strains were selected and transferred to fresh PDA plates for DNA extraction, followed by PCR using Internal Transcribed Spacers (ITS) and Translation Elongation Factor (TEF) primers. We successfully isolated and microscopically characterized several pathogens, including, but not limited to Fusarium spp., Colletotrichum coccodes, Sclerotinia sclerotiorum, Alternaria alternata, Alternaria solani, Verticillium dahliae, Rhizoctonia solani, Botrytis cinerea, Sordaria fimicola, Plectosphaerella cucumerina, Chaetomium globosum, Neonectria candida, Torula herbarum, and Lecanicillium psalliotae. Given the fact that many of these species are known to be potato pathogens, their identification and characterization provide valuable insights into the disease landscape affecting potato crops in Manitoba. Understanding the prevalence and characteristics of these pathogens is crucial for implementing effective disease management strategies to safeguard potato production and ensure food security in the region and beyond. Further research and collaborative efforts between agricultural stakeholders, researchers, and policymakers may be warranted to develop targeted interventions and mitigate the impact of these diseases on potato cultivation.

[P42] EXPRESSION OF SOYBEAN DEFENSE GENES ASSOCIATED WITH THE SALICYLIC AND JASMONIC ACIDS DEFENSE SIGNALING PATHWAY IN RESPONSE TO FUSARIUM GRAMINEAUM (Schw.). Nadia Garma[1], Rhodesia Xeloy[2], Mohammad Sayari[1], Mohamed El-Shetehy[1,3], Pawanpuneet Rehal[1], and Fouad Daayf[1]. [1]Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada; [2]Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre, AB, Canada; and [3]Department of Botany, Faculty of Science, Tanta University, Tanta 31527, Egypt
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Fusarium head blight (FHB) has been a devastating disease threatening cereal crops worldwide. In Central and Western Canada, where the wheat-soybean rotation is practiced, diseases caused by Fusarium species are also widely spread on soybeans. Different Fusarium species are associated with FHB in cereals, especially *Fusarium graminearum (Schw.), but this pathogen* has also been recently confirmed to cause soybean root rot. This represents a new potential threat to soybean production and requires more in-depth studies on the *F. graminearum*- soybean interactions. While defense mechanisms of wheat against F. graminearum have been largely investigated, no such studies were reported in soybean. To better understand this soybean-F.graminearum interaction, a differential soybean-F.graminearum system

consisting of two cultivars of soybean (susceptible; S and moderately resistant, MR) and two highly aggressive F.graminearum isolates was used to assess the expression of ten defense-related genes in soybean : Phenylalanine ammonia-lyase2 (PAL2), Isochorismate synthase1 (ICS1), Isochorismate synthase 2(ICS2), Allene oxide synthase 2 (AOS2), 12-Oxophytodienoate reductase 3 (OPR3), Nonexpressor of PR1(NPR1), Jasmonic acids-amido synthetase 1 (JAR1), Pathogenesis-related proteins 2 (PR-2), 3 (PR-3), and 4 (PR-4). These genes were selected because they are usually associated with either the salicylic acid (SA) or jasmonic acid (JA) defense signaling pathways. Expression of these genes was assessed in soybean roots at 6-,12- and 24-hour post-inoculation (hpi). We recorded a gradual increase in gene expression of PAL2, with significant induction at 24 hpi in both susceptible and moderately resistant lines. In contrast, gene expression of ICS1 and ICS2 was significant only at 6 and 12 hpi, respectively. This suggests that both the PAL and ICS pathways contribute to pathogen-induced SA response in soybean. Furthermore, gene expression of ICS1, ICS2, and PAL2 was more pronounced in moderately resistant lines compared to the susceptible ones. Additionally, we measured gene expression of AOS2, OPR3, and JAR1. AOS2 showed significant expression at 24 hpi, while JAR1 did at 6 hpi in moderately resistant line, along with OPR3. Gene expression of PR-3 and PR-4 was significantly induced at 24 hpi compared to the control. Additionally, the NPR1 gene exhibited significant expression at 6 hpi. These results indicate that the SA and JA pathways are involved in soybean defense against F. graminearum at different timings and add to the data gathered to elucidate the spatio-temporal signaling mechanisms in this host-pathogen interaction. If property integrated with knowledge on soybean responses to different Fusarium species, these data may contribute to reducing FRR effects on soybean yield.

[P43] LOSS OF CENTRAL METABOLIC GENES IN *PLASMODIOPHORA BRASSICAE*: A COMPARATIVE GENOMIC STUDY. A. Sedaghatkish[1], B. D. Gossen[2], and M. R. McDonald[1].
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Plasmodiophora brassicae Wor. is an obligate soil-borne Chromist that causes clubroot disease in brassica crops. Growing resistant cultivars is the best management strategy for producing canola in clubroot infested fields. However, the resistance is not durable and has been rapidly overcome by the pathogen. Obligate biotrophic pathogens such as *P. brassicae* strictly require living host cells to complete their life cycle. Cultivating *P. brassicae* in the lab would simplify gene discovery for breeding and contribute to other studies of the pathogen biology. It is not known what compounds must be supplied to this and other obligate biotrophs to allow growth on an artificial medium. Comparative genomic studies were conducted on the core genes responsible for central metabolites in *P. brassicae* to determine why it cannot grow and reproduce outside a living cell. A total of 120 essential genes in core metabolisms of *P. brassicae* were compared with 12 published plant pathogens including four fungi that can grow in culture (*Colletotrichum higginsianum*, *Magnaporthe grisea, Sclerotinia sclerotiorum,* and *Saccharomyces cerevisiae) and eight obligate plant pathogens such as rusts and* powdery mildews (*Blumeria graminis*, *Erysiphe necator*, *Erysiphe pisi*, *Erysiphe necator, Golovinomyces* orontii*, Puccinia graminis and Puccinia triticiana*) and the Oomycete , *Hyaloperonospora arabidopsidis*. *Plasmodiophora brassicae* lacks all 120 genes coding for essential core metabolites. These included important genes in nitrogen assimilation, thiamin biosynthesis, glutamate, glutathione, uracil, methionine, alcohol, and amino acid metabolism as well as channels and transporters and stress responses. The gene absence was similar to the powdery mildew pathogens examined (*B. graminis*, *E. necator*, *E. pisi*, and *G.* orontii). However, the two *Puccinia* species and Oomycete *H. arabidopsidis* posses some of these metabolic genes, which may explain why some rust pathogens such as *Puccinia* spp. have been cultured artificially, albeit with slow and poor growth. The lack of essential genes in *P. brassicae* demonstrates its inability to process inorganic compounds like nitrogen (e.g., ammonia, nitrate) provided in culture media, necessitating the provision of organic nitrogen compounds such as amino acids, amides, and vitamins. This deficiency in core metabolic genes explains many failed attempts to grow *P. brassicae in vitro*. Understanding the specialized nutritional requirements of *P. brassicae* will aid in developing a selective culture medium for this pathogen. Successful *in vitro* culture will enable the cultivation of pure isolates and lead to improved breeding for resistance and management strategies.

***[P44] FUNGICIDE TREATMENT EFFICACY FOR MITIGATING POWDERY SCAB AND PMTV IN ALBERTA POTATO FIELDS: A FIELD STUDY EVALUATION.** Muhammad Subhan Shafique[1], Michele Konschuh[1], Jennifer Foster[3], Michael Harding[2], and Dmytro Yevtushenko[1]. [1]Department of Biological Sciences, University of Lethbridge, Lethbridge, AB, Canada; [2]Alberta Agriculture and Irrigation, Brooks, AB, Canada; and [3]Syngenta Canada Inc., Guelph, ON, Canada.
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Powdery scab, a potato tuber disease caused by the plasmodiophorid pathogen *Spongospora subterranea* f.sp. *subterranea* poses a significant threat to the potato industry. It causes tuber lesions and root galls in potato plants. It is also the only known vector of potato mop-top virus (PMTV), which causes internal necrosis (spraing) in stored potato tubers. The powdery scab lesions on the tuber surface affect cosmetic appearance and reduce tuber quality for fresh market industries. It also poses challenges for French fry and chip production in Alberta because deeper peeling may be required. The lesions can also provide entry points for other pathogens, thereby affecting the long-term storage of potatoes. In the summer of 2023, fields with a history of powdery scab were sampled and tested for the presence of *S. subterranea* and PMTV using both morphological and molecular analyses. Trials were established in four fields with confirmed presence of *S. subterranea* using a paired-plot design with three different potato cultivars (Shepody, Russet Burbank, or Lady Claire) to evaluate the efficacy of five chemical treatments provided by Syngenta: A21008A, Allegro-low, Allegro-medium, Allegro-high, and A24367B. The fungicides were applied in-furrow at planting. Potato roots were evaluated for the presence and severity of galls during the growing season. Tuber samples were collected at harvest to determine yield and disease severity on tubers. Among the products tested, Allegro-medium demonstrated the best suppression of root galls, followed by A24367B, whereas A21008A had the least effect. All treatments showed significant scab suppression with Lady Claire, which was one of the most susceptible cultivars to powdery scab among those tested in this study. No significant differences in marketable yield were observed among treatments in any of the cultivars. The present findings have important implications for developing management approaches to mitigate potato powdery scab under regional environmental conditions.

[P46] AN EVOLUTIONARY LINEAGE OF *FUSRIUM OXYSPORUM* F.SP *CUBENSE*TR4 CAUSING NEW PANAMA DISEASE. Kyoko Watanabe[1], Shunsuke Nozawa[1], and Yousuke Seto[2]. [1]Graduate School of Agriculture, Tamagawa University, Machida, Tokyo 194-8610, Japan; and [2]Cancer Chemotherapy Center, Japanese Foundation for Cancer Research, 3-8-31, Ariake, Koto-ku, Tokyo 135-8550, Japan
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Fusarium oxysporum f. sp. *cubense* Tropical Race 4 (TR4) is the causal agent of New Panama Disease, which causes serious problems in banana production. The fungus is a single race of *Fusarium oxysporum* f. sp. *cubense* (FOC), sometimes referred to synonymously as *F. odoratissimum*. To understand the full extent of damage caused by this race and to develop disease control measures, we analyzed NGS data from 92 strains deposited in the genebank to determine what TR4 is.

Four thousand six hundred and three orthologous genes were analyzed, and the results showed that FOC is polyphyletic, but TR4 diverged earlier than other formae speciales with FOC STR4 and f. sp. *cucumerinum* clades, and the closest sister clade was STR4.Bayesian evolutionary analysis using a sampling tree based on 100 predicted gene sequences indicated that TR4 separated into four gropes. Most of the pathogens reported in different countries in recent years are grouped in one clade, originating from Malaysia. However, there are also strains in Colombia, India and China that are somewhat different, suggesting that they were not spread by a single invasion.

One of the characteristics of TR4 was that it encoded only the SIX8a gene, among the SIX8a and SIX8b homologs of the FOC. It was also thought that only TR4 encodes the SIX8a gene, which is thought to be involved in pathogenicity. On the other hand, the SIX8a gene was also reported to be present in F. sp. *sesami.* In our study, it was re-confirmed that TR4 encodes a copy of the SIX8a gene and that the SIX8a gene is also present in f. sp. *sesami*. Thus, the results support that the SIX8a gene is not unique to TR4. Furthermore, we found that there are TR4 strains encoding not only the SIX8a gene but also the SIX8b gene. We also reconfirmed the presence of multiple copies of the SIX8b gene in FOC race1, f. sp. *lycopersici*. The phylogenetic tree based on this gene did not match the genome-scale phylogenetic tree

and differed from TR4 in the evolutionary process; based on the comparison of sequences including upstream and downstream of the SIX8 gene, this difference is expected to be due to the horizontal and vertical distribution of the SIX8 gene in the past.

[P47] BACTERIAL ENDOPHYTES IN BARLEY CONTROL FUSARIUM HEAD BLIGHT PATHOGENS IN VITRO. Vinuri Weerasinghe[1,2,3], James Tucker[4], Ana Badea[1,4], Dilantha Fernando[1] and Champa Wijekoon[1,2,3]. [1]Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB, Canada, R3T 2N2; [2]Morden Research and Development Centre, Agriculture and Agri-Food Canada, Route 100, Unit 100-101, Morden, MB, Canada, R6M 1Y5; [3]Canadian Centre for Agri-Food Research in Health and Medicine, 351 Taché Avenue, Winnipeg, MB, Canada, R2H 2A6; and [4]Brandon Research and Development Centre, Agriculture and Agri-Food Canada, 2701 Grand Valley Road, P.O. Box 1000A, Brandon, MB, Canada, R7A 5Y3
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Barley (*Hordeum vulgare* L.) is the fourth most cultivated cereal crop in the world, and Canada is among the top ten barley producers. One of the major biotic threats to barley production is a fungal disease called fusarium head blight (FHB). The main pathogen, *Fusarium graminearum*, infects barley spikes and reduces the grain quality. FHB impacts several industries including livestock feed and malting, and may lead to significant economic losses. The plant microbiome consists of pathogenic as well as symbiotic and neutral microbial components. Host-microbe and microbe-microbe interactions play a role in maintaining a plant's health. Over the years, research interest in biological control of phytopathogens, particularly using endophytes has increased. Endophytes are microorganisms that inhabit healthy plant tissues without causing disease symptoms. Certain endophytes may be involved in defense against phytopathogens and plant growth improvement. Despite this, studies on endophytes of barley genotypes grown in Canada are limited. In this study, we investigated the antifungal effect of the bacterial endophytes isolated from barley on the pathogens of FHB. Bacterial endophytes were isolated from surface sterilized stems, roots, and grains of barley in bacterial culture media. The antifungal activity of the bacterial isolates against *F. graminearum* was screened using a dual culture plate assay (in vitro). A total of 16 bacterial antagonists were selected and the antifungal activity was evaluated by measuring the fungal radial growth and calculating the percentage of fungal growth inhibition in comparison to a control. Moreover, the selected bacteria were tested with *F. avenaceum*, *F. culmorum*, *F. oxysporum*, *F. poae* and *F. pseudograminearum*, previously isolated from barley plants grown in Canada. Polymerase chain reactions were performed to amplify the bacterial 16S rRNA gene and Sanger sequencing was carried out to identify the bacterial isolates. The antagonistic bacterial isolates identified from this study demonstrate the potential to be incorporated in the biological control of FHB in barley and other cereal crops.

[P48] PATHOGENIC AND GENETIC DIVERSITY OF *VERTICILLIUM LONGISPORUM* CAUSING VERTICILLIUM STRIPE OF CANOLA IN THE CANADIAN PRAIRIES. Longfei Wu[1], Rudolph Fredua-Agyeman[1], Godfrey Chongo[2], Ahmed Abdelmagid[3], Stephen E. Strelkov[1], and Sheau-Fang Hwang[1]. [1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada; [2]BASF Canada Inc., Saskatoon, SK S7K 3J9; and [3]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Rte 100 #100, Morden, MB R6M 1Y5
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Verticillium stripe, caused by *Verticillium longisporum*, poses an emerging threat to Canadian canola (*Brassica napus*) production. Initially detected in Manitoba, the pathogen has now been confirmed in various provinces across Canada. However, the genetic background and pathogenicity of *V. longisporum* populations from Alberta and Saskatchewan remain unknown due to limited availability of pure cultures of the fungus. To advance this understanding, isolations of *V. longisporum* were made from plant tissues samples collected in Alberta (7 isolates), Saskatchewan (12 isolates), and Manitoba (43 isolates). These were cultivated in pure culture, and genomic DNA was extracted from the fungal mycelium. Two species-specific primers targeting 18S rDNA intron region, VeruniF2/VeruniR3 and VlspF1/R4, were utilized to confirm the species designation of the isolates, while their lineages were determined using a multiplex PCR assay. Furthermore, five genes were sequenced, including the internal transcribed spacer (ITS), actin (ACT), elongation factor 1-alpha (EF), beta-tubulin (TUB), and mitochondrial oxaloacetate transport protein (OX) genes, to analyze the phylogenetic relationships among the isolates. The pathogenicity of

the isolates was evaluated under controlled conditions on canola at both the seedling and adult plant stages. All tested isolates were classified as belonging to the A1/D1 lineage of *V. longisporum*. The phylogenetic and pathogenicity analyses are in progress.

[P49] DIVERSITY OF SOIL NEMATODES FROM IRRIGATED AGRICULTURAL REGIONS OF SOUTHERN ALBERTA, CANADA. Maria Munawar and Dmytro P. Yevtushenko. Department of Biological Sciences, University of Lethbridge, 4401 University Drive W, Lethbridge, AB, Canada, T1K 3M4
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The soil is a vital component of the farming system, where soil-inhabiting nematodes play important ecological roles. Nematodes progress through a life cycle comprising egg, juvenile, and adult stages. These organisms feed on soil microbes, fungal propagules, or plant roots for growth and development. Whereas some nematode species contribute to soil health as beneficial organisms, others can pose significant economic threats as plant parasites; hence, understanding the presence and distribution of soil nematodes holds paramount importance. In the present work, we conducted a nematode inventory survey to understand the diversity of nematodes residing in the agroecosystems of southern Alberta. To this end, we collected samples from irrigated, cultivated fields, and adjacent areas covered with natural vegetation, to compare the abundance and host association of recovered nematodes. The survey indicated the presence of various groups, such as spiral, stunt, pin, and ring nematodes, as well as fungal- and root hair-feeding nematodes. We found that spiral, stunt, and pin nematodes were more abundant in cultivated field soil, as compared with undisturbed soils under natural vegetation. The coexistence of diverse nematode groups in cultivated regions does not inevitably lead to crop yield losses because not all nematode species exert detrimental effects on plants. However, we emphasize that the recognition and accurate taxonomical identification of detected species are important to assess potential future threats. Additionally, economically insignificant nematode species may evolve into parasites under altered habitat conditions, agronomic practices, cultivar choices, or rotation cycles. Therefore, proactive identification of overlooked nematode infestation issues, coupled with the continuous implementation of preventive crop protection and pest management measures, is crucial for sustainable agriculture.

[P50] EXPLORING THE MICROSCOPIC WORLD: IDENTIFICATION OF PLANT-ASSOCIATED NEMATODES WITH LIGHT AND SCANNING ELECTRON MICROSCOPY. Maria Munawar, Michele Konschuh, and Dmytro P. Yevtushenko. Department of Biological Sciences, University of Lethbridge, 4401 University Drive W, Lethbridge, AB, Canada, T1K 3M4
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Plant-parasitic nematodes represent a formidable threat to global agriculture, causing annual crop losses of up to eighty billion dollars. Precise identification of new or potentially harmful nematode species is crucial to the development of effective control and quarantine strategies. In our nematode studies, we employ a combined approach of light and electron microscopy to elucidate nematode characteristics. While molecular techniques offer valuable supplementary tools, sole reliance on them is limited, especially considering the lack of sequence data for many nematode species in public databases. As a result, morphological identification remains essential in nematode taxonomy. Light microscopy facilitates traditional morphological examination, enabling the calculation of morphometric ratios. Scanning electron microscopy (SEM) delivers high-resolution, three-dimensional images, unraveling intricate features, such as submedian lobes on lip regions, oral and amphidial apertures, cephalic annuli, and tail structures. In the present study, we identified *Mesocriconema curvatum*, *M. rusticum*, *Paratylenchus aculentus*, *P. goldeni*, *Helicotylenchus oscephalus*, and *Filenchus sandneri* in irrigated fields of southern Alberta, and recorded the first comprehensive documentation of these species through detailed light microscopy and SEM. SEM significantly enhanced nematode species identification, providing detailed, high-quality imaging for researchers and taxonomists. Our findings will aid in distinguishing closely related species and contribute to a better understanding of nematode biology and morphology.

[P51] PATHOGENICITY OF *VERTICILLIUM LONGISPORUM* ISOLATES ON CANOLA AT THE SEEDLING STAGE. Haitian Yu, Yixiao Wang, Sheau-Fang Hwang, Rudolph Fredua-Agyeman, and Stephen E. Strelkov. Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB T6G 2P5, Canada
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The fungus *Verticillium longisporum* is responsible for Verticillium stripe, a soilborne disease affecting canola (*Brassica napus*). Enhanced understanding of the pathogenicity of *V. longisporum* during the seeding stage could aid in the development of improved disease management methods. In this study, 62 isolates of *V. longisporum* were collected from infected plant tissue samples across Alberta, Manitoba, and Saskatchewan. These isolates were then evaluated for their effects on seedling emergence, plant height and vigor on the canola cv. 'Westar' under controlled conditions. Inoculations were conducted at seeding using low, medium and high concentrations of mycelial inoculum produced on potato dextrose agar. Seedling emergence was assessed at 7 days post-inoculation (dpi), while plant height and vigor were evaluated at 14 dpi. All three parameters declined following inoculation with *V. longisporum*, with some fungal isolates inducing more severe reductions at higher inoculum concentrations. Correlation analysis indicated that seedling emergence, plant height, and vigor were positively correlated with one another, with correlation indices ranging from 0.41 to 0.52. Principal component analysis showed that, collectively, these parameters explained 80% to 90% of the variation among isolates. There were no geographic or year effects on the pathogenicity of *V. longisporum* isolates across different inoculum concentrations. The work is ongoing, and disease severity will be assessed at 42 dpi. Nonetheless, the results so far suggest that this fungus can significantly reduce canola emergence and growth at the seedling stage.

[P52] ESTIMATING SOYBEAN YIELD LOSS TO WEED INTERFERENCE USING EARLY-SEASON REMOTE-SENSING TOOLS. RH Gulden[1], CJ Henry[2], N Badreldin[3], and DI Benaragama[1]. [1]Dept. Plant Science, University of Manitoba, Faculty of Agriculture and Food Sciences, 66 Dafoe Road, Winnipeg, MB, Canada R3T 2N2; [2]Dept. Computer Science, University of Manitoba, Faculty of Science, 75 Chancellors Circle, Winnipeg, MB, Canada R3T 2N2; and [3]Dept. Soil Science, University of Manitoba, Faculty of Agriculture and Food Sciences, 13 Freedman Crescent, Winnipeg, MB, Canada R3T 2N2
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Weed interference significantly reduces crop yield and blanket herbicide applications to manage these weeds have resulted in the selection of herbicide resistant (HR) weed biotypes. While the technology for site specific weed management exists, decision support systems that reduce the selection pressure for herbicide resistant biotypes by site specific applications of herbicides only where a yield loss threshold is met are lacking. Development of remote-sensed, site specific yield loss thresholds for data-driven decision support systems can contribute to more sustainable weed management and herbicide use. In 2023, a soybean additive-series experiment was established with increasing densities of either a surrogate HR broadleaf (canola) or a surrogate HR grassy weed (corn) sown in alternate rows to soybean to facilitate image segmentation. All other weeds were managed as needed with glyphosate. Multispectral digital images were captured using an Unmanned Aerial Vehicle (UAV) throughout the growing season to generate orthomosaic images of the experiment that were segmented into the ground cover of the respective crop and weed components for each experimental unit using a thresholding approach followed by manual correction. Soybean yield loss based on weed density followed the well-established rectangular hyperbola equation. Interestingly, the relationship between remote-sensed weed ground cover and soybean yield loss was a much simpler linear relationship for both weeds. The greatest regression coefficients for a single time point were obtained when yield loss was regressed against weed ground cover at the 4-leaf stage of soybean (Broadleaf R2 = 0.69, Grass R2 = 0.92) with different slopes between the two weed types. Inclusion of additional crop and weed ground cover data at other vegetative soybean developmental stages further improved the fit of the models. Overall, the preliminary results from this experiment show that early-season remote-sensed weed ground cover data is useful for predicting yield loss in soybean and shows promise towards using this technology to develop data-based, decision-support tools for weed management that can contribute to more sustainable crop production in a changing world.

[P53] ALTERNATIVE WEED MANAGEMENT OPTIONS IN ATLANTIC CANADIAN POTATO PRODUCTION. Andrew McKenzie-Gopsill[1], Ashley Nicolle MacDonald[1], Laura Anderson[1], Scott White[2], Aaron Mills[1], Aitazaz Farooque[3], Marie-Josée Simard[4], and Robert Nurse[5]. [1]Agriculture and Agri-Food Canada, Charlottetown Research and Development Centre; [2]Dalhousie University Department of Plant, Food, and Environmental Sciences; [3]University of Prince Edward Island School of Sustainable Design Engineering; [4]Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu Research and Development Centre; and [5]Agriculture and Agri-Food Canada, Harrow Research and Development Centre
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Potato producers across the Atlantic Canadian provinces of Prince Edward Island and New Brunswick rely on a few herbicides to provide the majority of their weed management. Increasing incidence of herbicide resistance in select species, a shift away from cultivation for weed control to minimize soil losses, and minimal investment in herbicide discovery, however, is challenging producers to develop novel methods of managing weeds in potato. Over the past several years researchers in Atlantic Canada have evaluated a suite of novel weed management tools and practices designed to target weeds in potato crops and in rotation to minimize their impact on productivity. This poster presents results from several of these efforts including the development of a real-time precision smart sprayer, testing suitability of crop-topping, the application of projectile abrasives, harvest weed seed control, and weed suppressive cover crops in rotation. Several of these technologies can provide acceptable control of weeds in a potato crop and more importantly provide significant reductions in additions to the weed seedbank. Further, we demonstrate that the use of cover crops can be important weed management tools by competing with weeds in rotation years and providing a carry-over effect following their incorporation.

***[P54] MORPHOLOGICAL AND GENETIC RESPONSES OF WATERHEMP TO ENVIRONMENTAL CONDITIONS.** Sreedevi Ramachandran, Rene Van Acker, and François Tardif. Department of Plant Agriculture, University of Guelph, Guelph, ON. N1G 2W1
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Waterhemp is a very competitive weed that has been spreading into Ontario in the last few years. Two varieties of waterhemp are recognized based on ecological and morphological characteristics: a riparian form, *A. tuberculatus* var. *tuberculatus* (tall waterhemp) and the agrestal form, *A. tuberculatus* var. *rudis* (common waterhemp). The agrestal form likely derived from the riparian form as it moved into fields, developing specific adaptations in the process. One question is whether these adaptations would allow var. *rudis* to be more adaptable than var *tuberculatus* to environmental conditions associated with climate change (e.g. temperature, drought, etc). We hypothesise that the agrestal form of waterhemp will show morphological and physiological variations demonstrating a greater capacity to adapt to the aforementioned factors compared to the riparian form. In this study, we grew two populations each of the riparian and the agrestal forms of common waterhemp in growth rooms under increased temperatures and reduced soil moisture conditions, such as could occur due to climate change. The growth and physiology of the plants were examined by measuring biomass accumulation, phenology, and reproductive allocation. Our preliminary results show that there is a significant decrease in plant height, biomass accumulation and reproductive allocation under high temperature and drought in all populations and riparian populations had less vegetative and reproductive biomass compared to the agrestal populations under high temperature and decreased soil moisture level. In addition, riparian populations were smaller plants and flowered earlier compared to agrestal populations under temperature and drought stress. We will identify and compare the drought and temperature-related microRNAs produced in all populations to identify the drought and temperature-responsive genes in the two varieties of waterhemp. The results of this study will help to predict the adaptive capacity of waterhemp to climate change, thereby contributing to developing appropriate management strategies to control this weed in the context of a changing climate.

***[P55] RESPONSE OF PROSTRATE SHRUB FUNCTIONAL TRAITS AND COMMUNITY NDVI TO LIMITING NUTRIENTS AND DEEP SNOW IN ARCTIC TUNDRA HEATH COMMUNITIES.** Liam Baron-Preston, John Markham, and James D. Roth. Department of Biological Sciences, University of Manitoba, Biological Sciences Building, 50 Sifton Road, Winnipeg, Manitoba, R3T 2N2
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Arctic prostrate shrubs are some of the relatively few plants that can survive the extreme conditions of Canada's North, where they dominate tundra heath ecosystems. As arctic temperatures continue to increase, the response of prostrate shrubs to changing environmental conditions will lay the groundwork for new succession regimes in the tundra. Arctic foxes (*Vulpes lagopus*) act as ecosystem engineers in tundra heath, where their den sites exhibit increased soil nutrients, atypical plant communities, and deeper snow. We treated tundra heath vegetation plots with N and P fertilizers and/or increased snow depth to examine how these den communities develop, and here we present how these treatments affected the leaf traits of 5 dominant prostrate shrub species (*Arctostaphylos rubra, Dryas integrifolia, Rhododendron lapponicum, Shepherdia canadensis, Vaccinium uliginosum*) after 5 years. We used ANOVA tests and principal components analyses (PCA) of leaf soluble protein content, leaf carbohydrate content, and specific leaf area (SLA) to show responses in leaf phenotype and abundance-weighted site means to evaluate these dominant species as a group. We found that the SLA of prostrate shrubs in plots that received fertilizer was ~50% higher than those in controls and this effect was doubled in plots with both fertilizer and snow fence treatments. The PCAs show an inverse relationship between SLA and soluble leaf protein content and highlight the effect of snow depth on leaf phenotype when nutrients are not limiting. The increase in specific leaf area is correlated with differences in the normalized difference vegetation index (NDVI) of each treatment plot, which shows significantly higher NDVI in all plots that received fertilizer compared to those that did not. Our results show that some arctic prostrate shrubs exhibit a productive phenotypic response to limiting nutrients independent from annual temperature and we add to the growing body of literature recognizing SLA and NDVI as key plant functional traits in a warming Arctic.

[P56] COMMUNITY OF PRACTICE FOR BUILDING HERBARIUM RESILIENCE, RELEVANCE, AND RELATIONSHIPS. Nadia Cavallin[1] and Jennifer Doubt[2]. [1]Royal Botanical Garden, 680 Plains Road West, Burlington, ON, Canada, L7T 4H4; and [2]Canadian Museum of Nature, 1740 chemin Pink, Gatineau, QC, Canada, J9J 3N7
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Herbaria vary in their histories and present-day activities, but many record the past two centuries or more of collecting plants, lichens, fungi and/or algae. They represent the cultures and priorities of the (mostly past) collectors and administrations that built them. Many institutional collections grew from colonial activities, through extractive and/or elitist practices, for exclusive purposes. Their holdings and methods still retain this history, creating barriers to new relationships and approaches, and limiting applications beyond those for which herbaria were originally conceived.

The power of herbaria as resources to address increasingly urgent, present-day challenges such as biodiversity loss, environmental change, and nature deficit - and their impacts on human health - grows with the continuous length of the specimen timeline, from past to future. With time, however, the *perceived* value of herbaria in many (particularly academic) institutions has diminished. Using essentially the same technology to collect and preserve specimens that were used 200 years ago, with holdings that reflect outdated worldviews, and with progressively fewer links to current programs or academic courses, herbaria can be wrongly dismissed as stagnant relics.

The key to resolving this disconnect lies, we believe, in relationships. The health and longevity of herbaria rely on the strength and diversity of their community relationships and on working *in* relationship to continually increase the ongoing relevance of their holdings.

With this poster, we invite interest in creating a community of practice oriented to building and sharing the public value of herbarium collections by diversifying and strengthening relationships, including communities that have been historically excluded. We propose to initiate a forum for sharing challenges, resources (literature, examples, experience), and ideas, and in doing so to support one another in building resilience and relevance within our networks of herbaria.

[P57] DRIVERS OF UNDERSTORY VEGETATION COMPOSITION AFTER NOVEL SILVICULTURAL TREATMENTS IN CANADIAN BOREAL FORESTS. Marion Noualhaguet[1], Enrique Hernández-Rodríguez[1], Miguel Montoro Girona[1,2]. [1]Groupe de recherche en écologie de la MRC Abitibi, Institut de recherche sur les forêts, Université du Québec en Abitibi-Témiscamingue, 445 boulevard de l'Université, Rouyn-Noranda, Québec, J9X 5E4, Canada; and [2]Universidad de Huelva, Calle Dr. Cantero Cuadrado, 6, 21004 Huelva, Spain
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Ecosystem-based management uses a wide diversity of harvesting practices to maintain forest ecosystem integrity by reducing differences between natural and managed forests. The success of this approach requires comprehensive assessments of forest community regeneration dynamics after harvesting. Understory vegetation plays a critical role in forest regeneration due to its major implications in biotic and abiotic interactions and is directly impacted by harvest. To guarantee the maintenance of biodiversity, a clear and long-term understanding of understory vegetation evolution post-harvest is crucial. We examined the impacts of novel harvesting patterns, in terms of intensity and spatial configuration of stem removal, over 18 years post-harvest, on understory vegetation diversity and composition in young and old stands of the Eastern Canadian boreal forests. Path analyses were used to assess the indirect impact of harvesting via soil substrate, light condition, live and dead wood covering a period of one year before and 18 years after harvesting. The understory vegetation was divided into the three layers: bryophytes, herbaceous and shrubs. The understory diversity response was delayed the first year after harvesting before reaching a peak 10-year post-harvest, leading to divergence based on harvesting level, then gradually becoming more similar to unharvested as the canopy regenerates. While species diversity can recover within 18 years of harvesting, composition takes longer, suggesting that this metric might be better for assessing long-term effects of harvesting on biodiversity. The path analysis revealed that trees, live or dead, were the primarily driver of understory community changes across the fist 10 years post-harvest whereas the preceding understory composition was the mainly influencing factor between 10- and 18-years post-harvest. These results highlight the complex biotic and abiotic interactions among understory species, underscoring the importance of considering both environmental factors and pre-existing understory composition when guiding sustainable forest management strategies aimed at balancing economic interests with ecological conservation.

[P58] DOES PHOTOPERIOD REGULATE METHANE EMISSIONS FROM PLANTS? Mirwais M. Qaderi[1] and Kate Burton[1]. [1]Department of Biology, Mount Saint Vincent University, 166 Bedford Highway, Halifax, NS, Canada, B3M 2J6
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Previous studies have shown that light quality and quantity affect methane emissions from plants. However, the role of photoperiod in plant-derived methane has not been addressed. We studied the effects of two photoperiods – long day (16h light/8h dark), and short day (8h light/16h dark) – on growth and methane emissions of lettuce (a long-day plant), mung bean (a short-day plant), and tomato (a day-neutral plant) under a temperature regime of 22/18°C and photosynthetic photon flux density of 300 µmol m^{-2} s^{-1}. All three species were grown under both light durations. First, seeds were germinated in Petri dishes for one week, then plants were transferred to pots and randomly assigned to one of the two experimental conditions. Under each condition, twelve plants were grown for 21 days; at that time, plant growth and physiological traits, including methane emissions, plant dry mass, growth index, photosynthesis, chlorophyll fluorescence, total chlorophyll, nitrogen balance index, flavonoids, and anthocyanin, were measured. The lettuce plants that were grown under short-day photoperiod had the highest methane emissions. The long-day plants that were exposed to short-day conditions and the short-day plants that were exposed to long-day conditions were stressed; day-neutral plants were also stressed under short days. All three species had decreased total dry mass under short-day conditions, most likely because of decreased photosynthesis and increased transpiration and stomatal conductance. Methane emission was positively correlated with shoot: root mass ratio, nonphotochemical quenching and anthocyanin, and negatively correlation with stem height, total dry mass, photosynthesis, water-use efficiency, total chlorophyll, and flavonoids. This study revealed that, besides light intensity and quality, light duration can also affect methane emissions from plants.

[P59] HUDSON BAY LOWLANDS BRYODIVERSITY: A NATIONAL HERBARIUM INITIATIVE REVEALING TAXONOMIC AND GEOGRAPHIC GAPS IN OCCURENCE DATA. Adam J. Storey[1] and Jennifer Doubt[1]. [1]National Herbarium of Canada, Natural Heritage Campus, Canadian Museum of Nature, 1740 Chemin Pink, Gatineau, QC, Canada, J9J 3N7
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The Hudson Bay Lowlands (HBL) form the largest wetland in Canada and the third largest wetland globally at 374,000 km^2. The region is known for its extensive peatlands — wetlands characterized by the accumulation of partially decayed plants, providing many regulatory services including sequestering and storing carbon. In arctic and northern boreal peatlands, bryophytes (mosses and liverworts) compose 90-100% of the ground cover, influencing all other plant and animal life. Their growth and decomposition rates, which are species- and climate-specific, heavily influence rates of carbon sequestration. Despite their functional diversity and ecological importance, the diversity and distribution of HBL bryophytes remain largely unassessed, even as development and other environmental changes call with increasing urgency for data that support management decision-making. The goals of this project are to (1) use existing data sources to generate the first bryophyte checklist for the entire HBL region and (2) produce a referenced dataset of known bryophyte species occurrences for the HBL region, to serve as primary resources for land managers. Bryophyte records from the HBL were compiled from 10,700 specimen records (e.g., CANM, UBC, NY, QFA, DUKE, MICH) and literature. These records were reviewed for errors and standardized to present-day taxonomy. At the Canadian Museum of Nature (CMN), these data are supplemented through the identification of thousands of previously unprocessed specimens from projects in Ontario's Ring of Fire region (CMN) and Wapusk National Park, Manitoba (University of Manitoba, Parks Canada). To date, 388 mosses (316 in CANM) and 145 liverworts (94 in CANM) are known for the HBL. The most diverse genera to date are *Sphagnum* (at least 40 species), *Dicranum* (20), and *Ptychostomum* (17) for mosses and *Scapania* (17), *Fuscocephaloziopsis* (7), and *Cephaloziella* (7) for liverworts. At least two species so far have not previously been reported from Manitoba. Four species are new to the HBL region due to taxonomic revisions, one of which is newly reported from Quebec, and another which is newly reported for Ontario and Manitoba. The resulting dataset will enable identification of geographical, taxonomic, and temporal gaps in search effort, and provide a foundation for future bryological work in the HBL. All specimens held at the CMN will be publicly accessible via the Global Biodiversity Information Facility. The checklist and occurrence records resulting from this study will be shared with project partners (Parks Canada, Mushkegowuk Council, Environment and Climate Change Canada) and conservation data managers in Manitoba, Ontario, and Quebec.

***[P60] TOTAL PHENOLIC COMPOUNDS AND HERBIVORE RESISTANCE IN HYBRID POPLAR EXPOSED TO SALINITY.** Sandamini Bandara[1], Trinity Bredardt[1], Caleb Lavallée-Shrupka[1], Sylvie Renault[1], and German Avila- Sakar[1,2]. [1]Biological Sciences, University of Manitoba, Winnipeg, Canada, R3T 2N2; and [2]Biology, University of Winnipeg, Canada, R3B 2G3
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Salinity and herbivory, two factors commonly faced by plants, are usually detrimental to their growth and reproduction. Salinity disrupts water and nutrient uptake and causes ionic and oxidative stress. Herbivory decreases plant photosynthetic area and triggers defensive biochemical pathways. The sequential exposure of plants to these factors may have contrasting outcomes. Plant responses to one stress may prime the biochemical pathways involved in their response to a second stress, thus lessening the detrimental effects of the latter. Alternatively, the allocation of resources involved in the response to one stress could decrease the effectiveness of the plant response to a second stress due to resource limitations. Phenolic compounds, known to provide plants with resistance against herbivores, are also elicited by salinity. Thus, exposure to salinity may prime plant resistance against herbivores via increased phenolic content. The objective of this study was to test whether hybrid poplar (*Populus*) cuttings exposed to salinity have higher concentrations of leaf phenolic compounds and greater resistance to a generalist herbivore, *Orgyia leucostigma*. Four-week-old hybrid poplar cuttings were irrigated with 0 or 100 mM NaCl for four weeks in a greenhouse. Leaf disc assays were used to determine constitutive resistance (prior to insect exposure) and induced resistance (after insect exposure). In-vivo feeding assays were also used to assess constitutive resistance. Constitutive and induced resistance were not affected by exposure to salinity. The total leaf phenolic content of plants exposed to salinity was greater than that of control plants

by about 30%. Additionally, salt-treated plants exposed to herbivory had total phenolic levels approximately 10% higher than those of control plants. Results of leaf disc and in-vivo feeding assays suggest that the responses triggered by salinity in hybrid poplar did not influence the feeding preference of *O. leucostigma*. Irrespective of salinity levels, hybrid poplar exhibited generally high resistance to *O. leucostigma* (constitutive and induced resistance values typically exceeded 80% and 85%, respectively). Despite the known involvement of phenolic compounds in plant responses to both salinity and herbivory, our study did not detect greater resistance linked to phenolic content elicitation by salinity.

[P61] REVISITING THE PERMANENT BIODIVERSITY MONITORING PLOTS IN THE NIAGARA ESCARPMENT BIOSPHERE. Natasha Hearn and Liette Vasseur. Brock University, Department of Biological Sciences, 1812 Sir Isaac Brock Way, St Catharines, On L2S 3A1
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Biodiversity is the basis for many ecosystem services that are important for human health and well-being, and the overall functioning of an ecosystem. Disturbances can disrupt this functioning and have devasting effects on the number and types of species that are present. Monitoring of permanent biodiversity plots can help understand how invasive species may affect species composition over time. In 2014, 10 permanent biodiversity monitoring plots were installed in two different forest ecosystems in the vicinity of Brock University campus, Niagara region, Ontario, through a field course entitled 'Biodiversity in the Biosphere Reserve'. One of the sites was a mature forest dominated by *Acer saccharum* (sugar maple) while the younger forest was dominated initially by *Fraxinus americana* (white ash). In 2014, the Emerald ash borer had started to invade the young forest leading to a dieback of the species. The present study aimed to first survey the plant diversity in those plots and then to assess the changes over the past nine years. Species surveys were completed during the summer of 2023 in the five plots located in a Mature forest and the five plots in the Young forest. Soil samples were also collected in all the plots to compare their composition. The results showed that diversities of trees, shrubs, and ground vegetation were generally higher in the Young (disturbed) forest than in the Mature (undisturbed) forest. In the young forest, the dominant species became *Fagus grandifolia* (American beech). Soil pH, nutrients and organic matter were significantly higher in the mature forest than in the young forest. The young forest had small ash tree saplings suggesting some recovery. The ground vegetation contained more invasive species than the undisturbed mature site. These findings indicate that plant diversity had increased in the young forest after the disturbance and these results may support the Intermediate Disturbance Hypothesis. It is likely that over time this forest will further change as sugar maple and other species such as *Carya ovata* and *Corylus americana* are also now present as small trees. Long-term monitoring through the field course will help assess how these forests may evolve considering the current and future disturbances in southern Ontario.

***[P62] UNRAVELLING THE DIVERSITY OF MICROBIOME IN PRUNUS SPECIES.** Vidya Venugopal[1], Manish N Raizada[1], and Jayasankar Subramanian[1]. Department of Plant Agriculture, Ontario Agricultural College, University of Guelph, Guelph, Ontario, N1G 2W1
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Plants are intricately associated with diverse microorganisms, forming a holobiont - the plant together with its associated microbial communities. This holistic approach contradicts the conventional understanding of plants as independent beings. These microbial partners play crucial roles in plant growth, development, and adaptation to environmental stresses through various mechanisms such as nutrient acquisition, pathogen protection, and stress tolerance. Therefore, unravelling the dynamics and composition of the plant microbiome is of cardinal importance. The objective of this study was to extensively characterize the endophytic microbiome of six major *Prunus* species (peach, Japanese plum, European plum, sweet cherry, sour cherry, and apricot). To elucidate the bacterial consortia associated with *Prunus* species, high-throughput amplicon sequencing of the 16S rRNA gene from leaf tissues was used, leveraging the Illumina MiSeq platform. Specifically, the hypervariable V4 region was targeted for amplification and subsequent sequencing, enabling comprehensive taxonomic profiling of the bacterial communities. Our results indicated that, different *Prunus* spp., shared unique bacterial assemblage. Interestingly, Proteobacteria was the most abundant phylum, followed by Actinobacteriota and Bacteroidota. To our knowledge this is the first study of this kind microbiome of *Prunus* spp. The findings from this study have

the potential to elucidate the interactions between the endophytic bacterial consortia and the genomes of *Prunus* species. This enhanced understanding could aid in identifying key endophytic bacterial taxa associated with stone fruit crops and unravelling their roles in conferring resistance against biotic and abiotic stresses.

[P63a] EXPLORING ROOT TRAITS OF DWARFING ROOTSTOCKS IN RELATION TO TREE VIGOR IN APPLE. Hao Xu, Danielle Ediger, Tom Forge, Paige Munro, and Lindsay King. Summerland Research and Development Centre, Agriculture and Agri-Food Canada
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Dwarfing rootstocks are widely used to control vigor in tree fruit production. Their hydraulic traits are different from their domesticated relatives. The restricted water transport capacity in rootstocks is hypothesized as an important dwarfing mechanism in apple (*Malus domestica*), which awaits to be tested using a set of rootstocks with contrasting vigor. In 2021, we investigated root volume and root xylem transport area in 11-year-old 'Honeycrisp' trees grafted on 15 rootstocks of different vigor, including 4 semi-dwarfing, 5 large-dwarfing, 3 moderate dwarfing, and 3 small dwarfing (n = 5), in a NC-140 rootstock trial in Summerland, British Columbia, Canada. Trees were cut at 10 cm below graft union; with the tree held in upright position, the cut end was submerged into 400 mL staining solution of 0.5% Safranin O dye (w/v) for 16 h to allow the solution to move upwards under transpiration; after staining, a clear cut was made at 5 cm below graft union; cross section was scanned using Samsung SCX; the area of Safranin-O stained tissue in the cross section was analyzed in ImageJ to assess the area of actively transporting xylem tissue at 5 cm below graft union. Roots in the top soil of 30cm depth were excavated and pulled out by shovel and back dozer; the excavated roots were photographed; root mass was estimated by area analysis in ImageJ. Scion trunk cross section area (TCSA) at 30 cm above graft union was the largest in semi-dwarfing rootstocks, followed by large dwarfing, moderate dwarfing and small dwarfing. There was a strong positive correlation between the scion TCSA and the estimated root mass in 30 cm deep top soil across the rootstock vigor classes ($r^2 = 0.95$). The area of Safranin-O stained xylem at 5 cm below graft union was significantly larger in semi-dwarfing rootstocks than in others; however, there was no significant difference between large, moderate or small dwarfing rootstocks (One-Way ANOVA, Tukey's test, pairwise comparison, $P \leq 0.05$). Tree vigor positively correlates with root volume which largely determines the soil resource availability to the plant. The study suggests root volume be evaluated as an important criterion for vigor potential and climatic adaptability, as the rootstocks with smaller root volume can effectively stunt tree growth and achieve higher planting density, whereas the rootstocks with larger root volume may exploit more soil resources, sequestrate more carbon, and enhance resilience against drought and heat.
Keywords: dwarfing rootstock, root volume, tree vigor, xylem transport

[P63b] TRANSCRIPTOMIC ANALYSIS OF ENHANCED FRUIT RETENTION BY HEXANAL IN 'HONEYCRISP' APPLES. Karthika Sriskantharajah[1], Alan Sullivan[2] Gopinadhan Paliyath[2†] and Jayasankar Subramanian[1]. [1]Department of Plant Agriculture, Vineland Research Station, University of Guelph, Canada; [2]Department of Plant Agriculture, University of Guelph, Canada; [†]Deceased
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Apple (*Malus domestica* Borkh) is prone to preharvest fruit drop (PFD), which is more pronounced in the cultivar, 'Honeycrisp'. To improve fruit retention and quality in 'Honeycrisp', an aqueous composition containing hexanal was applied 30 and 15 days before harvest. The effects of hexanal on fruit retention and quality were assessed using transcriptomic, physiological and biochemical approaches. At commercial maturity, hexanal substantially reduced Abscisic Acid (ABA) levels in the Fruit Abscission Zone (FAZ). At this stage, a total of 726 *Differentially Expressed Genes* (DEGs) were identified between hexanal treated and control FAZ. Functional classification of the DEGs showed that hexanal downregulated ethylene biosynthesis genes such as S-adenosylmethionine synthase (*MdSAM2*), 1-aminocyclopropane-1-carboxylic acid oxidases (*MdACO3, MdACO4*, and *MdACO4-like*), while it upregulated receptor genes such as *MdETR2* and *MdERS1*. Genes related to ABA biosynthesis such as *MdFDPS* and *MdCLE25* were also downregulated. Furthermore, hexanal downregulated the expression of genes related to cell wall degrading enzymes, including polygalacturonase (Md*PG1*), glucanase (endo-β-1,4-glucanase), and expansins (*MdEXPA1*, *MdEXPA6*, *MdEXPA10-like* and *MdEXPA16-like*). These findings revealed that hexanal reduces the sensitivity of FAZ cells to ethylene and ABA. Simultaneously, it

reduces cell wall degradation of FAZ cells by regulating genes involved in cell wall modifications. Thus, delayed fruit abscission by hexanal solution in 'Honeycrisp' is most likely achieved by minimizing ABA through an ethylene-dependent mechanism. Trees treated with the hexanal retained 18% more fruits compared to control trees. Fruit firmness also significantly improved by hexanal treatment, while fresh weight, and total soluble solids (TSS) remained unaffected in response to the treatment in the field. Further, at the end of the four months cold storage, hexanal also reduced the incidence of bitter pit by 17% compared to control. Thus, the application of hexanal is a promising technology to control fruit drop, bitter pit and enhance fruit qualities in 'Honeycrisp' apples.

***[P64] EFFECT OF MIR408 OVER-EXPRESSION ON PHOTOSYNTHETIC EFFICIENCY AND BIOMASS PRODUCTION IN ALFALFA.** Sameena Alam[1,2], Kimberley Burton Hughes[1], Udaya Subedi[1,2], Madeline Lehmann[1,2], Christie Stephen[1,3], Mohammed Musthafa Mukthar[1,2], Alicja Ziemienowicz[1], Guanqun Chen[2], and Stacy D Singer[1]. [1]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1 Ave S, Lethbridge, AB, Canada, T1J 4B1; [2]University of Alberta, Department of Agricultural, Food and Nutritional Science, 116 St and 85 Ave, Edmonton, AB, Canada, T6G 2R3; and [3]University of Lethbridge, Department of Biological Sciences, 4401 University Dr W, Lethbridge, AB, Canada, T1K 3M4
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The global population is projected to reach nearly 9.8 billion by 2050, which will pose a challenge for food security. Meeting this demand will not only require efforts to reduce food waste and establish equitable food distribution, but will also necessitate increased agricultural productivity. Unfortunately, yield gains across many crop species have stagnated in recent years, and improving photosynthetic efficiency could be pivotal for enhancing their yield potential. MicroRNA408 (miR408) has been shown previously to act as an important positive regulator of photosynthesis in several plant species, largely through the down-regulation of various genes encoding copper-containing proteins. In this project, my aim is to elucidate the function of miR408 in the context of photosynthesis in alfalfa, which is one of Canada's most valuable forage crops. MiR408 over-expression vectors were generated and successfully introduced into alfalfa using *Agrobacterium*-mediated transformation. To confirm the over-expression of miR408 in transgenic plants, both conventional and stem-loop quantitative reverse transcription PCRs (qRT-PCRs) were performed. Selected over-expression genotypes, along with the wild-type control, were assessed for changes in various morphological and growth parameters, as well as photosynthetic characteristics. To further our understanding of the transcriptional changes incurred through the modulation of miR408 expression, comparative RNA-Seq was carried out using RNA derived from the leaves of miR408 over-expression and wild-type genotypes, and the cleavage of putative miR408 target genes identified using *in silico* analyses will be validated using 5' RLM-RACE. Ultimately, the long-term goal of this research is to identify genes regulated by miR408 in alfalfa, which when knocked out using CRISPR/Cas9 could enhance photosynthetic efficiency and biomass production, thus contributing to global food security.

[P65] SPL9 REGULATES NODULATION AND DROUGHT RESPONSE IN *MEDICAGO SATIVA*. Abdelali Hannoufa[1,2], Vida Nasrollahi[1,2], Gamalat Allam[1,2], Alexandria Hanly[1,2], and Susanne E. Kohalmi[2]. [1]Agriculture and Agri-Food Canada, 1391 Sandford Street, London, Ontario, N5V 4T3; and [2]Department of Biology, University of Western Ontario, 1151 Richmond Street, London, Ontario, N6A 4B7
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Small non-coding RNAs, including miRNA156 (miR156), regulate gene expression at the posttranscriptional level to affect various aspects of plant growth and development. In *Medicago sativa* (alfalfa), miR156 silences at least 11 members of the SQUAMOSA PROMOTER BINDING PROTEIN LIKE (SPL) family of transcription factors, including SPL9. The aim of this study was to evaluate the role of SPL9 in regulating nodulation and response to drought stress in alfalfa. Examination of alfalfa plants with RNAi-silenced *SPL9* (*SPL9*-RNAi) showed that SPL9 positively regulates plant height, stem thickness, and internode length, while negatively regulating shoot branching. *SPL9*-RNAi alfalfa also exhibited an enhancement in tolerance to drought stress accompanied by elevated anthocyanin content and expression of DIHYDROFLAVONOL 4-REDUCTASE (DFR), an enzyme involved in anthocyanin biosynthesis. This finding suggests that SPL9-mediated downregulation of *DFR* may represent a strategy to regulate drought response. Moreover, phenotypic analyses of *SPL9*-RNAi plants showed that silencing of *SPL9* causes an increase in nodulation. Characterization of phenotypic and molecular parameters

revealed that SPL9 modulates nodulation under high nitrate concentration (10 mM KNO3) by regulating the nitrate-responsive genes *NR1*, *NR2*, and *NRT2.5*, as well as the AUTOREGULATION OF NODULATION gene, *SUNN*. Overexpression of SPL9 upregulated *SUNN*, *NR1*, *NR2*, and *NRT2.5*, while its silencing downregulated these genes and resulted in a nitrogen-starved phenotype. Taken together, these results demonstrate that SPL9 is a negative regulator of nodulation and response to drought stress, which makes it a promising molecular tool in biotechnological improvements of alfalfa and potentially other related crops.

[P66] SPL12 MODULATES NODULATION, NITROGEN FIXATION AND ROOT REGENERATION IN *MEDICAGO SATIVA*. Abdelali Hannoufa[1,2], Vida Nasrollahi[1,2], and Susanne E. Kohalmi[2]. [1]Agriculture and Agri-Food Canada, 1391 Sandford Street, London, Ontario, N5V 4T3, Canada; and [2]Department of Biology, University of Western Ontario, 1151 Richmond Street, London, Ontario, N6A4B7, Canada
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The root system architecture in plants is critical because of its role in controlling nutrient cycling, water use efficiency and resistance to biotic and abiotic stresses. Similar to most other phenotypic traits, root system architecture is controlled at the molecular level by many genes, some of which were recently identified, including some coding for transcription factors from the SQUAMOSA-PROMOTER BINDING PROTEIN-LIKE (SPL) family. We previously showed that transgenic *Medicago sativa* (alfalfa) plants overexpressing *microRNA156* (*miR156*) had increased nodulation, improved nitrogen fixation and longer roots. At least sixteen *SPL* genes, including *SPL12.* are targeted for silencing by microRNA156 in alfalfa. Thus, association of each target *SPL* gene to a trait or set of traits is essential for developing molecular markers for alfalfa breeding.
We determined the role SPL12 in root architecture and nodulation by investigating the phenotypic changes associated with altered expression of *SPL12* and by determining SPL12 targets. In this study, we used three *SPL12*-silencing and -overexpression alfalfa plants to investigate the role of SPL12. Furthermore, we conducted transcriptomics analysis of *SPL12* RNAi alfalfa roots and identified differentially expressed genes. Phenotypic analysis showed that alfalfa plants with reduced *SPL12* level had an increase in nodulation and root regeneration. Illumina next-generation sequencing-based transcriptomics in root tissues of *SPL12*-silenced genotypes also revealed SPL12 effects on genes involved in nodulation and nitrogen assimilation pathways. In addition, a gene encoding the transcription factor, AGAMOUS-like MADS box protein 6 (AGL6), was also identified as being directly silenced by SPL12 based on Next Generation Sequencing-mediated transcriptome analysis and chromatin immunoprecipitation assays, suggesting that AGL6 may be involved in regulating alfalfa nodulation. The present findings suggest that SPL12/AGL6 module regulates root development and nodulation, as well as nitrogen uptake and assimilation.

***[P67] GENE-EDITING FOR THE IMPROVEMENT OF PHOTOSYNTHESIS, GRAIN YIELD, AND LEAF RUST RESISTANCE OF WHEAT cv. 'FIELDER'**. Louie Cris Lopos[1], Igor Kovalchuk[2], Stacy Singer[3], and Andriy Bilichak[1]. [1]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Rte 100 #100, Morden, MB R6M 1Y5; [2]Biological Sciences Department, University of Lethbridge, 4401 University Dr W, Lethbridge, AB T1K 3M4; and [3]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1st Avenue South Lethbridge, AB T1J 4B1 Canada
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Wheat is a staple crop that faces plateauing yields and outbreaks from the rapidly evolving leaf rust pathogen *Puccinia triticina*. These factors compromise its ability to meet the growing human demand. Wheat improvement programs utilize genetic diversity from available germplasms to confer beneficial traits into elite wheat cultivars; unfortunately, the process is complex and lengthy, the genetic mechanisms of the desired traits are not yet fully understood, and oftentimes, the introgression of beneficial genes from wild relatives lead to linkage drag.

CRISPR-Cas9 and Prime-editing are RNA-guided gene-editing technologies that can introduce mutations into a targeted part of the genome for the purposes of gene functional discovery, genetic diversity expansion, and crop improvement. In this ongoing study, we aim to improve the grain yield and leaf rust resistance of wheat cv. Fielder using CRISPR-Cas9 and Prime-editing platforms, respectively. In order to improve grain yield, we are knocking-out the orthologs of previously identified rice microRNA408 targets:

OsUCL8 and *OsUCL30*, using CRISPR-Cas9. It was previously reported that the post-transcriptional regulator, microRNA408, downregulates the expression of genes that negatively affects photosynthetic efficiency and grain yield; its overexpression was shown to improve these traits in *O. sativa*, *A. thaliana,* and *N. benthamiana*. We generated plants with diverse insertion/deletion mutations that introduce premature stop codon in *TaeUCL8* and *TaeUCL30* coding sequence. Concurrently, we also generated TaemicroRNA408 overexpression plants under the control of the monocot constitutive *MAIZE UBIQUITIN* promoter. Both edited and microRNA408 overexpression plants will be evaluated in terms of grain yield, expression of photosynthetic genes, and other agronomic traits such as heading time, productive tiller number, and number of heads.

On the other hand, we intend to use and optimize a prime-editing strategy to fix the susceptible alleles of the leaf rust resistance genes *Lr21* and *Lr34* present in cv. Fielder. These alleles have naturally occurring insertion/deletion mutations resulting to truncated, ineffective protein products. We will use prime-editing to correct these causative mutations to recover complete open-reading frames and consequently, full and functional protein products. We will then evaluate these prime-edited plants by characterizing their resistance responses to the indoor inoculation of leaf rust causative pathogen, *Puccinia triticina.*

***[P68] DISCOVERING QUANTITATIVE TRAIT LOCI (QTL) ASSOCIATED WITH LODGING RESISTANCE IN *BRASSICA NAPUS* L.** H. Luu[1], H. Chawla[1], R. Gulden[1], C. McCartney[1], J. Morrison[2], and R. Duncan[1]. [1]Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB, Canada, R3T 2N2; and [2]Department of Biosystems, University of Manitoba, Winnipeg, MB
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Lodging is an agronomic challenge in canola production as it causes yield loss, alters oil and protein composition, can increase disease incidence, and increases harvest difficulties. Breeders need to continually select for lodging resistance in current parents and hybrids to maintain standability as they try to increase yield. The increase in pod load (i.e. seed yield) created greater force on the stem and roots during pod fill and ripening. Herein, a doubled-haploid population consisting of 198 lines derived from a cross between lodging susceptible (268-2 ZSDH6550 / LLHR10282-B-9-2) and lodging resistant (CB131037-6-8) parents was used to construct a high-density SNP map covering a genetic distance of 1000 cM, with an average marker interval of 0.21 cM. Phenotypic assessment for lodging using a lodging scale between one and five was conducted across four environments. Quantitative trait loci (QTL) analysis was performed using inclusive composite interval mapping (ICIM) to determine QTL for lodging resistance. QTL were detected and distributed on chromosomes A01, A03, A05, A07, A10, and C01. Phenotypic variation explained (PVE) ranged between 3.34 and 17.31%. Some of these QTL were detected in more than one environment. Co-localization between QTL for lodging and QTL for plant height, days-to-flower, and days-to-maturity were also highlighted in this study, indicating that QTL for lodging may have a pleiotropic effect or linkage with QTL controlling other traits. The QTL identified in this study could be instrumental in designing molecular markers for maintaining lodging resistance in *B. napus* as breeders strive to increase yield.

[P69] TOMATO CYSTATIN SLCYS8 AS A TRIGGER OF DROUGHT RESILIENCE AND TUBER YIELD IN POTATO. Maude Dorval, Marc-Antoine Chiasson, Thiago Gumiere, Marie-Claire Goulet, and Dominique Michaud. Centre de recherche et d'innovation sur les végétaux, Université Laval, 2480 boul. Hochelaga, Québec QC, Canada G1V 0A6
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Current climate change scenarios predict an increased incidence of drought episodes likely to affect potato crops worldwide. Potato exhibits a low-density, shallow root system that makes it particularly vulnerable to water shortage and any successful attempt to implement drought tolerance in cultivated potato varieties is potentially relevant from an agronomic standpoint. In this study, we assessed the potential of tomato cystatin SlCYS8 to promote drought tolerance in SlCYS8-expressing potato lines by induction of stress-related pleiotropy. Several recent studies have revealed a possible link between abiotic stress tolerance and the occurrence of plant cystatins in leaf tissue. SlCYS8-expressing plants grown in greenhouse exhibited an elevated root-to-shoot ratio, an indicator of drought tolerance, compared to the mother line used for genetic transformation. SlCYS8-potato lines also showed a high tuber yield compared to the control under both limiting and non-limiting water regimes, suggesting an

improved efficiency of the basal primary metabolism and the avoidance of a growth–stress response tradeoff as usually induced upon the establishment of a stress tolerance phenotype. Accordingly, SlCYS8 expression was associated with an altered leaf proteome explained by pleiotropic effects of the recombinant cystatin driving both the constitutive expression of stress-related proteins and the upregulation of growth- and yield-associated proteins. Drought tolerance indices (DTI) and yield performance indices (YTI) were calculated to determine whether higher tuber yields for the SlCYS8 lines upon water stress were primarily associated with an actual drought tolerance increase or, alternatively, with an improved metabolic status sustaining higher yields in water-limiting conditions resulting from upstream yield-promoting pleiotropic effects already giving the plant an advantage in non-limiting conditions. No significant difference was observed among the lines or the water irrigation treatments for the DTI indices, suggesting a general, drought-independent relative yield-promoting effect of the recombinant cystatin in SlCYS8-expressing lines under water deficit conditions. This conclusion was supported by YTI indices for the transgenic lines estimated at about two times the YTI indices of the control line under the water deficit treatments. Overall, our data suggest the potential of cystatins as molecular triggers of tuber biomass production and drought resilience in potato. Complementary studies will be warranted in forthcoming years to assess tuber yield and water stress resilience of the SlCYS8-lines in field conditions.

[P70] AN ENGINEERED, TRANS-ZEATIN-PRODUCING STRAIN OF *AGROBACTERIUM TUMEFACIENS* TO DOWNREGULATE DEFENSE RESPONSES AND PROMOTE RECOMBINANT PROTEIN PRODUCTION IN TRANSIENT EXPRESSION HOST *NICOTIANA BENTHAMIANA*. Adam Barrada, Louis-Philippe Hamel, Marie-Claire Goulet, and Dominique Michaud. Centre de recherche et d'innovation sur les végétaux, Université Laval, 2480 boul. Hochelaga, Québec QC, Canada G1V 0A6
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Different protein expression platforms have been developed over the years for the high-yield production of biopharmaceuticals in plants. One of these platforms involves leaf infiltrated-*Agrobacterium tumefaciens* as a vector to transfer foreign DNA in the transient expression host *Nicotiana benthamiana*. Despite rapid progress towards optimizing this system, *N. benthamiana* still presents inherent constraints for protein production and its full potential as an expression host has not been reached yet. One constraint is the strong stimulation of plant immunity upon agroinfiltration, which is key to the transfection process but which also implicates an important allocation of energy and metabolic resources to the production of endogenous defense proteins. Here, we show that “partially rearming” a disarmed, cytokinin-depleted agrobacterial strain by reintroduction of a trans-zeatin synthase (TZS) gene in the DNA backbone of its Ti plasmid may help temper the induction of the host plant defense response and, as a result, promote primary metabolism, including protein biosynthetic, functions in leaf tissue. TZStrain, an engineered strain carrying the TZS coding sequence and an extended version of its natural promoter, was developed and selected based on its ability to repress senescence and induce starch accumulation in *N. benthamiana* leaves upon leaf infiltration. TZStrain was combined with transformed agrobacterial strains carrying DNA sequences for GFP or mammalian IgG to assess its impact on recombinant protein expression. In brief, the cytokinin-producing strain upregulated both cytokinin titers and photosynthesis-associated gene expression in agroinfiltrated leaves, while by contrast reducing salicylic acid and jasmonic acid levels to downregulate the expression of defense-related genes naturally induced by these two defense elicitors. Most interestingly, TZStrain increased recombinant protein rates in leaf tissue, even more when transcription of the expressed transgene was driven by cytokinin-inducible promoters such as those of photosynthetic protein genes *RbcS* or *Plastocyanin*. Our data confirm that TZStrain added in the agroinfiltration medium of *N. benthamiana* may temper the growth-defense tradeoff triggered by agroinfiltration, with a positive impact on heterologous protein expression *in planta*.

***[P71] GENE EXPRESSION ANALYSIS OF *ARABIDOPSIS THALIANA* DEHYDRINS AND *IN SILICO* EXPRESSION PROFILING OF *BRASSICA NAPUS* DEHYDRINS IN RESPONSE TO CLUBROOT DISEASE.** Janani Radhakrishnan[1], Dinesh Adhikary[1], Habibur Rahman[1], and Nat N. V. Kav[1]. [1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada
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Clubroot disease caused by *Plasmodiophora brassicae* Woronin is a soil-borne disease which causes significant yield loss in economically important *Brassica* crops including, canola (*Brassica napus* L.). One

of the key strategies to manage clubroot is the use of genetic resistance. Previous multi-omics studies conducted in our laboratory to understand the host-pathogen interactions between *B. napus* and *P. brassicae* revealed the differential expression of a group of genes encoding dehydrins. Dehydrins belonging to the class II Late Embryogenesis Abundant (LEA) protein family, are known to protect plants during abiotic stresses like dehydration. However, there are limited studies conducted on the antimicrobial properties of dehydrins as well as their responses to biotic stresses. The objective of our research was to characterize the expression of various dehydrin genes in *Arabidopsis thaliana*, another susceptible host of *P. brassicae*, in response to infection by *P. brassicae*. The expression of ten known *A. thaliana* dehydrin genes were characterized in this study. The dehydrin genes that showed significant upregulation of expression in *Arabidopsis* roots and shoots in response to *P. brassicae* infection at four different time points (4, 7, 14, 21 days post inoculation (dpi)) were identified. Based on the results, dehydrin genes with significant increase in expression including *COR47, XERO1* and *RAB18* have been selected for constitutive overexpression in *A. thaliana* in order to determine whether they have any role in protecting plants from clubroot. In addition, a meta-analysis on the expression of *B. napus* dehydrins was conducted on the existing proteomics and transcriptomics datasets from our previous studies on incompatible *P. brassicae*-canola interactions in doubled haploid (DH) and near-isogenic lines (NILs) of canola with clubroot resistance. It is expected that our studies will reveal critical information on the expression patterns of *B. napus* dehydrins in response to *P. brassicae* infection, their cis-regulatory elements and sequence similarities with the *A. thaliana* dehydrins. These results will be presented and discussed within the context of the role of dehydrins in clubroot resistance.

[P72] ALTERED GROWTH AND DELAYED FLOWERING IN *SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1* (*SOC1A*) KNOCKDOWN ALFALFA. Madeline Lehmann[1,2], Guanqun Chen[2], Udaya Subedi[1,2], Christie Stephen[1,3], Kimberley Burton Hughes[1], D. Wade Abbott[1], and Stacy D. Singer[1]. [1]Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre, 5403 1st Ave S, Lethbridge, AB, Canada, T1J 4B1; [2]Department of Agricultural, Food and Nutritional Science, University of Alberta, 116 St and 85 Ave, Edmonton, AB, Canada, T6G 2P5; and [3]Department of Biological Sciences, University of Lethbridge, 4401 University Dr, Lethbridge, AB, Canada, T1K 3M4 Correspondence to: madeline.lehmann@agr.gc.ca

Alfalfa (*Medicago sativa)* is the most cultivated forage legume in the world. Commonly dubbed “the queen of forages” due to its high yield, nutritional value, and nitrogen-fixing capabilities, alfalfa is of vital importance as a forage, fodder, and silage in the beef and dairy industries. Forage quality is known to decrease in alfalfa during the transition from vegetative to reproductive growth, largely due to cell wall lignification and decreased leaf-to-stem ratios after flowering. This reduction in quality results in decreased digestibility and palatability as a feed. Thus, one proposed strategy to both extend the potential harvest window and improve forage quality in alfalfa is to utilize biotechnological tools such as RNA interference (RNAi) and CRISPR/Cas9 to target flowering time genes in order to delay flowering and potentially improve quality. *SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1* (*SOC1*) is a floral integrator gene responsible for integrating floral promotion and inhibition signals from several upstream pathways, and subsequently activating downstream floral meristem identity genes, thus inducing flowering. Down-regulation of *SOC1* in other plant species has resulted in delayed flowering and altered stem characteristics, but no such studies have been carried out in alfalfa up to this point. Therefore, in this study, RNAi and CRISPR/Cas9 vectors were designed to respectively knock down and knock out expression of *MsSOC1a*. These vectors were introduced into alfalfa by *Agrobacterium*-mediated transformation, and transgenic *MsSOC1a* knockdown and knockout genotypes were regenerated. Three *MsSOC1a*-RNAi genotypes with the greatest down-regulation in *MsSOC1a* expression were assessed for morphological alterations, including growth characteristics, vegetative biomass, and flowering time compared to a wild-type control. *MsSOC1a*-RNAi genotypes demonstrated significantly delayed flowering, decreased plant height, internode length, stem width, and biomass, and increased leaf-to-stem ratio compared to controls. Downstream, these *MsSOC1a*-RNAi genotypes will also be assessed for improvements in *in vitro* digestibility as well as metabolomic alterations. In addition, *MsSOC1a* CRISPR/Cas9 knockout genotypes will be evaluated in order to determine whether they share similar altered characteristics to the RNAi genotypes. Thus far, our preliminary results highlight the role of *MsSOC1a* in floral promotion and stem architecture, and may suggest a potential increase in forage quality in *MsSOC1a* knockdown alfalfa plants.

[P73] CHROMOSOME-LEVEL GENOME ASSEMBLY AND TRANSCRIPTOMIC ANALYSIS OF THE FORAGE LEGUME, SAINFOIN (*ONOBRYCHIS VICIIFOLIA* SCOP.). Cuong Nguyen[1], David Konkin[2], Rodrigo Ortega Polo[1], Bill Biligetu[3], Hari P. Poudel[1], and Stacy D. Singer[1]. [1]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1st Ave S, Lethbridge, AB, T1J 4B1; [2]Aquatic Crop Resource Development, National Research Council of Canada, 110 Gymnasium Place, Saskatoon, SK, S7N 0W9; and [3]Department of Plant Sciences, College of Agriculture and Bioresources, 51 Campus Dr, University of Saskatchewan, Saskatoon, SK, S7N 5A8
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Sainfoin (*Onobrychis viciifolia* Scop.), a perennial forage legume, is valued for its high nutritional content and resistance to pests and diseases, as well as its ability to reduce fermentation-related bloat in ruminants due to the presence of condensed tannins. Despite recent advances in the genomic characterization of sainfoin, further research is required to understand its genetic architecture, secondary metabolite pathways and potential for breeding. In order to expand our breeding toolkit for this species, we are carrying out the *de novo* genome assembly and comprehensive annotation of a genotype of the sainfoin cultivar AAC Mountainview (2n=4x=28). Using PacBio and Nanopore long-read sequencing technologies, as well as Illumina short-read sequencing, combined with Hi-C scaffolding, we have achieved highly contiguous, chromosome-level assemblies for the four haplotypes of this genome. In addition, we are performing extensive gene modeling and annotation, utilizing IsoSeq and RNAseq data from different tissues across various developmental stages to validate gene predictions and explore tissue-specific gene expression patterns. This study will also include the annotation of transposable elements and the investigation of epigenetic modifications, which play a crucial role in genome evolution and function. The findings from this study will provide a valuable genomic resource for sainfoin, facilitating further research and breeding programs aimed at improving this important forage crop.

***[P74] IN VITRO PROPAGATION AS A METHOD TO PRODUCE SPECIFIC ANTIOXIDANT COMPOUNDS IN LINGONBERRY**. Umanath Sharma[1,2], Abir U. Igamberdiev[2], and Samir C. Debnath[1]. [1]St. John's Research and Development Center, Agriculture and Agri-Food Canada, 204 Brookfield Road, St. John's, NL A1E 0B2, Canada; and [2]Department of Biology, Memorial University of Newfoundland 45 Arctic Ave. Room CSF 2211 St. John's, NL A1C 5S7, Canada
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Micropropagation is an advanced vegetative propagation technology employed to produce a large number of high-quality plants in a limited time and space and has been used extensively in *Vaccinium* species, including lingonberry (*Vaccinium vitis-idaea* L.). There is increased importance of the lingonberry as a health-promoting fruit crop containing a high number of antioxidant properties. Although most of the lingonberries are harvested from the wild, utilizing tissue culture techniques for rapid propagation and antioxidant compound production could benefit the commercial production of this crop. Two genotypes including one wild clone and one hybrid were used for the experiment. Plants in tissue culture were grown in semi-solid media in sigma bottles containing 1mg/L Zeatin as plant growth regulator and greenhouse grown plants were grown in plastic pots containing peat and perlite in the ratio of 2:1 V/V. Shoots from tissue culture plants and leaves from greenhouse-grown plants were sampled and frozen in liquid nitrogen until extraction. Antioxidant compound extraction was done with a methanolic solution containing formic acid. Eight commercially available compounds including Delphinidin 3,5-diglucoside, Delphinidin 3-O-β-D-glucoside, Cyanidine 3-galactoside, Petunidin 3-glucoside, Cyanidin 3-arabinoside, Pelargonidin 3-glucoside, Malvidin 3-glucoside and Procyanidin A2 were used as standards and to quantify the compounds. Mass spectrometric (MS) detection and separation using high-performance liquid chromatography (HPLC), identified four antioxidant compounds in lingonberry genotypes. Interestingly, proanthocyanidin A2 was found to be 16-22 times more prevalent in tissue culture plants than in greenhouse-grown plants. Similarly, cyanidin 3-galactoside was 7-14 times more in tissue culture plants. Although not all the compounds were detected in lingonberry, some of the individual compounds dramatically increased in tissue culture conditions, suggesting the potential implication of micropropagation in the specific antioxidant compound production.

[P77] INVESTIGATING MOLECULAR EFFECTS OF HUMALITE APPLICATION ON FIELD-GROWN WHEAT USING QUANTITATIVE PROTEOMICS. Lauren E. Grubb[1], Mohana Talasila[1], Maria Rodriquez Gallo[1], Linda Gorim[2], and R. Glen Uhrig[1,3]. [1]Department of Biological Sciences, University of Alberta, Edmonton, AB, CAN; [2]Department of Agriculture, Food and Nutritional Science, University of Alberta, Edmonton, AB, CAN; and [3]Department of Biochemistry, University of Alberta, Edmonton, AB, CAN
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An increasing global demand for food production has resulted in increased synthetic fertilizer application, with negative impacts on the environment. Biostimulants such as humalite are currently being applied as a strategy to increase nutrient use efficiency and minimize negative environmental effects in cropping systems. Humalite is a naturally-occurring coal-like substance found in mines in southern Alberta. Humalite deposits are unique, boasting exceptionally high ratios of humic acids (>70%) and micronutrients due to their unique freshwater depositional environment. Recently, local growers in Alberta have begun to apply humalite to their fields despite limited scientific data demonstrating the impacts of this product on yield across diverse crops. Some recent work has shown positive impacts on plant growth, yield and nutrient use, especially in dry years, with humalite application. However, there is a lack of research on the impacts of humalite on crops at the molecular level. As part of a larger agronomic project, we have taken a quantitative proteomics approach to identify systems-level molecular changes induced by the addition of different humalite application rates in field-grown wheat using three urea fertilizer application rates (zero, half and full recommended rate based on soil tests). Key results will be discussed and contextualized to provide insights into the protein-level changes associated with humalite application and its meaning for overall crop productivity.

[P78] CLASP-SORTING NEXIN 1 INTERACTION: A KEY DRIVER IN PLANT ADAPTATION TO ABIOTIC STRESS? Yexin Han, Dr. Laryssa Halat, and Dr. Geoffrey Wasteneys. Department of Botany, The University of British Columbia
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Microtubules form complex arrays in all eukaryotic cells, and are crucial for cell shape, the cell cycle, and intracellular transport. In plant cells, microtubules reorganize in response to external stimuli to help plants adapt to environmental changes. This process requires microtubule-associated proteins including CLASP (CLIP-ASSOCIATED PROTEIN). Previous work in our lab established that CLASP in the model plant *Arabidopsis thaliana*, like its homologues in other model eukaryotes, functions as a rescue factor, preventing the rapid disassembly of microtubules (Ambrose et al. 2011 Nat. Comm). In addition, we discovered that CLASP interacts directly with SORTING NEXIN 1 (SNX1), a protein associated with endosomal complexes. By tethering SNX1-endosomes to cortical microtubules, CLASP sustains the plasma membrane distribution of the auxin transporter PIN2 and the brassinosteroid receptor BRI1, which would otherwise be degraded in the lytic vacuole (Ambrose et al. 2013 Dev. Cell, Yuan et al., 2018 Current Biol.). Thus, in addition to its conserved role in microtubule dynamics, plants CLASP is a key player in mediating plant hormone signalling. Sequence analysis indicates that the CLASP-SNX1 interaction is plant-specific, and present in all land plant lineages, leading us to hypothesize that this interaction mediates plant resilience to environmental stress. Consistent with this, total loss of either CLASP or SNX1 expression results in hypersensitivity to salt and other abiotic stress, and the upregulation of reactive oxygen species-related genes. This total gene knock-out approach, however, is problematic because we cannot determine whether these effects are specific to CLASP's function in tethering SNX1 or its function in microtubule dynamics and organization. The objective of my project is to modify CLASP's SNX1-interaction motif to generate a version of CLASP that no longer interacts with SNX1 but retains its other functions. Using BLAST searches across land plants, I have narrowed down a 16 amino motif in an intrinsically disordered region that is highly conserved and using generative AI programs, I have been able to predict and model the structural interaction of CLASP and SNX1. Yeast 2-Hybrid is being used as a first step to confirm which amino acid substitutions can eliminate SNX interaction before engineering these changes in plant. By uncoupling CLASP-SNX1 interactions, this project will lead to new insight into plant abiotic stress tolerance mechanisms.

[P79] CHARACTERIZING THE CULM SKIN PIGMENTS OF BLACK BAMBOO: INTERGRATING TRADITIONAL AND MODERN METHODOLOGIES. Xinyi Huang[1], Xinchun Lin[2], and Shawn D. Mansfield[1]. [1]Department of Botany, University of British Columbia, 6270 University Boulevard, Vancouver, BC, Canada V6T1Z4; and [2]State Key Laboratory of Subtropical Silviculture, Zhejiang Agriculture and Forestry University, Hangzhou, Zhejiang Province, China
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Bamboo (*Bambusoideae*) is one of the most important non-timber forest products globally. With over 1400 species natively distributed across every continent except Europe and Antarctica, bamboo exhibits a high degree of morphological and genetic diversity. It is also the fastest growing grass, providing versatile resources as a promising answer to escalating concerns of climate change, food security, and energy demands. With its significant agricultural, economical, and cultural values, around 2.5 billion people cultivate and consume bamboo daily, generating an international trade reaching nearly $70 billion US per annum.

There is a great variation among bamboo species when it comes to the colour and pattern of their culms. In addition to most common green colouration, bamboo culms can also be light gray, yellow, cyan, and black, with or without stripes or spots of a secondary colour. For many species, culm colours can change depends on factors such as life stages and environmental conditions. Identifying these pigments and elucidating their biosynthetic pathways are not only important because of the cultural and aesthetic values of these bamboos, but also significant for taxonomical and evolutionary studies. Recent analyses suggest that the metabolites responsible for bamboo culm colour variations are most likely to be flavonoids, which could exhibit beneficial antioxidant properties, offering added values to downstream applications. *Phyllostachys nigra*, commonly known as black or purple bamboo, is a commercially available bamboo species native to China. It has been successfully imported and adapted to North America geography, and has been consistently grown in gardens and for industrial purposes. Its culms emerge green when young, but slowly accumulate purplish pigments first as dark purple spots, and then eventually become completely black across the whole culm. In this study, we aimed to identify the secondary metabolites responsible for this unique colour by analyzing the culm skin tissue of two bamboo varieties, *Phyllostachys nigra nigra* and *Phyllostachys nigra henonis*, grown at the Botanical Garden of the University of British Columbia. Traditional techniques such as UV-Vis spectroscopy and thin layer chromatography were employed to characterize the extracted pigments, in addition to untargeted metabolomic profiling via HPLC-QToF-MS/MS to compare young green tissue versus mature black tissue. Total chlorophyll and carotenoid contents were also quantified. These biochemical analyses will be coupled with transcriptomic sequencing to aid in the exploration of associated genes and pathways.

[P80] PURIFICATION AND DIFFERENTIATION OF YOHIMBINE AND ITS ISOMERS FROM YOHIMBE TREE BARK. Jaewook Hwang. University of New Brunswick
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Specialized metabolites, organic compounds produced by plants and other organisms, are highly valued in pharmacology and agriculture for their wide-ranging bioactive properties, finding applications in medicines, fragrances, flavorings, and pesticides. Among the specialized metabolites, Monoterpenoid Indole Alkaloids (MIAs) stand out as a significant class, notably abundant in plants from the Rubiaceae, Apocynaceae, and Loganiaceae families, from which numerous pharmaceuticals have been derived. The yohimbe tree, Pausinystalia johimbe apart of the Rubiaceae family, native to Western and Central Africa, is of particular interest due to its main active compound, yohimbine, traditionally used as an aphrodisiac and now prescribed for erectile dysfunction. Yohimbine is characterized by its complex molecular structure, including five chiral centers that lead to the formation of multiple stable isomers, such as rauwolscine, beta-yohimbine, corynanthine, and alo-yohimbine. Direct extraction from yohimbe bark was conducted for authentic analysis. Employing advanced techniques like thin-layer chromatography, high-performance liquid chromatography, mass spectrometry, nuclear magnetic resonance spectrometry, and polarimetry. The application of these methods not only ensures the accurate identification of the target compounds but also facilitates a deeper understanding of their structural intricacies. This research not only clarifies the compound profiles of yohimbine and its isomers but also lays the groundwork for exploring the enzymatic pathways involved in MIA biosynthesis, offering new perspectives for drug development and therapeutic innovations.

***[P81] DORMANCY RELEASE AND TRANSCRIPTIONAL REGULATION OF ABSCISIC ACID AND GIBBERELLIN METABOLISM GENES IN WHEAT SEEDS**. Riya Kalota[1], Pham Anh Tuan[1], Deepak Sharma[1], Santosh Kumar[2], and Belay T. Ayele[1]. [1]Department of Plant Science, University of Manitoba, Winnipeg, Manitoba, Canada; and [2]Brandon Research and Development Centre, Agriculture and Agri-Food Canada, Brandon, Manitoba, Canada
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Seed dormancy is an adaptive trait that influences the occurrence of preharvest sprouting (PHS), which is the germination of physiologically mature seeds on the spike before harvest. The presence of low dormancy in wheat seeds can result in PHS, leading to substantial losses in both yield and quality. The degree of dormancy in seeds is primarily regulated by two hormones, abscisic acid (ABA) and gibberellin (GA). To gain better insights into the molecular mechanisms regulating seed dormancy in wheat, this study conducted a comparative targeted transcriptomic analysis of ABA and GA metabolism genes between dormant and non-dormant (after-ripened) seeds derived from a highly dormant wheat genotype. After-ripening of the dormant seeds resulted in release of seed dormancy. The study revealed that genes involved in ABA biosynthesis such as *NCED1* and *NCED3* were significantly upregulated during imbibition of dormant seeds relative to the corresponding after-ripened seeds. On the other hand, genes involved in ABA catabolism such as *CYP707A1* and *CYP707A3* exhibited downregulation in the dormant seed samples. Moreover, genes involved in ABA signaling such as *SnRK3*, *SnRK10*, and *ABI5* exhibited higher expression levels during imbibition of dormant seeds relative to that found in after-ripened seeds. In contrast, genes involved in GA biosynthesis such as *GA3ox* and *GA20ox* were downregulated in the dormant seeds. The expression patterns of GA signaling genes including *GID1* and *GAMYB* was not consistent with the dormancy phenotype, and this might reflect post-transcriptional regulation of these genes.

***[P82] UNLOCKING NATURE'S PHARMACY: EXPLORING THE HIDDEN POTENTIAL OF *LESPEDEZA CAPITATA*.** Puneet Kaur[1] and Mehran Dastmalchi[1]. [1]Department of Plant Science, McGill University, 21111 Lakeshore Road, Ste-Anne-de-Bellevue, QC, Canada, H9X3V9
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The use of plant natural products for medicine, potions, and ointments predates human civilization and has profoundly influenced our very existence. The indigenous peoples of North America, including the Comanche, the Meskwaki, and the Pawnee, have made use of the plants from the Lespedeza genus, notably L. capitata. Significant uses include treating ailments such as rheumatism and neuralgia and as an antidote for poisoning. Metabolic profiling of Lespedeza spp. over two decades ago showed the presence of unique and obscure derivatives of the isoflavonoid scaffold. This class of compounds is associated, physiologically, with signalling to beneficial bacteria and protection against pathogenic microbes. Furthermore, they have immense potential in pharmacological applications as antioxidants and reno-protective and tissue regenerative medicines. Despite these promising findings, there is a notable gap in our understanding of the metabolic pathways and genetic underpinnings involved in the biosynthesis of these compounds. To fill this knowledge gap, I have undertaken a spatiotemporal approach to describing the metabolic profile and identifying the corresponding transcripts at various stages and tissue types of L. capitata. Tissues were harvested from early and mature roots, three stages of leaf development, stems, and nodules, homogenized and split into two samples: one for RNA and one for metabolite extraction. RNA isolation was challenging due to the high concentrations of phenolics and other recalcitrant compounds in the leaf samples, which required lengthy troubleshooting. These samples have been submitted to Génome Québec for RNA-sequencing using Illumina NovaSeq6000 and will be subsequently de novo assembled and annotated; followed by differential gene expression analysis to follow spatiotemporal trends. In parallel, I have used untargeted metabolomics (LC-QTOF/MS) to identify molecular features (predicted compounds) within these tissues, followed by fragmentation and comparison to authentic standards to quantify known peaks. This comprehensive transcriptomic-metabolomic dataset will be probed by a guilt-by-association approach, whereby genes co-expressed with metabolites, or their intermediates, are presumed to play roles in their biosynthesis, transport, or storage. Pinpointing these genes will provide an understanding of the complex and unique metabolic profile of the understudied Lespedeza genus, particularly of the biosynthesis of isoflavonoids.

***[P83] VARIATION IN LODGING TRAITS AND TRANSCRIPTIONAL REGULATION OF GIBBERELLIN METABOLISM GENES IN WHEAT.** Gurnoor Kaur[1], Ginelle Grenier[1], Douglas J. Cattani[1], Pham Anh Tuan[1], and Belay T. Ayele[1]. [1]Department of Plant Science, University of Manitoba, Winnipeg, Manitoba, Canada
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Wheat yield and quality are negatively affected by numerous factors including lodging, which refers to permanent displacement of a plant from its upright position that results in falling over of the plant or breakage of the stem. Plant height and stem mechanical strength are two of the major morphological traits that regulate lodging resistance. Crop management practices such as nitrogen fertilization affect these morphological traits and therefore the incidence of lodging. This study investigates if variation in lodging related morphological traits is associated with transcriptional regulation of gibberellin (GA) metabolism genes by using two wheat cultivars with contrasting plant heights that were grown under different nitrogen fertilization levels. Our data shows that elevated nitrogen levels resulted in 26% to 32% increase of plant height, 2.0- to 2.5-fold increase of bending moment and 1.8- to 2.7-fold increase of lodging index in both cultivars. However, the taller cultivar exhibited taller plant height, and higher bending moment and lodging index than the shorter cultivar. Changes in these morphological traits due to elevated nitrogen fertilization were associated with enhanced expression levels of the GA biosynthesis genes, *TaGA20ox4* and *TaGA3ox3*, and repression of the GA catabolism gene, *TaGA2ox3*. Treatment of the tall cultivar plants with a GA biosynthesis inhibitor led to the reduction of plant height by 10% to 22% irrespective of nitrogen fertilization levels. This decrease in plant height was associated with a reduction in bending moment by 26% to 37%, which led to a decrease in lodging index by ~25%.

***[P84] UNRAVELING THE INTERPLAY BETWEEN PHENYLPROPANOID BIOSYNTHESIS AND SALICYLIC ACID SIGNALING PATHWAYS IN MEDIATING PLANT IMMUNITY.** K. A. Dinithi Kumarapeli, Ken Wilson, and Yangdou Wei. Department of Biology, University of Saskatchewan, 112 Science Place, Saskatoon, SK, Canada, S7N 5E2
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The plant shikimate pathway is the entry to the biosynthesis of salicylic acid (SA) and phenylpropanoids. In Arabidopsis, SA, a key defense hormone, is predominantly synthesized through the isochorismate synthase (ICS1) pathway, with a partial residual amount synthesized through the phenylpropanoid pathway via the entry-point enzyme phenylalanine ammonia-lyase (PAL). PAL serves as a common precursor for partial SA biosynthesis and the formation of a whole set of phenolic metabolites, including monolignols, flavonoids, and phenolic esters. Monolignols contribute to lignin formation, providing a physical barrier against pathogen penetration, while SA acts as a signaling molecule orchestrating various defense responses. Our comparison of RNA-Seq-based transcriptome analysis revealed that upon pathogen infection, Arabidopsis mutant plants defective in cinnamate 4-hydroxylase (C4H), which catalyzes the second step of the general phenylpropanoids exhibited the delayed expression of pathogenesis-related genes (a marker for pathogen-induced SA production), suggesting a regulatory link between the two branches of shikimate pathways in mediating plant immunity. In this study, we generated a double mutant (ics1/c4h) with impaired SA production and phenylpropanoid biosynthesis to investigate the interplay between ICS1-mediated SA production and C4H-mediated phenylpropanoid metabolism in plant immune responses. Pathogenicity assays revealed increased susceptibility to the adapted powdery mildew (*Erysiphe cruciferarum*) in these double mutants, highlighting the significance of the coordination between two pathways in plant defense. Further research will emphasize on fine genetic dissection of C4H-mediated phenylpropanoid metabolisms and their associated molecular and cellular mechanisms that contribute to plant immunity.

[P85] THE EFFECT OF COPPER-INDUCED OXIDATIVE STRESS ON THE SYMBIOSIS BETWEEN MODEL LEGUME LOTUS JAPONICUS AND MESORHZOBIUM LOTI. Kathryn Lamoureux[1] and Sheila M Macfie[1]. [1]Department of Biology, University of Western Ontario, London, ON, Canada, N6A 5B7
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Legumes play an essential role in the nitrogen cycle due to their ability to fix atmospheric nitrogen (N). N-fixation is carried out by symbiotic bacteria called rhizobia, housed in root nodules. Rhizobia are

enveloped by a plant-derived membrane that maintains N-fixation under oxygenated conditions. The nitrogenase enzyme is deactivated by oxygen, so the nodule interior is compartmentalized and protected by antioxidant systems that scavenge free reactive oxygen species formed during bacterial respiration. Copper (Cu) is a common environmental pollutant, and can reduce nodulation and N-fixation in various legume species. Excess copper causes oxidative stress in plant tissues and destroys membranes essential to cellular function via lipid peroxidation, but it is not known if Cu-induced reductions in rhizobial activity are due to a reduced ability of a stressed plant to support the symbiont, or to oxidative stress within the nodule itself.

To determine the physiological mechanisms by which Cu inhibits nodulation and N-fixation, the model legume *Lotus japonicus* was inoculated with *Mesorhizobium loti* and grown in a sand-hydroponic system spiked with 0, 300 or 450 µM CuSO4. Cu uptake in roots, nodules, and shoots was confirmed by inductively coupled plasma-mass spectrometry. The concentration of Cu in the roots was up to 4-fold higher than in the nodules, and 11-fold higher than the shoots. A 30-40% decrease in both the mass and number of nodules was observed at both 300 and 450 µM CuSO4 compared to control. An acetylene reduction assay showed a 50% decrease in nitrogenase activity at 450 µM CuSO4 compared to control. A thiobarbituric reactive substances assay was used to determine lipid peroxidation in the roots and nodules, and showed 20-30% higher concentrations of malondialdehyde in roots compared to nodules, but no significant difference among Cu treatments.
These findings indicate that Cu does impact the health of the plant and its ability to form nodules. The nodules were both smaller and less numerous in Cu-treated plants, reducing total nitrogen fixation. The formation of malondialdehyde does not indicate that oxidative stress is occurring unduly in the nodules themselves. This, combined with the finding that nodules were relatively low in Cu compared to adjacent roots, suggests that Cu does not directly affect rhizobial activity within the nodule via oxidative stress, but rather that reduced N-fixation under Cu-stress is due solely to the plants having fewer and less developed nodules.

***[P86] RECOMBINANT INBRED LINES OF PLANTS ADAPTED TO EXTREME ENVIRONMENTS CAN HELP IDENTIFY THE GENETIC BASIS OF LOW-PHOSPHATE TOLERANCE IN CROPS.** Laura Li[1], Yong Li[2], Barbara Moffatt[2], and Elizabeth Weretilnyk[1]. [1]Department of Biology, McMaster University, 1280 Main St W, Hamilton, Ontario, Canada, L8S 4L8; and [2]Department of Biology, Waterloo University, 200 University Ave W, Waterloo, Ontario, Canada N2L 3G1
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Phosphorus is an essential nutrient for plants with many critical roles including energy transfer (ATP and photosynthesis) and as cellular components ranging from cell membranes to nucleic acids. Not surprisingly, agriculture relies on phosphate containing fertilizers to maximize crop yields and food security. However, decreasing global deposits of accessible rock phosphate for fertilizer production and excessive algal production from phosphate runoff makes it imperative to reduce our reliance on fertilizer use. *Eutrema salsugineum* is an extremophile crucifer and halophyte that is related to *Arabidopsis thaliana* and canola. An ecotype native to the semi-arid, subarctic Yukon, Canada, is tolerant to many abiotic stressors, including drought, freezing temperatures and low-phosphate conditions. In contrast, an ecotype from Shandong, China, an area that is more temperate, is sensitive to low-phosphate conditions. We are using recombinant inbred lines (RILs) produced by a cross between the Yukon and Shandong plants to identify traits associated with low-phosphate tolerance. For screening, we compared plants grown on a medium (agar or soil) supplemented with phosphate or a medium where phosphate addition was either low or absent. We identified lines that resemble their parents, either by displaying tolerance or sensitivity to low phosphate conditions. We measured several traits to rank low phosphate tolerance among the RILs including seedling root architecture, root and shoot biomass, rosette leaf area, and the expression of low-phosphate responsive genes. Among non-destructive measurements used on plants, chlorophyll fluorescence tests of non-photochemical quenching correlated well with low phosphate tolerance while quantum yield (Fv/Fm) values did not. Ongoing work is directed to identifying the physiological and genetic basis contributing to low phosphate tolerance in RILs displaying this tolerance to low phosphate. Identifying gene(s) associated with low phosphate tolerance in plants like Yukon *E. salsugineum* can help us generate crops that are more phosphate efficient to reduce our reliance on phosphate fertilizers.

***[P87] GENE EDITING WITH A TWIST; ENGINEERING CRISPR RESISTANCE INTO TRANSGENIC REPORTERS.** Magnus Macaulay[1], Tommy Kuo[1], Jose Alonso[2], and Geoffrey Wasteneys[1]. [1]Department of Botany, University of British Columbia, Vancouver, BC, Canada, V6T 1Z4; and [2]Department of Plant and Microbial Biology, Program in Genetics, North Carolina State University, Raleigh, North Carolina 27695
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Gene editing will play a key role in adapting crop plants to increasing climate-associated challenges. One approach is to introduce a modified version of a gene into a genome. This transgenic approach is problematic, however, because of competition from the unmodified endogenous gene. This is especially true for essential, single-copy genes because knocking out an essential gene has lethal consequences. In this study, we demonstrate a novel approach to generate modified transgenes that are CRISPR-resistant, so that CRISPR can subsequently knock out only the endogenous copy.

Our essential gene of interest is *MICROTUBULE ORGANIZATION 1* (*MOR1*), which encodes a microtubule-associated protein that is required for microtubule polymerization in *Arabidopsis*. Previous studies have analyzed MOR1 function through conditional mutants since knockout alleles are homozygous-lethal. The *mor1-1* allele, with a L174F single amino acid substitution, causes microtubule disorganization at temperatures above 29°C, resulting in conspicuous left-handed root twisting. While a yellow fluorescent protein-tagged reporter of *mor1-1* (*mor1-1*-3xYPet) enables live cell imaging of the *mor1-1* protein, the left-twisting phenotype is masked when the transgene is expressed in either wild-type or a T-DNA insertion mutant background, indicating that achieving a true null background is difficult. To overcome this challenge, we first used recombineering technology to modify a *MOR1* clone in a transformable bacterial artificial chromosome. In addition to adding a fluorescent protein-encoding sequence, and introducing the *mor1-1* point mutation, we introduced silent nucleotide substitutions at two CRISPR protospacer-adjacent motif (PAM) sites near the 5'-end of the MOR1 coding sequence. The CRISPR-resistant transgenic reporter was then introduced into wild-type *Arabidopsis* by *Agrobacterium*-mediated transfection, and lines homozygous for the transgene were selected in the T2 generation using antibiotics and fluorescence microscopy. Next, seedlings carrying the CRISPR-resistant *mor1-1*-3xYPet were transfected with a CRISPR/Cas9 construct targeting the PAM sites still present in the endogenous *MOR1* gene. Finally, plants with CRISPR/Cas9-induced indels in the endogenous *MOR1* gene were identified by sequencing. Sequencing results confirmed the CRISPR construct only knocked out the endogenous *MOR1*. Importantly, we found that expression of the CRISPR-resistant *mor1-1-3xYPet* transgene reporter generated the characteristic temperature-dependent left-handed root twisting of *mor1-1* mutants only after CRISPR was introduced.

Our study demonstrates that it is possible to engineer CRISPR-resistant transgenes, an innovative approach that could have widespread applications for both understanding the function of essential genes in any organism, and for modifying specific genes in crop species.

[P88] MONOTERPENE INDOLE ALKALOIDS PURIFICATION AND IDENTIFICATION FROM PLANTS *VINCA MINOR* AND *TABERNAEMONTANA LITORALIS*. Zhan Mai and Yang Qu. University of New Brunswick, department of chemistry, Fredericton, NB, Canada E3B 5A3
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Monoterpene indole alkaloids (MIAs) are one of the largest classes of alkaloids with diverse bioactivities. The MIAs are rich in Apocynaceae, Loganiaceae, and Rubiaceae plant families and many MIAs are used commercially owing to their medicinal values, such as anticancer vinblastine and antimalarial quinine. To futher understand MIA chemistry and biochemistry, we investigated MIA metabolites in two Apocynaceae species *Vinca minor* and *Tabernaemontana litoralis*. We obtained plant total alkaloids by standard acid-base extraction from total plant materials. We then used thin Layer Chromatography (TLC) to efficiently separate and purify MIAs. We used Liquid Chromatography-Mass Spectrometry (LC-MS/MS) to identify MIA masses and possible skeletons. We further identified major MIAs in these plants by ^{1}H and ^{13}C Nuclear Magnetic Resonance (NMR), and the identification was further supported by comparing to literature values. 2D-NMR analyses included Correlation Spectroscopy (COSY), Heteronuclear Multiple Bond Correlation (HMBC), Heteronuclear Single Quantum Correlation (HSQC), and Nuclear Overhauser Effect Spectroscopy (NOSEY).

[P89] TEACHING SCIENTIFIC OBSERVATION AND VISUAL COMMUNICATION USING BOTANICAL DRAWINGS. Miranda J. Meents[1]. [1]Biological Sciences Department, Simon Fraser University, 8888 University Drive, Burnaby, BC, Canada V5A 1S6
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OBSERVATION & COMMUNICATION SKILLS: Observation and communication skills are an important part of undergraduate education in biology. In lab courses especially, close observation of plant specimens by eye or using dissecting or compound microscopes is an important tool in student development of a solid understanding of anatomy and diversity. Careful observation can be guided by student preparation of sketches and drawings of specimens. Drawing activities can also contribute to development of effective visual communication skills that are widely transferrable to other contexts. This approach is an especially good fit for plant biology courses because botanical drawing preparation has a long history both in the study plants and for recording and communicating this knowledge.
TEACHING USING BOTANICAL DRAWING: In a third-year Plant Biology course (including lecture and lab) I use botanical drawings as a framework to guide student learning of plant anatomy and to expand their toolkit of observation and visual communication skills. This approach has 4 key components. (1) WEEKLY GOAL SETTING & PRACTICE: Each week in lab students make their own goals for what observation or drawing skills the want to work on, complete a drawing activity related to the topic of the lab, and then receive one-on-one feedback on their goals and drawing from the teaching team. (2) FINAL BOTANICAL DRAWING: At the end of the term the students choose one weekly activity to recreate as a full-colour, large botanical drawing. They also submit draft images and sketches to document their process and an Artist Statement discussing their work. (3) PUBLIC SHOWCASE: All the botanical drawings are celebrated in a public showcase at the end of the term, including food, drinks, and voting on the best drawing. (4) REFLECTIONS: Students supplement their weekly goal setting and reflections with a mid-semester check-in, and a final reflection on their learning and skill-development progress.
RESULTS: This approach is now a highlight of the course! We notice a marked improvement in the quality of students' observation and visual communication skills. The students corroborate this in their feedback, but also report that these activities and assignments improve their understanding of plant biology, that the goal-directed and feedback-focused approach to skill development is highly effective, and that they developed a deeper appreciation for plants as a result.

[P90] SKINNY MAIZE - DRIVING *ZEA MAYS* GENOME CONTRACTION THROUGH CAS9 DELETION OF HIGH COPY NUMBER LTR ELEMENTS. Mark A. A. Minow[1], Ankush Sangra[1], and Robert J. Schmitz[1]. [1]Davison Life Sciences Complex, University of Georgia, Genetics, 120 E Green St, Athens, GA, USA, 30602
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Eukaryotic genomes are replete with repetitive, parasitic transposable elements (TEs) that serve little known benefit to their hosts. The *Zea mays* (maize) genome is ~85% TE-derived, with most maize TE sequence originating from Long Terminal Repeat (LTR) retrotransposons; the four most prolific LTR TE families alone encompass ~0.52 Giga-bases or ~23.7% of the genome. These high copy number LTR TEs retain family-level sequence conservation, providing an opportunity to use a limited number of *CRISPR* guide RNAs (gRNAs) to elicit largescale genome-wide TE deletion. From the four most prolific maize LTR TE families, we generated consensus sequences from which we extracted all possible *CRISPR* gRNA sequences and found all the complementary sites in the genome. These TE-derived gRNAs had up to 65,755 targets in the reference. A selection of these gRNAs will be combined with pollen specific *SpCAS9* expression to trigger rounds of widespread TE deletion. By editing in the male gametophyte, lethal edits will be screened out in pollen and seed populations (n ~10^6 and ~10^2 per plant, respectively). Moreover, pollen-specific editing facilitates choosing between more deletions, by crossing with male flowers, or pausing edits, by using the female ear. The LTR targets largely exist between genes, allowing edits at different, but linked, TEs to also delete the intervening genic sequences. Through repeated rounds of deletion, we will gradually diminish LTR TE copy number and remove non-lethal genes. Beyond investigating potential TE-to-gene regulatory interactions, this deletion scheme will reveal which genes and regulatory sequences can be lost without losing viability, providing insights into the 'minimal' maize genome.

[P91] PURIFICATION, IDENTIFICATION, AND INVESTIGATION OF THE BIOSYNTHETIC PATHWAYS OF MONOTERPENOID INDOLE ALKALOIDS IN *HAMELIA* PATENS. Alyssa Seveck[1] and Yang Qu[1]. [1]Department of Chemistry, University of New Brunswick, 3 Bailey Drive, Fredericton, NB, Canada, E3B 5A3
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Monoterpene indole alkaloids (MIAs) are specialized metabolites naturally produced by plants when they face abiotic or biotic stressors. There are over 3000 of these bioactive alkaloids that have been identified, and they can be found in plant families including:
Rubiaceae, Apocynaceae, and Loganiaceae. Some MIAs have been found to have numerous therapeutic benefits. One such example is the MIA vinblastine, a commercial chemotherapeutic drug that derives from the plant, *Catharanthus roseus*. In *Hamelia patens*–a plant species that falls in the Rubiaceae family–several of these MIAs can be found. *Hamelia patens*, a plant that is native to southern Florida, Mexico, Central and South America has been employed over the centuries to treat things such as inflammation, menstrual disorders, and wound healing. Due to the possible medicinal benefits of these MIAs present in *Hamelia patens,* it is advantageous to study the biosynthetic pathway(s) of these compounds. In this study, several MIAs are/have been successfully extracted and identified using LC-MS, 1D and 2D NMR data. These isolated MIAs will be later used as standards. To identify the biosynthesis of these MIAs, candidate CYPs will be utilized to perform a possible oxidation reaction(s) on potential substrates.

[P92] ELONGATION OF THE BASAL INTERNODES OF SOYBEAN AND ITS ASSOCIATION WITH THE EXPRESSION PATTERNS OF GIBBERELLIN METABOLISM GENES. Ankita Thapar[1], Pham Anh Tuan[1], Deepak Sharma[1], and Belay T. Ayele[1]. [1]Department of Plant Science, University of Manitoba, Winnipeg, Manitoba, Canada
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Lowest pod height, which refers to the distance between the tip of the lowest/first pod and the soil surface, in crops such as soybean is closely associated with the length of basal internodes. Lowest/first pods that are lower than the reach of the combine cutter are usually lost during harvesting and this results in significant yield loss. Therefore, it is necessary to develop strategies that enhance the elongation of basal internodes or develop soybean cultivars with longer basal internodes that are able to set their first pods at higher heights. This study investigated the role of gibberellin in the elongation of basal internodes using a cultivar characterized by short pod height and also examined the transcriptional regulation of gibberellin biosynthesis and catabolism genes in the basal internodes of two cultivars exhibiting shorter and longer first pod heights. Seed treatment with biologically active gibberellin increased the lengths of the basal internodes in the cultivar with short pod height as compared to the control plants derived from untreated seeds. However, the same treatment did not have significant effect on the thickness of the internodes and their bending strength. Basal internodes of the two cultivars with contrasting first pod height showed variation in their elongation, and this variation in internode lengths is associated with the expression patterns of GA biosynthesis genes including *GA20ox* and *GA3ox* and those involved in its catabolism, the *GA2ox*s.

***[P93] BIOCONTROL ACTIVITY OF *BACILLUS SP*. OF PHYTOMICROBIOME AGAINST *BOTRYTIS CINEREA* IN *CANNABIS* SATIVA.** Haleema Tariq[1], Anja Geitmann[1], and Donald Smith[1]. [1]Department of Plant Science, Macdonald Campus, McGill University, Montreal, QC, Canada
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Cannabis is a promising medicinal plant that is used for relieving pain, relaxing muscles, improving sleep, and treating many neurological disorders. Cannabinoids such as cannabidiol (CBD) and tetrahydrocannabinol (THC) are important secondary metabolites produced by *Cannabis* and have been used as analgesics. *Botrytis cinerea* is a fungal pathogen that affects a wide range of crops worldwide including *Cannabis*. It compromises the ability of *Cannabis* producers to achieve the desired secondary metabolite profiles and overall productivity. Controlling this fungus using fungicides costs more than $1 billion annually, and the residual fungicides on plants lead to health concerns for consumers. Gray mold caused by *B. cinerea* causes significant losses in both indoor and outdoor production systems and decreases *Cannabis* yield by up to 32%. With the rapid expansion of the cultivation of *Cannabis*,

especially in North America, there is a need to focus on pathogen attacks in this crop plant. Plant growth-promoting rhizobacteria have a potential role in sustainable food production, particularly in the presence of biotic and abiotic stresses, including those associated with global climate change, to feed our growing global population. Plant-beneficial microbes provide an alternative and can be suitable tools for *Botrytis* control and enhance overall crop productivity in an environmentally sustainable way. The current study focuses on the biocontrol activity of bacteria against *Botrytis cinerea* of the cannabis plant. Morphological analysis and scanning electron microscopy helped us determine the interaction between biocontrol (microbes) and *Botrytis.* Microbiological studies performed to characterize the selected beneficial bacteria for their ability to produce lytic enzymes involved in plant pathogenic inhibition and plant growth stimulation revealed cellulase, protease, lipase, amylase, ACC-deaminase and phosphatase activity. The study allowed the detection of several enzymatic mechanisms involved in plant growth and protection and revealed the potential of members of phytomicrobiomes as a biocontrol and biostimulant in cannabis plants. The current project aims to reduce fungal pathogen infection (*Botrytis cinerea*) in *Cannabis* plants using plant-beneficial microbes which will help the producers and sellers in reducing the limitations of *Cannabis* production and limit the use of synthetic fungicides that are harmful to human health and increase greenhouse gas emission.

***[P94] GENOME-WIDE ASSOCIATION STUDY OF PREHARVEST SPROUTING ASSOCIATED ALPHA- AMYLASE ACTIVITY IN BARLEY.** Rui Wang[1], Gurkamal Kaur[1], Marta S. Izydorczyk[2], Dean Spaner[3], Aaron D. Beattie[4], Ana Badea[5], and Belay T. Ayele[1]. [1]Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada; [2]Grain Research Laboratory, Canadian Grain Commission, Winnipeg, MB R3C 3G8, Canada; [3]Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton Canada; [4]Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada; and 5Brandon Research and Development Center, Agriculture and Agri-Food Canada, Brandon, MB R7A 5Y3, Canada
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Barley production is significantly affected by preharvest sprouting (PHS), which refers to the germination of seeds on the mother plant before harvesting due to humid and rainy conditions. Most of the modern barley cultivars in Canada exhibit a low level of seed dormancy and are susceptible to PHS, which activates alpha- amylase activity and starch degradation in the seeds and therefore causes substantial yield and quality losses. Therefore, there is a need to develop PHS resistant barley cultivars. The main objective of this study is to identify genomic regions/candidate genes associated with PHS induced alpha-amylase activity in barley seeds using genome-wide association study (GWAS). Seeds of the mapping panel, which consists of 160 diverse barley genotypes, harvested from four field tests were examined for variations in alpha- amylase activity using Rapid Visco Analyser (RVA). The mapping panel was also genotyped using a 50K Illumina Infinium iSelect genotyping array. After filtration, a total of 30,494 polymorphic single nucleotide polymorphisms (SNPs) were considered for GWAS using mixed linear model with Kinship (MLM+K). Our analysis identified 10 significant markers representing one quantitative trait loci (QTL) on chromosome 5H based on the linkage disequilibrium (LD) decay 2.81cM and false discovery rate (FDR) threshold of $\alpha = 0.05$. Each of the 10 significant markers explain 13% to 18% of the phenotypic variation. The markers associated with the alpha-amylase activity might have the potential to enhance marker-assisted selection in the development of PHS resistant barley cultivars.

[P95] EVALUATING SEASON EXTENSION TECHNOLOGIES ACROSS BOREAL NORTHERN AGRICULTURAL REGIONS. Julia Wheeler, Karen Compton, Dena Wiseman, and Linda Elizabeth Jewell. St. John's Research and Development Centre, Agriculture and Agri-Food Canada, 204 Brookfield Road, St. John's, NL A1E 0B2
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Northern boreal communities depend on complex food systems that are frequently highly reliant on outside exports. Obtaining fresh, high-quality produce is often extremely difficult in these communities, as their long supply chains are frequently disrupted. Ongoing climate changes, such as increased frequency of extreme weather events, disrupt these supply chains and increase food insecurity in Northern boreal communities. Local vegetable production represents an important component of the food system, but there are numerous barriers to agriculture in Boreal Northern regions, one of which is short growing seasons with frequent frosts in both spring and fall.

Season extension technologies (e.g. row covers, plastic mulches, thermal tunnels) can help address short growing seasons by providing a warmer and more sheltered root-and-shoot-zone microclimate for germinating and growing crops, particularly in the colder shoulder seasons. Season extension technologies can accelerate development and increase crop yield; however, they can also provide ideal conditions for pests and pathogens. Despite their potential importance for local vegetable production in Northern boreal communities, there is a lack of systemic evaluation of season extension technologies for production in these climates.

The overall goal of our research was to evaluate season extension technologies across a range of Northern boreal sites (Whitehorse, YK; Happy Valley-Goose Bay, NL; St. John's NL) to determine their effects on phenology, yield and damage by pests and pathogens in two vegetable crops. First, we evaluated combinations of degradable bio-plastic mulches (which warm soils and trap moisture) and low tunnels (which warm air temperatures and maintain humidity) for a model warm-climate crop (green beans; *Phaseolus vulgaris*). Second, we evaluated bio-plastic mulch for potato (*Solanum tuberosum*) production; potatoes are a staple Northern boreal root crop, which are strongly impacted by low soil temperatures.

We found that bioplastic mulches significantly increased damage to crops by both pests and pathogens; neither bioplastic mulches nor low tunnels had a consistent positive effect on yield relative to controls in any of the sites across three years. Bioplastic mulches also showed poor breakdown at the NL sites, which impacted plant growth, likely by providing shelter to insect pests. However, mulch breakdown was better at the Yukon site, which was the only site that demonstrated positive effects of mulch on yield in some years. This suggests specific climate conditions (potentially longer daylight) alters the effect of some season extension technologies in Northern boreal growing systems, which indicate further avenues for investigation.

[P96] BENEFIT: BIO-INOCULANTS FOR THE PROMOTION OF NUTRIENT USE EFFICIENCY AND CROP RESILIENCY IN CANADIAN AGRICULTURE. George C diCenzo, Matthew G Bakker, Terrence H Bell, Derek G Brewin, Olivia Wilkins, and Ivan J Oresnik. [1]Queen's University, Canada; [2]University of Manitoba, Canada; [3]University of Toronto Scarborough, Canada
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Chemical fertilizers have contributed to the dramatic rise in global crop yields over the past 50 years. However, they also account for as much as 20% of all greenhouse gas emissions associated with Canadian agriculture. In the case of nitrogen fertilizer, only 40-50% of applied nitrogen is assimilated by plants, with the lost nutrient becoming run-off or converted to nitrous oxide. To reduce the climate impact of growing crops, suitable alternative methods of promoting crop nutrition without reducing crop yields should be developed. Microbes have great promise to become a key and widespread tool in reducing greenhouse gas emissions from agriculture through nitrogen fixation, phosphorus solubilization, and promoting root development. However, inoculants have often failed to reach their potential outside of lab conditions and often behave unpredictably in different fields, thereby limiting their use by farmers. To overcome these limitations, the BENEFIT project is undertaking a genomics-driven approach to develop microbial inoculants supporting wheat, barley, canola, kale, bean, and pea nutrition in Canada.

***[P97] RENSEQ-BASED REFINEMENT OF *BRASSICA NAPUS* NLROME.** Jiaxu Wu[1-5], Soham Mukhopadhyay[1-5], Coreen Franke[6], and Edel Pérez-López[1-5]. [1]Département de phytologie, Faculté des sciences de l'agriculture et de l'alimentation, Université Laval, Quebec City, QC, Canada; [2]Centre de recherche et d'innovation sur les végétaux (CRIV), Université Laval, Quebec City, QC, Canada; [3]Institute de Biologie Intégrative et des Systèmes (IBIS), Université Laval, Quebec City, QC, Canada; [4]L'Institute EDS, Université Laval, Quebec City, QC, Canada; [5]Centre SÈVE, Université de Sherbrooke, Sherbrooke, J1K 2R1, QC, Canada; and [6]Nutrien Ag Solutions Canada, Saskatoon, SK, S4N 4L8, Canada
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Canola (*Brassica napus* L.) is primarily cultivated as an oilseed crop with significant economic value. However, the emergence of devastating diseases such as clubroot and blackleg threatens the canola industry. Nucleotide-binding and leucine-rich repeat (NLR) genes play a crucial role in initiating a robust

immune response upon perceiving pathogen-secreted effectors. Therefore, accurate annotation of *NLR* genes in *B. napus* is essential for understanding their functions and engineering elite cultivars in the future. In this study, we selected the 'Westar' cultivar of *B. napus* for NLR re-annotation, which is widely used in genetic mapping and transformation studies in Canada and elsewhere. A high-quality genome, based on long-read sequencing, was selected for further analysis. Querying the annotated reference protein sequences against the Pfam database indicated the presence of only 336 genes with domain signatures associated with NLR proteins. To re-annotate the full NLR repertoire in *B. napus* cv. 'Westar,' we applied the resistance gene enrichment sequencing (RenSeq) method. By combining RenSeq mapping, the NLR-Annotator tool, and *de novo* gene prediction of problematic regions using AUGUSTUS, we increased the number of annotated NLR genes from 336 to 774. Intriguingly, the majority of newly identified NLR genes belong to unannotated or wrongly annotated regions in the reference genome. Moreover, we compared the 'Westar' NLRome with those of other elite cultivars like 'ZS11' and 'Darmor-bzh' to investigate the intraspecific diversity of NLR genes in terms of chromosome location, phylogenetic relationships, integrated domains (IDs), and orthogroups (OGs) identification. We further applied RenSeq and Oxford Nanopore whole-genome sequencing to annotate *NLR* genes in five clubroot-resistant *B. napus* inbreed homozygous lines (IH1-IH5) with different resistance profiles. The results show 612, 600, 601, 601, and 597 *NLR* genes in these five lines, respectively. Taken altogether, the re-annotated *NLR* genes in these *B. napus* susceptible and resistant lines provide a crucial resource for breeders and researchers to improve disease-resistant gene discovery and evolutionary studies among Brassicaceae.

***[P98] SEED GERMINATION UNDER STRESS - MECHANISTIC INSIGHTS INTO THE EARLY LIFE OF LONG-LIVED PLANTS.** Michael Yankov[1,2], Oscar Felipe Nunez-Martinez[1,2], Stefan Heinen[2], and Katharina Bräutigam[1,2]. [1]Cell and Systems Biology, University of Toronto, Toronto, ON, Canada, [2] Department of Biology, University of Toronto Mississauga, Mississauga, ON, Canada
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Seeds are critical for the propagation of individual plants, the persistence of plant populations and the maintenance of terrestrial ecosystems. Seeds safely package the plant embryo for dispersal, and successful germination is strongly influenced by environmental factors. With climate change and increased anthropogenic activities such as mining or irrigation practices, soil salinity has increased drastically and has removed thousands of hectares of land from use in agriculture and agroforestry in Canada and worldwide. At the same time, little is known about the effect of salinity on seed germination in many prominent forest trees.

Here, we systematically study the effect of increased salinity on seed germination in *Populus*, i.e. trees of central importance for Canada's forest and economy. Poplar seeds were exposed to increasing concentrations of salt under controlled environmental conditions. Different ions and osmotic conditions were studied. High salt concentrations can affect seeds and seedlings mechanistically through two means: osmotic forces and toxic effects of ions. To discriminate between these two effects, salinity treatments were compared to non-salt iso-osmotic controls. The effects on seed germination were tracked over a period of ten days and threshold concentrations for seed germination were determined, which, notably differed depending on the identity of the ions in the salts. We also introduced the criterion of maximum harm that quantifies seedling damage post successful germination. In order to assess the impacts of salinity on early plant development, germinated seedlings were classified into four distinct developmental stages and monitored daily over the full period of the study. Finally, biomass production was analyzed to assess plant growth during the early seedling establishment phase. Interestingly, it was partially uncoupled from development, depending on the identity of the ions in the salt treatments.
Our findings contribute to the mechanistic understanding of germination and early plant development under salt stress and can be critical for the selection of strategies, species, or genotypes in ecosystem regeneration and land reclamation efforts.

***[P99] IDENTIFYING THE GENOMIC VARIABILITY OF DIVERSE WHITE MOULD (*SCLEROTINIA SCLEROTIORUM* (LIB.) DE BARY) ISOLATES.** Marysia Zaleski-Cox[1], Laura Esquivel-Garcia[1], and Valerio Hoyos-Villegas[1]. [1]McGill University – Macdonald Campus, 21111 Lakeshore Rd, Sainte-Anne-de-Bellevue, Quebec H9X 3V9
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Sclerotinia sclerotiorum (Lib.) de Bary (Ss) is a cosmopolitan, fungal plant pathogen that can greatly reduce the yield of important crops such as *Phaseolus vulgaris* L. (common bean, Pv). Pv's resistance to Ss is quantitative and no cultivar with complete resistance has been identified. Ss does not have a universal effect on common bean, as some isolates are more aggressive than others and an isolate by host cultivar interaction has been observed. Our objective is to characterize the genomic diversity of Ss within a geographically diverse set of isolates and identify loci potentially linked to variable aggressivity. This will be done using whole genome sequencing of Ss to identify subpopulations within the collected isolates followed by inoculation of diverse common beans with a representative of each Ss subpopulation. Inoculation will provide phenotypic aggressivity information. The collected genotypic and phenotypic data will be linked with an analysis of polymorphisms within regions associated with Ss aggressivity and a multi-trait genome wide association study (GWAS) of Ss resistance in Pv. Ss isolate collection, sequencing and analysis of variance are underway. This work will improve standard Ss screening procedures in breeding laboratories by identifying appropriately diverse Ss isolates to be used during inoculation of new breeding material. Additionally, a multi-trait GWAS will help uncover pleiotropic resistance determinants in Pv. Ultimately, this will facilitate the development of Pv lines harbouring improved Ss resistance.

***[P100] BREAKING FREE: INSIGHTS INTO AUXIN AND ETHYLENE CONTROL OF ABSCISSION ZONE PATTERNING IN ARABIDOPSIS.** Risham Osahan[1] and Shelley R. Hepworth[1]. [1]Department of Biology and Institute of Biochemistry, Carleton University, 1125 Colonel By Drive, Ottawa, ON, Canada, K1S 5B6
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Abscission is a critical developmental process that leads to the detachment of plant organs. In *Arabidopsis thaliana*, pollination triggers the abscission of floral organs by signaling cell separation responses in abscission zones (AZs) at the base of sepals, petals, and stamens. As abscission approaches, AZ cells form a proximal separation layer that secretes hydrolytic enzymes and a distal lignified layer that serves as a mechanical brace. Phytohormones auxin and ethylene play an important role in regulating abscission by inhibiting and promoting organ detachment, respectively. How these hormones influence AZ structure and differentiation has been unclear. Experiments in wild-type plants showed that AZs form their distinct layered structure about one position before organs detach. By manipulating hormone pathways, our findings reveal that auxin is essential in ordering the cellular architecture of AZs. Exogenous application of auxin caused disorganized AZs and inhibited layer differentiation, whereas the inhibition of auxin transport led to the earlier formation of AZ layers. By contrast, ethylene influenced the timing of abscission and layer formation without changing AZ morphology. In ethylene-treated plants, AZ layers formed in unopened flower buds suggesting that AZs are responsive to ethylene before pollination. Our research highlights distinct roles for auxin and ethylene in AZ differentiation. Future work will explore how boundary genes that define and organize AZ cell structure interact with auxin and ethylene to control the timing of AZ layer differentiation.

[P101] THE PURIFICATION AND IDENTIFICATION OF MONOTERPENE INDOLE ALKALOIDS IN ALSTONIA SCHOLARIS. Scott Mann and Dr. Yang Qu. University of New Brunswick
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Monoterpene Indole Alkaloids (MIAs) are a class of metabolites found in many plant families including Apocynaceae, Rubiaceae, and Nyssaceae. MIAs have become popular in pharmaceutical research due to their wide range of bioactivities, stemming from their diverse structure. Although medicinally valuable, the synthesis of MIAs has proven difficult due to their complex structures. Therefore, the elucidation of MIAs biosynthetic pathways is a crucial step to making these metabolites a pharmaceutically viable option. The first step in understanding these biosynthetic pathways is to purify and Identify MIAs from plant extracts. Alstonia scholaris, a tree species native to southeast Asia, has been previously

documented to synthesize important MIAs. In this project, the purification and identification of MIAs synthesized by Alstonia scholaris was attempted, yielding four MIAs.

***[P102] MANAGING VERTICILLIUM STRIPE DISEASE IN CANOLA THROUGH GENETICS, OMICS, AND UNDERSTANDING THE *BRASSICA NAPUS - VERTICILLIUM LONGISPORUM* INTERACTION.**
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Canola (*Brassica napus*) is a highly demanding and economically valuable crop in Canada, contributing approximately $29 billion to revenue. Canola in Canada faces several devastating diseases, including blackleg, clubroot, and sclerotinia stem rot. Among the most common diseases, Verticillium stripe disease, a newly emerged disease caused by the soilborne fungal pathogen *Verticillium longisporum*, has caused drastic damage to canola yields. Nevertheless, fungicidal application, crop rotation, or cultural control measures offer inconsistent and expensive disease management options that do not facilitate control. Additionally, resistant varieties, as an effective control measure, are currently unavailable. Therefore, this study will focus on the impact of *V. longisporum* on changes in the expression of genes involved in plant growth hormone biosynthesis and antioxidant enzyme activity, as it is poorly studied and understood in canola. RNA-Seq data will express the behavioral changes of the genes responsible for the activities of antioxidant enzymes and plant growth hormones during the disease progression. By narrowing down the differentially expressed gene pool identified, a few critical genes will be selected and used for functional characterization at the seedling stage of *B. napus* plants against the disease. CRISPR/Cas9 will be applied to knock out the negatively regulating candidate genes in *B. napus* resistance in response to *V. longisporum* infection. Furthermore, the resistant evaluation of *V. longisporum*-infected canola plants will be assessed concurrently. Spectrometric outputs will outline the behavior of significant antioxidant enzymes such as superoxide dismutase, peroxidase, and catalase. The most effective genes identified, as well as phenotypic evaluation and antioxidant enzyme production analysis, will be employed in future breeding strategies to produce *B. napus* varieties that have resistance against *V. longisporum*, as well as for a better understanding of disease progression and aiding in effective disease management strategies in the field.

***[P103] ASSESSING THE INFLUENCE OF COVER CROP MIXTURES ON SOIL HEALTH IN FABA BEAN PRODUCTION SYSTEM IN BOREAL CLIMATE.**
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Low soil fertility, extreme weather conditions, and a short growing season are the major factors of low crop production in Newfoundland and Labrador (NL). Winter cover crops (CCs) are known to be grown for their ability to establish quickly and survive in extreme environmental conditions. Early frost and low temperatures during fall significantly delay harvesting of primary crops and seeding of CCs), hence CC establishment. CCs are known to enhance soil carbon (C) pools, reduce erosion, increase soil organic matter (SOM), add nitrogen (N), improve soil physicochemical properties, and enrich active microbial population and abundance. The present research examines how the establishment of CC mixtures impacts on labile carbon pools, mineral nitrogen, and the active microbial population in soil within faba bean (Vicia faba L.) production systems situated in a boreal climate.
During the 2022 and 2023 growing seasons, a field trial was conducted in Pasadena, NL. Faba beans were planted on June 6, 2022, and June 30, 2023, and harvested on August 25, 2022, and October 18, 2023. CC mixtures were planted after harvesting faba beans, on August 31, 2022, and harvested on June 27, 2023. The 14 CC mixtures were two- and three-crop combinations of legumes (hairy vetch (HV), red clover (RC), berseem clover (BC), and bird's foot trefoil (BT)) and grasses (triticale (TR), fall rye (CR), and annual ryegrass (AR)). Soil sampling was done from the top-20 cm after harvesting CC mixtures to determine permanganate-oxidizable carbon (POX-C), particulate organic matter nitrogen (POM-N) and carbon (POM-C), microbial biomass carbon (MBC) and nitrogen (MBN) and mineral N. Phospholipid fatty acid analysis (PLFA), was performed to determine the active microbial community structure and abundance.

Results showed that CC mixtures had significant effects on MBC whereas no significant effects on POX-C, POM-N, POM-C, MBN, or soil mineral N. Higher soil MBC was observed in BT+AR mixture compared to the lowest was recorded in the RC+CR mixture. The PLFA analysis showed that the RC+TR mixture produced a higher gram-negative population (93.08 nmol/g) compared to the lowest (88.68 nmol/g) was recorded in control. Contrarily, the highest gram-positive bacteria population and total bacteria population was observed in NCC. However, CC mixtures had no significant effects on fungi and protozoa populations. We may conclude that the CC mixtures demonstrated not much progress in improving soil health parameters due to short term experiment. Hence, long-term field research is necessary to examine how the establishment of CC mixtures affects the population of active microbial communities, levels of labile C pools, enzyme activities, and N dynamics in podzolic soil within a boreal climate.

***[P104] ASSESSING THE IMPACTS AND POTENTIAL OF COVER CROP ESTABLISHMENT ON WEED CONTROL, YIELD CONSISTENCY, AND FABA BEAN QUALITY IN A BOREAL CLIMATE.**
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Newfoundland and Labrador (NL) face challenges with achieving high crop yields due to short growing seasons and low soil fertility. Low crop heating units influence the growing season, resulting in a significant delay in primary crop harvest. Cover crops (CCs) are known to provide soil cover, reduce soil erosion, enhance soil quality and health, suppress weeds, and offer additional forage to the farmers. Current research investigates the potential of CC establishment and how they might positively affect weed suppression, yield stability and forage quality of faba bean under boreal climate.

A field research trial was conducted in Pynn's Brook, NL during the 2022 and 2023 growing seasons. Faba beans were seeded on June 6, 2022, and June 30, 2023, and harvested on August 25, 2022, and October 18, 2023. After harvesting, grass-legume CC mixtures were seeded on August 31, 2022, and harvested on June 27, 2023. The 14 CC mixtures were two- and three-crop combinations of legumes (hairy vetch, red clover, berseem clover, and bird's foot trefoil) and grasses (triticale, fall rye, and annual ryegrass), arranged in a randomized complete block design with four replications. Faba bean and CC biomass were measured from 0.5 m x 0.5 m quadrat. The plant samples were ground, and a sub-sample of 50 g from each treatment was analyzed for forage nutritional quality.

Results showed that the hairy vetch/-cereal rye mixture produced the highest total biomass (2.4 Mg/ha), whereas the lowest (0.7 Mg/ha) was measured from the bird's foot trefoil-annual rye mixture. Faba bean forage yield harvested after CCs (2023) was 30% less than faba bean harvested before CCs (2022), mainly because of the abiotic stress (high precipitation and low temperature) and delayed sowing in the year 2023. Legume/grass proportions varied among treatments. CCs had significant effects on faba bean quality i.e. acid detergent fibers, neutral detergent fibers, net energy for gains, net energy for maintenance, net energy for lactation, total digestible nutrients, and relative feed value. All CCs led to weed suppression >60% compared to the control, the highest being in the hairy vetch-cereal rye mixture. This research demonstrates that CC mixtures could be established successfully after harvesting faba beans in a boreal climate, leading to significant weed suppression. Long term studies are required to determine the yield stability of faba bean and establishment of CCs in a boreal climate.

[P105] THE EFFECT OF HUMIC ACID ON ROOT NODULATION AND PLANT GROWTH OF RED CLOVER (*Trifolium pratense* L.).
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Legumes are crucial for sustainable agriculture, forming symbiotic relationships with *Rhizobium* bacteria to fix atmospheric nitrogen, reducing the need for nitrogen fertilizers, and promoting ecologically friendly cropping systems. Establishing a fully functional symbiosis is a complex process and suboptimal nodulation can hinder nitrogen fixation, necessitating effective strategies to optimize it. Humic-based

products, rich in humic acid (HA), are recognized as valuable organic amendments and vital plant biostimulants, known for enhancing soil physicochemical properties, crop health, yield, and stimulating microbial growth. The primary aim of this study was to assess the effect of HA on the phenotypic traits of red clover. This experiment was conducted under controlled environmental conditions using a hydroponic system with five different concentrations of HA [0.025%, 0.05%, 0.1%, 0.2% and 0.4% (v/v)] in 0.25X N-free Hoagland's solution. After seven weeks of growth, plants were harvested, and data were collected on nodule number, nodule dry weight, shoot and root dry weight, root volume, root surface area, and root length. In this study, all parameters tested exhibited a notable increase in plants treated with the highest concentration of HA (0.4% (v/v)) compared to the untreated control. Across root parameters, a consistent upward trend was observed in both root surface area and length with increasing HA concentrations. Relative to the control, a significant improvement in root surface area was observed at HA concentrations of 0.1% (49%), 0.2% (61%), and 0.4% (106%), while significant increases in root length were observed at HA concentrations of 0.2% (53%) and 0.4% (115%). Notably, a significant improvement in root volume and dry weight was observed solely at the highest HA concentration, with increments of 112% and 44%, respectively, compared to the control. Moreover, plants treated with the 0.4% HA showed 43% higher shoot dry weight compared to the control. Additionally, both nodule number and nodule dry weight exhibited an upward trend with increasing HA concentration, showcasing significantly higher results in plants grown at the highest HA concentration, with increments of 68% and 101%, respectively. However, the average nodule dry weight showed no significant difference across different HA treatments. These findings emphasize the positive impact of HA on red clover nodulation and growth.

[P106] TILLER AGE RELATIONSHIP TO FLOWERING PROPENSITY IN INTERMDIATE WHEATGRASS. Douglas J Cattani. Depasrtment of Plant Science, University of Mantioba
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Flowering in perennial grasses may be impacted by age of the individual tiller. Using different fall seeding times to stage main stem development prior to vernalization, we tested the likelihood to produce an inflorescence, the timing of anthesis and relative potential reproductive effort in intermediate wheatgrass (Thinopyrum intermedium). This was tested at four site-years with seeding in 2020-2022. Growing seasons were variably influenced by drought. In general, earlier seeding dates resulted in larger main stem inflorescences (weight and floret number) and initiated flowering more uniformly and earlier. Fall development at the fifth leaf stage on the main stem was required for a similar flowering time and inflorescence yield potential as an established crop.

***[P107] PROLONGED NITROGEN FIXATION DURING PERIODIC MOISTURE STRESS TO ENHANCE YIELD AND PROTEIN ACCUMULATION IN SOYBEAN.** Larissa Cottick[1], Malcolm Morrison[2], and Yvonne Lawley[1]. [1]Department of Plant Science, University of Manitoba, Winnipeg, Manitoba, Canada; and [2]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6
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Drought is among the most problematic abiotic factors challenging soybean production in Canada. Regular precipitation, specifically during flowering to pod-fill stages, is crucial for high seed protein and yield. Adapting drought tolerant cultivars for Canadian growing conditions is an important research priority. This project tests for the presence of prolonged nitrogen fixation (PNF) traits in backcrossed derived short season soybean lines selected for adaptation to Ontario and Manitoba growing conditions. Field experiments were conducted from 2021 to 2023 at the AAFC Ottawa RDC and from 2022 to 2023 at the University of Manitoba Carmen Research Farm. Yield and protein accumulation of fourteen soybean lines and two paired check lines (nodulating and non-nodulating) grown under ambient and supplemented moisture growing conditions were arranged in a split plot design with irrigation treatment as the main plot and soybean line as the sub plot in four replicates. Irrigated treatments were supplemented using sub-surface drip tape installed 4 inches deep in between soybean rows. Seed and protein yield was used to identify lines that were more capable of fixing N under periodic moisture stress conditions. The difference between soybean lines grown under irrigation and natural precipitation is called the Delta Yield and was used as an indicator of the presence of PNF traits in the tested soybean lines. Six of the lines tested had lower Delta Yield than the mean of Ottawa and at Carman site years. These six lines had the lowest

difference in protein yield per ha when the non-nodulating control protein was subtracted from the line protein. Based on the results of these field trails, these lines may have the PNF traits. They should continue to be tested to help soybean crops in Canada reman profitable and adapt to changing climates.

***[P108] IMPACT OF DROUGHT STRESS ON MIXED RED CLOVER-GRASS STANDS VERSUS GRASS MONOCULTURE.** Chathuranga De Silva[1], Hari P. Poudel[2], and Malinda S. Thilakarathna[1]. [1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada T6G 2P5; and [2]Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre, Lethbridge, AB, Canada T1J 4B1
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Drought stress significantly impacts forage production, underscoring the need to deepen our understanding of how forage plants respond to such conditions. The primary aim of this study was to assess the response of legume-grass forage mixed stands to drought stress compared to grass monoculture. A greenhouse pot experiment was conducted by exposing a mixed stand of red clover (*Trifolium pratense* L.)–timothy grass (*Phleum pratense* L.) and a timothy monoculture stand to severe drought (20% field capacity–FC), moderate drought (40% FC), and well-watered (80% FC) conditions for four weeks at the early flowering stage. Following the drought phase, plants were subjected to a four-week recovery period by restoring the soil moisture level to 80% FC. Results show that the total biomass and shoot total nitrogen content of the legume-grass mix stand was notably higher than the grass monoculture stand at the end of the drought and recovery phases. However, shoot biomass of the mixed stand was significantly reduced under moderate (16.7%) and severe drought (21.7%) conditions compared to the well-watered plants, while no significant difference was observed in the timothy monoculture under different FC levels. Red clover–timothy mixed stand subjected to moderate drought recovered shoot growth during the recovery phase, showing no significant difference between moderate drought and well-watered treatments for shoot biomass. Although the total nitrogen content in shoots was significantly higher in the grass-legume mixed stand compared to the grass monoculture, moderate and severe drought significantly reduced the red clover shoot nitrogen content at the end of drought and recovery phases. In terms of nitrogen fixation, severe drought stress reduced the percentage of nitrogen derived from the atmosphere of red clover by 8.3% and 4.6% in the drought and recovery phases, respectively. In the drought phase, total fixed nitrogen in red clover shoots was significantly reduced by 27% (in moderate) and 47% (in severe) drought compared to control. Furthermore, total nitrogen fixed in shoots following the recovery phase was lower under moderate (17.5%) and severe drought (29.5%) conditions compared to the well-watered condition. In general, grass in the mixed stand exhibited a significantly higher shoot nitrogen content compared to grass monoculture. Overall results indicate that drought has deleterious effects on forage production and nitrogen fixation inputs under legume-grass mixtures.

[P109] CHILLING CHALLENGES: EARLY SEASON COLD STRESS AFFECTS GERMINATION, NODULATION, AND PLANT GROWTH IN PEA (*Pisum sativum* L.). Dhanuja N. Abeysingha[1] and Malinda S. Thilakarathna[1]. [1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada T6G 2P5
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Early seeding poses a significant challenge in regions with shorter growing seasons, mainly due to cold spring weather. Ultra-early seeding has demonstrated promising outcomes for certain agricultural crops, such as spring wheat. Being a cool season crop and benefiting from hypogeal germination, pea crops may potentially aid in their resilience against spring frosts compared to other crops. This study aims to evaluate the effects of early-season cold stress on germination, nodulation, plant growth, and yield parameters in field pea. Pea seeds (cultivar CDC Meadow) were inoculated with *Rhizobium leguminosarum* bv. *viciae* (3841) and grown in two separate fully controlled growth chambers, maintaining the temperature at 8°C (cold stress) and 15°C (control). A subset of plants (n=10) in each treatment was harvested at five weeks to evaluate the impact of cold stress on root and nodule parameters and shoot growth. The remaining plants (n=10) were transferred to a greenhouse and grown till maturity to assess yield parameters. Cold stress delayed seed germination by 6 days and markedly reduced the nodule

number by 100%, shoot dry weight by 88%, root dry weight by 45%, root length by 83%, root surface area by 75%, and root volume by 64% at the 5-week-old stage compared to the plants grown at 15°C. Although plants appeared to partially recover from early season cold stress during the latter growth till maturity, significant reductions were observed in yield parameters compared to control plants, including shoot weight (by 36%), pod number (by 32%), pod weight (by 16%), seed number (by 18%), and seed weight (by 15%). The effect of early-season cold stress on symbiotic nitrogen fixation will be measured using the ^{15}N dilution method. Conducting further experiments with diverse cultivars, including cold-resistant cultivars, may lead to a more conclusive understanding.

[P110] ASSESSING COLD PLASMA'S POTENTIAL TO IMPROVE PEA (*Pisum sativum*) CROP GROWTH, PRODUCTIVITY, AND NITROGEN FIXATION UNDER CONTRASTING WATER AVAILABILITY. Dhanuja N. Abeysingha[1], M. S. Roopesh[1], Thomas D. Warkentin[2], and Malinda S. Thilakarathna[1]. [1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada T6G 2P5; and [2]Crop Development Centre, University of Saskatchewan, Saskatoon, SK, Canada S7N 5A8
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Expanding global food production to meet the needs of the increasing population while maintaining environmental sustainability is a pressing challenge. In this context, Cold Plasma (CP), a green and innovative technology, emerges as a potential solution. It has shown promise in enhancing crop productivity and stress resilience. Comprising a diverse blend of energized atoms, molecules, ions, and radicals, CP can alter the seed's physical properties and regulate gene expression, potentially resulting in sustained effects on crop growth and productivity. Our study aims to test the hypothesis that CP seed treatment can increase root nodulation, root and shoot growth, symbiotic nitrogen fixation, and seed yield in pea under varying water availability conditions. The pea seeds, both CP-treated (treatment using a dielectric barrier discharge unit at atmospheric pressure for 6 min.) and untreated (control), of the cultivar CDC Meadow were inoculated with *Rhizobium leguminosarum* bv. *viciae* (3841) and grown under controlled environmental conditions at 30% and 80% field capacity (FC) levels. The effect of CP on root parameters, nodule parameters, nitrogen fixation parameters, linear electron flow, and relative leaf chlorophyll content was evaluated at the 50% flowering stage (BBCH 65) (n=10). Furthermore, yield and nitrogen fixation parameters were assessed at the maturity stage (BBCH 97) (n=10). Under 80% FC level, plants derived from CP-treated seeds showed significant increases in root length (28%), root surface area (32%), root volume (38%), pod weight (41%), seed number (26%), seed weight (47%), seed total nitrogen content (69%), and total fixed nitrogen content (66%) compared to the plants derived from the untreated seeds. Drought stress substantially reduced all the tested parameters; however, the CP treatment did not ameliorate the stress effects. Overall, the findings indicate the potential of CP-seed treatment in enhancing plant growth, productivity, and seed quality in pea plants under well-watered conditions. Additional experiments are needed to validate the potential of this pioneering technology in agronomic applications.

***[P111] IDENTIFICATION OF QUANTITATIVE TRAIT LOCI FOR POD SHATTER TOLERANCE IN *BRASSICA NAPUS* L.** Lauren Gislason[1], Harmeet Singh Chawla[1], Robert H. Gulden[1], and Robert Duncan[1]. [1]Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB, Canada R3T 2N2
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Seed loss resulting from pre-harvest pod shatter is a significant threat to canola (*Brassica napus* L.) producers. Pod shatter is a quantitative trait, primarily genetically controlled, but highly influenced by environmental conditions, including hail, heat, humidity, precipitation, and wind. Pod shatter is of dual concern; economically, seed loss decreases yield, resulting in lost revenue; agronomically, dropped seeds become a competitive weed in future growing seasons. In the light of climate change and increasingly extreme weather events on the Canadian prairies, pod shatter tolerant canola hybrids are preferred to ensure sustainable crop production. The primary goal of this research project is to identify genomic regions and molecular markers using quantitative trait loci (QTL) analyses, aiming to help breeders select genotypes with improved pod shatter tolerance in *B. napus*. In this research, a doubled haploid (DH) population (SH1) consisting of 192 genotypes, was developed from a pod shatter-susceptible female (13R4497) and a pod shatter-tolerant male (13R3973). The population included the

pod shatter resistant commercial hybrid, as a control. Genotypes were replicated three times in a randomized complete block design at two Manitoba field sites in 2022 and 2023. Pod shatter tolerance was assessed using a rating scale of one (susceptible) to nine (tolerant), following an artificial high-speed wind event simulated with a leaf blower. Phenotypic variation for pod shatter tolerance was observed in the DH population at all field sites. The mean male parent tolerance ratings ranged from 3.73 to 6.93, mean female parent tolerance ratings ranged from 1.20 to 3.06 and mean DH genotype ratings ranged from 1.17 to 8.21. Genomic DNA was extracted from leaf samples using the Qiagen DNeasy® Plant Mini kit. Parental and DH genotypes were genotyped using the *Brassica* 90K Illumina Infinium™ SNP array. SNP marker data was used to construct a genetic linkage map anchored to the Darmor-bzh v.10 *B. napus* reference genome. ANOVA, conducted with PROC GLIMMIX in SAS v.9.4, identified genotype and genotype by environment interaction as statistically significant factors influencing phenotypic expression of pod shatter tolerance. The inclusive composite interval mapping (ICIM) method was applied in QTL IciMapping indicating 11 additive-effect QTL in the SH1 population, located on chromosomes A03, A05, A06, A09, C03, C04 and C09. The male allele was found to be increasing pod shatter tolerance in nine of the 11 QTL, explaining 4.93 to 17.00 % of phenotypic variation observed in the population.

[P112] UNVEILING FLAVOR DIVERSITY IN RICE GRAINS: VOLATILE ANALYSIS OF 137 CORE ACCESSIONS SELECTED FROM GLOBAL COLLECTION. Kanphassorn Wimonmuang[1] and Young-Sang Lee[1,2]. [1]Quality Control Institute for Agricultural Products, Soonchunhyang University, Asan 31538, Republic of Korea; and [2]Department of Medical Biotechnology, Soonchunhyang University, Asan 31538, Republic of Korea
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Rice flavor, a key determinant of both consumer preference and market value, arises from the complex interplay of volatile organic compounds (VOCs) within the grain. In this study, profiles of volatiles in brown rice among 137 accessions of a core set, heuristically selected from a worldwide collection of 10,368 accessions, were investigated using headspace solid phase microextraction (HS-SPME) coupled with gas chromatography-mass spectrometry (GC-MS). A total of 159 volatiles were identified, comprising 3 acids, 25 alcohols, 21 aldehydes, 8 bases, 23 esters, 4 ethers, 3 furans, 52 hydrocarbons, 17 ketones, and 3 phenols. Among these, 88 were categorized as odor-active volatiles with distinct odor descriptions, while 71 were odor-inactive. The five odor-active volatiles with the highest peak areas observed across all 137 rice accessions were butylated hydroxytoluene, nonanal, methyl salicylate, D-limonene, and 1-octanol. Conversely, eucalyptol and 2-methylbutanal were infrequently detected. Genetic variation among tested accessions, assessed through the relative standard deviation (RSD %) of peak area, identified benzothiazole as the highest variation (RSD 268%), while dibutyl phthalate as the lowest (RSD 18%). Partial least squares discriminant analysis (PLS-DA) revealed that volatile profiles may not effectively differentiate indica and japonica rice ecotypes, nor distinguish fragrant from non-fragrant rice accessions. All these results revealed qualitative and quantitative diversity of volatile flavor compounds in rice, offering valuable breeding information for developing superior flavor profiles.

[P113] LOW-COST PHOTOGRAMMETRY RIG FOR 3D CROP MODELLING AND PLANT PHENOMICS. Joe Hrzich[1], Christopher P. Bidinosti[1], Michael A. Beck[1], Christopher J. Henry[2], Kalhari Manawasinghe[3], and Karen Tanino[3]. [1]University of Winnipeg; [2]University of Manitoba; and [3]University of Saskatchewan
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Photogrammetry, the science of generating 3D models from 2D digital photographs, offers a comprehensive method for acquiring, studying, and analyzing detailed information about the structure of objects. Despite their utility, high-quality 3D scanners remain relatively expensive for many researchers and practitioners within the agricultural sector. In response, we have developed a low-cost, close-range photogrammetry rig, priced at $2,600 CAD, to support agronomists, plant scientists, and breeders. This work outlines the development of our device, which integrates a multi-camera system featuring the Arducam 64MP Autofocus Quad-Camera Kit, a rotary table from Ortery, and a Raspberry Pi for comprehensive control and processing.

Our scanner efficiently captures detailed 3D data, offering a valuable tool for non-destructive, automatic, and robust 3D phenotyping. It is possible to use our device across various applications, including growth

monitoring and the extraction of plant traits. Specifically, we have leveraged the device to measure the canopy volume of different wheat genotypes by computing the convex hull from the 3D point clouds. Furthermore, we have developed a high-throughput, quantitative trait index for wheat to identify distinct planophile and erectophile canopy architectures. We also plan to develop customized, plug-and-play systems tailored to the specific needs of researchers, which can be operated with minimal expertise.

***[P114] ASSESSING THE ROLE OF CANOPY ARCHITECTURE OF WHEAT (*Triticum aestivum* L.) FOR DROUGHT AND HEAT TOLERANCE.** Kalhari Manawasinghe[1] and Karen Tanino[1]. [1]Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada
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Wheat (*Triticum aestivum* L.) is one of the key staple crops worldwide. Even though future demand for wheat is estimated to increase by 60% by 2050, wheat production might drop by 29% due to climate change since it impacts soil water availability and ambient air temperature, which leads to stress on the plants. Canopy architecture influences yield, and erect canopies produce a higher yield than planophile plants. The purpose of this research is to identify how different canopy architectures and their significant traits improve yield stability under high temperature and drought stress conditions. This research was conducted in a new unique system of 12 field-established, environmentally controlled high tunnels (30 ft x 50 ft each) with a randomized complete block experimental design. Five selected wheat genotypes were grown in each tunnel. Plants were exposed to four treatments, including control (ambient air temperature with 90% field capacity), drought (ambient air temperature with 30% field capacity), heat (ambient air temperature +12 °C with 90% field capacity), and combined drought and heat stress (ambient air temperature +12 °C with 30% field capacity) at the heading stage. Canopy architecture was graded according to the visual UPOV scoring scale, and grain yield was obtained at the end of the growing period. Promising physiological traits related to different canopy architectures under stress will be presented. This represents the first step towards developing drought- and heat-tolerant crops of high yield that will be beneficial not only to crop producers but also to wheat breeding programmes and the consumer.

[P115] PERFORMANCE OF SOYBEAN-BASED ROTATIONS IN MANITOBA. Ramona Mohr[1], Yong Min Kim[1], Mohammad Khakbazan[1], Debbie McLaren (ret'd)[1], and Byron Irvine (ret'd)[1]. [1]Brandon Research and Development Centre, Agriculture and Agri-Food Canada, Box 1000a RR#3, Brandon, MB, Canada, R7A 5Y3
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Soybeans have become an integral part of Manitoba crop rotations over the past 15 years. Traditionally grown on a limited acreage, soybean production has expanded rapidly with the introduction of better-adapted cultivars. From 50,000 acres in 2001, Manitoba's annual soybean acreage has increased to between one and two million acres since 2013, making soybean one of the most widely grown crops in Manitoba along with wheat and canola. As a result of this rapid expansion, research regarding the longer-term effects of including soybean in rotation is limited for this region. In order to determine the relative productivity of soybean-containing rotations, a randomized, replicated field study consisting of five rotations (soybean-canola; soybean-wheat; soybean-wheat-canola; soybean canola-wheat; soybean-soybean-wheat) was established on a Newdale clay loam north of Brandon, Manitoba in 2014, with each phase of each rotation present in each year. Effects of rotation on crop yield and quality were determined for all crops on an annual basis from 2016 through 2021, which represented three cycles of the 2-year rotations and two cycles of the 3-year rotations; 2014 and 2015 were considered stubble establishment years. Conditions varied markedly over this period with growing season precipitation ranging from 60% to 160% of the long-term average. While rotation influenced soybean yield in 4 of 6 years during this period, no single rotation consistently outyielded the others, although lower yields were associated with the stacked rotation of soybean-soybean-wheat in some cases. Over this same period, rotation had no effect on wheat yield and limited effects on canola yield. Higher seed protein was evident in wheat or canola that followed soybean in rotation in select cases; however, rotation had limited effects on test weight and seed size for all crops. Although findings to date suggest that some differences are beginning to emerge

among rotations, additional rotation cycles are required to identify and confirm trends as effects of rotation often occur slowly over time with changes in the plant-soil system.

[P116] EVALUATION OF COVER CROP OPTIONS FOR POTATO CROPS IN MANITOBA. Oscar Molina[1], Steve Sager[1], Layton Dyck[1], and Meagan Gould[1]. [1]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB, Canada R6M 1Y5
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Nature based climate-smart crop production solutions, particularly cover crops, are getting lot of interest among potato growers who are looking for ways to improve soil health, management of soil-borne pathogens and carbon sequestration. In short-season growing regions like the Canadian Prairies, selecting the most suitable cover crop is an important step in the adoption process. However, adoption of cover crop is limited due to the short growing season, arid and cold climates and lack of experience with cover crops in potato systems. In this 3 year crop rotation study, we evaluated the effect of two cover crops annual mix and mustard, and three shoulder cover crops fall rye, red clover and the mix peas/oats on potato yield, plant and soil health. Preliminary results indicated that the limited precipitation reduced the ability of cover crops to produce sufficient biomass to provide the ecological benefits and opportunities for adoption in potato systems.

***[P117] INVESTIGATION ON MULTIPLE HERBICIDE RESISTANCE TO PHOTOSYSTEM II AND HPPD INHIBITORS IN REDROOT PIGWEED (*AMARANTHUS RETROFLEXUS* L.).** Isabelle Aicklen, François Tardif, and Malavika Nair. Department of Plant Agriculture, University of Guelph, Crop Science Building, University of Guelph, Ontario, Canada N1G 2W1
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The increased and constant use of herbicides for weed management is a strong selection pressure for herbicide resistance. Globally, there are 530 unique cases of herbicide resistance in 272 species. Pigweed species (*Amaranthus* spp.) have shown an extraordinary ability to evolve resistance to herbicide from groups 2, 5, 6 and 14 among others. Herbicides inhibiting 4-hydroxyphenylpyruvate dioxygenase (HPPD, group 27) are often seen as the last resort to control multiple herbicide resistant pigweeds. In 2022, an *Amaranthus retroflexus* L. (redroot pigweed) population from Chatham, Ontario survived field applications of HPPD and photosystem II (PS II) (groups 5 and 6) inhibiting herbicides. Our objective was to confirm resistance and determine the pattern of multiple resistance in this suspected resistant (R) redroot pigweed population. Greenhouse screening confirmed resistance to PS II and HPPD inhibitors but not to acetolactate synthase inhibitors (group 2). The application of atrazine (group 5) at a discriminating rate of 1000 g a.i. ha^{-1} led to 100 % survival and limited biomass reduction in R, while it completely killed a reference susceptible (S) population. Dose-response experiments assessed differences in survival and biomass accumulation between R and S populations when treated with bromoxynil (group 6), topramezone, and mesotrione (group 27). Analysis of the dose-response curves for biomass and survival showed that R has 2.8-fold resistance to bromoxynil and 1.8-fold resistance to mesotrione, but appeared to be susceptible to topramezone. This is the first report of group 27 resistance in redroot pigweed in Canada. Multiple resistance to groups 5, 6 and 27 severely limits the options available to growers to manage this species.

[P118] MAPPING OF A MAJOR PRE-HARVEST SPROUTING RESISTANCE QUANTITATIVE TRAIT LOCI IN WHEAT. Raman Dhariwal[1], Simranjeet Kaur[1], Gagandeep Kaur Brar[1], Purnima Kandpal[3], Colin Hiebert[2], Jaswinder Singh[3], and Harpinder S. Randhawa[1]. [1]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1st Avenue South, Lethbridge, Alberta, Canada T1J 4B1; [2]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, Manitoba, Canada R6M 1Y5; and [3]Department of Plant Science, McGill University, Ste-Anne-de-Bellevue, QC Canada H9X 3V9
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Pre-harvest sprouting (PHS) poses a significant challenge to wheat production, leading to yield loss, reduced quality, and diminished seed viability. In Canada alone, PHS costs approximately $100 million annually to spring wheat production. Despite the recognized importance of developing PHS-resistant cultivars, progress in breeding PHS-resistant wheat has been impeded by the lack of suitable molecular

markers. To address this, we utilized a doubled haploid mapping population (N=184) derived from crossing PHS-susceptible cv Sadash with a PHS-resistant spring wheat germplasm line P2711. Phenotyping of the population for PHS in 2022 and 2023, and genotyping using a 15K SNP chip followed by quantitative trait loci (QTL) mapping revealed a major PHS resistance QTL on wheat chromosome 4A. This QTL explains up to 27% phenotypic variation (LOD = 12.0). The results of this study will be discussed.

[P119] DEVELOPMENT OF A BREEDER-FRIENDLY MOLECULAR MARKER FOR REDUCED DEOXYNIVALENOL CONTENT IN WHEAT. Raman Dhariwal[1], Maria A. Henriquez[2], Colin Hiebert[2], and Harpinder S. Randhawa[1]. [1]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1st Avenue South, Lethbridge, Alberta, Canada T1J 4B1; and [2]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, Manitoba, Canada R6M 1Y5
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Fusarium head blight (FHB), primarily caused by Fusarium graminearum, poses a significant threat to wheat production, leading to yield and quality losses. Developing FHB-resistant cultivars is crucial for managing FHB and minimizing economic losses. While type-II resistance QTL and their markers have been identified, markers for deoxynivalenol (DON) resistance, a type-III resistance are yet to be developed in wheat. Recently, we identified a major type-III resistance QTL, QDon.lrdc-2D from FHB-resistant wheat cultivar AAC Tenacious. QDon.lrdc-2D explains up to 34.5 % of phenotypic variation for DON content and co-localizes with loci controlling FHB disease incidence, severity, visual rating index, fusarium damaged kernels, and increased total number of spikelets but no any other traits such as days to anthesis, plant height, etc. Our analysis showed that the AAC Tenacious-type allele at QDon.lrdc-2D region had 43.9% lower DON content than the susceptible parent (AAC Innova) allele ($P < 0.05$). Thus, to utilize this QTL in breeding wheat, we developed a tightly lined KASP molecular marker, KASP-G7295A, from this locus and validated it in diverse cultivars. This KASP marker holds significant promise for facilitating the selection of FHB resistance in wheat breeding programs. The results of this study will be discussed.

***[P120] CHELATE ASSISTED PHYTOEXTRACTION OF MULTI-METAL(LOID) CONTAMINATED SOILS USING INDIAN MUSTARD.** Ruchini Sovis[1], Nora Casson[2], and Srimathie Indraratne[3]. [1]Department of Biology, University of Winnipeg, Winnipeg, Manitoba, R3B 2E9, Canada; [2]Department of Geography, The University of Winnipeg, Winnipeg, Manitoba, R3B 2E9, Canada; and [3]Department of Environmental Studies and Sciences, The University of Winnipeg, Winnipeg, Manitoba, R3B 2E9, Canada
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Phytoextraction is an environmentally friendly remediation method that uses plants to extract metal(loid)s from soil and accumulate them in harvestable plant parts. Indian mustard (*Brassica juncea* L.) was identified as an effective candidate for phytoextraction due to its high biomass production, rapid growth rates, and tolerance to high metal(loid) levels in soils. The use of chelators enhances the phytoextraction potential of plants by forming chelate-metal complexes and increasing the metal(loid) bioavailability. Despite the proven effectiveness of the synthetic chelator Ethylenediaminetetraacetate (EDTA) in remediating metal(loid)-contaminated soils, its significant drawbacks make it unsuitable for field application. As an alternative, natural organic acids such as citric acid (CA) and oxalic acid (OA) can be used in phytoextraction. However, studies testing the success of CA and OA compared to EDTA are limited, and a knowledge gap exists in the combined application of these chelators for phytoextraction of multi-metal(loid) contaminated soils. The objective of the study was to evaluate the phytoextraction effectiveness of EDTA, CA, and OA chelators alone or in combination in multi-metal(loid) contaminated (As, arsenic; Cd, cadmium; Cu, copper; Pb, lead; Ni, nickel; and Zn, zinc) acidic soils using Indian mustard as the hyper-accumulator. A greenhouse pot experiment was conducted for 10 weeks, applying six treatments with three replicates as control (contaminated soil), soil amended with EDTA, CA, OA, and combinations of EDTA with CA, and EDTA with OA. Chelators were applied twice at monthly intervals, and plants were harvested 10 days after the second application. Pore water was collected three times: initially, 10 days after the addition of the first round of chelators, and at the end of the greenhouse experiment. After harvesting, plant growth parameters (biomass, height) were recorded, and plant

chlorophyll and enzyme activity will be analyzed. The metal(loid)s and nutrients of pore water samples, harvested plants, and soil were measured using inductively coupled plasma-atomic emission spectroscopy (ICP-AES). EDTA treatment alone or in combination significantly affected plant biomass and height, leading to rapid senescence within a few days of application and demonstrating toxicity symptoms of leaf necrosis and chlorosis. Conversely, CA and OA treatments showed minimal impact on plant growth. Sole or combined applications of EDTA increased the bioavailability of metal(loid)s (Cu, Cd, Ni, Zn, As, Pb) to toxic levels for Indian mustard. Although OA application showed the greatest increase in Pb bioavailability, application of natural chelators alone exhibited limited phytoextraction potential in acidic multi-metal(loid) contaminated soils using Indian mustard.

***[P121] KEY FACTORS AFFECTING THE WINTER SURVIVAL OF FALL-DORMANT-SEEDED SPRING CROPS: SEED CHARACTERISTICS AND WATER UPTAKE.** Prerana Upretee[1], Manjula Bandara[2], and Karen K. Tanino[1]. [1]Department of Plant Sciences, University of Saskatchewan, Saskatoon, S7N 5A8, Canada; and [2]MCB Agric-Research Consulting,106-204 17th Street E, Brooks, Alberta, T1R 1R1, Canada
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In 2023, spring field crops across the Canadian prairies were seeded to 53.85 million hectares [1], with a 7.5% decrease in the total production compared to 2022, due primarily to adverse growing conditions [2]. One proposed strategy to recover yield loss is the implementation of fall-dormant-seeding (seeding in late October), which offers prominent benefits over spring seeding, such as early crop maturity, increased grain yield, reduced frost-damage risk, and increased seed oil concentration [3]. However, this seeding practice was not adopted by producers due to the failure of the crop establishment the following spring. This study, therefore, aimed to identify the key factors affecting the loss of freezing tolerance of seeds. Experiments were designed and conducted under different growing conditions, considering lentil as a model plant due to its inherant variation in physical characteristics of the seed, such as cotyledon color, seed coat color, seed size (TSW), seed surface area and seed volume. Thirty-eight lentil cultvars/lines, as well as five spring wheat cultivars, eight field pea cultivars, five canola culivars, one cultivar from each brown and yellow mustards, five carinata mustard lines and three coriandar cultivar/lines were included. Water uptake rate and amount, germination rate and percentage of the seeds of these crops were assessed under cool (+2^{O}C), and ambient temperatures. The amount of water absorption had a significant positive linear relationship with TSW for all crop species, except for spring wheat. Thus far we found that the amount of water uptake into lentil seeds was positively and linearly related with seed surface area and volume. However, additional factors are being investigated. Furthermore, tests were conducted to determine the freezing tolerance of imbibed lentils, field peas, wheat and canola seeds (LT_{50} and LD_{50}). While the link between water uptake and freezing tolerance maybe simply related to seed surface area and volume in lentil, this aspect is not universal across all crops and we are further investigating how water uptake is regulated at the anatomical, biochemical and physiological levels to understand why some high water uptake seeds are still freezing tolerant. The potential answers to these questions are being addressed through characterization of the testa and seed biochemical properties, seed priming with ABA and GA_3 as well as an examination of the pathway of water into the seed.

[P122] THE ORANGE BLOSSOM WHEAT MIDGE IN WESTERN CANADIAN GRAIN. Tiffany Chin[1], Kerri Pleskach[1], Tyler Wist[2], Curt McCartney[3], Alejandro Costamagna[3], Bin Xiao Fu[1], Janice Bamforth[1], Niradha Withana Gamage[1], Tehreem Ashfaq[1], Mayantha Shimosh Kurera[1,3], and Sean Walkowiak[1,3]. [1]Canadian Grain Commission, Winnipeg, MB, R3C 3G8, Canada; [2]Agriculture and Agri-food Canada, Saskatoon, SK, S7N 0X2, Canada; and [3]University of Manitoba, Winnipeg, MB, R3T 2N2, Canada
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The orange blossom wheat midge, *Sitodiplosis mosellana* (Géhin) (Diptera: Cecidomyiidae), is a pest of wheat in North America. Infestation by midge reduces wheat yield, quality, and grade, and outbreaks can result in significant economic loss. Cultivars that carry the *Sm1* gene produce phenolic acids in response to midge-larval feeding on the developing kernel which are unpalatable to larvae. Single-gene resistance such as *Sm1* have a high possibility of resistance breakdown and loss of this trait. Additionally, whether *Sm1* reduces midge damaged kernels (MDK) on production scale farms and if any resistance breakdown occurred has not been comprehensively examined across different cultivars, environments, and years. In this study, we report annual and regional trends of midge incidence and severity in western Canada using

Harvest Sample Program (HSP) data from 1995-2023 for Canadian Western Red Spring (CWRS) and Canadian Western Amber Durum (CWAD). We also examine midge damage to cultivars that carry and do not carry *Sm1* for CWRS and CWAD. Overall, MDK in Canada showed periodic spikes in midge incidence and severity for CWAD and CWRS across the western provinces, with CWAD having higher midge incidence compared to CWRS, with a peak in midge incidence in 2012. In contrast, CWRS had higher MDK severity compared to CWAD, with Saskatchewan having a peak in MDK severity during 2007. As midge damage is considered a grading factor in Canada, the need to mitigate the effects of midge damage is essential for sustaining crop quality. In the case of CWRS and CWAD, there are years of low midge severity, with many samples categorized as Grade 1, and instances for a grade downgrade occur during spikes of midge incidence. For CWRS cultivars carrying *Sm1*, there is a reduction in midge damage compared to non-*Sm1* cultivars, and this pattern is consistent across regions and years ($p < 0.05$; one-way ANOVA). However, for CWAD, there is a similar level of midge damage on *Sm1* and non-*Sm1* cultivars across all cultivars irrespective of years and regions ($p > 0.05$; one-way ANOVA). Together, our results indicate that *Sm1* is an effective control mechanism for midge in CWRS, more so than CWAD. The study also highlights the value of continuous datasets in monitoring of grain quality factors, such as the HSP data. Further research could examine the affects of midge on grain quality as well as model midge damage in wheat as a tool for predicting and mitigating disease.

[P123] HYPERSPECTRAL IMAGING TO DETECT CLUBROOT IN COMMERCIAL CANOLA FIELDS.
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The objective of this research was to determine if small patches of clubroot (*Plasmodium brassicae* Wor.), an economically important disease of canola (*Brassica napus* L.), could be detected from the air using a drone mounted hyperspectral camera. Early detection, before the disease is permitted to spread, would be of economic value to producers, but clubroot symptoms don't generally develop until after the onset of flowering when detailed scouting is difficult. In 2021, 12 canola fields were imaged during the early flowering stage across northern Alberta using a DJI M600 remotely piloted aircraft system (RPAS) outfitted with a Headwall nano-hyperspec camera. This research-grade camera captures 270 spectral bands ranging from 399 to 1000 nm wavelengths. Two additional fields were captured under similar circumstances in northern Alberta in 2022, and 7 more fields were sampled across northern Saskatchewan in 2023. Each RPAS mission included an imaged area of 1–2 ha and all data was calibrated using a reflectance tarp included within the scene. Follow-up ground surveys were conducted after swathing by plant pathologists on each sampled field. A disease severity index was used to assess the extent of clubroot infestation using 10 randomly selected plants in at least 20 spots within the heart of the area judged most likely to be infected. Research fields proved to be especially valuable since the co-operators were often willing to share disease severity indices for imaged areas. Supervised classification was used to differentiate the spectral signatures of clubroot infected and non-infected areas. Principal component analysis in combination with logistic regression and quadratic discriminant analysis provided variable results. Subsequent analysis using predictive analytics and machine learning helped reinforce earlier detected trends while providing additional data insights. Stochastic gradient boosting offered the most consistent and reliable results, outperforming binary logistic regression, classification and regression trees, and random forests with misclassification rates among test data less than 5%.

***[P124] ADOPTION OF IP-FREE GENE EDITING SYSTEM IN WHEAT.**
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Gene editing technologies have revolutionized plant breeding and crop improvement by offering precise and predictable genetic modifications. The CRISPR (Clustered Regularly Interspaced Short Palindromic

Repeats) gene editing systems, such as CRISPR/Cas9 and CRISPR/Cas12a, are widely used for gene editing in plants. In 2017, a biotechnology company named Inscripta released the MAD7 nuclease, a Cas12a-like nuclease enzyme, freely available as a royalty-free tool for both academic and commercial use, eliminating licensing constraints or royalty payments and enabling users to capitalize on their results. The novel MAD7 was discovered in the Eubacterium rectale bacteria found in the human gut microbiome of rural Madagascar resident.

The project utilized the CRISPR/MAD7 gene editing system in the spring wheat cultivar 'Fielder', with a primary focus on drawing conclusions regarding its editing efficiency using different Crispr-RNAs (crRNAs) with distinct Protospacer Adjacent Motifs (PAM) sequence recognition, targeting the same gene. MAD7 nuclease recognizes T-rich PAM sequence (YTTN, where Y = T or C, N = A, C, or G). Additionally, we will explore the impact of Matrix Attachment Regions (MARs, Tobacco RB7 MAR) on the transgene expression in wheat. MARs are unique regulatory DNA sequences, 100 – 3000 bp AT-rich fragments, which can bind to the nuclear matrix. The research goal is to mutate the lycopene ε-CYC gene to redirect the carotenoid pathway towards the accumulation of β-carotene in wheat. We employed the GoldenBraid cloning system for constructing MAD7 plasmids and used Agrobacterium-mediated transformation, followed by tissue culture and putative transgenic plants cultivation under controlled conditions. So far, genomic DNA extraction and PCR confirmed the presence of the MAD7 transgene in 35 out of 57 putative T0 transgenic plants.

Further assessment involved qPCR and Cleaved Amplified Polymorphic Sequence (CAPS) assay to confirm edits at the target regions. Notably, crRNA (lab# AB341) demonstrated promising results, with 25 out of 30 positive transgenic plants exhibiting edits confirmed by CAPS assay. These samples will be re-verified by Long-Read Sequencing. The transgene copy number was measured using digital droplet PCR, with 8 out of 25 having a low transgene copy number (<5). Conversely, qPCR analysis of samples with crRNA (lab# AB339) did not reveal evident mutations, which was confirmed by Illumina Next Generation Sequencing. Overall, we aim to use different crRNAs and incorporate specific MARs with the CRISPR/MAD7 system to enhance gene editing efficiency in wheat.

[P125] IDENTIFICATION OF QTLS FOR PREHARVEST SPROUTING RESISTANCE IN SPRING WHEAT (*TRITICUM AESTIVUM* L.). Ramanpreet Ramanpreet[1], Gurkamal Kaur[1], Muhammad Iqbal[2], Curt A. McCartney[1], Dean Spaner[2], and Belay T. Ayele[1]. [1]Department of Plant Science, University of Manitoba, Winnipeg, Canada; and [2]Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton Canada
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Wheat grain quality is significantly affected by pre-harvest sprouting (PHS), which refers to the germination of seeds on the mother plant due to the occurrence of wet and humid conditions prior to harvest. PHS is primarily controlled by seed dormancy, an adaptive trait that blocks the germination of seeds under optimal environmental conditions. Thus, a low level of seed dormancy leads to increased susceptibility to PHS. Given that PHS and seed dormancy are polygenic traits governed by multiple genes, identifying specific genomic regions related to these traits holds significant promise in addressing the problem of PHS in wheat. Therefore, the objective of this study was to identify QTLs and genetic markers regulating PHS and seed dormancy through genome-wide association analyses of a mapping panel that consists of diverse wheat genotypes grown over five different environments. Mature seeds of the association mapping panel were characterized for their germination index (GI), which exhibited significant variation in seed dormancy levels among the genotypes. Genotyping of the mapping panel was performed using a 90k Illumina iSelect SNP array. Mixed linear model (MLM_Q+K) identified 14 significant markers located on chromosomes 4A, 5B and 5D. These significant markers explained phenotypic variations ranging from 10.22% to 20.82%. A total of three QTLs associated with the 14 significant SNPs were detected on those chromosomes. The loci and markers identified to be associated with seed dormancy could be used for the development of wheat cultivars with enhanced resistance to PHS.

[P126] DISCOVERY OF YIELD QTL IN CANADIAN SPRING WHEAT. Santosh Kumar[1], Jasdeep Kaur[1], Clare Workman[1], and Kirby Nilsen[1]. [1]Brandon Research and Development Centre, Agriculture and Agri-Food Canada, 2701 Grand Valley Road, Brandon, MB, Canada, R7A 5Y3
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The northern Prairie region of Canada has a shorter growing season, which impedes the yield potential due to insufficient growing degree days. Yield is the most important factor in the farm scale adoption and profitability of a new variety. Among yield contributing factors, days to maturity and yield are negatively corelated. To understand the yield contributing factors, a doubled haploid population was developed from a cross between AAC Wheatland (mid-season) and breeding line PT485 (early maturing). Both AAC Wheatland and PT485 are semi-dwarf premium quality wheat varieties but differ in AAC Wheatland being Orange Blossom Wheat Midge tolerant, which provides yield advantage. The DH population was grown as yield plots at Brandon, MB and Saskatoon, SK. The data on yield components (height, maturity, yield, test weight and thousand kernel weight) were recorded. Genotyping was performed on the mapping population using Affymetrix 25K SNP Chip through SGS North America. The linkage map was constructed using MSTmap resulting in 36 linkage groups using 4552 polymorphic loci. The QTL analysis was performed on Qgene software. A yield QTL was detected in both environments on chromosome 7. The closest SNPs AX-158544327 and TGWA25K-TG0227 are at 7.1 cM and 1 cM from the QTL peak respectively suggesting close linkage. The poster will describe the potential QTL for yield and the underlying genomic loci with genes of interest.

[P127] MAGNETIC BEAD BASED PLASMID ISOLATION PROTOCOL FOR HIGH-YIELD SEQUENCING GRADE PLASMID DNA. Ankita Talla, Sneha Thakur, Lalitha S., Vishal Mane, Radha Hariharan, Sujata Hajra, Kavita Khadke, and Rajas Warke. HiMedia Laboratories Pvt. Ltd.
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The recombinant DNA technology has demonstrated unique impacts in bringing advancement in human life. This technology has various applications and potential to deal with important aspects of life, for instance, improving health, enhancing food resources, and resistance to various environmental effects. Particularly in agriculture, the genetically modified plants have increased resistance to harmful agents, enhanced product yield, and shown increased adaptability for better survival.

The basic steps of molecular cloning includes vector digestion, insert preparation, ligation, transformation and Clone selection. Hence, Plasmid vectors and clones with high yield and good purity are always in high demand. In HiMedia, we have indigenously developed one automated magnetic bead-based system which consistently isolates recombinant plasmids having high yield and purity.

This study signifies using Insta NX® Automated extraction platform for plasmid DNA extraction from small volume of cultures. HiPurA® Pre- filled Cartridges for Plasmid DNA Extraction MB508PC16 along with Insta NX® Mag16^{Plus} provides the fastest and easiest way to purify plasmids of varying size under affordable cost and less time. This extraction method is found to be most efficient and suitable for applications in PCR, library screening, sequencing, etc. The DNA purification procedure comprises of three steps viz. adsorption of DNA to the magnetic beads, removal of residual contaminants and elution of pure plasmid DNA. HiMedia's Insta NX® Mag16^{Plus} can be used for processing small amount of samples volumes (from 500µl to 5ml) for plasmid DNA extraction. An average yield upto 50ng/µl and purity (A_{260}/ A_{280}) in range of 1.7-1.9 is achieved by MB508PC16 - HiPurA® Pre- filled Cartridges for Plasmid DNA Extraction kits.

The number of steps involved in manual plasmid DNA extraction are minimized with the help HiMedia's Magnetic Automated extractor and HiPurA® Pre-filled kits. The HiPurA® Pre- filled Cartridges for Plasmid DNA Extraction kit provide a high quality and quantity of plasmid DNA required for Recombinant Protein expression, PCR analysis, Library preparation followed by Sequencing and other downstream molecular applications.

[P128] ESTABLISHING A NOVEL, AUTOMATED, MAGNETIC BEAD-BASED METHOD FOR EXTRACTION OF SEQUENCING GRADE NUCLEIC ACID FROM DIFFERENT PLANT SAMPLES.
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Extraction of Nucleic acid from plant sample is essential for molecular biology, in identifying, isolating, and extracting the desired gene to replicate in successive generations of plants. It is a crucial pre-analytic step in the development and performance of any successful molecular diagnostic method and ensures reliable result. Molecular techniques are mainly based on PCR assays, therefore a good quality of DNA and RNA is prerequisite for any tools to be used. A variety of Nucleic acid extraction methods and kits are available, however they are costly, low yield, and time consuming. The present study shows a Novel, Automated, Magnetic bead-based platform and reagents for efficient extraction of Plant Nucleic Acid (DNA & RNA) from different plant samples like Maize, Soyabean, Wheat, Tomato, Pigeon pea, Chick pea, Tobacco, Mustard, Potato, Spinach, Scallions, Millets etc.

Hi-Media's HiPurA® pre-filled cartridge-based extraction kits, MB507PC16 & MB571PC16 for DNA extraction and MB603PC16 for RNA extraction along with the Automated Magnetic extraction system, Insta NX® Mag16^{Plus} is found to be the most efficient nucleic acid extraction method, capable to provide high yields with better quality, affordable cost and less time. The extracted high-quality nucleic acid is suitable for PCR assays, library preparation followed by sequencing. We have recorded an average yield of upto 100 ng/µl and purity (A_{260}/ A_{280}) in range of 1.7-1.9 for the extracted DNA and for RNA upto 500ng/µl of yield and purity (A_{260}/A_{280}) in range of 2.0-2.2. As compared to competitor kit used, the data was found to be better than competitor.

Overall, Insta NX® Mag16^{Plus} Automated extractor along with the pre-filled kits will be advantageous for researchers working in this field. Using minimum amount of starting material (upto 200mg), good PCR amplifiable, Sequencing Grade DNA can be extracted which can help in further downstream assays.

[P129] LACCASE GHLAC14-3 REGULATES CELL WALL DEFENSE TO CONFER RESISTANCE AGAINST VERTICILLIUM WILT BY INTERACTING WITH GHMAPKKK2 IN COTTON.
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Verticillium wilt (VW), caused mainly by *Verticillium dahliae*, is one of the most important diseases of cotton. Lignification of the cell wall, triggered by pathogen invasion, is an inherent defensive mechanism. Laccases in plants are recognized for their function in lignifying secondary cell walls. However, their role in cotton resistance to *V. dahliae* remains unclear. In our previous study, numerous differentially expressed genes (DEGs) were identified in the transcriptome and metabolome of *Arabidopsis thaliana* infected with *V. dahliae*. In the present study, we successfully characterized a laccase GhLAC14-3 and identified it as a positive regulator associated with cotton resistance against *V. dahliae*. The expression of *GhLAC14-3* in cotton plants, significantly elevated at the early stage of *V. dahliae* invasion, was transiently silenced, accompanied by a higher disease index, a reduction in lignin content, and the expression of lignin-related genes, thereby obviously enhancing the VW susceptibility. In contrast, ectopic expression of *GhLAC14-3* in *Arabidopsis* conferred enhanced resistance to VW. The interaction between GhLAC14-3 and GhMAPKKK2, a mitogen-activated protein kinase, was further determined in the cell membrane using a yeast-two-hybrid screen and the bimolecular fluorescent complementation. GhMAPKKK2 expression was significantly induced by *V. dahliae*, and its constitutive expression enhanced the resistance of *Arabidopsis.* These results demonstrate that GhLAC14-3 interacted with GhMAPKKK2 in the plant membrane, modulates cell wall defense, and contributes to cotton resistance against *V. dahliae,* suggesting its potential applications in molecular breeding programs designed to enhance VW resistance.

[P130] OPTIMIZATION OF A RAPID, SENSITIVE AND HIGH THROUGHPUT ASSAY TO MEASURE CANOLA PROTOPLAST RESPIRATORY METABOLISM AS A MEANS OF SCREENING NANOMATERIAL CYTOTOXICITY. Zhila Osmani[1,2], Muhammad Amirul Islam[2], Feng Wang[2], and Marianna Kulka[1,2]. [1]Faculty of Medicine, University of Alberta, Edmonton, Alberta, Canada; and [2]Quantum and Nanotechnologies Research Centre, National Research Council Canada, Edmonton, Alberta, Canada
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Introduction:
Plant genetic engineering using nanomaterials is a versatile method of developing new cultivars for food production. However, a key challenge is that many nanomaterials are reactive and toxic to cells at concentrations needed for efficient transformation. Protoplasts, plant cells lacking a cell wall, are often used in nanomaterial-mediated genetic engineering but due to their fragility, protoplasts are particularly sensitive to nanomaterial treatment. Therefore, it is necessary to utilize a rapid, sensitive, and high throughput method to measure the cytotoxicity of various nanomaterials on protoplasts. Conventional methods of measuring protoplast viability are technically challenging, require specialized instrumentation and are labour intensive. We have developed a rapid, cost-effective and high throughput assay to measure respiratory metabolism of protoplasts using the reduction of resazurin, a non-toxic dye that is converted to highly fluorescent resorufin during cell respiration. Although resazurin has been used extensively to study cell viability in mammalian cells, its applicability to protoplasts has not been tested.

Methods and Results:
Initial optimization revealed that both glucose and mannitol directly reduce resazurin, and thus W5 buffer lacking glucose was chosen as the ideal buffer for this assay. Next, we determined whether protoplasts could reduce resazurin as a sign of their metabolic activity. We isolated protoplasts from hypocotyl canola (*Brassica napus* L.) using cellulase (15 mg/ml) and macerozyme (6 mg/ml) for 16 h at 22 ^{o}C. We incubated healthy protoplasts with resazurin at different cell densities, for varying times and at different temperatures and determined that the most sensitive parameters for the detection of protoplast viability occurred when 20,000 cells were incubated with 40 uM of resazurin at room temperature for 3 hours. Next, we determined the applicability of our assay to nanomaterial cytotoxicity measurement. We incubated protoplasts with silver nanospheres, silica nanospheres, a cholesteryl-butyrate nanoemulsion, and lipid nanoparticles and measured protoplast viability using our optimized resazurin protocol. Silver and silica nanospheres had no effect on protoplast viability even at the highest concentration of 500 ng/µl. However, the cholesteryl-butyrate nanoemulsion and lipid nanoparticles were toxic to the protoplasts at 500 ng/µl.

Conclusions:
In conclusion, the resazurin assay offers a precise, rapid, and high throughput method for assessing canola protoplast viability, enabling more accurate analysis of nanomaterial effects on protoplasts. The versatility of this approach and its scalability make it a valuable tool for nanomaterial cytotoxicity screening prior to the use of nanomaterials for genetic engineering of protoplasts.

[P131] DEVELOPMENT OF A MOBILE, HIGH-THROUGHPUT, AND LOW-COST IMAGE-BASED PLANT GROWTH PHENOTYPING SYSTEM. Li'ang Yu[1], Hayley Sussman[1], Olga Khmelnitsky[1], Maryam Rahmati Ishka[1], Aparna Srinivasan[1], Andrew D L Nelson[1], and Magdalena M Julkowska[1]. [1]Boyce Thompson Institute, Cornell University, Ithaca, NY 14850, USA
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Nondestructive plant phenotyping forms a key technique for unraveling molecular processes underlying plant development and response to the environment. While the emergence of high-throughput phenotyping facilities can further our understanding of plant development and stress responses, their high costs greatly hinder scientific progress. To democratize high-throughput plant phenotyping, we developed sets of low-cost image- and weight-based devices to monitor plant shoot growth and evapotranspiration. We paired these devices to a suite of computational pipelines for integrated and straightforward data analysis. The developed tools were validated for their suitability for large genetic screens by evaluating a cowpea (Vigna unguiculata) diversity panel for responses to drought stress. The observed natural

variation was used as an input for a genome-wide association study, from which we identified nine genetic loci that might contribute to cowpea drought resilience during early vegetative development. The homologs of the candidate genes were identified in Arabidopsis (Arabidopsis thaliana) and subsequently evaluated for their involvement in drought stress by using available T-DNA insertion mutant lines. These results demonstrate the varied applicability of this low-cost phenotyping system. In the future, we foresee these setups facilitating the identification of genetic components of growth, plant architecture, and stress tolerance across a wide variety of plant species.

[P132] REGULATION OF A SINGLE INOSITOL 1-PHOSPHATE SYNTHASE HOMOLOGY BY HSFA6B CONTRIBUTES TO FIBER YIELD MAINTENANCE UNDER DROUGHT CONDITIONS IN UPLAND COTTON. Li'ang Yu[1], Anna C. Nelson Dittrich[1], Xiaodan Zhang[1], Venkatesh P. Thirumalaikumar[1,5], Giovanni Melandri[2], Aleksandra Skirycz[1], Kelly R. Thorp[3], Lori Hinze[4], Duke Pauli[2,6], and Andrew D.L. Nelson[1]. [1]Boyce Thompson Institute, Cornell University, Ithaca, NY 14850, USA; [2]School of Plant Sciences, University of Arizona, Tucson, AZ 85721, USA; [3]United States Department of Agriculture-Agricultural Research Service, Arid Land Agricultural Research Center, Maricopa, AZ 85138, USA; [4]United States Department of Agriculture-Agricultural Research Service, Southern Plains Agricultural Research Center, College Station, TX 77845, USA; [5]Current address: Purdue Proteomics Facility, Bindley biosciences, Purdue University, West Lafayette, IN, 47907, USA; and [6]Agroecosystem Research in the Desert (ARID), University of Arizona, Tucson, AZ 85721
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Drought stress substantially impacts crop physiology resulting in alteration of growth and productivity. Understanding the genetic and molecular crosstalk between stress responses and agronomically important traits such as fiber yield is particularly complicated in the allopolyploid species, upland cotton (*Gossypium hirsutum*), due to reduced sequence variability between A and D subgenomes. To better understand how drought stress impacts yield, the transcriptomes of 22 genetically and phenotypically diverse upland cotton accessions grown under well-watered and water-limited conditions in the Arizona low desert were sequenced. Gene co-expression analyses were performed, uncovering a group of stress response genes, in particular transcription factors GhDREB2A-A and GhHSFA6B-D, associated with improved yield under water-limited conditions in an ABA-independent manner. DNA affinity purification sequencing (DAP-seq), as well as public cistrome data from Arabidopsis, were used to identify targets of these two TFs. Among these targets were two lint-yield associated genes previously identified through genome-wide association studies (GWAS) -based approaches, *GhABP-D* and *GhIPS1-A*. Biochemical and phylogenetic approaches were used to determine that *GhIPS1-A* is positively regulated by GhHSFA6B-D, and that this regulatory mechanism is specific to Gossypium spp. containing the A (old-world) genome. Finally, a SNP was identified within the GhHSFA6B-D binding site in *GhIPS1-A* that is positively associated with yield under water limiting conditions. These data lay out a regulatory connection between abiotic stress and fiber yield in cotton that appears conserved in other systems such as Arabidopsis. This regulatory mechanism highlights how sub-genome dynamics contribute to phenotypic stress-response plasticity in cotton.

[P133] MOLECULAR SCREENING OF BACTERIA IN CANADIAN GRAINS. Tehreem Ashfaq[1], Niradha Withana Gamage[1], Janice Bamforth[1], and Sean Walkowiak[1]. [1]Grain Research Laboratory, Canadian Grain Commission, 196 Innovation Drive, Winnipeg, MB, Canada, R3T 2N2
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Bacteria are prevalent and play a vital role in maintaining global biodiversity. They can either be beneficial to our health as gut microbiome which exists symbiotically within the human digestive system, can be harmful to humans and animals by causing disease, or can coexist as neutral members of the microbiome. Studying the bacteria within grains is important for understanding the potential risks and benefits of them, ensuring the grain quality and safety. We monitor bacteria on grains according to Health Canada's MFLP-52 protocol, with some modifications, and have established a procedure that allows us to test hundreds of raw grain samples including wheat, barley, soybean, corn, canola and etc. for the presences of different bacteria each year. Our protocol involves culturing and enriching bacteria from the grains. This process begins with measuring 25g of each sample, placed in a sterilized pulsified bags. The grains are first soaked in Buffered Peptone Water (BPW) followed by 100% Tryptic Soy Broth (TSB). Then the samples are incubated at 42°C to promote the growth of bacteria. After 20-24 hours of

incubation, a sample with bacterial community is isolated for DNA extraction using the Takara NucleoSpin 96 Tissue kit. Following DNA extraction, we check the quality of randomly selected DNA extracts. The DNA of each sample is then tested for the presence of different bacteria using high-throughput real-time polymerase chain reaction (PCR) (Takara SmartChip system), capable of screening 216 samples for a primer panel composed of 24 different targets. The samples are also being tested for community structure using Illumina short read sequencing and PacBio single molecule, real-time (SMRT) technology (Kinnex 16S rRNA kit for full-length 16S sequencing). The results showed that most of samples were free from harmful pathogens but contained many commensal bacteria that are common in the environment, including those promoting plant growth. This method allows us to continue to monitor bacteria associated with Canadian grain as part of grain quality and safety assurance.

[P134] DNA EXTRACTION METHODS AND COMPARATIVE GENOMICS FOR *PARASTAGONOSPORA SPP*. Janice Bamforth[1] and Sean Walkowiak[1]. [1]Microbiology and Grain Genomics, Grain Research Laboratory, Canadian Grain Commission, 196 Innovation Drive, Winnipeg, MB, Canada, R3T 2N2
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Septoria leaf and glume blotch are destructive crop diseases caused by fungal pathogens formerly classified under the genus *Septoria*. Recent taxonomical revisions have led to the reclassification and renaming of these fungi, some of which are now under the genus *Parastagonospora* of taxonomical family *Phaeosphaeriaceae*. The Canadian Grain Commission (CGC) houses a substantial fungal culture collection comprising over 6700 specimens, including isolates morphologically identified as species from the former genus *Septoria* that were isolated from Canadian wheat, durum and barley. In this study, we characterized 10 *Parastagonospora* isolates from the CGC fungal culture collection. DNA extraction methods were explored to prepare fungal extracts suitable for sequencing using the Oxford Nanopore platform. Freezing fungal mycelia at -140°C served as a viable substitute for liquid nitrogen for the initial grinding of mycelia when preparing DNA extracts. DNA was extracted using a cetyltrimethylammonium bromide (CTAB) and chloroform-isoamyl alcohol method as well as purification and size selection using the Blue Pippin. Whole genome sequencing was performed using Oxford Nanopore Technologies long-read platforms and genome assemblies were generated using Flye and polished with Illumina short-reads with BWA-MEM and Pilon. To determine the relationship between these isolates and similar fungi that have been previously characterized, we aligned the newly assembled genomes to 389 genomes from taxonomical families containing *Septoria*-related genomes obtained from NCBI using NUCmer. Comparative genomic analysis revealed that the CGC isolates clustered discretely with either *Parastagonospora nodorum* (n = 5), or *Parastagonospora avenae f. sp. Tritici* (n = 5), which are causative agents of glume blotch. Both species were isolated from wheat and barley and only the latter was isolated from durum. None of the cultural isolates were found to be similar to NCBI genomes from other *Phaeosphaeriaceae*, and taxonomical families *Mycosphaerellaceae*, *Massarinaceae* where former *Septoria spp*. have been reclassified, including *Zymoseptoria tritici*, the causative agent of Septoria Tritici Blotch. In summary, the CGC has a large fungal culture collection of historically important fungi. Here we sequenced and assembled the genomes of *Parastagonospora spp*., and genomes will be made available to enable further research on diseases which causes reduced yields in cereals in Canada and worldwide.

[P135] ASSESSING CHANGES IN AGGRESSIVENESS OF *FUSARIUM AVENACEUM* ISOLATES FOLLOWING PASSAGE THROUGH PEA AND WHEAT. Anas Eranthodi[1], Michelle Hubbard[2], David Overy[3], Linda Harris[3], Timothy Schwinghamer[1], Syama Chatterton[1], and Nora Foroud[1]. [1]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403-1st Avenue South, Lethbridge, AB, Canada, T1J 4B1; [2]Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, 1 Airport Road, Swift Current, SK, Canada, S9H 3X2; and [3]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6
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Fusarium avenaceum is a causative agent in pulse root rot and cereal head blight. In a recent study, we found that *F. avenaceum* isolates from pea were more aggressive on pea and wheat than isolates obtained from lentil or wheat. It is thus hypothesized here that cereal-pulse rotation can influence *F. avenaceum* aggressiveness and that completion of the life cycle in one crop type might influence

aggressiveness in the other. Two *F. avenaceum* isolates recovered from pea (AET-070 and AET-093) and one from wheat (FaLH29), all with moderate levels of aggressiveness in durum wheat, pea and lentil, were selected and an hygromycin expression cassette was inserted into these isolates using CRISPR. One hygromycin resistant strain from each isolate with growth and disease phenotype similar to their respective wild-type was used to inoculate pea, CDC Meadow, by a soil inoculation method. Root rot disease severity, shoot length and emergence were assessed 14 days post inoculation. The inoculated strains were re-isolated from infected pea roots on potato dextrose agar medium with hygromycin to select for the strains and streptomycin sulfate and Penicillin G potassium salt to prevent bacterial growth. Single spore isolates were obtained from the isolated strains. The inoculation and re-isolation were repeated two more times in CDC Meadow, and each time root rot disease severity, shoot length and emergence were recorded. For the first and second passage, there were no statistically significant differences for disease severity, shoot length or emergence between the strains that were passed through pea roots and their respective hygromycin resistant strains. The third passage is underway. The strains re-isolated from the third passage will be inoculated onto durum wheat, lentil and pea to assess whether the serial passage through pea roots alters aggressiveness in these hosts. Similarly, the hygromycin strains will be passed through durum wheat spikes three times and the strains after the third passage will be assessed for changes in aggressiveness in the aforementioned cultivars.

[P136] INVESTIGATING THE REGULATORY MECHANISMS OF TRICIN BIOSYNTHESIS IN RICE.

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Tricin is a 3',5'-dimethoxyflavone belonging to a large family of plant secondary metabolites named flavonoids which is characterized by a diphenyl propane (C6-C3-C6) backbone. Tricin has been studied as *O*-conjugates for decades due to its widespread distribution in the grass family (Poaceae) and its protective effects against pathogenic fungi and weeds. Tricin has also been reported to possess pharmacological bioactivities including anti-inflammatory activity. Recently, tricin is identified as an insoluble component in lignin polymer to form secondary cell wall in grasses.

In rice (*Oryza sativa*), the biosynthetic pathway of tricin has been elucidated in our laboratory. The biosynthesis begins with the formation of naringenin chalcone by chalcone synthase which is then isomerized by chalcone isomerase to form naringenin. To generate flavone, CYP93G1 functions as flavone synthase II to convert naringenin into apigenin which is hydroxylated by flavonoid 3'-hydroxylase (CYP75B4) to form luteolin. To generate tricin, luteolin goes through several methylation and hydrolyzation reactions catalyzed by ROMT9 and CYP75B4, respectively.

The underlying regulatory mechanisms for tricin biosynthesis have remained unclear. In recent years, a group of transcription factors (TFs) named Myeloblastosis (MYB) proteins has been reported to regulate the biosynthesis of phenylpropanoid-derived compounds, including flavonoids, in many plant species. Here, an MYB protein (provisionally named M14) with similar gene expression patterns to those of tricin biosynthetic genes has been selected for investigations. To identify the potential physical interaction between M14 and the tricin biosynthetic genes, yeast one-hybrid assay was conducted. M14 was found to bind to the promoters of *CYP75B4* and *ROMT9*. The results of DAP-seq also supported that M14 directly bound to the promoters of *CYP75B4* and *ROMT9.* Meanwhile, electromobility shift assay showed M14 directly bound to ACII motif on the promoters. Also, the results of dual-luciferase reporter assay suggested that M14 has transcriptional activating activity by interacting with the promoters of *CYP75B4* and *ROMT9*. To understand the role of M14 playing on tricin accumulation, *CRISPR/Cas9* mutant lines were generated. By LC-MS/MS analysis of the flavone profile, it was found that the mutation in *M14* led to a significant reduction in tricin content in the shoots during seedling and heading stages. Further analyses will be done to characterize the regulatory role of M14 on tricin biosynthesis in rice.

In general, better understanding of the regulatory mechanisms of tricin biosynthesis will provide new insights into tricin bioengineering for improvement of plant performance and biomass utilization.

[P137] CHARACTERIZATION AND GENOME ASSEMBLY OF PATHOGENIC *COLLETOTRICHUM* SPP. OF MANGO. Dr. Md. Mynul Islam[1], Dr. Tofazzal Islam[2], and Dr. Andrew Sharpe[3]. [1]Senior Scientific Officer, Plant Pathology Division, Bangladesh Agricultural Research Institute, Gazipur and Postdoctoral Fellow, Global Institute of Food Security, University of Saskatchewan, Canada; [2]Professor, Institute of Biotechnology and Genetic Engineering, Bangabandhu Sheikh Muzibur Rahman Agricultural University, Salna, Gazipur; and [3]Bangabandhu Research Chair in Food Security, Global Institute for Food Security (GIFS), University of Saskatchewan, Canada
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Mango (*Mangifera indica* L) is a major fruit crop with an immense economical relevance in South Asian countries, especially Bangladesh. It has high demand in the local as well as the global market due to its taste and nutritional quality. There are many constraints of mango production in Bangladesh, however, anthracnose disease caused by several pathogenic *Colletotrichum* spp. is the most damaging postharvest issue. The disease causes about 30% yield loss in India. Molecular tools are used widely to identify the species of *Colletotrichum* responsible for the disease. Twenty five isolates of *Colletotrichum* spp. (*C. gloeosporioides, C. asianum and C.siamense*) from mango fruits were collected, isolated and purified from 11 mango growing regions in Bangladesh during May 2023 to July 2023. Pathogenicity tests of the isolated pure cultures were conducted using BARI mango-3 as a host. DNA of the isolates were extracted, ITS rDNA gene was amplified, sequenced and blasted to confirm the pathogen species. Whole genome sequencing of the *Colletotrichum* spp. isolates is being carried out using an Oxford MinION long read sequencer. Genome assembly and gene annotation will be undertaken, and unique primers will be designed to identify species and for the development of a rapid diagnostic kit.

[P138] BRASSINOSTEROIDS AND SALICYLIC ACID MUTUALLY ENHANCE ENDOGENOUS CONTENT AND SIGNALING TO SHOW A SYNERGISTIC EFFECT ON PATHOGEN RESISTANCE IN ARABIDOPSIS THALIANA. Jeehee Roh, Yeon Ju Park, Ji-Hyun Youn, and Seong-Ki Kim. Department of Life Science, Chung-Ang University, Seoul 06974, Republic of Korea
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The crosstalk mechanism regulating content and signal transduction between brassinosteroids (BRs) and salicylic acid (SA) for plant defense was investigated in Arabidopsis. Compared to the wild type, an increased bacterial resistance was observed in bzr1-1D, a dominant mutant of the BR transcription factor BZR1. In bzr1-1D, SA biosynthetic gene ICS1 expression and endogenous SA content greatly increased upon Pst DC3000 infection, and the direct binding of BZR1 to the ICS1 promoter was confirmed through EMSA and ChIP. In bzr1-1D where NPR1 expression was almost absent, expression of PR genes was increased, and both BZR1 and PR5 expressions increased after SA treatment. EMSA and ChIP verified that BZR1 binds directly to the cis-element present in the PR5 promoter and a pull-down assay showed that TGAs, SA transcription factors upstream of PR genes, interact with BZR1 at the protein level. Crude enzyme assays demonstrated that BR C-6 oxidase activity, a CYP85A1 function, greatly increased during Pst DC3000 infection. In the tga1 tga4 double mutant lacking SA transcription factors TGA1 and TGA4, BR biosynthetic gene CYP85A1 expression was significantly reduced. EMSA and ChIP confirmed that both TGA1 and TGA4 bind to the cis-element present in the CYP85A1 promoter, and castasterone (CS), a bio-active BR, was significantly reduced in tga1 tga4. Taken together, the upregulation of ICS1 expression by BZR1 and CYP85A1 expression by TGA1/4 mutually enhanced endogenous level of BR and SA in Arabidopsis. Furthermore, TGAs and BZR1 interaction at the protein level induces SA-induced immunity through the upregulation of PR5 expression, increasing bacterial resistance in the plant. These results explain the mutual control mechanisms of the synergistic effects BR and SA have on plant defense and confirm BR's effect on plant defense and growth promotion in A. thaliana.

[P139] APPLICATION OF PACBIO KINNEX RNA KIT TO SOIL DNA SAMPLES FOR 16S AND ITS RRNA AMPLICONS FROM CROPLANDS. Sung-Jong Lee, Tiffany Chin, Janice Bamforth, Niradha Withana Gamage, and Sean Walkowiak. Grain Research Laboratory, Canadian Grain Commission, 196 Innovation Drive, Winnipeg, MB, Canada, R3T 2N2
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Soil microbiome studies using amplicon-based metagenomics for 16S and ITS rRNA are widely conducted in various soil types, including croplands. 16S and ITS sequences act like barcodes that can

be compared to databases to identify the bacteria and fungi to different levels of taxonomic resolution, depending on which variable regions of the rRNA are sequenced. Most studies that perform rRNA analysis use short-read sequencing technologies that can target a limited number of variable regions due to restrictions on sequencing read length. Recently, the long-read sequencing platform offered by PacBio has enabled the sequencing of several variable regions on a single reaction, increasing the resolution of taxonomic identification. New advances in PacBio sequencing have also increased throughput, with the release of the high-yield PacBio Kinnex full-length RNA kit. In this study, we applied the Kinnex rRNA kit to long (1200-1500 bp) and short length (300-450 bp) 16S and ITS rRNA regions, respectively, to the same soil microbiome DNA samples. In order to perform ITS sequencing as well as shorter amplicon sequencing, we modified the Kinnex protocols and adapted them for sequencing different amplicons. The DNA samples were extracted from soil obtained from different field crops grown in Saskatoon, Saskatchewan. We observed differences in DNA quality (intactness and yield) and microbiome profiles based on different crop types, DNA extraction methods, and amplicon length. Using these latest state-of-the-art approaches, we are able to identify both bacteria and fungi within complex soil communities with high resolution and throughput.

***[P140] LOCALIZATION OF ALKALOID BIOSYNTHETIC ENZYMES IN *LOPHOPHORA WILLIAMSII* CACTUS.** Ginny Li and Peter J. Facchini. University of Calgary, 2500 University Drive N.W., Calgary, AB, Canada, T2N 1N4
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Peyote (*Lophophora williamsii*) is a cactus known to the phenethylamine protoalkaloid mescaline. Consuming peyote 'buttons' has been used in Indigenous ceremonies for at least six millennia owing to the psychedelic effect of mescaline. Recently, hallucinogenic compounds such as psilocybin have been used to treat mental health disorders including depression, anxiety, or post-traumatic stress disorder. Mescaline is currently undergoing clinical assessment for its potential therapeutic benefits.

The biosynthetic pathway converting L-tyrosine to mescaline, and related phenethylamines and tetrahydroisoquinoline (THIQ) alkaloids, was recently elucidated in our laboratory. L-Tyrosine is first hydroxylated by a cytochrome P450 (LwCYP76AD94) to form L-DOPA, which is then decarboxylated by a tyrosine/DOPA decarboxylase (LwTYDC) to yield dopamine. A specific *S*-adenosylmethionine-dependent *O*-methyltransferase (LwOMT2) subsequently produces 3-methoxytyramine, which undergoes hydroxlation and subsequent *O*-methylation at the 5 position and a final *O*-methylation by LwOMT10 at the 4 position to yield mescaline. The diversity of metabolites associated with this core pathway include THIQ alkaloids resulting from the Pictet-Spengler condensation of phenethylamines, and *N*-methylated derivatives of corresponding phenethylamine and THIQ compounds formed via a unique *N*-methyltransferase (LwNMT).

Polyclonal antibodies were raised against LwTYDC, LwOMT10 and LwNMT as tools to investigate the cellular localization of phenethylamine and THIQ biosynthesis in peyote. Based on based on the use of matrix-assisted laser desorption/ionization mass spectrometry imaging, mescaline was reported to accumulate primarily in, or near, the epidermis of aerial organs. Immunoblot analyses of total protein extracts from shoots sectioned longitudinally or cross-sectionally detected all three enzymes in all parts of the aerial organs, with the relative abundance increasing from bottom to top, and from the inside out. Liquid chromatography-mass spectrometry (LC-MS) analysis of corresponding sections showed that the phenethylamine and THIQ content was generally higher in apical and peripheral tissues, although mescaline levels were relatively consistent in regions of the shoot. Total RNA was also extracted from aliquots of each sectional sample to perform qRT-PCR, which showed that, in contrast to the immunolocalization results, *LwOMT10* and *LwNMT* transcript levels were highest in the apex, but declined sharply in other areas of the shoot, whereas *LwTYDC* transcripts showed an inverse localization pattern with higher levels in basal region.

Immunolocalization in fixed tissue sections showed that LwTYDC and LwNMT are associated with chloroplasts, whereas LwOMT10 is associated with the nucleus. Sucrose density gradient fractionation followed by immunoblot analysis of each fraction confirmed that LwOMT10 and LwNMT were associated with cellular fractions with the same density as nuclei and chloroplast, respectively, although both

enzymes were also detected in the cytoplasmic fraction. A model for the cellular localization of mescaline biosynthesis in peyote will be presented.

[P141] A UNIQUE PATHOGEN-INDUCIBLE STILBENE *O*-METHYLTRANSFERASE IN SORGHUM.

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Stilbenes are characterized by the 1,2 -diphenylethylene nucleus. They belong to a small family of plant-specialized metabolites which have been extensively investigated for their valuable pharmaceutical effects and antimicrobial activities. Simple stilbenes can be glycosylated, methylated, or oligomerized by specific enzymes, giving rise to different structural derivatives. Notably, *O*-methylated stilbenes produced by methylation of a hydroxyl group are prominent nutraceuticals but rarely produced by crop plants.

In this study, several stilbene compounds including resveratrol, piceid (resveratrol 3-*O*-glucoside), and *O*-methylated resveratrol derivatives, i.e. pinostilbene (3-*O*-methylated stilbene) and pterostilbene (3,5-bis-*O*-methylated resveratrol), were detected in sorghum seedlings following infection by the anthracnose pathogen *Colletotrichum sublineola*. In particular, the resistant genotype SC748-5 accumulated 9 times more pterostilbene than the susceptible genotype BTx623. In vitro spore germination and mycelial growth assays further demonstrated the superior inhibitory effects of pterostilbene over pinostilbene and resveratrol towards *C*. *sublineolum*, highlighting the importance of stilbene *O*-methylations during defense responses in sorghum.

In silico expression dataset for *Bipolaris sorghicola*-infected sorghum leaves and our in-house transcriptome dataset for *C. sublineola*-infected sorghum seedlings were analyzed. Two pathogen-inducible *O*-methyltransferase (OMT) genes, SbSOMT (*Sb07g004710*) and SbOMT4 (*Sb07g004590*), potentially involved in stilbene *O*-methylation were identified. In recombinant enzyme assays, SbSOMT converted resveratrol to pinostilbene and pterostilbene successively while SbOMT4 showed minimal SOMT activity. Transient co-expression of SbSOMT with sorghum stilbene synthase (SbSTS1) genes in *Nicotiana benthamiana* resulted in the production of pterostilbene in the agro-infiltrated leaves. To investigate the in planta role of SbSOMT in planta, *sbsomt* mutants were generated via CRISPR/CAS 9-mediated genome editing in sorghum genotype TX430. Following *C. sublienola* infection, *sbsomt* mutants accumulate resveratrol and piceid but not pinostilbene or pterostilbene while wild-type plants accumulate different both stilbene *O*-methylated derivatives, hence establishing the indispensable role of SbSOMT in the *O*-methylation of resveratrol to form pinostilbene and pterostilbene.

Phylogenetic analysis further revealed that SbSOMT homologs are restricted to *Sorghum* spp. including *S*. *bicolor* and *S*. *halapense* (Johnson grass). Apparently, the genus-specific stilbene *O*-methyltransferases were recruited from canonical caffeic acid *O*-methyltransferases (COMTs) after the divergence of *Sorghum* spp. from *Saccharum* spp.

Overall, our work presents SbSOMT as a unique SOMT that may be exploited for bioengineering of bioactive *O*-methylated stilbenes. presents SbOMT as a novel target for bioengineering of stilbene *O*-methylation via transgenic technology or synthetic biology.

[P142] TRANSCRIPTIONAL REGULATION OF ABSCISIC ACID AND GIBBERELLIN METABOLISM GENES DURING SEED DEVELOPMENT IN BARLEY (*HORDEUM VULGARE* L.). Pham Anh Tuan, Tran-Nguyen Nguyen, Parneet K. Toora, and Belay T. Ayele. Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada
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Seed development is a complex physiological process which is partly regulated by abscisic acid (ABA) and gibberellins (GAs). However, regulation of the metabolism of these hormones during barley seed development is not well understood. This study investigated spatiotemporal changes in the expression patterns of ABA and GA metabolism genes and endogenous levels during development of barley seeds. Elevated levels of ABA and GA were observed in both embryo and endosperm tissues during the early/main seed filling (SF) phase, suggesting the role of ABA and GA in embryo development, organ expansion and accumulation of storage reserves. During transition from early to physiological maturity (PM) phase, endospermic ABA level showed an increase and this is associated with expression patterns of *NCED*s and *CYP707A2* genes while GA level showed a decrease and this is regulated by downregulation of *GA3ox2* and upregulation of *GA2ox* genes during the same period. Low levels of ABA and no GAs were detected in the endosperm during post-PM. The PM stage, which is known to exhibit high level of dormancy, is associated a peak in embryonic ABA level that is regulated mainly by the expression of *NCED* genes, and a low level of GA, which is controlled by *GA20ox*, *GA3ox* and *GA2ox* genes. The embryo during post-PM phase is characterized by the detection of certain amount of ABA but not GA, suggesting the role of ABA in desiccation tolerance. Our study indicates that spatiotemporal changes in ABA and GA levels, which are mediated by transcriptional regulation of specific genes involved in their respective metabolic pathways, regulate physiological processes during barley seed development.

[P143] BACILLUS CEREUS IN CANADIAN GRAIN: MICROBIAL COMMUNITY PROFILING. Niradha Withana Gamage[1], Tehreem Ashfaq[1], Tiffany Chin[1], Janice Bamforth[1], and Sean Walkowiak[1]. [1]Grain Research Laboratory, Canadian Grain Commission, Canada
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Grain and grain products can become contaminated with microorganisms derived from various sources including plants, insects, water, soil, fertilizers, and animal feces. Bacteria such as *Bacillus cereus* can survive for extended periods of time in these low moisture foods. *Bacillus cereus* is a facultative anaerobic, Gram-positive, rod-shaped, spore forming bacterium widely distributed in nature. However, these bacteria have demonstrated a crucial role as beneficial bacteria in plants while some have been reported as harmful pathogens causing food poisoning in consumers. Studies showed that some species of *B. cereus* have influenced plant growth and crop yield by acting as plant growth promoting bacteria (PGPB) and by inhibiting broad range of plant pathogens and insect pests. Adversely, *B. cereus* has gained special attention worldwide as a foodborne pathogen due to their potential of producing toxins causing gastrointestinal illnesses. The purpose of this study was to investigate the *B. cereus* community profile associated with raw grain samples received at the Canadian Grain Commission. We screened (n = 508) wheat samples received in 2018 and (n = 636) of wheat and flax samples received in 2017 and analysed them using molecular techniques. Grain bacteria were isolated by enriching samples as per a modified protocol (Health Canada MFLP-52). Pure colonies were isolated and confirmed using Chromogenic culture media and their DNA was tested with real-time PCR and by Illumina sequencing. The overall *B.cereus* isolation rate in the current study was 56.3% in 2018 and 85.2% in 2017. Comparative genomics of 109 presumptive *B. cereus* isolates divided most of them into two genetically distinct groups. Additionally, molecular characterization revealed that the *B.cereus* population in grain was composed of diverse genetic elements including: enterotoxin genes causing gastrointestinal illnesses (nheA and hbID), antimicrobial resistance genes and genes involved in the production of insecticidal proteins (Cry). Our study investigated the composition of *B. cereus* in Canadian grain in two different harvest years and the results shows the value of surveillance of bacteria naturally occurring in raw grain. Ongoing research is being conducted to screen *B. cereus* isolates associated with grain that may pose a risk for consumers in term of food safety and also to investigate the possible *B. cereus* candidates as beneficial biocontrol agents or PGPB in plants.

[P144] ASSESSING AMMONIA VOLATILIZATION LOSSES WITH DIFFERENT NITROGEN SOURCE, TIMING, AND PLACEMENT. Jongwon Kang[1], Jason DeBruin[2], Rebecca Hensley[3], and Joshua Nasielski[1]. [1]Department of Plant Agriculture, University of Guelph, Guelph, Ontario, N1G 2W1, Canada; [2]Corteva Agriscience, Johnston, Iowa, USA, Johnston, Iowa, IA 50131, USA; and [3]Corteva Agriscience, Windfall, Indiana, IN 46076, USA
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Given the economic and environmental costs associated with ammonia (NH_3) losses from nitrogen (N) fertilizer applications, there is significant interest in evaluating various N management practices to reduce NH_3 volatilization. The aim of this study was to provide N management recommendations to enhance N use efficiency and minimize ammonia losses. A three-year field study (2021-2023) was conducted at five locations in Canada and the US to measure NH_3 volatilization from different N sources (urea and UAN with/without urease inhibitor), placements (broadcast and injection), and application timings (V5 and V13) in corn fields, using the dositube method. Both urease inhibitors and tillage were found to reduce volatilization losses for urea (average 39.2 kg N ha^{-1}) and UAN (average 5.6 kg N ha^{-1}), although losses with UAN were already low even when applied on the surface. Application timing (V5 or V13) did not significantly affect total NH_3 loss, except in the case of surface-applied urea, which had higher losses at V13 than at V5. Soil texture was a significant factor in that soils with high sand content were more prone to N losses due to rapid downward movement of N following rainfall events. However, this can raise the potential risk of increasing other N losses, such as N leaching (pollution swapping).

***[P145] METABOLOMICS TO INVESTIGATE PLANT ADAPTATATIONS TO CLIMATE CHANGE: AN EXAMPLE FROM THE ARTIC.** Daniel A. Gaudet[1], Susan J. Murch[1], and Lauren A.E. Erland[1,2], [1]University of British Columbia, Okanagan, 3247 University Way, Syilx Okanagan Nation Territory, Kelowna, BC, Canada V1V 1V7; and [2]University of the Fraser Valley, Stó:lō Temexw, Chilliwack, BC, Canada, V2S 7M8
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Inuit Nunangat and Canada's Arctic are experiencing warming at up to 4X the rate of Southern regions in a phenomenon known as Artic amplification. Plant species growing in these regions are highly adapted to growth at low temperatures and long day-lengths and are experiencing relatively rapid changes in their environments. To better understand the metabolomic changes occurring in Artic plant species, field samples of aerial tissues of *Cerastium regelii* (Ostenf.) and *Stellaria longipes* (L.) were collected in Qausuittuq, Nunavut. We hypothesized that plants collected from northern regions respond to changing temperatures by activation of specific metabolic pathways. Metabolomics is the untargeted analysis of any biological sample. We used an untargeted metabolomics approach to detect and identify metabolites in C. regelii and S. longipipes seedlings grown in tissue culture in controlled environment chambers with three climate setting (12°C, 24°C or 28°C). Data on physiological responses was collected after three weeks. In vitro-grown tissues were collected, flash frozen and extracted in a stabilizing buffer. Metabolites were separated by reverse phase chromatography (Thermo UHPLC; BEH C18 column; gradient elution) and high-resolution mass spectrometry (Q-Exactive orbitrap). A set of 50 known plant growth regulators was used as a standard mixture to ensure data quality. Data were exported, aligned, and verified through MZMine version 3.0. Multivariate statistical approaches and data visualization algorithms including PCA, PLSDA and SAM were used to determine significant differences and eliminate false discoveries in the data. Compound ID, HormonomicsDB, and pathway deconvolution algorithms were used to predict specific compounds and mechanisms. Growing temperature significantly affected 222 features in *C. regelii* and 110 features in *S. longipes*. Important biosynthetic pathways that are responsive to temperature in these species include the GOGAT pathways, shikimic acid biosynthesis pathways, polyamine metabolism and cytokinin biosynthesis. Interestingly, dihydrozeatin-O-glucoside and meta-topolin metabolism were induced by temperature increases and associated with increased growth. The data proposes several new hypotheses for plant adaptation mechanisms that may be important factors in plant resiliency or vulnerability to climate change.

***[P146] SOMETHING SWEET: SUGAR MEDIATED CHANGES IN CELL PROLIFERATION VIA TOR-BRASSINOSTEROID SIGNALLING REQUIRE THE MICROTUBULE ASSOCIATED PROTEIN *CLASP*.**
Sean P.A. Ritter, Dr. Laryssa Halat, and Dr. Geoffrey Wasteneys. The University of British Columbia
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To survive, organisms need to be able to coordinate energy-demanding processes, such as growth, with prevailing environmental conditions. In plants, sugars are the major energy source utilized to power cellular processes. Thus, plants must be able to perceive sugar levels, and enact appropriate cellular responses. TARGET OF RAPAMYCIN (TOR) is a conserved protein kinase activated by growth factors and inactivated by energy deprivation, thereby acting as a master regulator of metabolic pathways in all eukaryotes. In plants, TOR has been shown to alter cell proliferation and growth in response to changing light levels and sugar availability. While numerous targets of TOR kinase activity have been identified, such as the brassinosteroid-responsive transcription factor BRASSINAZOLE RESISTANT 1 (BZR1), how TOR kinase activity is translated into altered growth at the cellular level remains unclear. I propose that the microtubule-associated protein CLIP-ASSOCIATED PROTEIN (CLASP) is a crucial component of the TOR signaling pathway, providing a mechanism by which sugar affects root meristem activity and growth. *CLASP* expression is altered by both BZR1 activity and light availability, resulting in microtubule-dependent fine-tuning of cell proliferation in response to environmental conditions. In addition, CLASP also modulates meristem activity through its direct interaction with SORTING NEXIN 1 (SNX1). This interaction maintains the plasma membrane distribution of the auxin transporter PIN2, a known target of TOR. My research shows that *CLASP* null mutant plants have greatly reduced sensitivity to pharmacological inhibition of TOR at the organ, cellular and subcellular levels, and fail to increase cell proliferation in response to sugar. Furthermore, in the absence of CLASP both PIN2 levels at the plasma membrane, and auxin distribution patterns are unaltered by TOR inhibition. This effect is mediated by the brassinosteroid signalling pathway, as both constitutively active BZR1 and mutation of the BZR1 binding site within the *CLASP* promoter prevent TOR-dependent changes in CLASP expression, and root growth. Together, these findings indicate that CLASP is required for TOR-mediated meristem activity. Through characterization of the interaction between CLASP, TOR and plant hormones, this work provides insight on how the sugar provision is translated into altered root development, thereby furthering our understanding of how plants perceive and respond to their changing environment.

***[P147] TRACKING HOP LATENT VIROID (HLVD) IN HOP (HUMULUS LUPULUS (L).) TISSUE.**
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Hop Latent Viroid (HLVd) is a mechanically transmitted pathogen of hop (*Humulus lupulus*) and cannabis (*Cannabis sativa*) which impacts yield and secondary metabolites. Symptoms vary from severe, causing ‘dudding disease’ as in cannabis, to latent and symptomless as in reservoir species such as stinging nettle (*Urtica dioica*). HLVd is a member of the genus *Cocadviroid*, family Posiviroidae, and forms a stable self-complementary RNA structure 256-nt in length. Currently, a sound agricultural management strategy for viroids would include beginning a hop yard with clean plant germplasm. To evaluate clean plant material, a sensitive and specific diagnostic and sampling strategy is required. Mapping distribution of HLVd in plant tissue will assist in developing a method to sample plants with a diagnostic, leading to higher yields and better-quality products. In silico characterization of the HLVd genome discovered motifs including the conserved region, pathogenicity region, and functional hairpins. A survey for viroid presence and titer among tissue types was conduced on 20 randomly selected mature (3 year old) hop plants (10 ‘Centennial’, 10 ‘Chinook’) at the Ontario Crop Research Center yard near Simcoe, Ontario. Field samples were taken of leaf, cone and root tissue to compare viroid titer using RT qPCR, due to the latent nature of HLVd in hop. Of the 20 hop plants randomly selected for the survey, HLVd was detected in 100% of sampled units with variable titer and tissue distribution. A two way ANOVA revealed statistically significant differences in titer between hop tissue types but not cultivar ($F(2, 33) = [5.368]$, $p = 0.009$) where root tissue had significantly lower titre than leaf and cone tissue ($p = 0.007$, 95% C.I = [0.83, 4.24]). Inconsistent spread of HLVd in tissues may have explanations founded in mode of transmission,

symptom induction, and interference of cellular components. Based on these results, vegetative propagation of hop may be limited in its success of reducing HLVd spread with prior detection, suggesting a need for further preventative action.

[P148] OPTICAL DENSITY ASSAY TO ASSESS THE SENSITIVITY OF *PYTHIUM* AND *GLOBISPORANGIUM* ISOLATES TO MEFENOXAM. Umbrin Ilyas[1], Lindsey J. du Toit[2], and Mary Ruth McDonald[1]. [1]Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada, N1G 2W1; and [2]Department of Plant Pathology, Washington State University, Mount Vernon, WA, USA, 98273 Correspondence to: uilyas@uoguelph.ca

Cavity spot of carrot is an economically important disease caused by several species of *Pythium* and *Globisporangium*. Disease management in conventional production primarily relies on applications of the fungicide mefenoxam. Frequent reports in Ontario of severe disease even with mefenoxam applications suggest prevalence of mefenoxam resistance in populations of the pathogen. The objectives of the study were to (1) develop a fast and accurate optical density (OD) assay to assess mefenoxam sensitivity (2) evaluate the sensitivity of *Pythium* and *Globisporangium* isolates to mefenoxam (3) determine if mefenoxam sensitivity varies among species. OD assays are used routinely to screen for antibiotic resistance in bacteria, but there are challenges with filamentous oomycetes. To account for variability in growth using an OD assay, the growth was measured at nine positions per well in a 96-well plate at 600 nm, and the readings averaged. Z-scores (>0.4) and growth curves were used to confirm the isolate was growing actively as isolates of different species grow at different rates. Validity of the method to assess mefenoxam sensitivity was confirmed by comparing growth inhibition and half maximal effective concentration (EC_{50}) values from the OD assay with those from the standard assay of measuring colony growth on mefenoxam-amended agar medium. A total of 188 isolates collected from 13 carrot fields in the Holland Marsh, Ontario, in 2020-23 belonged to seven species: *P. sulcatum*, *G. violae*, *G. rostratifingens*, *G. intermedium*, *G. sylvaticum*, *G. irregulare*, and *G. ultimum*. A 2-mm-diameter mycelial plug of each isolate was transferred to mefenoxam-amended V8 broth with six concentrations (0.1 – 100 µg/mL). The positive control treatment included five isolates of *G. ultimum* resistant to mefenoxam and one isolate of this species sensitive at 10 µg/mL. The optimum time for determining mefenoxam sensitivity for slow-growing species (<20 mm/day) was 72 hours, and for fast-growing (>20 mm/day) was 48 hours based on the z-score and growth curves with the OD assay. There was a significant positive correlation (r= 0.94 and 0.74) and linear relationship (R^2_{adj}= 0.97 and 0.97) between EC_{50} and growth inhibition values calculated for the OD and agar medium assay. All isolates tested were sensitive to mefenoxam at 10 µg/mL. The percentage inhibition at 1 µg/mL varied significantly among species, with isolates of *G. irregulare* most sensitive, and isolates of *P. sulcatum* least sensitive. This optimized OD assay is an efficient and accurate method to monitor mefenoxam resistance in filamentous oomycetes.

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