The Canadian Tri-Society meeting

JUNE 17-21 2023, Ottawa

Agroecosystem resiliency under a changing climate.

Message from the Chair of the Organizing Committee

Dear colleagues, on behalf of the Organizing Committee, I am honoured and delighted to welcome you to this Canadian Tri-Society 2023 Conference with the Canadian Phytopathological Society (CPS), the Canadian Society of Agronomy (CSA) and the Canadian Society for Horticultural Science (CSHS) on June 17th to 21st 2023 at the Delta hotel, Ottawa, ON. This meeting will bring together researchers in plant science with a thematic on “Agroecosystem resiliency under a changing climate.” There will be scientific workshop tours on Sunday and Wednesday, Special sessions, Plenary session, Symposium and 14 sessions programmed daily from Monday to Wednesday from 8am to the evening with 2 poster sessions in the evening on Monday, Tuesday. Our program features talks from keynote speakers and societies awardees on the topics of Plant-Soil health and Innovations in Agronomy, Genetics biotech and breeding, Climate change, Disease Management of Horticultural Crops, Nutrient Management, Sustainable Disease management tools, Clubroot, Biotic and Abiotic Challenges, Emerging/novel tools for plant pathogen diagnosis, Obligate biotrophic pathogens and soil borne diseases, Biovigilance and approach for emerging and novel phytopathogens, and Long-term studies: Soil and plant. We will have special sessions and activities which will offer opportunities for professionals working in plant sciences to discuss the latest research, learn from peers and expand their knowledge. These networking opportunities can help move research forward and enhance the careers of the participants. There will be rooms for students to have competitions, oral and poster sessions and a special 3 minute talks activities and scientific paper workshop. We will also have rooms with planned student activities, reception and banquet. I want to thank all the meeting committees and chairs and our sponsors who have helped to support our event. We could not have a successful conference without you. Thanks a lot for your participation in this meeting that was originally planned in 2021. We received over 200 abstracts and will have a program very full to allow everyone to present with more than 100 talks and 100 posters and will see over 250 attendees. Your participation makes this event a success, thank you! I wish you a great week in Ottawa conference and hope you will also enjoy visiting the National Capital region. Very happy to see you in person. Have a good meeting!

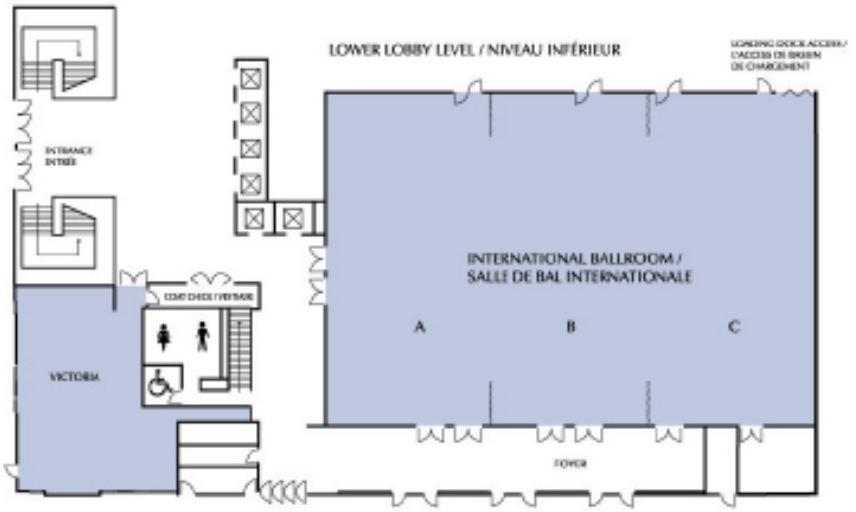
Dr. Guillaume J. Bilodeau

Chair of the Organizing Committee

Program at a glance

Pre-meeting	Sunday June 18th	Monday June 19th		Tuesday June 20th		Wednesday June 21st	
	8:00—14:00	**8:00—10:20**		**8:00—9:30**		**8:00—9:30**	
	Tour 1: Ottawa RDC Herbaria, culture & insect collections ***Load bus:*** Delta Lobby	**Plenary session: Agroecosystem resiliency under a changing climate (Ballroom A)** ***10:00—10:20.** Coordination in Plant Health (Brittany Day & Jaimie Schnell) ***10:20—10:35.** D-mark L7 Informatics (Vasu Rangadass)		**Symposium 1-CPS:** Emerging/novel tools for plant pathogens diagnostics-**1** **(Ballroom AB)**		**Symposium 2- CSHS:** Controlled Environment Agriculture CSHS - **(Ballroom AB)**	
		10:40—12:10		**9:30—11:00**		**9:30—11:00**	
		Session 1: Plant-Soil health and Innovations in Agronomy-**1** (**Ballroom A**)	**Session 2 :** Genetics, biotechnology, and breeding-student-**1** (**Panorama**)	**Session 5a :** Nutriments Management **(Pinnacle)**	**Session 5b :** Sustainable Diseases management tools: Bioproducts, cultural practices and prediction modeling-**1** (**Panorama**)	**Session 9 :** Sustainable Diseases management tools: Bioproducts, cultural practices and prediction modeling-**2** (**Pinnacle**)	**Session 10:** Plant soil health and innovation in agronomy-**2** (**Panorama**)
				11:00—12:30 Special session: Communicating our science to the general public and policymakers **(Ballroom AB)**		**11:00—12:30 Equity, Diversity and Inclusion (EDI) (Ballroom AB)**	
		12:00—13:00 **Lunch (Ballroom AB foyer)**		**12:30—14:30-Lunch (Ballroom AB foyer)** CPS Business Meeting (**Ballroom AB**) CSHS Business Meeting (**Pinnacle**) 12:30—13:15: CSA Business Meeting (**Panorama**)		**12:30—14:30** **Lunch (Ballroom AB foyer)** Incoming CPS meeting: Board members only (Bytown room)	
	8:00—19:00 **Registration desk open** **18th -21st**			13:15—14:30 CSA-Distinguished Agronomist & Genetics and Breeding 1b (**Panorama**)		**13:00—16:00 Workshop 2-CSA-Tour**	
		13:15—14:45		**14:30—15:45**		**14:30—16:00**	
		Session 3: Climate change and biodiversity (**Panorama**)	**Session 4:** Disease Management of Horticultural Crops (**Pinnacle**)	**Workshop 1-CSA:** Practical carbon capture/ GHG emission measurements: Methods, Implementation and Uses (**Panorama**)	**Session 6:** Clubroot disease (**Pinnacle**)	**Session 11:** Obligate biotrophic pathogens and soil-borne diseases (**Pinnacle**)	**Session 12:** Biovigilance approach for Emerging and novel phytopathogens (**Panorama**)
	16:00—1800	**15:00—16:00**		**15:45—17:15**		**16:00—17:30**	
	Outgoing board CPS - Board members only **(Capitale)**	**Scientific Paper Workshop** - Canadian Journal of Plant Science: Improve your chance of getting published (**Ballroom A**)		**Session 7:** Biotic and Abiotic Challenges (**Panorama**)	**Session 8:** Emerging/novel tools for plant pathogens diagnostics-**2** (**Pinnacle**)	**Session 13:** Genetics, biotechnology, and breeding-**2** **(Pinnacle)**	**Session 14 :** Long-term studies: Soil and plant **(Panorama)**
		16:00—17:00 **Book launch & Networking** (Keith Seifert) (**Ballroom A**)	**16:15—18:00** **Poster session 1** **(Grand Salon)**	**17:15—19:00** **Poster session 2** (**Grand Salon**)		**17:35—18h:20** **Closure of the meeting** **(Ballroom AB)**	
18:00-21:00 Board members only CPS- FAC **(Capitale)**	**19:00—22:00** Welcome reception (**Ballroom A**)	**18:00—19:00** **Student activity 3 min talks** (**Ballroom A**)		**19:00—22:00** **Banquet** **Ballroom AB**)		**18:15—19h:00** **Posters removal**	
		20:00—23:30 **Student social**					

Floor plan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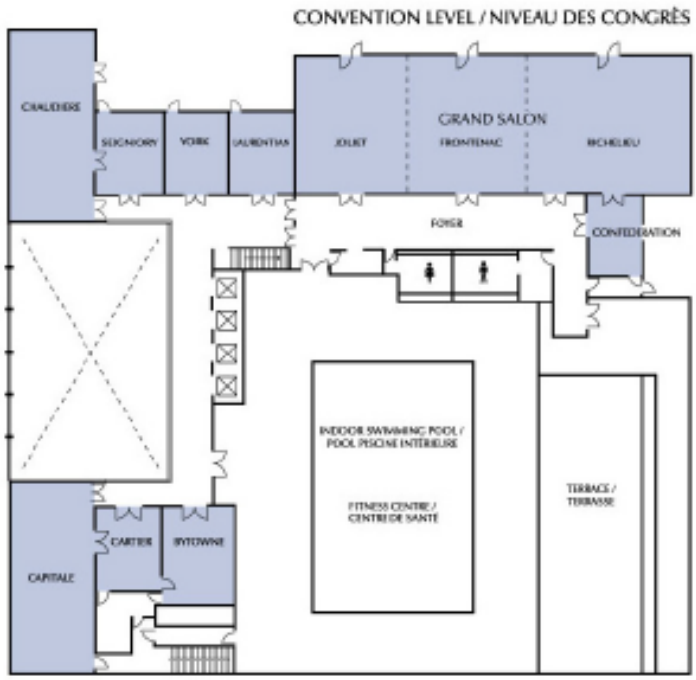
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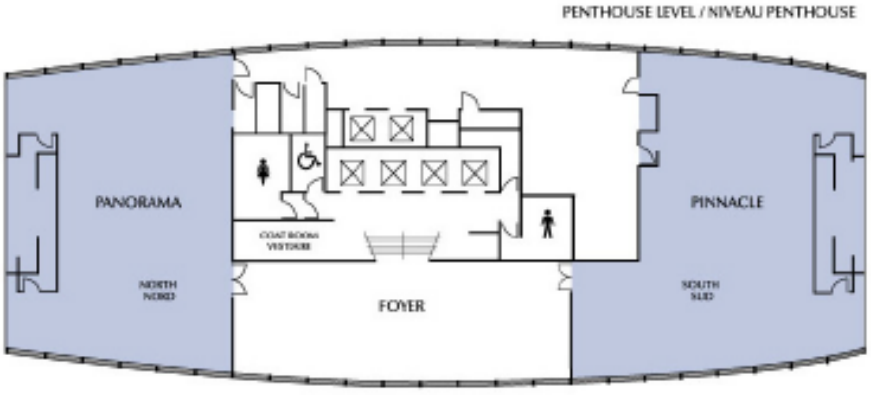
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Scientific Program Schedule Saturday, June 17

Pre-meeting

Time	Saturday, June 17	Location
18:00–21:00	Board members only CPS-FAC	Capitale room

Scientific Program Schedule Sunday, June 18

Time	Sunday, June 18	Location
8:00–14:00	**Tour 1:** Ottawa RDC Herbaria, culture & insect collections	***Load bus:*** Delta Lobby
8:00–19:00	Registration desk open	
16:00–18:00	Outgoing board CPS * Board members only	Capitale room
19:00–22:00	Welcome reception	Ballroom A

Scientific Program Schedule Monday, June 19

Time	Abst. no.	Monday, June 19	Location
8:00–10:20		**Plenary session: Agroecosystem resiliency under a changing climate** Moderators: Guillaume Bilodeau (Welcome), Mamadou L. Fall, Youbin Zheng and Jamie Larsen	Ballroom A
8:00	1	Amélie Gaudin – Building Agroecosystem Resiliency to a Changing Climate	
8:45	2	Neil Mattson – Optimizing plant quality, environmental, and socioeconomic outcomes of controlled environment agriculture crops	
9:30	3	Mario Tenuta – The Evolving Role of Nitrogen Management in Crop Production	
10:00–10:20		Brittany Day & Jaimie Schnell – Coordination in Plant Health	
10:00–10:35		Vasu Rangadass – D-mark L7 Informatics	
10:40–12:10		**Session 1: Plant-Soil health and Innovations in Agronomy-1** Moderators: Raphael Ofoe and Kelly Turkington	Ballroom A
10:40	4	Thomas (Kelly) Turkington – The impact of row spacing, seeding rate, and fungicide timing on the severity of leaf disease, fusarium kernel damage, deoxynivalenol, and productivity of spring wheat.	
10:55	5	Thomas Forge – Utility of organic amendments for managing root-lesion nematodes prior to replanting apple orchards	
11:10	6	Natalie LaForest – Investigating the role of *Pterostichus melanarius* in agricultural pest predation in wheat (*Triticum aestivum*) and hemp (*Cannabis sativa* L.) in Alberta	
11:25	7	Efoo Bawa Nutsukpo – Quality indices of grape juice can be altered by varying rates of pyroligneous acid	
11:40	8	Raphael Ofoe – Metabolomic analysis revealed coordinated regulation of central carbon metabolism in pyroligneous acid-treated tomato under aluminum stress	
11:55	9	Griffin Bailey – Potato Early Dying Complex: management and identification in Ontario potato soils	
10:40–12:10		**Session 2: Genetics, biotechnology, and breeding-student-1** Moderators: Jaswinder Singh and Bourlaye Fofana	Panorama
10:40	10	Yishan Zhang – Genetic mapping of aggressiveness in *Fusarium graminearum*, the cause of Fusarium head blight in durum wheat	

10:55	11	Vincent Fetterley – Introgression of stripe rust resistance from spelt wheat to Canada Western Red Spring (CWRS) wheat is complicated by segregation distortion	
11:10	12	Keval Shah – Identification of resistance in hexaploid *Brassica* against Leptosphaeria maculans and introgression in *Brassica napus*	
11:25	13	Sijan Pandit – RNAseq study of partially resistant and susceptible pea lines upon *Aphanomyces euteiches* infection	
11:40	14	Erika Dort – Development of plasmid transformation and CRISPR/Cas9 gene editing systems in forest *Phytophthora* pathogens	
11:55	15	Ana Laura Achilli – Genetic gains in grain yield and agronomic traits in Argentinian durum wheat	
12:00–13:00		**Lunch**	Ballroom AB foyer
13:15–14:45		**Session 3: Climate change and biodiversity** Moderators: Claire Gahagan and Wen Chen	Panorama
13:15	16	Xiaoyang Zhu – Corn disease shifts in Ontario from 1998 to 2022	
13:30	17	Jazeem Wahab – SWEET POTATO: Climate Change Opens a New Opportunity for the Prairies	
13:45	18	Bourlaye Fofana – Diploid potatoes in changing climate biotic and abiotic challenges	
14:00	19	Claire Gahagan – Tillage and crop rotation effects on soil static abiotic properties and oomycete communities in different soil layers.	
14:15	20	Malina Thilakarathna – Effect of drought stress on symbiotic nitrogen fixation, soil nitrogen availability, and soil health parameters in forage legumes	
14:30	21	Chunxiao Yang – Genome-wide association studies (GWAS) of root architectural traits in a large collection of *Brassica* accessions	
13:15–14:45		**Session 4: Disease Management of Horticultural Crops** Moderators: Maria Roy and Shawkat Ali	Pinnacle
13:15	22	Lawrence Kawchuk – Blackleg diversity and biocontrol in potato from western Canada	
13:30	23	Shawkat Ali – Plant defense elicitors can reduce the use of chemical fungicides and alter the microbiome structure and composition of apple fruit	
13:45	24	Maria Roy – Evaluating biocontrol potential of fungal endophytes isolated from healthy mature apple (*Malus domestica*) trees against apple replant disease	
14:00	25	Andrea Rether – Cross-resistance of *Clarireedia jacksonii* to DMI fungicides	

14:15	26	Ethan Stratford – Determining the identity and frequency of foliar pathogens on *Vicia faba* L. in Saskatchewan.	
14:30	27	Zohralyn Homulle – Intercropping as a sustainable alternative to reduce late blight infestation in potato – a search for mechanisms.	
15:00–16:00		**Scientific Paper Workshop** - Canadian Journal of Plant Science: Improve your chance of getting published	Ballroom A
16:00–17:00		**Book launch & Networking by Keith Seifert**	Ballroom A
16:15–18:00		**Poster session 1 (P1 to P50)***	Grand Salon
18:00–19:00		**Student 3 Minute Thesis Session**	Ballroom A
20:00–23:30		**Student Trivia and Networking Night**	Spin Kitchen & Bar

*** Posters need to be installed on Monday morning and removed on Tuesday morning. Grand Salon will be accessible only on Sunday for Sponsors or poster setup and not Saturday.**

🤝**For AAFC attendees, please join us for an informal gathering organized by the Plant Health Protection portfolio team. The gathering will be held in the Capital room.**

Message from François Chretien.

Time and location: Monday June 19th, 17:00–18:30, Capital room.

Scientific Program Schedule Tuesday, June 20

Time	Abst. no	Tuesday, June 20	Location
8:00–9:30		**Symposium 1-CPS: Emerging/novel tools for plant pathogens diagnostics-1** Moderator: Guillaume Bilodeau and Vahid Jalali Javaran	Ballroom A-B
8:00	28	Guillaume Bilodeau – High throughput sequencing: Overview, challenges perspectives for plant pathogens diagnostic	
8:15	29	Jayasankar Subramanian – Black Knot resistance in plums: A multi-omic approach to address genetic resistance for an unusual disease	
8:30	30	Junye Jiang – Development and evaluation of a loop-mediated isothermal amplification (LAMP) method for *Synchytrium endobioticum* (potato wart) detection	
8:45	31	Chamath Minuka Hewapathirana – High throughput sequencing (HTS) of Bees and Pollen for Bio-surveillance of Agricultural and Invasive Pathogens	
9:00	32	Sachithrani Kannangara – RNAseq-based identification of a novel virus and novel virus variants in farmed blueberries in British Columbia	
9:15	33	Vahid Jalali Javaran – Optimizing dsRNA extraction toward rapid virus detection using nanopore sequencing	
9:30–11:00		**Session 5a: Nutriments Management** Moderators: Yutong Jiang and Hiroshi Kubota	Pinnacle
9:30	34	Mumtaz Cheema – Effects of nitrogen stabilizers on the growth, yield, and forage quality of crops grown in short rotation on podzols in boreal climate	
9:45	35	Anagha Pradeep Kumar – Seafood biostimulant effect on seed germination, plant growth, and productivity of Kale (*Brassica oleracea* var. *sabellica*)	
10:00	36	Hiroshi Kubota – Yield and pre-malting grain quality of malting barley varieties in response to increasing nitrogen rates in western Canada	
10:15	37	Farzana Yasmin – Effect of cover cropping strategies on subsequent grain corn (*Zea mays* L.) yield in no-till and fall strip-till systems.	
10:30	38	Polly Musayidizi – Long-term impacts of cover crops on nitrogen dynamics in grain corn (*Zea mays* L.) in southwestern Ontario.	
10:45	39	Yutong Jiang – Water-conducting roots responsible for nitrogen uptake in maize (*Zea mays*)	
9:30–11:00		**Session 5b: Sustainable Diseases management tools: Bioproducts, cultural practices and prediction modeling-1**	Panorama

		Moderators: Imane Laraba and Jim Menzies	
9:30	40	Meaghan Mechler – Mitigating apple replant disease with biocontrol soil treatments	
9:45	41	Chloe Shum – Metabolomics-based Profiling of Resistant Japanese Plums Infected with Black Knot Fungus	
10:00	42	Mercy Akuma – CRISPR/Cas9 gene knockout studies reveal the involvement of phenazine production in the antifungal activity of the novel *Pseudomonas chlororaphis* strain S1Bt23	
10:15	43	Leticia Reis – Thinning response of gala to metamitron applied at different stages of fruitlet development	
10:30	44	Emily McFaul – Insensitivity of *Stemphylium vesicarium* to two FRAC 7 fungicides in Ontario in 2021–2022.	
10:45	45	Haitian Yu – Enhancing soil health and root rot suppression in canola (*Brassica napus*): an investigation into fungal communities and chemical-physical properties of field soils	
11:00–12:30		**Communicating our science to the general public and policymakers**	Ballroom A-B
12:30–14:30		**Lunch (Participants will need to bring their lunch to the business meeting room)**	Ballroom AB foyer
12:30–14:30		**Lunch:** CPS Business Meeting	Ballroom A-B
12:30–14:30		**Lunch:** CSHS Business Meeting	Pinnacle
12:30–13:15		**Lunch:** CSA Business Meeting	Panorama
13:15–14:30		**CSA-Distinguished Agronomist & Genetics and Breeding 1b**	Panorama
13:15	46	Pierre Hucl – The rewards of tilting at research dogma	
13:45	47	Anjan Neupane – Genetic analysis of yield and yield stability traits in spring wheat across diverse Canadian environments	
14:00	48	Helen Booker – Underlying Mechanisms of FHB Susceptibility and Resistance in Wheat: Insights from a Transcriptome-Based Analysis	
14:15	49	Raja Khanal – Pathogenicity of *Fusarium graminearum* and *F. poae* causing Fusarium head blight in barley under controlled conditions	
14:30–15:45		**Workshop 1-CSA:** Practical carbon capture/ GHG emission measurements: Methods, Implementation and Uses	Panorama
14:30–15:45		**Session 6: Clubroot disease** Moderators: Emilee Stofie and Stephen Strelkov	Pinnacle
14:30	50	Stephen Strelkov – Clubroot in the Canadian canola crop: two decades into the outbreak	

14:45	51	Yoann Aigu – Understanding the fitness cost of resistance-breaking capacity in *Plasmodiophora brassicae*	
15:00	52	Sandra Marcela Velasco Cuervo – Efficient identification of *Plasmodiophora brassicae* pathotypes using molecular tools	
15:15	53	Emilee Storfie – The identification of an improved heterologous protein expression system for assessing the function of *Plasmodiophora brassicae* effectors	
15:30	54	Keisha Hollman – The virulence of *Plasmodiophora brassicae* on canola varieties with 'second-generation' clubroot resistance in Canada	
15:45–17:15		**Session 7: Biotic and Abiotic Challenges** Moderators: Rylie McConachie and Jatinder Sagha	Panorama
15:45	55	Jesse MacDonald – Sudden apple decline in British Columbia: a potential link between fungal cankers, invasive Sesiidae moths, and abrupt hydraulic failure.	
16:00	56	Sharandeep Singh – Genetic mapping of resistance to Fusarium head blight and DON accumulation in wheat landrace Wat.1190580	
16:15	57	Mohammed Antar – Microbe-coating fertilizers for sustainable biomass production and yield enhancement: Corn and potato case studies	
16:30	58	Riley McConachie – Winter wheat genotype-*Fusarium graminearum* isolate interactions using the detached wheat head bioassay method	
16:45	59	Vinuri Weerasinghe – Changes in barley seed bacterial endophytes under Fusarium head blight infection	
17:00	60	Roksana Saleh – Yield, Quality, and Antioxidant Enzyme Activities of Microgreens in Response to different Blue: Red LED Light Ratios and Growing Media	
15:45–17:15		**Session 8: Emerging/novel tools for plant pathogens diagnostics-2** Moderators: Edward McNab and Sean Li	Pinnacle
15:45	61	Jonathan Griffiths – Metagenomics monitoring of plant viruses in Canadian agricultural fruit production systems through honey bee pollination	
16:00	62	Shimaila Ali – In search of a decision support system: A rapid assay to detect a soil's potential to cause Aphanomyces root rot	
16:15	63	Edward McNab – A Novel Field Assay to Detect DMI Fungicide Resistance in *Clarireedia jacksonii*	
16:30	64	Ziwei Tang – ER-localized Heat shock protein 70s facilitate Turnip mosaic virus infection in Arabidopsis	
16:45	65	Xiang (Sean) Li – Closely-related pathogen classification using Clasnip.com based on gene or genomic sequences	
17:15–19:00		**Poster session 2 (P51 to P100)****	Grand Salon

19:00–22:00		**Banquet**	Ballroom A-B

**** Posters need to be installed on Tuesday morning and removed on Wednesday by 19:00.**

Scientific Program Schedule Wednesday, June 21

Time	Abst. no	Wednesday, June 21	Location
8:00–9:30		**Symposium 2- CSHS: Controlled Environment Agriculture CSHS** Moderator: Neil Mattson	Ballroom A-B
8:00	66	Youbin Zheng – Controlled environment cultivation of *Cannabis sativa*	
8:15	67	Ashleigh Ahrens – Flowering *Cannabis sativa* under photoperiods longer than 12-h can increase yield and potency	
8:30	68	Serge Levesque – Optimization and Scalability of Regenerative in situ Electrochemical Hypochlorination for Closed-Loop Hydroponics	
8:45	69	Ajwal Dsouza – Optimizing environment conditions enhances yield and nutritional quality of hydroponic barley (*Hordeum vulgare* cv. Esma) fodder	
9:00	70	Sparsha Chada – Central carbon metabolic response of Mexican mint (*Plectranthus amboinicus*) to varying watering regimes	
9:15	71	Valerie Gravel – Effect of light quality and extended photoperiod on flower bud induction during transplant production of day-neutral strawberry cultivars	
9:30–11:00		**Session 9: Sustainable Diseases management tools: Bioproducts, cultural practices and prediction modeling-2** Moderators: Anas Eranthodi and Sara Stricker	Pinnacle
9:30	72	Zayda Morales Moreira – *Pseudomonas brassicacearum* control of the root rot pathogen *Aphanomyces euteiches* via a novel nitroimidazole antibiotic	
9:45	73	Anas Eranthodi – Cereal-pulse rotations and *Fusarium avenaceum* pathogenicity	
10:00	74	Maria Oviedo-Ludena – Effect of diverse crop sequences on Fusarium head blight and leaf spot diseases of wheat in the Canadian Prairies	
10:15	75	Liam Buirs – Suppression of Botrytis cinerea Pers. induced bud-rot on greenhouse cultivated cannabis (*Cannabis sativa* L.) via enhanced air circulation and Rootshield-HC (*Trichoderma harzianum* Rifai.) spray applications	
10:30	76	Joshua Molligan – Investigating the impact of LED lighting on *Botrytis cinerea* in a controlled environment: A photomorphogenic approach	
10:45	77	Zamir Punja–Spread and impact of Hop Latent Viroid on growth and quality of cannabis (Cannabis sativa L.) plants	
9:30–11:00		**Session 10: Plant-soil health and innovation in agronomy-2** Moderators: Keisha Hollman and Kui Liu	Panorama

9:30	78	Kui Liu – Improving cropping system performance through rotation diversification with pulse crops	
9:45	79	Dhanuja Abeysingha – Cold plasma seed treatment as a potential agronomic application to increase plant growth, development, and yield in Pea (*Pisum Sativum*)	
10:00	80	Laura Van Eerd – Corn (*Zea mays* L.) grain yield gains from long-term cover cropping: evidence of increase nitrogen availability possibly due to increased soil organic matter.	
10:15	81	Joshua Nasielski – Linking plant-level measurements to crop-level outcomes: plant growth regulator effects on lodging in winter wheat	
10:30	82	Pramod Rathor – Humic acid improves the growth of wheat seedlings by modulating the expression of genes involved in auxin and cytokinin biosynthesis pathways	
10:45	83	Tarlok Sahota – Effect of Apex, Top Phos, EXCELIS MAXX and Bio-Stimulants on canola in Northwestern Ontario	
11:00–12:30		**Equity, Diversity and Inclusion (EDI)**	Ballroom A-B
12:30–14:30		**Lunch**	Ballroom AB foyer
12:30–14:30		**Lunch** Incoming CPS meeting: Board members only	Bytown room
13:00–16:00		**Workshop 2-CSA-Tour**	Panorama
14:30–16:00		**Session 11: Obligate biotrophic pathogens and soil-borne diseases** Moderators: Umbrin Ilyas and Dilantha Fernando	Pinnacle
14:30	84	Dilantha Fernando – Understanding the interaction between *Verticillium longisporum* and canola, causing verticillium stripe: the new soil-borne disease creating challenges to the industry	
14:45	85	Vikram Bisht – Verticillium wilt early dying status in Manitoba potatoes, 2020-2022	
15:00	86	Brian Duarte – Unravelling the life cycle of *Cronartium ribicola*, the causal agent of white pine blister rust	
15:15	87	Atta Ur Rahman – Understanding the causative agents of potato early dying disease in Alberta: a focus on *Verticillium dahliae*, *V. albo-atrum*, and *Colletotrichum coccodes*	
15:30	88	Kun Lou – Race characterization and strain-level disease diagnosis of the *Puccinia striiformis* f. sp. *tritici* population in western Canada from 2017 to 2022	
15:45	89	Umbrin Ilyas – Soil microbiome and calcium content in relation to the risk of cavity spot on carrots	

14:30–16:00		**Session 12: Biovigilance approach for Emerging and novel phytopathogens** Moderators: Jeffrey Pepin and Odile Carisse	Panorama
14:30	90	Odile Carisse – Challenges and possible solutions for moving towards sustainable crop protection: How can biovigilance help to structure the transition?	
14:45	91	Émilie D. Tremblay – Fungal diversity, surveillance and incidence forecasting of crop-associated phytopathogens using metabarcoding of aerial spore and suction traps	
15:00	92	Xiang (Sean) Li – Finding a needle in a haystack Using NGS and associated bioinformatics toolkit	
15:15	93	Tom Hsiang – Naturally occurring propiconazole-tolerant fungal isolates in the phyllosphere of *Agrostis stolonifera*	
15:30	94	Jeffrey Pepin – Screening of grain and oilseed using a combination of long read sequencing and qPCR assays for bio-surveillance of phytopathogens	
15:45	95	Bradley Calder – Assessing the variability of *Sclerotinia sclerotiorum* isolates collected from different host crops across Canada	
16:00–17:30		**Session 13: Genetics, biotechnology, and breeding-2** Moderators: Sparsha Chada and Lord Abbey	Pinnacle
16:00	96	Sepideh Torabi – Unravelling resistance mechanisms: Dual RNA sequencing of soybean and soybean Cyst Nematode (SCN)	
16:15	97	Raman Dhariwal – Insights from the first FHB-resistant wheat cultivar AAC Tenacious	
16:30	98	Soren Seifi – Cannabis landraces and exotic germplasm as a great source for resistance breeding against powdery mildew disease	
16:45	99	T. Fatima Mitterboeck – Understanding Potato Greening through ‘omics approaches	
17:00	100	Hari Poudel – An insight into sainfoin breeding in western Canada: challenges and achievements.	
17:15	101	Yousef Papadopoulos – Evaluation of new breeding lines of alfalfa, birdsfoot trefoil and red clover for adaptation to low pH soil conditions	
16:00–17:30		**Session 14: Long-term studies: Soil and plant** Moderators: Atta Ur Rahman and Sean Westerveld	Panorama
16:00	102	Syama Chatterton – Changes in pea yield and root rot levels in field trials naturally-infested with *Aphanomyces euteiches* in Alberta and Saskatchewan	
16:15	103	Sean Westerveld – Survey and management of plant parasitic nematodes in Ontario ginseng	

16:30	104	Noureddine Benkeblia – Climate change and crops health in the Caribbean: Threats and challenges	
16:45	105	Bruce Gossen – Survival of *Plasmodiophora brassicae* over time in trials on the Canadian Prairies	
17:00	106	Michelle Hubbard – Pea-brassica intercropping does not ameliorate root rot in pea, but sometimes provides yield benefits	
17:15		**Closure of the meeting**	Ballroom A-B
18:15–19:00		**Poster removal**	Grand Salon

THE CANADIAN PHYTOPATHOLOGICAL SOCIETY
LA SOCIÉTÉ CANADIENNE DE PHYTOPATHOLOGIE

The Canadian Phytopathological Society

The Canadian Phytopathological Society (CPS) is a scientific society for plant pathologists established in 1929 to encourage research, education, and the dissemination of knowledge on the nature, cause, and control of plant diseases. The society has around 300 members in Canada and abroad, including graduate students, postdoctoral fellows, research associates, technical assistants, extension plant pathologists, research scientists and university professors. In addition, several grower organizations and private companies are sustaining members. CPS members have expertise in all facets of plant pathology from applied field research to investigations of host-pathogen interactions at the molecular level. The society presents several types of awards to members, including 'Award for Outstanding Research', 'Career Recognition Award', 'Outstanding Young Scientist Award' and several awards for graduate students.
The society's work is guided by a Board of Directors, several committees and eight regional societies. For 2022-2023 the Board consists of:

President:	Sheau-Fang Hwang
President Elect:	Gary Peng
Vice President:	Guillaume Bilodeau
Past President:	Lone Buchwaldt
Secretary:	Tom Fetch
Treasurer:	Kenneth Conn
Membership Secretary:	Vikram Bisht
CJPP Editor in Chief:	Linda Jewell
Senior Director at Large:	Wen Chen
Junior Director at Large:	Sara Stricker
CPS Website Editor:	Michael Holtz
Student Representative:	Minuka Hewapathirana

Publications
The CPS oversees the publication of the Canadian Journal of Plant Pathology with the help of many Section and Associate Editors who ease the flow of manuscripts through the review process. CPS publishes two books, 'Diseases of Field Crops in Canada' and 'Diseases and Pests of Vegetable Crops in Canada', the latter in both English and French. Other publications include the annual 'Pest Management Research Reports' and the 'Canadian Plant Disease Survey', which celebrated its' 100th anniversary in 2019. The society also distributes a Newsletter, maintains a web site https://phytopath.ca/ and has a presence on both Facebook and Twitter.

Annual meetings and collaboration with other societies
The CPS oversees the publication of the Canadian Journal of Plant Pathology with the help of many Section and Associate Editors who ease the flow of manuscripts through the review process. CPS publishes and updates two books, 'Diseases of Field Crops in Canada' and 'Diseases and Pests of Vegetable Crops in Canada', the latter in both English and French. Other publications include the annual 'Pest Management Research Reports' and the 'Canadian Plant Disease Survey', which celebrated its' 100th anniversary in 2029. The society also distributes a Newsletter, prepares online workshops, maintains a web site https://phytopath.ca/ and has a presence on both Facebook and Twitter.

Canadian Society of Agronomy
La Société Canadienne d'Agronomie

The Canadian Society of Agronomy

The Canadian Society of Agronomy (CSA) is a non-profit, educational and scientific society. 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, and to provide opportunities for members to communicate news and scientific findings to the scientific community. More information can be found at AgronomyCanada.com

CSA Executive Members (2022-2023)

President	Jamie Larsen
Executive Director	Marcie Wilson
Past President	Mumtaz Cheema
President-Elect	Harpinder Randhawa
Secretary-Treasurer	Gurcharn Singh Brar
Western Directors	Hiroshi Kubota
	Kui Liu
Eastern Directors	Milad Eskandari
	Kathleen Glover
Student Representative	Nate Ort
Industry Representative	Jagroop Gill Kahlon
Canadian Journal of Plant Science Representative	Ben Thomas

Acknowledgements:
The Graduate Student Pest Management Award Student is supported in part by Bayer Canada – Crop Science Division. The CSA is grateful for their support.

Contact Information:
For more information on CSA Membership or our awards program contact Marcie Wilson, Executive Director 30 Tallgrass Crescent, Winnipeg, MB, R3X 0C9 Phone: 204-228-8508, csagronomy@gmail.com or visit our website at agronomycanada.com and follow us on Twitter and Facebook @agronomycanada.

Canadian Society for Horticultural Science

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 (2022-2023)

Horticulture production in Canada is extremely diverse and one of the main priorities of the CSHS is to make sure that this is reflected in the activities of the Society. Again this year, the CSHS has a pan-Canadian representation on its board of directors, with members coming from coast to coast. While we practice a progression within the board, our members are encouraged to submit their candidacy to any position available. Terms are for 2 years with the possibility of 2 consecutive terms at the same position. Please contact the current CSHS secretary (Lord Abbey at LAbbey@Dal.Ca) and visit our website) if you are interested in joining the CSHS executive board or if you are interested in becoming a member and participating in specific activities.

CSHS Student Committee

Students are an integral part of the CSHS and their involvement in the Society is important and valued. A Student committee was implemented in 2016 within the Society to support students' initiatives. To know more, 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 Student Committee. If you are interested, contact the current Student Committee Chair (email address is listed on our website).

Becoming a member of the CSHS

Numerous benefits are offered to CSHS members including:

• A significantly reduced registration fee at the annual CSHS conferences and at the Plant Canada Conference•

Reduced page charges to publish in the Canadian Journal of Plant Science

• Timely direct mail alerts to jobs, grant opportunities, etc.

• Eligibility to the Most Cited CJPS Paper award for horticulture (which comes with an invitation to be a conference speaker)

In addition, for students, benefits also include:

• Eligibility for the Awards for oral and poster presentation

• Eligibility for Travel Awards to the annual conference

• Community & Extension Funding, which supports student activities in introducing any form of Horticulture science in communities

• Network between members, sharing of experiences about studies and research

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

Keynote speakers

Dr. Amélie Gaudin

Dr. Amélie Gaudin is Associate Professor and Endowed Chair of Agroecology in the Department of Plant Sciences at the University of California Davis. She obtained a Ph.D. in Plant Agriculture at the University of Guelph (Canada) and worked as an agronomist and crop physiologist at various CGIAR centers to sustainably intensify staple food crop production in smallholder farming systems. She currently leads a dynamic and diverse team of students and postdoctoral researchers to characterize outcomes of regenerative agricultural models that have conservation of natural resources, agrobiodiversity, and ecosystem services as a basis for improvements. She engages communities with the science of agricultural ecology by collaborating with and learning from a diverse group of students, growers, advisors, and policy advocates. Her research integrates concepts and methodologies from various disciplines to measure multifunctional outcomes of ecological intensification and regenerative strategies on soil health, C sequestration and drought resilience. She is also interested in better understanding root system and rhizosphere ecology and their potential to harness improvements in soil health, sequester carbon and decrease crop water and nutrients requirements. More information here: http://gaudin.ucdavis.ed

Dr. Neil Mattson

Dr. Neil Mattson is Professor and greenhouse extension specialist within the Horticulture Section, School of Integrative Plant Science at Cornell University. Prior to joining Cornell in 2007, Dr. Mattson completed his PhD in Plant Biology and UC Davis and his M.S. in Horticulture at the University of Minnesota. Dr. Mattson researches technologies to reduce natural resource use in greenhouse floriculture and vegetable production while maintaining or improving profitability. Particular interests include plant responses to light quantity and quality, energy efficient light control strategies, and optimizing crop nutrient management. Dr. Mattson has authored or co-authored 69 peer-reviewed journal articles, 15 book chapters, 169 extension articles and has given more than 300 outreach presentations to more than 16,000 greenhouse industry members. Dr. Mattson is the director of Cornell University's Controlled Environment Agriculture program. nsm47@cornell.edu

Dr. Mario Tenuta

Dr. Mario Tenuta P.Ag., is the Natural Science and Engineering Council/Western Grains Research Foundation/Fertilizer Canada Senior Industrial Research Chair in 4R Nutrient Stewardship and Professor of Applied Soil Ecology at the University of Manitoba. His training includes a B.Sc. in Botany and Physical Geography, an M.Sc. in Soil Fertility, a Ph.D. in Plant Pathology, and Post-Doctoral research in Nematology. The 4R Industrial Research Chair Program is advancing research in 4R nitrogen management practices to give farmers and industry solutions to achieving nitrous oxide emission reductions and improved soil health and crop productivity. A key feature of the Chair program is conducting farm-based research with particular attention to the outreach of findings to farmers, industry and policy-makers. A key feature of the Chair program is conducting farm-based research with particular attention to the outreach of findings to farmers, industry and policy-makers. mario.tenuta@umanitoba.ca
Twitter: @soilecologyUMan

To learn more about Mario and the Chair program, please visit www.soilecology.ca

Tours of the national collections at Ottawa Research and Development Centre

960 Carling Ave., Ottawa, ON, Canada

[June 18, 2023, Sunday, 8:30 am – 1:30 pm]

Schedule:

08:20 – 08:30 am	Bus pick up at the Delta Hotel, take attendance. Get split into 3 groups of 10.
08:30 – 09:00 am	Travel to K.W. Neatby building (960 Carling Ave.)
09:00 – 09:30 am	Drop off visitors at the lobby of K.W. Neatby. Sign in with security. One group to walk over to Saunders for DAO/DAOM tour; one group to wait in the lobby for DAOMC tour; one group to go to the third floor for CNC tour
09:30 – 10:00 am	Tour 1.
10:00 – 10:15 am	Buffer & travel time.
10:15 – 10:45 am	Tour 2.
10:45 – 11:00 am	Buffer & travel time.
11:00 – 11:30 am	Tour 3.
11:30 – 12:40 pm	Gather in Salon A for lunch and social.
12:40 – 01:00 pm	Sign out of K.W. Neatby building. Get on the bus at K.W. Neatby entrance.
01:00 – 01:30 pm	Travel back to Delta Hotel.

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Click the following links to read more about the national collections at Ottawa Research and Development Centre

Canadian Collection of Fungal Culture (DAOMC)

Canadian National Mycological Herbarium (DAOM) ***and*** ***National Collection of Vascular Plants (DAO)***

Canadian National Collection of Insects, Arachnids, and Nematodes (CNC)

Field Tour at CFIA Fallowfield & Central Experimental Farm, Ottawa R&D Centre, AAFC

[June 21, 2023, 12:30 – 16:00]

Tentative schedule:

12:30 Bus pick up at the Delta Hotel, take attendance. Box lunch for registered attendees.

13:00 Arrive CFIA Fallowfield Site

13:00 GHG emissions Measurement Demonstration Andy VanderZaag & Luc Pelletier

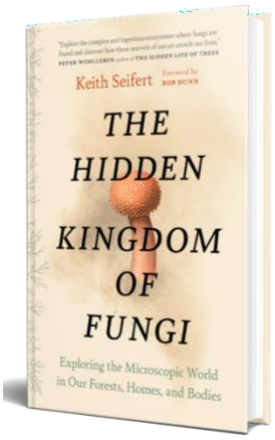
13:50 Depart CFIA Fallowfield Site

14:10 Arrive CEF Ash Lane @ Field Central 9a

14:15 Presentations:

- Elroy Cober - Introgressing wild germplasm into elite soybean;
- Malcolm Morrison - Phenomics data capture; and
- Others
- 15:30 - Depart CEF for Delta Hot

Book Launch and Networking: [June 19, 2023, Monday, 4 – 5 pm]



Join **Dr. Keith Seifert** and celebrate the launch of his enlightening new book,

The Hidden Kingdom of Fungi: Exploring the Microscopic World in Our Forests, Homes, and Bodies

published by Greystone Books, which explores how fungi affect the environment and our daily lives.

==========

Keith is a retired mycologist after an esteemed career at Agriculture & Agri-Food Canada. His research expertise was the taxonomy of the asexual fungi known as Hyphomycetes, especially genera such as *Fusarium* and *Penicillium* that produce mycotoxins. His research involved the collection and culturing of fungi from agricultural (especially those producing mycotoxins) and other ecosystems (such as forests or the indoor environment), microscopy, DNA-based phylogenetics, the description of new species and genera, and the development of identification systems that can be used by other people scientists, based on either DNA or microscopy. He was very active in fungal DNA barcoding, which has led to a later interest in environmental metagenomics and fungal genomics.

Keith's specimens and cultures are deposited in the Canadian National Mycological Herbarium and the Canadian Collection of Fungal Cultures. Keith is now a freelance writer and writing books on the impact of science on human affairs.

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Draft agenda (Ballroom A):

⇒ Welcome remarks –Dr. C. André Lévesque [5 min]

⇒ Short presentation – Keith [20 min]

⇒ Q&A – [10 min]

⇒ Networking

Panel Discussion:

Communicating our science to the general public and policymakers

[June 20, 2023, Tuesday, 11 AM – 12:30 PM]

Introduction: Agriculture and forestry intensification, global trade, and climate change increase the incidence and spreading of existing, emergent, and invasive diseases, threatening agricultural production and natural ecosystems. The general public and stakeholders expect the scientists, regulators, and policymakers to speak up on timely and long-standing issues that have profound impacts on the health, economy, environment, and their daily lives. Scientists are expected to provide independent advice to policy and decision makers with the best-available evidence and are being asked to make statements on science-related issues through their scientific publications but also through mainstream media (e.g., magazine, radio and TV interviews, documentary broadcasting, etc.), online forums and social media, citizen science, as well as teaching activities.

To ensure food safety and security, protect the forests, the biodiversity, and the environment, and maintain ecological goods and services, plant pathologists need to engage the public, stakeholders, and policymakers and raise awareness about the damages caused by plant pests and pathogens, the control measures and strategies, and risk forecasting and management schemes for plant protection. There is an increasing need for effective science communication targeted to decision-makers but also to make key science findings more readily identified and accessible to the general public.

Panelists

Moderator:

- C. André Lévesque – Former research scientist, CPS President, and science executive in the public service, with leaderships in developing programs and policies for large R&D centers and Canada-wide R&D initiatives.

Panelists:

- Bill (William) Anderson - Executive Director, Plant Health Science Directorate of the Canadian Food Inspection Agency (CFIA). Bill was previously the Executive Director of the Plant Health and Biosecurity Directorate in the CFIA's Policy and Programs Branch.

- Gilles Saindon – Assistant Deputy Minister, Science and Technology Branch, Agriculture and Agri-Food Canada.

- Kelly Turkington – Plant Pathologist with the Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, in Lacombe, Alberta.

2023 Canadian Phytopathological Society-Canadian Society of Agronomy-Canadian Society for Horticultural Science (CPS-CSA-CSHS) Tri-Society Meeting

Workshop:

Practical Carbon Capture/GHG Emission Measurements: Methods, Implementation and Uses

[June 20, 2023, Tuesday, 2:30PM-3:45 PM]

Introduction:

The Tri-Society meeting theme is "Agroecosystem Resiliency Under a Changing Climate". This theme was selected by the organizing committee based on the importance of addressing climate change challenges in Agriculture. Recognizing the need to quantify agronomic management impacts on our climate, this workshop was developed to provide practical information to researchers considering incorporating greenhouse gas and carbon capture quantification methods into their research.

The format of this workshop will be similar to an informal classroom lecture setting. This workshop will discuss using chamber-based and microscale meteorology (MicroMet) methods to capture Nitrous oxide and Ammonia emissions, as well as challenges, time lines, equipment and labour to implement these methods. Methods to measure carbon capture will also be discussed. Modelers will provide information on how this data is used and gaps in current datasets where further research would be useful to properly model agriculture emissions. A brief demonstration of the Holos Model, a whole-farm model and software program that estimates greenhouse gas (GHG) emissions will be provided.

Presenters

- Mario Tenuta-Senior Industrial Research Chair in 4R Nutrient Management and Professor (Soil Ecology), Professor, University of Manitoba
- Andy VanderZaag-Research Scientist, Agriculture and Agri-Food Canada, Ottawa Research and Development Centre
- Sarah Pogue-Model Developer (Holos), Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre
- Aaron McPherson-Computer Programmer (Holos), Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre

2023 Canadian Phytopathological Society-Canadian Society of Agronomy-Canadian Society for Horticultural Science (CPS-CSA-CSHS) Tri-Society Meeting

Panel Discussion:

Equality, Diversity, and Inclusion (EDI) [June 21, 2023,Wednesday, 11 am – 12:30 pm]

Introduction: Equity, Diversity and Inclusion (EDI) are essential in the research context because they allow to provide opportunities to all potential researchers, where they can reach their full potential, providing impactful results in science. But EDI is also relevant because of the social implications of research and the need for fairer society.

As in other settings, disparities can have deep effects in the research environment. Providing a fair environment where differences are accepted and recognized, and where individuals are provided with all tools to reach their goals is conducive to team success. An environment where EDI is placed as part of the core values provides a better sense of belonging and safety, allows to provide ideas from different perspectives leading to innovation, and opens the door for more diverse collaborations and recruitment.

In the research context, EDI needs to be taken into consideration not only when assembling a team but also for the research project itself. The people who will be impacted by the development and results of a project need to be part of the conversation at all project stages. This approach provides a clearer picture of the real needs of stakeholders and generates better cooperation towards reaching targets.

The current panel will discuss the positive impact of an equitable and diverse research environment, the organizational changes needed to make that environment really inclusive, and the current challenges and potential avenues for improvement.

Panelists

Moderator (Confirmed):

- Leonardo GalindoGonzalez – Research Scientist with the Canadian Food Inspection Agency. Worked in formal and non-formal science communication and in committees for improvement of workplace culture.

Panelists (Invitees):

- Diane Allan - VP Science Branch and Chief Diversity Officer, Canadian Food Inspection Agency.
- Jaclyn Brusso - Professor & Vice-Dean of Equity, Diversity, Inclusion and Professional Development, Department of Chemistry and Biomolecular Sciences, Faculty of Science, University of Ottawa
- Rowan Thomson - Professor & Associate Dean (Equity, Diversity, and Inclusion), Department of Physics, Faculty of Science, University of Carleton
- Adrian Chan - Professor and Director, Research and Education in Accessibility, Design, and Innovation (READi); Department Systems & Computer Engineering, Faculty of Engineering and Design, University of Carleton.

- Emilee Storfie - Ph.D. Candidate, Financial Manager and Reporter, Women in Science, Engineering and Research (WiSER); Department of Agricultural, Food and Nutritional Science, Faculty of Agricultural, Life and Environmental Studies.

Draft agenda:

- Opening – welcome remarks.
- Introduction of panelists.
- Topics:
    - Positive impact of a diverse research environment (the presence of different points of views and ideas in research).
    - How to generate real inclusive environments (looking at diverse backgrounds, idiosyncrasies and culture to create pro-active research).
    - Providing tools for everyone to succeed (looking at differences to reach equity)
    - Largest barriers for EDI in research.
    - Potential actions for present challenges.
- QA session (open to audience).
- Closing remarks.

Improve Chances of Getting Published!

Workshop by Canadian Journal of Plant Sciences

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Monday June 19th
4pm—5pm
Delta Hotels Ottawa City Centre

Trivia Night & Social

Students are invited to a fun night of trivia!
Groups of 3-4 will compete for trivia glory!
Trivia winner will be announced!

Networking and social will follow!

REGISTER to reserve a drink ticket : https://forms.gle/tmYdh35iGXsJiD3n8

Monday June 19th
8pm-10pm
Spin Kitchen & Bar , 100 Kent St, Ottawa

3 Minute Thesis

Canadian Tri–Society Meeting

June 17th— 21st 2023

Agroecosystem resiliency under climate change

1st, 2nd, 3rd, and Peoples Choice Prizes

June 19th 7pm—8pm

Students are invited to present a topic of their choice which relates to the theme of the symposium for **3 minutes**

Max slide limit: 3 slides

A panel of judges (SSC) will judge the contestants

Delta Hotels by Marriott Ottawa City Centre

Organized by the Student Social Committee

Moderator: Emily McFaul, CPS Co-chair of the Student Social Committee

Judges:

Minuka Hewapathirana, CPS Co-chair

Simon Lackey, CSA Co-chair

Raphael Ofoe, CSHS Co-chair

3MT Competitors

Keval Shah
University of Manitoba
Identification of resistance in hexaploid Brassica against *Leptosphaeria maculans* and introgression in *Brassica napus*.

Riley McConachie
University of Guelph
High-Throughput Phenotyping of Fusarium Head Blight Symptoms in Winter Wheat

Sharan Dhaliwal
University of British Columbia
Genetic mapping of resistance to FHB and DON accumulation in wheat landrace

Natalie LaForest
University of Alberta
Genetics & generalist predators: Can an introduced insect be beneficial in agroecosystems?

Ronak Samadpour
University of Padova
Exploration of grapevine research

Anagha Pradeep Kumar
Dalhousie University
Seafood Biostimulant effect on Seed Germination, Plant Growth, and Productivity of Kale (*Brassica oleracea* var. *sabellica*)

Yakob Ghirmay Ghilamichael
University of Florence
Combined effect of different levels of remediated wastewater and biochar as a substrate in tomato (*Solanum lycopersicum*) in Firenze, Italy

Mercy Akuma
University of Ottawa
CRISPR/Cas9 gene knockout studies reveal the involvement of phenazine production in the antifungal activity of the novel *Pseudomonas chlororaphis* strain S1Bt23

Fernando Guerrero Zurita
University of Alberta
Identifying superior photosynthetic traits in canola *Brassica napus* gene pool

Caio Rodrigues-Correa
University of Guelph
Dissecting Bacterial Brown Spot and Common Bacterial Blight Resistance in Common Bean

Eliassaint Josue
Université Quisqueya
TBD

Josenel Floradin
UNASMOH
Impact de la maladie des plantes en milieu tropical.

Bawa Nutsukpo
Dalhoulsie University
Influence of biostimulants in carbon-nitrogen metabolism in plants

Vincent Bishop

Performance: Tuesday, June 20th at the banquet

In concert, this young Franco-Ontarian, originally from Vancouver, abounds with positive energy. His versatile loop pedal arrangements, performed on guitar, bass, banjo or a capella, always leave the audience wanting more. His 3rd album “L’amour serait bienvenu” was released last year. Produced by John-Anthony Gagnon-Robinette (Kaïn, Reney Ray, Brittany Kennell), his new opus is a vibrant collection of original works inspired by French-Canadian “chansons à répondre”. With a good dose of trad, a little country, pop singalongs and some beatboxing to boot, describing this album and his concerts only as “festive” would be a serious understatement!

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Acknowledgements

Committee Members Organizing The Canadian Tri-Society Meeting, 2023

Executive Group

Guillaume Bilodeau	Chair of tri-society meeting, CPS
Gary Peng	Executive for CPS
Mumtaz Cheema	Executive for CSA
Jamie Larsen	CSA President elect
Ken Conn	CPS Treasure (Finance)
Youbin Zheng	President for CSHS
Bourlaye Fofana	Executive for CSHS

Portal for registration, Website

Michael Holtz	Chair: Web site master for CPS (CPS webpage, registration abstract)
Ken Conn	Treasurer for CPS
Diane Edwards	Treasurer for CSHS
Shahrokh Kanizadeh	Webmaster for CSHS
Gurcharn Brar	Treasurer for CSA
Kui Liu	CSA tech support

Hotel Committee

James Tambong	CPS
Wen Chen	CPS
Ken Conn	Treasurer for CPS
Guillaume Bilodeau	CPS
Émilie Tremblay	CPS (Menu-Foods)

Scientific Committee including the Executive Group

Mamadou L. Fall	CPS Co-chair
Youbin Zheng	CSHS Co-chair
Jamie Larsen	Keynote/Plenary-CSA
Hervé Van der Heyden	CPS
Guillaume Bilodeau	CPS
Harvinder Bennypaul	CPS
Bourlaye Fofana	CSHS
Shawkat Ali	CSHS
Wen Chen	CPS
Lord Abbey	CSHS
Harpinder Andhawa	CSA (Scientific program oral pres.)
Mumtaz Cheema	CSA (Student program pres.)

Workshops Committee and Special sessions

Wen Chen	CPS Chair
Hai Nguyen	Co-Chair CPS
Shawkat Ali	CSHS Co-chair
Jamie Larsen	CSA
Andrew Burt	CSA
Sara Stricker	CPS
Bourlaye Fofana	CSHS
Lord Abbey	CSHS
Leonardo Galindo	CSA
André Lévesque	CSA

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Shawkat Ali	CSHS Co-chair
Lord Abbey	CSHS
Sean Westerveld	CSHS/CPS
Jim Menzies	CPS

Society Awards Committee

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Mumtaz Cheema	CSA
Vasantha Rupasinghe	CSHS
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Emily McFaul	CPS Co-Chair
Nate Ort	CSA Co-Chair
Simon Lackey	CSA Co-Chair
Raphael Ofoe	CSHS Chair

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Youbin Zheng	CSHS
Valerie Gravel	CSHS
Fouad Daayf	CPS
Jagroop Gill Kahlon	CSA

Communications and Advertising

Vikram Bisht	CPS membership secretary
Marcie Wilson	CSA
Milad Eskandari	CSA
Hiroshi Kubota	CSA
Valerie Gravel	Communications for CSHS
Bourlaye Fofana	Communications for CSHS
Linda Jewell	CPS Newsletter

Program Book Committee

Sarah Drury	CPS
Guillaume Bilodeau	CPS
Mamadou Fall	CPS

Committee for Technical Support, Printing, Registration desk, Animation…

Sarah Hambleton	CPS
Sara Stricker	CPS
Andrea Botero	
Sandra Marcela	
Velasco Cuervo	
Kui Liu Kui	CSA
Emily Giroux	CPS

Session moderators

Raphael Ofoe	CSHS
Jaswinder Singh	CSA
Claire Gahagan	CPS
Maria Roy	CSHS
Yutong Jiang	CPS
Imane Laraba	CPS
Emilee Stofie	CPS
Rylie McConachie	CPS
Edward McNab	CPS
Anas Eranthodi	CPS
Nate Ort	CSA
Umbrin Ilyas	CPS
Jeffrey Pepin	CPS
Sparsha Chada	CSHS
Atta Ur Rahman	CPS
Kelly Turkington	CSA
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Jatinder Sagha	CPS
Sean Li	CPS
Sara Stricker	CPS
Kui Liu	CSA
Dilantha Fernando	CPS
Odile Carisse	CPS
Lord Abbey	CSHS
Sean Westerveld	CPS/CSHS
Guillaume Bilodeau	CPS
Mamadou L. Fall	CPS
Jamie Larsen	CSA
Youbin Zheng	CSHS
Neil Mattson	
Vahid Jalali Javaran	CPS

Abstracts

Plenary session: Agroecosystem resiliency under a changing climate

1. Building Agroecosystem Resiliency to a Changing Climate A. GAUDIN *Department of Plant Sciences at the University of California Davis, Davis, California, U.S.A.*

Diversifying and re-designing cropping systems based on agroecological principles can provide new avenues to mitigate climate risks in agriculture. I will share the resilience building potential of several strategies implemented and tested by California and Midwest farmers and discuss some of the mechanistic underpinnings. I will conclude with research needs to enhance adoption and impacts.

2. Optimizing plant quality, environmental, and socioeconomic outcomes of controlled environment agriculture crops N. MATTSON *School of Integrative Plant Science, horticulture section at Cornell University, Ithaca, New York, U.S.A.*

The production of high nutrient density crops in controlled environment agriculture (CEA, i.e., greenhouses and vertical farms) allows for high yielding, year-round food production. CEA is one tool to address food system resiliency under a changing climate. CEA has seen increased attention from investors but there is a lack of information on successful models, especially urban production, and vertical farming. Mattson leads an NSF-funded project that seeks to better understand the benefits and constraints of urban CEA including: economics, natural resource use, carbon footprint, and nutrition. Mattson will discuss related research that seeks to optimize crop performance and energy/water use through strategic LED lighting and light spectrum and precise control algorithms for light and carbon dioxide. Engaging the next generation of CEA workers is crucial if the industry is to expand. Mattson will discuss efforts of the NSF project to define workforce development needs by the nascent CEA industry and a new USDA workforce development project to expand training opportunities in CEA for 2-year colleges and lifelong learners.

3. The Evolving Role of Nitrogen Management in Crop Production M. TENUTA *Department of Soil Science, University of Manitoba, Winnipeg, Manitoba, Canada*

Nitrogen (N) supply to crops is one of the most important determinants of crop yield and input cost for farmers. Further nitrogen availability is for the quality of crop products, plant health and disease tolerance. There is no doubt of synthetic nitrogen fertilizers' great contribution to increasing global food production. However, the greater use of nitrogen in cropland has ramifications for water and atmospheric quality, greenhouse gas emissions and deposition (fertilization) of natural systems. Understandably nitrogen management in croplands has been more concerned with productivity and, to a lesser extent, environmental consequences. With a necessity for reducing greenhouse gas emissions (GHG) and achieving net zero emissions, the objectives of nitrogen management are changing. The N fertilizer supply chain accounts for 2.1% of global GHG emissions (1% of each production and soil emissions and 0.06% transportation of fertilizers). However, this doesn't account for livestock manure emissions, where about half of the nitrogen animals consume comes from fertilizers. We are using fertilizer N in croplands better. Improvements in nitrogen use efficiency in highly productive-input systems, such as Canada, are evident. Important regions with poor use efficiency, such as China, are also beginning to improve. However, there will be 1.75-2 billion more people by 2050, with increases greatest for sub-Saharan Africa and Central and South Asia. Areas depend on importing grains and oilseeds and using relatively low amounts of N fertilizer. To feed the global population in 2050, an increase of 37% in nitrogen addition to cropland is required. Farmers have always considered the return on investment of nitrogen cost, but that interest ebbs and flows depending on the cost of fertilizer. Recently fertilizers have reached unprecedented high costs.

Unsurprisingly, how farmers manage N fertilizer is changing, with more attention given to minimizing environmental consequences, improving nitrogen use efficiency, and increasing return on investment. The 4 R Nutrient Stewardship framework of applying nutrients at the right rate, source, placement and timing gives farmer and researcher a means to manage N better.

Research by the 4R Industrial Research Chair Program over the past 12 years has shown that for highly productive, input-intensive agriculture, such as in Western Canada, applying the 4Rs doesn't usually increase yields. However, the 4Rs significantly reduce N losses to the environment, which is critical to achieving Canada's GHG reduction targets for 2030. We have found reductions in nitrous oxide (N2O) emissions from cropland to be reduced in order Legumes > Split N Application > Nitrification inhibitors > Controlled Release N Fertilizer. Moving forward, it is important to dedicate research and outreach to reduce losses, GHG emissions and improve the use efficiency of N fertilizer because N rates applied to cropland will continue to go up as yields increase. Greater attention will be given to reducing indirect emissions of N2O from ammonia volatilization and leaching of fertilizers. There is much room for increased use of 4R practices by farmers. Though the adoption of 4R practices may not result in yield increases, it should allow the use of N additions more efficiently and reduce rates, by how much we know. Developing more sophisticated 4R practices is underway, particularly in the area I term Precision 4R Management. Here fields are managed for N individually with attention to management zones and landscape positions within fields. 4R practices cost farmers money and are a significant barrier to greater adoption of

practices. Recently governments have rolled out cost-sharing programs to offset the cost of implementing 4R practices. Another means of offsetting increased costs is selling GHG credits to C markets, though such a market mechanism is not developed in Canada. An exciting means to reduce GHG emissions from the production of N fertilizer is using renewable energy, primarily electricity, to produce "green ammonia" instead of natural gas. Lastly, change in consumer preference and behaviour to greater pulse and plant protein consumption will lessen demand for synthetic N and more reliance on biologically produced N, which has a lot less GHG emissions."

Session 1: Plant-Soil health and Innovations in Agronomy-1

4. The impact of row spacing, seeding rate, and fungicide timing on the severity of leaf disease, fusarium kernel damage, deoxynivalenol, and productivity of spring wheat T. K. TURKINGTON, H. KLEIN-GEBBINCK, K. XI, S. REHMAN, B. BERES, R. ABOUKHADDOUR, P. LOKURUGE, A. MULENGA, G. PENG, W. MAY, R. MOHR, G. TELMOSSE, D. PAGEAU, A. FOSTER, B. BLACKWELL, H. KUBOTA, B. TIDEMANN, AND G. SEMACH *(T.K.T., H.K., B.T.) Lacombe Research and Development Center, Agriculture and Agri-Food Canada, Lacombe, AB T4L 1W1, Canada; (H.K.G.) Beaverlodge Research Farm, Agriculture and Agri-Food Canada, Beaverlodge, AB T0H 0C0, Canada; (K.X., S.R.) Field Crop Development Centre, Olds College, Lacombe, AB T4L 1W8, Canada; (B.B., R.A.) Lethbridge Research and Development Center, Agriculture and Agri-Food Canada, Lethbridge, AB T1J 4B1, Canada; (P.L., A.M.) Scott Research Farm, Agriculture and Agri-Food Canada, Scott, SK S0K 4A0, Canada; (G.P.) Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, Saskatoon, SK S7N 0X2, Canada; (W.M.) Indian Head Research Farm, Agriculture and Agri-Food Canada, Indian Head, SK S0G 2K0, Canada; (R.M.) Brandon Research and Development Center, Agriculture and Agri-Food Canada, Brandon, MB R7A 5Y3, Canada; (D.P., G.T.) Normandin Experimental Farm, Agriculture and Agri-Food Canada, Normandin, QC G8M 4K3, Canada; (A.F.) Crops and Livestock Research Centre, Agriculture and Agri-Food Canada, Charlottetown, PEI C1A 4N6, Canada; and (B.B.) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa, ON K1A 0C6, Canada*

The impact of row spacing, seeding rate, and fungicide on spring wheat was assessed at seven research sites in 2018, 2019, 2021 and 2022. Narrow and wide row spacings were only set up at four sites, while seeding rates (SR) of 200 and 400 seeds m^{-2} were used at all sites. Fungicide (Prosaro XTR) timings included: no treatment; the start of anthesis (early); 7-10 days after the start of anthesis (late); and both early and late applications (dual). Leaf spot, fusarium damaged kernel (FDK) and deoxynivalenol (DON) levels varied depending on site and year. Overall, SR and fungicide tended to have the most consistent impacts on agronomic and disease parameters. The impact of SR was likely via an influence on canopy microenvironment, inter-plant competition, improved weed competition, or the production of a more uniform crop stand that reduced the window for potential FHB infection and/or provided a more uniform fungicide target. The impact of fungicide varied depending on site as to whether single early or late, or dual fungicide applications were better for reducing leaf spots, FDK severity and DON, while improving grain yield and kernel parameters. At some sites delaying fungicide application to the single late timing allowed for further leaf spot development on upper canopy leaves. For FDK and DON, results suggested there was no consistently ideal fungicide timing in terms of comparing single applications at the start of anthesis or 7-10 days later. In addition, the dual timing tended to more consistently reduce FDK an DON levels.

5. Utility of organic amendments for managing root-lesion nematodes prior to replanting apple orchards T. A. FORGE, P. MUNRO, K. FULLER, V. LEVESQUE, AND S. ALI *Summerland Research and Development Centre, Agriculture and Agri-Food Canada, 4200 Highway 97, Summerland, British Columbia, V0H 1Z2, Canada; and (K.F., V.L., S.A.) Kentville Research and Development Centre, 32 Main Street, Kentville, NS B4N 1J5, Canada*

Root-lesion nematodes, particularly the species *Pratylenchus penetrans* (Cobb) Filipjev & Schuurmans-Stekhoven, are cosmopolitan pests of horticultural crops. They have long been associated with poor growth of juvenile apple and cherry trees replanted into old orchard sites where populations have built up. In an effort to provide sustainable alternatives to soil fumigation for the management of root-lesion nematodes, we have conducted a series of greenhouse and field experiments to determine the effects of several organic soil amendments on the infestation of roots by *P. penetrans* and the growth of apple rootstock trees in old orchard soils. Biochar suppressed *P. penetrans* infection of apple roots in two separate greenhouse experiments, and a mustard seed meal amendment with biofumigant properties similarly suppressed *P. penetrans* infection in a greenhouse experiment. Compost suppressed *P. penetrans* infection in a field experiment in Nova Scotia, which is consistent with prior research on cherry replant in British Columbia. Additional field experiments were established in Nova Scotia and British Columbia in 2022 to compare the efficacy of biochar, compost, and mustard seed meal under field conditions. None of the treatments suppressed *P. penetrans* populations in soil relative to non-treated control plots; data on infection of roots will be obtained in the spring of 2023 and discussed.

6. Investigating the role of *Pterostichus melanarius* in agricultural pest predation in wheat (*Triticum aestivum)* and hemp (*Cannabis sativa* L.) in Alberta N. B. LAFOREST AND B. A. MORI *Department of Agricultural, Food, and Nutritional Science, University of Alberta, 4-16C Agriculture/Forestry Centre, 9011 – 116 St NW Edmonton, AB, T6G 2P5, Canada*

Ground beetles (Coleoptera: Carabidae) are a diverse group of beneficial insects that consume various arthropod pests and weed seeds. *Pterostichus melanarius* (Illiger, 1798) is a ground beetle that was unintentionally introduced to North America in the 1920s and is now widespread throughout the United States and Canada. Although *Pterostichus melanarius* is a habitat generalist, it is a valuable polyphagous predator in agroecosystems. Here we investigate the potential impact of semi-natural habitat and crop type on *P. melanarius* abundance, and how this species can contribute to the ecosystem service of pest predation. To sample *P. melanarius* abundance, pitfall traps (n = 5) were placed in the crop edge (1 m) and interior (100 m) of wheat (*Triticum aestivum*) and industrial hemp (*Cannabis sativa* L.) fields near Redwater, Alberta, during the summers of 2021 and 2022. In 2021, crop type had a significant effect on *P. melanarius* abundance, but not transect location. In 2022, there

was a significant effect of crop type and transect location on *P. melanarius* abundance. To determine the prey items of *P. melanarius* within these agroecosystems, gut contents will be analysed using multiplex PCR with species-specific primers targeting the trn-L chloroplast coding region for plants and the CO1 mitochondrial region for insects. This research will identify the trophic interactions of this species of ground beetle and will determine if agronomically significant pests are being consumed by *P. melanarius* within wheat and hemp crops.

7. Quality indices of grape juice can be altered by varying rates of pyroligneous acid E. B. NUTSUKPO, L. R. GUNUPURU, R. OFOE, S. M. N. MOUSAVI, S. K. ASIEDU, C. EMENIKE, AND L. ABBEY *Department of Plant, Food, and Environmental Sciences, Faculty of Agriculture, Dalhousie University, B2N 5E3, Nova Scotia, Canada*

Pyroligneous acid (PA) biostimulant effect on plants has been extensively studied, but not yet on grapes (*V. vinifera* cv. KWAD7-1). A study was conducted to assess the effect of different concentrations of PA (0, 2, 4, 8, and 12%) on quality indices of grape juice. The results revealed that all PA concentrations had no significant ($p > 0.05$) effect on grape juice pH. The total soluble solids in the juice ranged between 14.8 °Brix for the 12% PA and 16 °Brix for the 8% PA. The 4% PA significantly ($p < 0.05$) increased salinity of grape juice by approximately, 0.2-fold; while total dissolved solids and electrical conductivity increased by approximately, 0.14-fold as compared to the control. The 4% PA significantly ($p < 0.05$) decreased titratable acidity by approximately, 0.50-fold as compared to the control. All PA treatments significantly ($p < 0.05$) increased total phenolics and flavonoid. The 4% PA resulted in approximately 0.21-fold and 0.40-fold respectively, followed by the 8% PA at approximately 0.13-fold and 0.34-fold respectively, and finally, the 12% PA at 0.11-fold and 0.16-fold respectively compared to the control. A 2D principal component analysis showed that the 4% PA had the strongest effect on juice quality and the 12% PA had the least effect. In conclusion, PA application improved quality indices of grape juice, particularly the 4% PA. Further studies should be conducted to evaluate the effect of PA on grape juice sensory quality.

8. Metabolomic analysis revealed coordinated regulation of central carbon metabolism in pyroligneous acid-treated tomato under aluminum stress R. OFOE, R. H. THOMAS, S. K. ASIEDU, AND L. ABBEY *Department of Plant, Food, and Environmental Sciences, Faculty of Agriculture, Dalhousie University, 50 Pictou Road, Bible Hill B2N 5E3, Nova Scotia, Canada; and (R.H.T.) Department of Biology, Faculty of Science, Western University 2025E Biological & Geological Sciences Building, 1151 Richmond Street, London N6A 5B7, Ontario, Canada*

Aluminum (Al) toxicity is a major threat to global crop production on acidic soils. Pyroligneous acid (PA) is an aqueous reddish-brown liquid with numerous bioactive compounds that can promote plant growth and resilience to diverse environmental stresses. However, its effects in regulating plant central carbon metabolism (CCM) under Al stress is unknown. In this study, we investigated the effect of varying PA rates (0, 0.25 and 1% PA/ddH_2O (*v/v*)) on CCM responses of tomato (*Solanum lycopersicum* L. 'Scotia') seedlings under varying Al stress (0, 1 and 4 mM $AlCl_3$). A total of 48 differentially expressed metabolites of CCM were identified in the leaves of both control and PA-treated plants under Al stress. The Calvin-Benson cycle and pentose phosphate pathway (PPP) metabolites were considerably reduced in PA-treated plants and in both control and PA-treated plants under 4 mM Al stress. Contrarily, PA treatment markedly increased the glycolysis and tricarboxylic acid cycle (TCA) metabolites compared to the control. Although the glycolysis metabolites of 0.25% PA under Al stress were comparable to the control, 1% PA-treated plants accumulate the highest glycolysis metabolites while all PA treatment increased TCA metabolites under Al stress. Moreover, the electron transport chain metabolites were higher in PA-treated plants alone and under 1 mM Al but were reduced under 4 mM Al. Furthermore, these findings showed that PA stimulates alteration in plant metabolism to modulate energy production and organic acids biosynthesis for Al stress tolerance.

9. Potato Early Dying Complex: management and identification in Ontario potato soils G. BAILEY, M. TENUTA, K. E. DUNFIELD, D. VAN DYK, AND K. S. JORDAN *Department of Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1, Canada; (M.T.) Department of Soil Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada; (K.E.D.) School of Environmental Sciences, University of Guelph, Guelph, ON N1G 2W1, Canada; and (D.V.D.) Horticulture Crops Division, Ontario Ministry of Agriculture, Food and Rural Affairs, Guelph, ON N1G 4Y2, Canada.*

Potato Early Dying (PED) is a disease complex caused by the fungal pathogen *Verticillium dahliae* and exacerbated by the plant parasitic nematode *Pratylenchus penetrans*. When PED becomes severe during the tuber bulking stage, the result can be up to a 50% reduction in tuber size. Both causal pathogens of PED are native in Ontario soils and are conventionally managed by soil fumigation which has been shown to negatively impact the long-term health of agricultural soils. The objectives of this study are to determine how populations of the causal agents of PED influence disease and potato yield, determine the effects of farm management on pathogen inoculum, and to develop improved strategies to control PED through the enhancement of soil health. Field trials are being conducted over a three-year period in Simcoe, Ontario to test various crop rotations and the use of cover crops and biofumigants compared to conventional PED management practices. The influence on PED development and potato yields is assessed. Results show that the severity of PED increased when plants endured water stress under field conditions. Impacts on soil health and resiliency to PED resulting from farm management practices are being measured as changes in soil organic matter, fertility, microbial community composition and changes in pathogen inoculum levels in the soil over time. This study will assess whether populations of PED causal pathogens can be brought to manageable levels without the use of soil fumigants and the implications such treatments will have on potato yields and disease severity.

Session 2: Genetics, biotechnology, and breeding-student-1

10. Genetic mapping of aggressiveness in *Fusarium graminearum*, the cause of Fusarium head blight in durum wheat Y. ZHANG, C. POZNIAK, G. S. BRAR, AND E. SARI *Faculty of Land and Food Systems, The University of British Columbia, 2357 Main Mall, Vancouver, BC V6T 1Z4, Canada; (C.P.)*

Crop Development Centre, University of Saskatchewan, College of Agriculture and Bioresources, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada; and (E.S.) Department of Microbiology and Plant Pathology, University of California Riverside, Boyce Hall 1463, Riverside, CA 92521, USA

Fusarium graminearum, the predominant causal agent of Fusarium head blight (FHB) in cereal crops, impacts the Canadian wheat industry through reduced yield and seed contamination with mycotoxins. According to the type of mycotoxins produced by *F. graminearum*, the strains can be classified into 3-acetyl-deoxynivalenol (3ADON) and 15-acetyl-deoxynivalenol (15ADON) chemotypes. A highly virulent population producing 3ADON is becoming more prevalent in North America, compared to the historically dominant population producing 15ADON. It indicates the increasing risk of FHB to more western part of the wheat growing region in Canada. Decoding the genetic determinants of aggressiveness and evolution among field populations by identifying effective QTL markers is necessary for studying the wheat-*Fusarium* interactions. This project aims to map QTL conferring aggressiveness (Fg-QTL) in *F. graminearum* using a bi-parental population developed from Nit-5 (derived from the 15ADON isolate PH-1) and SK-17-97 (a 3ADON isolate with a high level of aggressiveness). A high-density genetic map of the bi-parental population and their phenotypic data of aggressiveness toward durum wheat was linked to reveal aggressiveness loci and the magnitude of Fg-QTL's expression in the population. The pan-genome analysis of a Nested Association Mapping Population of *F. graminearum* (FgNAM), reflecting phenotypic variations among the field populations, will be combined with the transcriptome analysis of the bi-parental population to narrow down the Fg-QTL interval and the list of candidate genes. This study will provide a better understanding of the virulence mechanism in *F. graminearum* and the genetic basis of aggressiveness variations among field populations in North America.

11. Introgression of stripe rust resistance from spelt wheat to Canada Western Red Spring (CWRS) wheat is complicated by segregation distortion V. FETTERLEY, C. J. POZNIAK, P. HUCL, AND G. S. BRAR *(V.F., G.S.B.) Faculty of Land and Food Systems, The University of British Columbia, 2357 Main Mall, Vancouver, BC V6T 1Z4, Canada; and (C.J.P., P.H.) Crop Development Center, College of Agriculture and Bioresources, 51 Campus Drive, Saskatoon, SK S7N 5A8*

Wheat stripe rust is among the five priority one wheat diseases in Canada. Each infection cycle produces trillions of *Puccinia striiformis* f. sp. *tritici (Pst)* spores, which accumulate mutations that threaten to evade host recognition and overcome disease resistance. Resistance bred into new cultivars is often defeated within a decade, and novel sources of stripe rust resistance are needed to limit yield losses. Wheat relatives like spelt are reservoirs of resistance genes that can be mined for improving elite cultivars. Two spelt wheat lines: 'CDC Silex' and '10Spelt17' have shown near immunity at the adult plant stage to several *Pst* isolates over multiple field seasons. When crossed with 'Avocet' (susceptible bread wheat), resulting F_2 and $F_{2:3}$ populations of each resistant spelt did not show expected Mendelian segregation ratios for stripe rust resistance. Interestingly, when crossed with various CWRS elite cultivars, both resistant spelt lines generated susceptible F_1 progeny, but the F_1 from 'CDC Silex' and 'CDC Origin' (susceptible spelt wheat) were stripe rust resistant. Currently, we are conducting mapping experiments to develop DNA markers associated with the resistance loci in 'CDC Silex' by using BSA-seq on a bi-parental population of 'CDC Silex' and 'CDC Origin'. We will also phenotype F_6 RILs of the 'Avocet' crosses with the resistant spelt lines in field nurseries, genotype using the markers we generate, and attempt to identify region(s) responsible for distortions in segregation. This may permit the introgression of novel stripe rust resistance into elite cultivars and reduce CWRS yield losses in Canada.

12. Identification of resistance in hexaploid *Brassica* against *Leptosphaeria maculans* and introgression in *Brassica napus* K. SHAH, D. WANG, G. LI, L. ZHAO, D. FERNANDO, C. STASOLLA, C. MCCARTNEY, AND R. W. DUNCAN *66 Dafoe Road, Department of Plant Sciences, University of Manitoba, Fort Garry campus, Winnipeg, Manitoba, R3T 2N2*

Canola (*Brassica napus* L.) is an important oilseed crop with global production of 70 Million Metric Tones. Blackleg disease is caused by the fungal pathogen *Leptosphaeria maculans* (Desm.) Ces. et de Not. and can cause up to 50% yield loss (Gugel et al., 1992). Various management strategies are used, including resistant cultivars, which are effective and eco-friendly. Brassica species containing the B-genome, such as *Brassica juncea* L. Czern & Coss, *Brassica carinata* A. Braun, and *Brassica nigra* (L.) Koch, are highly resistant to blackleg. Synthetic hexaploid *Brassica* sources have been reported to be a useful source of resistance. In this study, crosses between *B. napus* and synthetic hexaploid *Brassica* were inoculated with a highly virulent *L. maculans* isolate, *AvrLm2*, *5-9*, *6*, *10*, and *11*, to test for resistance against blackleg disease. Phenotyping was performed at 7, 9, and 11 days post-inoculation. Resistant plants were backcrossed with the susceptible recurrent parent until the BC_5 generation and selfed until the BC_5F_4 generation. Resistance was identified using publicly available molecular markers specific to *B. juncea* (AABB) and *B. carinata* (BBCC). Plants were then phenotyped with *L. maculans* isolates containing *AvrLm5 AvrLm6*, *avrLm5 AvrLm6*, and *avrLm5 avrLm6*. The results suggest the presence of resistance in hexaploid *Brassica* and the introgression into *B. napus*. The genotypes containing resistance against highly virulent *L. maculans* can serve as a source of resistance in spring canola/rapeseed breeding. This study highlights the potential of using synthetic hexaploid *Brassica* species as a source of resistance against blackleg disease.

13. RNAseq study of partially resistant and susceptible pea lines upon *Aphanomyces euteiches* infection S. PANDIT, R. GOYAL, T. WARKENTIN, R. ORTEGA POLO, N. Z. Lim, AND S. CHATTERTON *University of Lethbridge, 4401 University Drive, Lethbridge, AB, T1K 3M4, Canada; (S.P., S.C., R.O., N.Z. L.) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403–1 Avenue South Lethbridge, AB, T1J 4B1, Canada; (R.G.) Lacombe Research and development center, Agriculture and Agri-Food Canada, 6000 C and E trail, Lacombe, AB, T4L 1W1; and (T.W.) University of Saskatchewan, College of agriculture and bioresources, 51 Campus Drive, Saskatoon SK, S7N 5A8, Canada*

Aphanomyces root rot (ARR), caused by the oomycete *Aphanomyces euteiches*, is one of the most devastating soil-borne diseases of field peas (*Pisum sativum*). ARR can cause complete yield loss, and disease management options are limited. The objective of this study was to understand plant responses conferring partial resistance that has been observed in some breeding lines. We evaluated changes in gene expression by performing RNAseq in partially resistant and susceptible pea lines inoculated with *A. euteiches* isolate Ae1. Seven germplasm lines, including five partially resistant - PI 660736, PI 660729, PI 557500, 5001, and 7084F1-7-7, and two susceptible - CDC Meadow and CDC 4053-4 were planted in a standard greenhouse. After 14 days of growth, the plants were inoculated with zoospores of *A. euteiches,* and the controls were treated with a mineral salt solution. For RNAseq analysis, the root tissue was sampled at 2, 6, 12, and 24 hours post-inoculation. The roots infected with *A. euteiches* were rated for disease severity at 14 days post-inoculation. Significantly less ARR severity was observed in all of the partially resistant lines only when compared with a susceptible cultivar, 4053-4, but not in comparison with CDC Meadow. RNAseq revealed a total of 24000 genes were differentially expressed in all the lines and cultivars at all time points. Significantly different numbers of genes were expressed among all time points for all the germplasm lines. Detailed analysis of the trends of genes differentially expressed between partially resistant and susceptible lines is underway and will be presented.

14. Development of plasmid transformation and CRISPR/Cas9 gene editing systems in forest *Phytophthora* pathogens E. N. DORT, N. FEAU, AND R. C. HAMELIN *Faculty of Forestry, University of British Columbia, 2424 Main Mall, Vancouver, BC V6T 1Z4, Canada; and (N.F.) Pacific Forestry Centre, Canadian Forest Service, Natural Resources Canada, 506 West Burnside Road, Victoria, BC V8Z 1M5, Canada*

CRISPR/Cas9 genome editing is now a well-established molecular tool for plant pathology. The CRISPR/Cas9 systems developed for several agricultural phytophthoras have led to an improved understanding of the diseases they cause. However, a CRISPR/Cas9 system has yet to be established in any forest phytophthoras. We sought to develop a CRISPR/Cas9 protocol in several forest *Phytophthora* species, including the sudden oak death pathogen *P. ramorum* Werres, de Cock & Man in't Veld. There were no published transformation protocols for any of our selected species, so our first task was to establish polyethylene glycol-calcium (PEG/$CaCl_2$) protoplast transformations using CRISPR/Cas9 plasmids developed for *P. sojae* Kaufm & Gerd . Transformations succeeded in *P. ramorum*, though efficiency was low, with only two to four transformants produced per transformation. We switched to *P. cactorum* (Lebert & Cohn) Schröter, a pathogen causing root rot on conifers for which PEG/$CaCl_2$ transformations had already been established. We successfully co-transformed *P. cactorum* with an antibiotic selection plasmid and a CRISPR/Cas9 ribonucleoprotein complex targeting the gene for an oxysterol-binding protein-related protein (ORP) previously linked to oxathiapiprolin fungicide resistance in agricultural *Phytophthora* pathogens. We screened 47 transformants and found two heterozygous mutants, the first with a one base pair (bp) insertion at the Cas9 cut site and the second with a one bp deletion. Currently, we are testing growth of the mutants on oxathiapiprolin-supplemented medium relative to wildtype cultures. Our experiments highlight the challenges in developing CRISPR/Cas9 gene editing in forest phytophthoras and lay the groundwork for future research.

15. Genetic gains in grain yield and agronomic traits in Argentinian durum wheat A. L. ACHILLI, P. RONCALLO, AND V. ECHENIQUE *(A.L.A., P.R., V.E.) Centro de Recursos Naturales Renovables de la Zona Semiárida (CERZOS-CONICET), Camino de la Carrindanga km 7, Bahía Blanca 8000, Argentina; (A.L.A., P.R., V.E.) Departamento de Agronomía, Universidad Nacional del Sur (UNS), San Andrés 800, Bahía Blanca 8000, Argentina; and (A.L.A.) Faculty of Land and Food Systems, University of British Columbia (UBC), 2357 Main Mall, Vancouver, BC V6T 1Z4, Canada*

Understanding the basis of genetic gains in grain yield and yield-related traits is essential for designing future crop breeding strategies. The aims of this study were to assess (1) the population structure and the genetic diversity of the Argentinian durum wheat germplasm, (2) the genetic gains in grain yield achieved by durum wheat breeding in Argentina and (3) the agronomic traits associated with these gains. To this end, a wide set of Argentinian cultivars was phenotyped in three field trials and genotyped with 3,565 genome-wide SNPs and with functional markers in order to determine the allelic variation at two genes: *Rht-B1* (semi-dwarfism) and *Ppd-A1* (photoperiod insensitivity). Population structure analyses revealed the presence of three main groups, composed of old (<1980), and modern cultivars with either European or CIMMYT ancestry. The semi-dwarfism *Rht-B1b* and the photoperiod insensitivity *Ppd-A1a* (*GS105*) alleles were associated with increases in grain number per spike, grain number per spikelet, harvest index, decreases in plant height, grain protein content and earlier heading date although only the cultivars carrying the *Rht-B1* variants showed differences in grain yield. A significant linear trend (R^2 = 0.55) was observed between the grain yield and the year of cultivar release, with an increase of 26.94 kg ha^{-1} yr^{-1} from 1934 to 2015. The increases in grain yield were mostly associated with increases in harvest index and grain number. Overall, the genetic gains were mostly associated with the incorporation of semi-dwarfism into the germplasm in the 1980s, with low genetic gains after that.

Session 3: Climate change and biodiversity

16. Corn disease shifts in Ontario from 1998 to 2022 X. ZHU, A. Z. KEBEDE, T. WODEMARIAM, AND A. U. TENUTA *Agriculture and Agri-Food Canada, Ottawa Research and Development Centre, Ottawa ON, K1A 0C6; and (A.U.T.) Ontario Ministry of Agriculture, Food and Rural Affairs, P.O. Box 400, Ridgetown ON, N0P 2C0*

The purpose of this study is to identify the impact of environment (regional/local), seed treatments and hybrid selection over the past 25 years in Ontario based on annual corn disease surveys from 1998 to 2022. Northern corn leaf blight (NCLB), the most epidemic disease, caused losses every year, up to 80-97% sampled fields during 2010 to 2018. A total 1027 NCLB samples collected from 2006 to 2021 were found to have 17-26 races identified with 5 *Ht* genes. Head smut, a sporadic disease, caused yield losses up to 65%. Large weather events (wind/rainfall) increased incidences and severities of NCLB, common rust, eyespot, northern leaf spot, anthracnose leaf blight, gray leaf spot (GLS), and tar spot. An epidemic pathway from Mexico, passes Texas, Kansas, Iowa, Indiana, Ohio, Michigan, brought GLS, southern rust, and tar spot to Southern Ontario and GLS to Eastern Ontario. A dry condition in autumn increased top-die back, anthracnose and Fusarium stalk rot. Precipitation in September increased Fusarium/Gibberella ear rot, and Pythium stalk rot. Most epidemic areas were located near lake, river, hill, or surround by trees. Ear injury and exposed ear favored common smut. Stewart's wilt (SW) was prevalent in sweet and seed corn fields early in survey, ELISA test positive on leaf, husk, stalk, kernel, and corn flea beetle (CFB) adults, but insecticide seed treatments have been highly effective in controlling SW/CFB. Hybrid resistance advancements has reduced crazy top, maize redness (stolbur phytoplasma), Maize Dwarf Mosaic Virus, Sugarcane Mosaic Virus, and Wheat Streak Mosaic Virus.

17. SWEET POTATO: Climate Change Opens a New Opportunity for the Prairies M. N. J. WAHAB, R. L. LEMKE, R. Y. SOOLANAYAKANAHALLY, C. WIJEKOON, E. SVENDSEN, AND E. K. MUPUNDWA *Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2; and (C.W.) Canada Centre for Agri-Food Research in Health & Medicine, 351 Tache Ave., Winnipeg, MB R2H 2A6*

The relatively short, cool growing environment of the Canadian prairie is a major constraint for producing higher-value warm-season crops. However, if the effects of climate-change-influenced warmer temperatures, longer growing seasons, and in-season soil moisture deficit can be mitigated with irrigation, it would be possible to grow warm-season vegetables such as sweet potato on the prairies. The increasingly popular sweet potato is high in nutrients and has diverse markets. It is a long-season (100-130 days) crop and grows best between 25°C-30°C. Cultivars Radiance, Vineland Early Orange, and Orleans were evaluated under high-tunnel and open-field (with and without plastic mulch -bare ground) production systems at the Canada-Saskatchewan Irrigation Diversification Centre, Outlook, SK during the 2022 growing season. Agronomic studies included irrigation and harvest management. The overall marketable yield ranking was high-tunnel > open-field-mulch > and open-field-bare ground. On average, high-tunnel produced 46 t ha^{-1} comprising 'Petite' (35-60 mm), 'USA No. 1' (45-90 mm) and 'Jumbo' (>90 mm) roots. Open-field-mulch produced 19 t ha^{-1} of 'Petite' and 'USA No. 1' roots (no 'Jumbo'). While, the open-field-bare ground produced the lowest total yield of 13 t ha^{-1} of only 'Petite' grade roots. Preliminary agronomic studies indicated (i) marketable root yield ranked Vineland Early Orange > Radiance > Orleans, (ii) moderate moisture stress did not impact root yield, and (iii) mechanical or chemical vine-kill did not adversely affect yield or quality. Root yield, grade size distribution, and quality attributes in response to production system, cultivar, irrigation and harvest management will be discussed.

18. Diploid potatoes in changing climate biotic and abiotic challenges B. FOFANA, D. MAIN, M. ZAIDI, AND B. BIZIMUNGU *(B.F., D.M., M.Z., B.B.) Charlottetown Research and Development Centre, Agriculture and Agri-Food Canada, 440 University Avenue, Charlottetown, Prince Edward Island, C1A 4N6, Canada; and (B.B.) Fredericton Research and Development Centre, Agriculture and Agri-Food Canada, 95 Innovation Road, PO Box 20280, Fredericton, NB E3B 4Z7*

With climate change, plants face increased challenges by biotic and abiotic stresses. Among these stresses, drought and common scab (*Streptomyces scabies*) are serious threats to the cultivated potato's (*Solanum tuberosum* L.) productivity and quality. Currently, the major proportion of the potato untapped genetic diversity remains within the diploid potatoes which, compared to the cultivated tetraploid potato (*Solanum tuberosum* L.), is regarded as little potatoes in many aspects, including morphological and genetic features, tuber size, and yield. However, have more attention and resources been deployed for diploid breeding and agronomy as have been done for the cultivated potatoes? Our research intended to provide some answers to these questions by developing and characterizing a mutant diploid potato population. We will show that some diploid potatoes are as competitive with cultivated potatoes both in terms of tuber size, yield potential, and quality. Further, we will show that diploid potatoes have the genetic architecture that confers resistance to drought and common scab, while maintaining the genetic armors for maturity and quality traits. Based on the findings, diploid potatoes are not as little as generally thought and we anticipate a bright and promising future for diploid potato in commercial production if more resources are deployed in its cultivar development and agronomy.

19. Tillage and crop rotation effects on soil static abiotic properties and oomycete communities in different soil layers A. C. GAHAGAN, Y. SHI, D. RADFORD, M. J. MORRISON, E. GREGORICH, S. ARIS-BROSOU, W. CHEN *(A.C.G., Y.S., D.R., M.M., E.G., W.C.) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling ave., Ottawa, ON K1A 0C6, Canada; and (A.C.G, S.A.B., W.C) Department of Biology, University of Ottawa, Ottawa, 60 Marie Curie Prv., Ottawa, ON K1N 6N5, Canada*

The soil microbiome is influenced by the physicochemical properties of the soil, which vary with depth. Soil-borne oomycetes species rely on mobile zoospores to infect hosts, making them susceptible to disruptions caused by tillage and crop rotation. To understand how oomycete communities respond to such changes, soil samples were collected from post-harvested fields in 2018 at two different depths profiles (0-15 cm and 15-30 cm) in a split-plot experimental field with conventional tillage [CT] and no till [NT]) as the main plot factor and monocultures of soybean, corn, or wheat, and corn-soybean-wheat rotation as the subplot factor. Total carbon and nitrogen were higher in the top layer under NT,

but not under CT, while pH was higher in the lower layer in general. The oomycete community contained 292 Amplicon Sequence Variants (ASVs) representing 34 species, predominantly in the genera *Globisporangium* (81.0% in abundance) and *Pythium* (14.0%). Oomycete diversity did not differ significantly between the two soil depths, but at 0-15 cm in depth, it was higher under CT than under NT, and was negatively correlated with total nitrogen and available potassium. The community compositional structure differed significantly between the two soil depths, with a more prominent difference observed under NT than CT, likely due to increased aeration and mixture of the soil layers following CT. Our study suggests that tillage had a greater impact on nutrient levels and oomycete communities in the surface soil layer, with NT potentially promoting soil general suppressiveness through nutrient preservation and enrichment of beneficial microorganisms antagonistic oomycetes pathogens.

20. Effect of drought stress on symbiotic nitrogen fixation, soil nitrogen availability, and soil health parameters in forage legumes M. S. THILAKARATHNA, D. DOLLETE, AND R. LUMACTUD *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada*

Climate change has made drought more prevalent and persistent and is predicted to continue contributing to drought severity in the near future. We hypothesize that drought stress can negatively impact plant growth, root nodulation, and symbiotic nitrogen fixation (SNF) in forage legumes, thus influencing soil nitrogen availability and soil health parameters. In this study, we evaluated the effects of drought stress on nodulation, plant growth, SNF, soil nitrogen availability, soil extracellular enzyme activities, and soil microbiome of alfalfa (*Medicago sativa*) and red clover (*Trifolium pratense*) under controlled environmental conditions. The drought treatments were imposed at the flowering stage, where the soil moisture contents were maintained at 20% field capacity (FC) (severe drought), 40%FC (moderate drought), and 80%FC (well-watered) for three weeks. Severe drought had significant negative effects on nodulation, root and shoot growth, and SNF. Soil available nitrogen was significantly increased under severe drought conditions. The extracellular enzyme assay showed that drought stress reduced the N-acetyl-glucosaminidase in alfalfa and β-D cellobiosidase activity in red clover. Microbiome data showed differential responses of the two forage plant species under drought conditions. While drought did not affect β-diversity in both plant host species, α-diversity was affected in alfalfa only. Furthermore, we observed a decrease in the relative abundances of Acidobacteria in alfalfa, whereas, enrichment of *Nocardiodes* in red clover. Overall results indicate that drought has deleterious effects on nodulation, plant growth, and carbon and nitrogen cycling enzyme while positively impacting soil nitrogen availability and some specific soil microbial taxa.

21. Genome-wide association studies (GWAS) of root architectural traits in a large collection of *Brassica* accessions C. X. YANG, R. FREDUA-AGYEMAN, S. F. HWANG, S. E. STRELKOV, AND L. Y. GORIM *Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB T6G 2P5, Canada*

Root system architecture (RSA) is critical for plant growth and development given the function of roots in water and nutrient uptake, anchorage, and storage of resources. However, the evaluation of root traits is tedious and time-consuming. *Brassica* is an important genus of the *Brassicaceae* family and includes many field crops and vegetables. The *Brassica* root system is complex, and comparative RSA studies that combine morphological and genetic analyses are limited. In this study, eight RSA traits were evaluated in 377 *Brassica* accessions representing six species (*B. napus*, *B. juncea*, *B. carinata*, *B. oleracea*, *B. nigra* and *B. rapa*). The phenotypic data indicated that *B. napus* and *B. oleracea* have the most complicated and largest root systems among these species, with relatively larger values for six of the eight traits measured; in contrast, *B. nigra* had the smallest root systems. In addition, 313 of the *Brassica* accessions were genotyped using a 19K *Brassica* single nucleotide polymorphism (SNP) array. After removing monomorphic and low-coverage site markers, markers with MAF ≤ 0.05 and those missing data for >5% of the accessions, 6213 SNP markers, comprising 5103 markers on the A genome and 1110 markers on the C genome, were selected for the GWAS analyses. Several mixed linear models (MLM) were tested to identify the genomic regions and SNPs associated with the RSA traits. This study will improve understanding of the diversity of *Brassica* root systems and help to determine whether development of cultivars with improved RSA is an important breeding objective.

Session 4: Disease Management of Horticultural Crops

22. Blackleg diversity and biocontrol in potato from western Canada B. PAGENI, K. GNAM, M. KONSCHUH, J. NEILSON, AND L. KAWCHUK. *Lethbridge Research Centre, Agriculture and Agri-Food Canada, 5403 – 1 Avenue South, Lethbridge, AB T1J 4B1, Canada; and (M.K.) Department of Biological Sciences, 4401 University Drive, University of Lethbridge, Lethbridge, AB T1K 3M4, Canada*

Pectobacterium species are Gram-negative pectolytic pathogens that may cause blackleg and soft rot in potato. Blackleg is a seed-borne disease that is distributed largely by movement of varieties within and between potato growing areas. Analysis of diseased potato samples from western Canada between 2021 and 2023 by PCR and multi-locus sequence typing (MLST) revealed an increase in the *Pectobacterium* Waldee species diversity and confirmed the absence of the relatively aggressive *Dickeya* Samsun et al. species. Previous studies reported that blackleg and soft rot were caused mostly by *Pectobacterium atrosepticum* (van Hall) Gardan et al. An increase in the number of *Pectobacterium carotovorum* (Jones) Waldee, *Pectobacterium polare* corrig. Dees et al., and *Pectobacterium parmentieri* Khayi et al. was observed in the present study. An expanding industry that increases disease pressure and seed movement between regions, together with climate change, appear to be contributing to

blackleg incidence and impact. Isolation and genomic sequencing of endemic lytic bacteriophage from samples identified members of the Podoviridae, Myoviridae, and Siphoviridae. Occurrence of clustered regularly interspaced short palindromic repeats (CRISPR) Cas 4 RecB-like nuclease in some suggests the phage are capable of defeating the pathogen defensive capabilities. Laboratory and field trials confirmed that the phage reduced disease incidence and severity and increased yields by over 30% as an environmentally friendly biocontrol treatment.

23. Plant defense elicitors can reduce the use of chemical fungicides and alter the microbiome structure and composition of apple fruit S. ALI, M. S. MCLAUGHLIN, S. N. YURGEL, AND P. A. ABBASI *(S.A., M.S.M., P.A.A.) Agriculture & Agri-Food Canada, Kentville Research and Development Centre, Kentville, NS B4N 1J5, Canada; (M.S.M.) Department of Plant, Food, and Environmental Sciences, Faculty of Agriculture, Dalhousie University, Truro, Nova Scotia, Canada; and (P.A.A) United States Department of Agriculture, Agricultural Research Service, Grain Legume Genetics and Physiology Research Unit, Prosser, WA, 99350, USA*

Chemical fungicides are the primary means of controlling fungal disease in apple orchards, typically requires 12-14 applications in one crop season. These fungicides increase production costs and adversely impact the environment, animal and human health, and soil sustainability, leading to increased scrutiny of their use. As the use of fungicides are increasingly restricted, additional, eco-friendly and cost-effective disease management tools are necessary. In this study, the plant defense elicitor, Salicylic Acid (SA), was integrated into a conventional chemical fungicide program for the management of fungal diseases on 'Honeycrisp' apples. Experiments were conducted at apple orchards in Kentville Research and Development Centre and commercial orchards in Nova Scotia, New Brunswick and Prince Edward Island. At the experimental orchard, the same level of disease control was observed using either conventional chemical fungicide or the integrated program of SA and fungicides on foliage diseases throughout the growing season, on apple fruit at harvests and 3 months post storage. Similar results were obtained in apple fruit harvested from commercial orchards, with the exception of the New Brunswick orchard, in which the integrated spray program performed better against black rot than the conventional chemical fungicide. We also investigated the impact of chemical fungicides and SA on the fungal communities of apple fruit from a single orchard over two consecutive growing years. We observed variations in fungal community structure and composition, including shifts in the abundance of key fungal genera among tissue types, growing seasons, and treatments. Furthermore, we demonstrate a loss in fungal network complexity as a result of fungicide treatment.

24. Evaluating biocontrol potential of fungal endophytes isolated from healthy mature apple (*Malus domestica*) trees against apple replant disease M. ROY, S. ALI, A. WALKER, H. WRIGHT, K. FULLER, M. SUMARAH, J. RENAUD, AND J. TANNEY *(M.R., S.A., H.W., K.F.) Kentville Research and Development Centre, Agriculture and Agri-food Canada, 32 Main Street, Kentville, NS B4N 1J5*; *(M.R., A.W.) Department of Biology, Acadia University, 33 Westwood Avenue, Wolfville, NS, B4P 2R6*; *(M.S., J.R.) Agriculture and Agri-Food Canada, London Research & Development Centre, 1391 Sandford Street, London, Ontario, Canada, N5V 4T3*; and *(J.T.)* Pacific Forestry Centre, 506 Burnside Road West Victoria, British Columbia, V8Z 1M5

Apple Replant Disease (ARD) negatively affects young apple trees (*Malus domestica*), replanted on a site that was previously used to cultivate apple or related plant species, and results in root necrosis and reduction in plant growth and vigour. Additionally, ARD reduces fruit yield and delays fruit bearing which adversely affects growers' return. The deregistration of harmful, chemical fumigants, the conventional way to address ARD in the past, has created a demand for eco-friendly alternative treatments. We are exploring fungal endophytes from healthy, mature apple roots as potential biocontrol agents to treat ARD and reduce the need for chemical fumigants. Forty-eight fungal endophytes were isolated from apple root and tested in dual culture assays *in vitro* for inhibitory properties against *Pythium ultimum* and *Rhizoctonia solani,* two pathogens associated with ARD. All endophytes were able to inhibit pathogens to some extent and four different types of endophyte-pathogen interactions were observed. From the results of these assays, five biocontrol candidates were selected for further investigation. High resolution liquid chromatography–mass spectrometry (LC-MS) was used to analyze the metabolites produced by these endophytes in dual culture. The filtrate from liquid cultures of these isolates demonstrated a range of inhibition potential against four fungal pathogens, with an endophyte isolate identified as *Mortierella* sp. inhibiting all four pathogens to the greatest extent. The five biocontrol candidates were also tested for phosphate solubilization ability, optimal growth temperature and through an initial anti-ARD trial with micropropagated apple rootstocks in the greenhouse.

25. Cross-resistance of *Clarireedia jacksonii* to DMI fungicides A. RETHER, K. YU, AND T. HSIANG *School of Environmental Sciences, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada*

Dollar spot, caused by *Clarireedia jacksonii* Salgado, is the most common turfgrass disease in Eastern North America. It is often managed by repeat applications of demethylation inhibiting (DMI) fungicides each season, and decreased sensitivity to the DMI propiconazole to *C. jacksonii* has been reported. Cross-resistance, where an organism shows resistance to multiple pesticides with the same mode of action, was evaluated in lab studies for *C. jacksonii* in Ontario over 20 years ago with DMI fungicides available at that time. The purpose of this study was to compare sensitivity levels among 20 isolates of *C. jacksonii* that have demonstrated varying sensitivities to propiconazole (very sensitive to highly resistant to propiconazole) to 11 DMI fungicides including propiconazole. EC_{50} values (effective concentration for 50% inhibition of hyphal growth) were generated for each combination of isolate by fungicide, and these values were subjected to pairwise correlation analysis. Among the fungicides examined in amended agar tests, correlation coefficients (R values) ranged from 0.54 to 0.99 (all $p \leq 0.01$), suggesting that there is significant cross-resistance in *C. jacksonii* among all the DMI fungicides tested. Future research will determine if these results are similar in the field.

26. Determining the identity and frequency of foliar pathogens on *Vicia faba* L. in Saskatchewan E. STRATFORD AND S. BANNIZA *(E.S.) Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada*

Foliar diseases can cause large reductions in yield of faba bean (*Vicia faba* L.) in Saskatchewan. *Botrytis fabae* Sard. and *Stemphylium botryosum* Wallr. are considered to be the causal species of the majority of lesions observed in the field, and both have been isolated from faba bean in Saskatchewan. In 2022, potted susceptible faba bean plants were placed in faba bean plots in Rosthern and Melfort, SK, to collect natural inoculum. Plants were retrieved from the field and incubated under high humidity for 72 h and disease severity was assessed 14 days after returning from the field. Presumptive diagnosis and disease severity were recorded based on lesion characteristics and leaf area affected. A multiplex PCR assay was used to detect the presence of five causal pathogen species and one causal species complex from the DNA of lesions. *Alternaria alternata* (Fries) Kiessl. was detected in a large percentage of lesions; however, those lesions only accounted for a small proportion of disease severity, suggesting that it lives epiphytically and may be an opportunistic pathogen. *Stemphylium* spp. were detected in a large percentage of samples from both locations and caused moderate disease severity. *Botrytis fabae* was not detected in any sample tested, however, the predominant symptoms resembled those caused by *B. fabae*. Due to inconsistencies between visual assessment and molecular analysis, diagnosis of causal pathogens may not be possible by visual assessment and further molecular work is required to fully realize which pathogen species cause disease in the field.

27. Intercropping as a sustainable alternative to reduce late blight infestation in potato – a search for mechanisms Z. HOMULLE, N. P. R. ANTEN, T. J. STOMPH, W. VAN DER WERF, AND J. C. DOUMA *Wageningen University, Centre for Crop Systems Analysis, 6708 PE Wageningen, The Netherlands*

Crop diversification, through intercropping, is often reported to reduce disease pressure, and could thus be a sustainable component of integrated crop protection. Nevertheless, the question of how exactly intercropping reduces diseases is not clear. Intercrop field experiments were conducted in the Netherlands, where potatoes (*Solanum tuberosum* L.) were strip-cropped with contrasting companion crops (either grass (*Lolium perenne* L.) or maize (*Zea mays* L.)) to quantify their effect on potato late blight (*Phytophthora infestans* (Mont.) de Bary). Next to data on disease severity, data was collected related to various disease suppressive mechanisms, such as the microclimate in the potato canopy, and incoming particles. Significant reductions in disease severity were observed in both the grass and maize intercrop treatment, compared with potato monoculture. Furthermore, the duration of a high relative humidity (>90%) was reduced in the potatoes intercropped with grass, whereas reductions in the number of incoming particles were observed in the maize intercrop treatment. The greatest reductions in disease severity were observed in the grass intercrop treatment, indicating that the choice of the companion crop is important for disease suppression. The effect of the short grass on the microclimate in the potato canopy might have been stronger for reducing late blight development than the effect of the tall maize as a barrier for incoming spores. Enhancing our understanding of the various mechanism at play in intercrop systems could help us to better optimise intercrop designs to reduce potato late blight, and potentially other diseases.

Symposium 1-CPS: Emerging/novel tools for plant pathogens diagnostics-1

28. High throughput sequencing: Overview, challenges perspectives for plant pathogens diagnostic G. J. BILODEAU AND M. L. FALL *(G.J.B.) Ottawa Laboratory Fallowfield, Canadian Food Inspection Agency, 3851 Fallowfield Road, Ottawa, ON K2H 8P9, Canada; Saint-Jean-sur-Richelieu Research, and (M.L.F.) Development Centre, Agriculture and Agri-Food Canada, 430 Gouin Boulevard, Saint-Jean-sur-Richelieu, Quebec J3B 3E6 Canada*

In the past decade, the advent of high-throughput sequencing technology (HTS), with some sequencing instrument as little as a USB thumb drive, has allowed efficient characterization and monitoring of the plant pathogens. By mining the genomes of closely-related pests and comparing them to one another, we are able to design molecular markers that can be used by diagnostics labs to distinguish them from one another or to find appropriate genomic regions. Furthermore, metagenomics, metatranscriptomics, metaviromics or metabarcoding tools coupled with custom bioinformatic pipelines can be used to evaluate potential sampling methods for pathogens biosurveillance in forestry and agriculture and contribute to identify spreading pathways for different types of plant pathogens (virus, bacteria, fungi, nematodes, parasites). These tools have opened the door to design novel approaches for rapidly developing molecular methods that can facilitate detection and identification of the pathobiome and improve the efficiency of our regulatory activities. However, use of these technologies can be challenging, specially with the tsunami of data that they generated and their requirements in terms of standard and non standard analysis and reference databases, which are more developed for some pathogens than others. Consequently, user guidelines have been recently published and aim to get consensus between multiple users for diagnostic purposes. Broader adoption of HTS in plant science can take different forms to evaluate pesticide resistance, develop quick detection tools, biosurveillance, identification of a novel virus or organisms and optimization of nucleic acid preparation for great use are a few examples.

29. Black Knot resistance in plums: A multi-omic approach to address genetic resistance for an unusual disease J. SUBRAMANIAN, R. SHINDE, C. SHUM, W. EL KAYAL, V. VENUGOPAL, D. TORKAMANEH, G. PERRY, D. AHMAD, I. EL SHARKAWY, M. M. AYYANATH, M. SHUKLA AND P.

SAXENA *(J.S., R.S., C.S., V.V., G.P., M.M.A., M.S., P.S.) University of Guelph, Guelph, Canada; American; (W.E.) University of Beirut, Beirut, Lebanon; (D.T.) Universite Laval, Laval, Canada; and (D.A., I.E.) Florida Agricultural and Mechanical University, Tallahassee, Florida*

Black knot is a serious cancer of plums. It is caused by a fungus *Apiosporina morbosa*. Since the disease takes multiple seasons to develop fully there is no known *in vitro* assay to check for resistance. Thus, the existence of genetic resistance is either unavailable or analysed properly. We used a multi-pronged 'omics' based approach to understand the mechanism of resistance in a genetically diverse population of Japanese and European plums, which were left to allow BK infestation to flourish in the orchard. Whole-genome sequencing followed by common variant analysis in 2 of the resistant and susceptible genotypes resulted in the identification of 52 BK resistance (R and PRR), and 31 pathogenicity-related (PR) genes with linked functional variants in the Japanese plum. Further, we also found that chromosomes 1, 4, and 6 had the highest number of R, PRR, and PR genes, and the variants linked with these genes suggest that they may have a critical role in conferring BK resistance. Metabolomic analyses revealed that 2 anti-microbial compounds are differentially present in the 2 resistant genotypes tested. Phytohormone analyses of the black knot disease and progression suggested that auxin-cytokinins interplay, possibly driven by *A. morbosa* is vital in disease progression by hampering the plant defense system. Further, contrary to the conventional reports, both Salicylic acid and Jasmonic acid levels were elevated in the susceptible genotypes, the reason for which is being currently investigated. Collectively our results have made significant progress in our understanding black knot in plums and the possibility of a genetic, metabolomic and hormonomic marker to identify BK resistance is closer.

30. Development and evaluation of a loop-mediated isothermal amplification (LAMP) method for *Synchytrium endobioticum* (potato wart) detection J. JIANG, W. FEINDEL, S. BAJEMA, AND J. FENG *(J.J., W.F., S.B.) Potato Growers of Alberta, Edmonton, AB T5Y 6H3, Canada; and (J.J., W.F., J.F.) Alberta Plant Health Lab (APHL), Edmonton, AB T5Y 6H3, Canada*

Potato (*Solanum tuberosum*) wart, caused by the biotrophic fungal pathogen *Synchytrium endobioticum*, is a serious disease of cultivated potatoes. In October 2021, suspect potatoes from two farms of Prince Edward Island (PEI), Canada, were confirmed with the infection of potato wart; therefore, a rapid and accurate diagnostic method needs to be developed. In this study, we described the development and evaluation of a loop-mediated isothermal amplification (LAMP) method to detect the pathogen *S. endobioticum*. Four sets of LAMP primers were designed. Their specificity were preliminarily verified by *in silico* analysis and on DNA of one *Plasmodiophora brassicae* isolate and 24 fungal species, and their sensitivity was tested on a gBlock. All the four primer sets were specific to *S. endobioticum*. One primer set showed a higher sensitivity with a detection limit at 7-8 DNA molecules per reaction. On sensitivity, the LAMP was comparable to qPCR (probe and SYBR based) and about 10 times more sensitive than conventional PCR. Considering the convenience of operation, this LAMP protocol is accurate and robust and fdiagnosis for potato wart.

31. High throughput sequencing (HTS) of Bees and Pollen for Bio-surveillance of Agricultural and Invasive Pathogens C. M. HEWAPATHIRANA, M. E. ROTT, M. M. GUARNA, S. F. PERNAL, J. F. GRIFFITHS, AND G. J. BILODEAU *(C.M.H.) Canadian Food Inspection Agency (CFIA), 3851 Fallowfield Road, Ottawa, ON, K2H 8P9, Canada; (M.E.R.) Canadian Food Inspection Agency (CFIA), 8801 East Saanich Road, North Saanich, BC, V8L 1H3, Canada; (M.M.G, S.F.P.) Agriculture and Agri-Food Canada (AAFC), 1 Research Road, Beaverlodge, AB, T0H 0C0, Canada; (J.G.) Agriculture and Agri-Food Canada (AAFC), 4902 Victoria Avenue North, Vineland Station, ON, L0R 2E0, Canada; and (G.J.B.) Canadian Food Inspection Agency (CFIA), 3851 Fallowfield Road, Ottawa, ON, K2H 8P9, Canada*

Due to their role in pollination, the European honey bee (*Apis mellifera*) is a vital component of agricultural systems. Bees come into contact with plant pathogens (from pollen and spores in the air) during their foraging trips. Bees are wide-ranging, capable of rapidly visiting and sampling individual plants in an agricultural setting. Managed bee species represent a central hub in agriculture that can be utilized to monitor multiple agriculturally-related pathogens. This project proposes to examine the presence of pathogens during the interactions of bees and plants by using bees and bee-collected pollen to monitor both plant and bee pathogens. Over 250 bee-specific samples have been obtained from experimental tree fruit farms across British Colombia, Ontario and Alberta. HTS technologies (ION Torrent™) are utilized to sequence barcode regions - Internal transcriber spacer (ITS) region for fungal identification and 16S ribosomal DNA for bacterial identification. Bioinformatics pipelines are being developed to identify pathogenic species (fungal or bacterial) that demonstrate a high risk towards the health of the plant pollinator ecosystem. Preliminary results show bee bread as a rich source for fungal pathogen detection with identifications such as *Podosphaera leucotricha* (Powdery mildew - apples) and *Monilinia vaccinia-corymbosi* (Mummy berry disease - blueberries). Bee pathogens identified in the samples include - *Ascophaera apis* (Chalkbrood disease) and *Melissococcus plutonius (*European foulbrood disease). This pilot study aims to evaluate the potential and limitations in using honeybees as a biomonitoring species for identifying major pathogenic threats to beekeeping and the Canadian agricultural sector.

32. RNAseq-based identification of a novel virus and novel virus variants in farmed blueberries in British Columbia S. KANNANGARA, J. RODRIGUEZ, A. GILEWSKI, G. DE VILLIERS, P. ELLIS, E. GERBRANDT, AND J. MATTSSON *(S.K., J.R., A.G., J.M.) Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada; (G.D.V., P.E.)Phyto Diagnostics Company Ltd., 9381, Ardmore Drive, North Saanich, BC V8L 5G4, Canada; and (E.G.) BC Blueberry Council, 275 32160 South Fraser Way, Abbotsford, BC V2T 1W5, Canada*

Blueberry scorch and shock viruses negatively impact on production of highbush Blueberries in British Columbia. Correct diagnosis is important as scorch virus-infected plants will die and should be removed, whereas shock virus-infected plants recover over time. In recent years, about 20% of diseased plants tested negative for both viruses by ELISA and PCR. Potential explanations are that these plants may be infected by novel variants that escape detection, or that a novel virus causes similar symptoms. We applied high-throughput sequencing of RNA isolated from 77 diseased plants collected across the BC lower mainland. While obtained shock virus sequences differed little from known sequences, we identified extensive variation in the scorch genome. Sanger sequencing of the coat protein-encoding region showed variation that compromised PCR detection of variants by published primers. Predicted coat protein also differed with extensive variation, especially in the amino terminus, which split analyzed sequences into two major clades, potentially compromising ELISA detection. Moreover, we identified a novel virus belonging to the luteovirus family. This virus genome (~5 kbp) contains open reading frames for an RNA-dependent RNA polymerase, a coat protein, and RNA polymerase. This virus is present in nearly all tested plants, suggesting it does not cause disease. However, since a population of diseased plants test negative for scorch, shock, and other viruses by deep sequencing but do harbor the luteovirus, we cannot rule it out as a cause of disease. In summary, we have identified novel scorch virus variants and a novel virus in diseased blueberry plants.

33. Optimizing dsRNA extraction toward rapid virus detection using nanopore sequencing V. J. JAVARAN, A. POURSALAVATI, P. LEMOYNE, M. LUSSIER-LÉPINE, P. MOFFETT, AND M. L. FALL *(V.J.J., A.P., P.L., M.L.F.) Laboratoire d'expertise et de diagnostic en phytoprotection, Saint-Jean-sur-Richelieu Research and Development Centre, Agriculture and Agri-Food Canada, St-Jean-sur-Richelieu, QC J3B 3E6, Canada*; *and (V.J.J., A.P. , M.L.-L., P.M.) Centre SÈVE, Département de Biologie, Université de Sherbrooke, Sherbrooke, QC J1K 2R1, Canada*

Plant viruses cause significant yield losses and reduce crop quality, making their early detection and identification essential for proper management and control of viral diseases. Double-stranded RNA (dsRNA) serves as an intermediate replicative RNA during replication and transcription of plant viruses, making it a reliable target for virus detection. However, the conventional dsRNA purification protocol is a lengthy and laborious process, taking up to eight hours to complete, which can delay virus detection and hinder effective management strategies. The objective of this study was to develop a rapid dsRNA purification protocol from different plant species for virus detection. We modified the conventional dsRNA purification protocol by incorporating chromatography columns and cellulose to shorten the purification time. The new protocol takes only 1.5 hours to complete. We successfully extracted dsRNA from grapevine, bell pepper, and celery using the modified protocol. The extracted dsRNAs were sequenced using nanopore sequencing technology and compared to Illumina Miseq sequencing as a standard method to evaluate the efficiency of the modified protocol. Both sequencing technologies produced comparable results, validating the modified protocol's efficacy in detecting plant viruses in different plant species. Our modified protocol offers significant advantages over the conventional dsRNA purification protocol, including reduced extraction time and simplified steps. This protocol can be a valuable tool for plant pathologists and diagnostic labs for rapid and efficient detection of plant viruses, which can aid in developing timely management strategies. Additionally, the modified protocol's simplicity, reliability, and efficiency make it a viable alternative for dsRNA purification from various plant samples.

Session 5a: Nutriments Management

34. Effects of nitrogen stabilizers on the growth, yield, and forage quality of crops grown in short rotation on podzols in boreal climate T. A. N. MBITE, Y. KATANDA, M. NADEEM, S. ELLSWORTH, R. THOMAS, L. GALAGEDARA, AND M. CHEEMA *(T.A.N.M., Y.K., M.N., L.G., M.C.) School of Science and the Environment, Memorial University of Newfoundland, Corner Brook, NL, A2H 5G4, Canada; (S.E) Government of Newfoundland and Labrador, Dept. of Fisheries, Forestry and Agriculture, Corner Brook, NL, A2H 7E1, Canada; and (R.T.) Department of Biology, Faculty of Science, Western University, London, Ontario, N6A 5B7, Canada*

Intensive agriculture production demands substantial nitrogen (N) fertilizer application to boost yield but poses higher risks of N losses. N stabilizers, such as urease and nitrification inhibitors (UIs and NIs, respectively), are known to reduce N losses, enhance N uptake, and consequently crop growth and yield. Field trials were conducted in 2019 - 2020 to evaluate the effects of urea (UR) stabilized with N-(n-butyl) thiophosphoric triamide (NBPT), nitrapyrin, and dicyandiamide (DCD) on the growth, dry matter yield (DMY), and forage quality of crops grown in a two-year rotation. Silage corn was seeded in 2019 followed by faba beans, oats + peas mixture, wheat, or canola in 2020. The N fertilizer treatments were: 1) control (CTRL), 2) urea (UR), 3) AgrotainTM (AG, urea with NBPT), 4) eNtrenchTM (EN, urea with nitrapyrin), and 5) SuperUTM (SU, urea with DCD and NBPT). There were significant yield responses to N fertilization in all crops. Silage corn DMY responses were highest in plots treated with SU, increased by 253% and 124% in 2019 and 2020, respectively. Compared to UR, SU produced 4.7% greater net energy for lactation from silage corn whereas AG significantly increased seed protein content in canola. Overall, there were no significant effects of UIs or NIs on growth, yield, N uptake, and NRE in all crops. Split-applying UR to canola significantly increased N uptake, seed protein content, and NRE. The results suggest that UIs and NIs have limited effects on agronomic performance, but potential nutritional quality benefits for silage corn and canola.

35. Seafood biostimulant effect on seed germination, plant growth, and productivity of Kale (*Brassica oleracea* var. sabellica) A. PRADEEP KUMAR AND L. ABBEY *Department of Plant, Food, and Environmental Sciences, Faculty of Agriculture, Dalhousie University, 50 Pictou Road, Bible Hill, B2N 5E3, NS, Canada*

The use of organic and sustainable agricultural practices has become increasingly important to reduce environmental impact while ensuring food security. The potential use of sea minerals and fish hydrolysate as natural alternative to synthetic biostimulants in sustainable agriculture has not been comprehensively explored. In this study, we investigated the effect of three sea minerals (SM1, SM2 and SM3) and fish hydrolysate (FH) at four different concentrations (0.25, 0.5, 1 and 2%) on seedling and plant growth of kale (*Brassica oleracea* var. sabellica). The results showed that the application of 0.25% SM3 increased seed germination rate by *ca.* 78% while 2% FH increased the mean germination time by *ca.* 35% compared to the control. Root length and surface area were increased with 0.25% SM2 while the shoot length and surface area were increased with 0.25% FH application. Both shoot and root volume of seedlings were increased with 0.25% SM3 and 0.25% SM2, respectively. Plants treated with 2% FH showed an overall increase in plant height and number of leaves, resulting in increased fresh and dry weights of plant tissues. Application of 2% FH increased chlorophyll content, stomatal conductance of CO_2, transpiration and photosynthetic rate. However, maximum photochemical efficiency, and rate of quantum conversion were observed for 1% SM3. In conclusion, 2% FH was the most effective for plant height and weight, but 1% SM3 is recommended for optimal photochemical efficiency. The findings of this study support the potential use of these natural resources in sustainable agriculture.

36. Yield and pre-malting grain quality of malting barley varieties in response to increasing nitrogen rates in western Canada H. KUBOTA, J. O'DONOVAN, B. TIDEMANN, N. HARKER, K. TURKINGTON, W. MAY, C. GRANT, E. JOHNSON, B. BERES, C. VERA, M. IZYDORCZYK, L. OATWAY, P. JUSKIW, AND Y. KABETA *Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, 6000 C and E Trail, Lacombe, AB T4L 1W1, Canada; (W.M.) Indian Head Research Farm, Agriculture and Agri-Food Canada, PO BOX 760, 1 Government Road, Indian Head, SK S0G 2K0, Canada; (C.G.) Brandon Research and Development Centre, Agriculture and Agri-Food Canada, Box 1000a, R.R. #3, Brandon, MB R7A 5Y3, Canada; (E.J.) University of Saskatchewan, Agriculture Building 51 Campus Drive Saskatoon, SK S7N 5A8, Canada; (B.B.) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1st Avenue South, Lethbridge, AB T1J 4B1, Canada; (C.V.) Melfort Research Farm, Agriculture and Agri-Food Canada, Star City No. 428, SK S0E 1A0, Canada; (M.I.) Canadian Grain Commission, 303 Main St, Winnipeg, MB R3C 3G7, Canada; and (L.O., P.J., Y. K.) Olds College Field Crop Development Centre, 40227 Range Road 27-0 Hwy 2A South Lacombe AB T4L 2N1, Canada*

Successful malt barley pays a premium over feed barley; however, meeting malting quality standards is challenging due to the strict quality parameters for malting. The risk of rejection for malting due to high protein levels caused by high N fertilizer rates discourages producers from malting barley production. A 4-year field study (2013-2016) was conducted at seven sites across the Canadian prairies (Beaverlodge, Lacombe and Lethbridge, AB; Melfort, Scott and Indian Head, SK; and Brandon, MB) to assess the performance of malting barley varieties to increased N rates. Four newer varieties ('Cerveza', 'CDC Kindersley', 'AAC Synergy', and 'ABI Voyager') were compared to 'AC Metcalfe' at four N rates (0,25,50, and 100 kg/ha). Compared to 'AC Metcalfe', all newer varieties yielded higher (4 to 10% higher) while maintaining lower grain protein levels (1 to 4% lower). The exception was 'CDC Kindersley', which had a similar protein level to 'AC Metcalfe'. Grain yield and protein increased with increasing N rates; however, responses to increasing N rates varied among varieties. 'AAC Synergy' and 'ABI Voyager' were more responsive in yield to increasing N rates while they maintained lower protein levels. In contrast, 'CDC Kindersley' and 'AC Metcalfe' had comparatively small yield responses but steep increases in protein levels to increasing N rates. All tested varieties had decreased kernel plumpness as N rates increased; however, reductions with 'AAC Synergy' and 'ABI Voyager' were less. These findings suggest that producers could increase N rates with 'AAC Synergy' and 'ABI Voyager' and still maintain acceptable pre-malt qualities.

37. Effect of cover cropping strategies on subsequent grain corn (*Zea mays* L.) yield in no-till and fall strip-till systems F. YASMIN, J. NASIELSKI, K. SCHNEIDER, AND L. L. VAN EERD. *School of Environmental Sciences, University of Guelph Ridgetown Campus 120 Main Street East, Ridgetown, ON, N0P 2C0, Canada; and (J.N. and K.S.) Department of Plant Agriculture, University of Guelph 50 Stone Road East, Guelph, ON, N1G 2W1, Canada.*

Cover crops (CC) provide numerous ecosystem services, but their effects on subsequent cash crop yield must be neutral for wider adoption. CC effect on corn yield mainly depends on the type of CC species used, biomass accumulated, and termination timing. A study was conducted at four Ontario site-years in a soybean-winter wheat-CC-corn rotation with a split-plot design (four replications; alpha=0.05). The main-plot factors consisted of overwintering and winter-terminated CC species in mono-, bi-, and polycultures (4, 8, 12 species) and controls with/without nitrogen applied to corn (NoCC+N/NoCC0N). The split-plot factor was no-till vs. fall strip-till. Bicultures or polycultures tended to accumulate greater fall biomass than monoculture species, likely because grass and legume CCs were always included together. The exception was at New Liskeard and Winchester in 2020, when the radish (*Raphanus sativus* L. var. *Longipinnatus*) (1080±95 and 3240±235 kg ha^{-1}, respectively) accumulated significantly more fall aboveground biomass than other CC treatments. In the corn year at Ridgetown, CC treatments were not different than NoCC+N (12.5±0.68 Mg ha^{-1}) and all yielded >3.8 Mg ha^{-1} than NoCC0N. At Winchester in both 2020/2021, all CC treatments had similar grain yield to NoCC+N (11.5±0.57 Mg ha^{-1}) but in 2020, poor termination of red clover (*Trifolium pratense* L.) reduced yield (4.28 ± 0.57 Mg ha^{-1}). At New Liskeard, N availability did not appear to affect yield as NoCC+N and NoCC0N controls were not different (8.09 and 8.20±0.71 Mg ha^{-1}). Interestingly, tillage systems did not impact corn yield, indicating the importance of CC selection.

38. Long-term impacts of cover crops on nitrogen dynamics in grain corn (*Zea mays* L.) in southwestern Ontario P. MUSAYIDIZI, A. BISWAS, and A. BERG, AND L L. VAN EERD *School of Environmental Sciences, University of Guelph, Ridgetown Campus, ON N0P 2C0, Canada; and (A.B.) School*

of Environmental Sciences, University of Guelph, Guelph, ON N1G 2W, Canada; and (A.B.) Geography, Environment & Geomatics, University of Guelph, Guelph, ON N1G 2W1, Canada

The role of cover crops (CCs) on the fate of N in the CC and subsequent seasons have been well documented. However, less is known on how long-term cover cropping impacts N dynamics during corn growing season. This long-term split-plot (four replicates) experiment has two side-by-side sites established in 2007 and 2008, respectively at Ridgetown, Ontario. Main-plot treatments were a control (no-CC), and annual CCs were grown 11 out of 15 years: OAT (*Avena sativa* L.), radish (RAD*; Raphanus sativus* L. var. *Longipinnatus*), winter cereal rye (RYE; *Secale cereal* L.) and RAD+RYE mix. Sub-plot factor was winter wheat straw retained or removed. In 2022, corn N status (SPAD meter and hand-held optical sensor NDVI), plant N uptake, soil moisture (Time-Domain Reflectometry sensor) were assessed during the corn season, and soil mineral N content prior to planting (n=40; alpha=0.05). Starting at V6 (collar method), corn grown in RAD and RAD+RYE plots were greener (mean NDVI= 0.7 and; SPAD= 50.4 and 50.4, respectively) and 26-to-31 cm taller at V8 than OAT and no-CC (NDVI=0.6 and 0.6; SPAD=45.9 and 44.7, respectively), indicating N deficiency which continued to harvest. Overall, OAT and no-CC plots had 15% and 22% greater soil moisture than the RAD and RAD+RYE, suggesting that crop growth was limited by N availability rather than plant-available water in the no-CC and OAT (less so in RYE) plots, compared to RAD and RAD+RYE. More results will be forthcoming on corn yield and plant N uptake and the experiment will be repeated in 2023.

39. Water-conducting roots responsible for nitrogen uptake in maize (*Zea mays*) Y. JIANG AND J. K. WHALEN *Department of Natural Resource Sciences, McGill University, 21111 Lakeshore Road, Ste-Anne-de-Bellevue, Quebec, Canada H9X 3V9*

Maize (*Zea mays*) root systems have embryonic primary and seminal roots, and post-embryonic crown roots. Embryonic roots have a smaller diameter and fewer xylem vessels than the crown roots. This means that crown roots should pull more water and dissolved nutrients from the soil pores to the plant. However, root hydraulic conductance will be affected by the soil water potential because it is harder to pull water from a dry soil than a wet soil environment. This study will determine the relative importance of embryonic and crown roots of maize to acquire NO_3^-, a mobile dissolved nutrient, in relatively wet and dry soil conditions. We hypothesized that crown roots acquire more NO_3^- than embryonic roots in a relatively wet soil (-5kPa), whereas more NO_3^- is obtained from embryonic than crown roots in a relatively dry soil (-30 kPa). Maize was grown in a split-root pot to segregate the embryonic roots and crown roots. Nitrate acquisition was the amount of ^{15}N labelled KNO_3 fertilizer that migrated from soil to the maize plant at V3 and V6 growth stages. A partial nitrogen mass balance was determined by destructively sampling shoots, roots, and soils after 0, 24 and 48 h after ^{15}N-KNO_3 fertilizer application. We measured the hydraulic conductance, xylem area and number, and morphology of embryotic and crown roots. Relationships between root characteristics and N uptake by maize plants will be discussed.

Session 5b: Sustainable Diseases management tools: Bioproducts, cultural practices and prediction modeling-1

40. Mitigating apple replant disease with biocontrol soil treatments M. A. A. MECHLER AND J. A. CLINE *Ontario Agricultural College, Department of Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1, Canada.*

Apple replant disease (ARD) can increase apple tree (*Malus domestica* Borkh) mortality, delay production, and impair yield, resulting losses of up to $60 K/ha over an orchard's lifespan. Common fumigation treatments harm human and environmental health, have variable effectiveness, and disrupt beneficial soil microbial activity and processes. This project aims to reduce long-term ARD in Ontario orchards with commercially available plant growth-promoting (PGP) microbial biocontrols. Experiments were carried out at three commercially managed apple orchards in Norfolk County, Ontario using a randomized block design with five treatments: untreated control, fumigation control (chloropicrin 164 L ha^{-1}), PGP fungi (PGP-F), PGP rhizobacteria (PGP-R), and a mix of PGP-F and PGP-R. Tree growth and soil health was monitored seasonally with several plant, chemical and ecological soil assessments. Differences in soil bacterial and fungal communities were observed among treatments. PGP treatments impacted plant growth at two of the orchards. At the Simcoe Research Station, PGP-R produced the greatest mean root mass (181 g), followed by the chemical fumigation (150 g). PGP-F treatments accumulated less root biomass (130 g) than the untreated control (137 g). Chemical fumigation resulted in the greatest above-ground biomass tree growth (307 g) followed by the PGP-R (252 g), whereas PGP-F (218 g) accumulated less biomass than the untreated control (237 g). At a commercial orchard, the chemical fumigation resulted in the largest annual trunk diameter growth between 2020-2021 with 2.27 cm, followed by the combination PGP-F & R treatment (1.91 cm). The untreated control had the least growth (0.91 cm).

41. Metabolomics-based Profiling of Resistant Japanese Plums Infected with Black Knot Fungus C. SHUM, W. EL KAYAL, D. AHMED, I. SHARKAWY, AND J. SUBRAMANIAN *Department of Plant Agriculture, Ontario Agricultural College, University of Guelph, ON N1G 2W1, Canada; (W.E.K.) Faculty of Agricultural and Food Sciences, American University of Beirut, Beirut, 1107, Lebanon; and (D.A., I.S.) Center for Viticulture & Small Fruit Research, College of Agriculture and Food Sciences, Florida A&M University, FL 32308, United States of America*

Japanese plums (*Prunus salicina*) are debilitated by a fungus, *Apiosporina morbosa* which causes Black Knot (BK) disease. It is a difficult disease to study, due to unpredictable epidemic cycles and long duration before symptoms to appear. Spores germinate on young branches, and over time,

the cankers from which girdle the branches and eventually cause death. We hypothesized that there are metabolic differences among genotypes that confer disease resistance. Thus, we determined the metabolites involved in BK resistance to provide a marker-based profiling method to accelerate breeding efforts. An untargeted metabolomic study using 2 resistant varieties ('Shiro' and 'Vampire') and 2 susceptible varieties ('Redcoat' and 'Underwood') was performed. Extracts of stems of each genotype were analysed using liquid chromatography mass spectrometry (LC-MS). The analysis was conducted with Principal Components Analysis (PCA) and Variable of Importance (VIP) scores to generate associations. 471 metabolites in total were discovered, while 6 metabolites were found in greater concentrations solely in the resistant varieties which included polyphenols, benzaldehydes and aromatic compounds. Two unique compounds, Catechin and 3,4 Dihydroxybenzaldehyde were identified in resistant genotypes which are known plant defense metabolites. HPLC analysis of the samples further confirmed the higher presence of these compounds in resistant genotypes. This research paves the way for generating a metabolite marker-based selection of BK resistance in breeding plums and also elucidating mechanisms behind BK resistance.

42. CRISPR/Cas9 gene knockout studies reveal the involvement of phenazine production in the antifungal activity of the novel *Pseudomonas chlororaphis* strain S1Bt23 M. AKUMA, S. I. CHI, R. XU, V. PLANTE, M. HADINEZHAD, AND J. T. TAMBONG *Agriculture and Agri-Food Canada, Ottawa, Ontario, K1A 0C6; (M.A.) University of Ottawa, Ottawa, Ontario, K1N 6N5; (S.I.C.) Canadian Blood Service, Ottawa, Ontario, K1G 4J5; and (J.T.T.) Department of Plant Science, University of Manitoba, Winnipeg, MB. R3T 2N2*

Canadian field and greenhouse crop yields suffer significant losses annually due to fungal pathogens. The use of chemical pesticides to alleviate this issue poses major public health and environmental safety concerns. Biological pesticides are promising alternatives to the use of synthetic chemicals. In 2015, a novel *Pseudomonas* strain S1Bt23 was isolated from Canadian woodland soils. Taxonomic characterizations by electron microscopy, 16S rRNA, multi-locus sequence analysis and whole-genome analysis identified S1Bt23 as a potential new subspecies of *Pseudomonas chlororaphis*. Strain S1Bt23 displayed antifungal activity against five major fungal/oomycete phytopathogens (*Alternaria solani*, *Pythium ultimum, Pythium arrhenomanes*, *Rhizoctonia solani* and *Sclerotinia sclerotinium*) but the secondary metabolites involved remained unknown. Genome analysis of S1Bt23 revealed the presence of a complete phenazine cluster. Thin-layer chromatography (TLC) and high-performance liquid chromatography analyses of extracts of S1Bt23 confirmed the production of phenazine-1-carboxylic acid (PCA), a potent antifungal compound. CRISPR/Cas9-mediated deletion of either *phz*B or *phz*F gene from the phenazine cluster in S1Bt23 completely abolished PCA production based on TLC analysis. This indicates that *phz*B and *phz*F are essential for PCA production. Importantly, both PhzB-/- and PhzF-/- S1Bt23 strains lost antagonistic activity against *Pythium ultimum*, a pathogen of tomato. Furthermore, metabolic extracts from the wild-type displayed antifungal activity but not those from PhzB-/- and PhzF-/- mutants. This study demonstrated that PCA plays a major role in the potent *in vitro* antifungal activity of *P. chlororaphis* S1Bt23. Greenhouse experiments will be conducted to test the effectiveness of strain S1Bt23 to control *Pythium ultimum* in the presence of tomato plants.

43. Thinning response of gala to metamitron applied at different stages of fruitlet development L. A. C. REIS AND J. A. CLINE *Ontario Agricultural College, Department of Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1, Canada*

Cultural management of fruit load of apple trees is critical challenge to optimize fruit size, quality, and reduced biennial bearing. Carbaryl is a common chemical fruitlet thinner for apple trees, but it is banned in Europe due to its potential negative impacts on human health and its neurotoxic effect on bees. Carbaryl has been subjected to continuous risk assessment by the PMRA in Canada, hence finding thinning alternatives has generated interest in studying new compounds that are efficacious in thinning. Metamitron (MET) is a photosynthesis II inhibitor being evaluated for thinning. The objective of this research was to investigate the optimal time to apply MET during early fruitlet development. Trees were treated with 438 mg/L MET applied at 5, 8, 14.5, 18.5, 22.5 mm fruitlet diameter and compared to an untreated control in a randomized complete block design with five replications. Fruit set, yield, number of fruits/trees, fruit weight, and crop load were evaluated in 2021 and 2022. MET applied when fruitlets were between 11 and 18.5mm reduced fruit set, number of fruits/tree and crop load of Gala trees in both years. In 2021, fruit weight was 14%, 18%, and 15% higher compared with the untreated control when MET was applied at 7, 11 and 15 mm, respectively. In 2022, when MET was applied at 5, 8, 14.5, 18.5 and 23.5 mm, fruit weight increased 4%, 12%, 17%, 11% and 6% compared to the untreated control, respectively. Further benefits of MET as an effective thinning product will be discussed.

44. Insensitivity of *Stemphylium vesicarium* to two FRAC 7 fungicides in Ontario in 2021–2022 E. MCFAUL, B. D. GOSSEN, AND M. R. MCDONALD *Department of Plant Agriculture, University of Guelph, 50 Stone Road E, Guelph, ON N1G 2W1, Canada; and (B.D.G.) Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada*

Stemphylium leaf blight (SLB), caused by *Stemphylium vesicarium* (Wallr.) E.G. Simmons, is an important fungal disease of onion in North America. SLB causes premature defoliation and reduced sprout inhibitor efficacy, bulb quality and yield. Commercial onion cultivars are not resistant to *S. vesicarium* and calendar-based fungicide applications (10–14-day intervals) do not provide adequate SLB reduction. Previous studies reported insensitivity in *S. vesicarium* to fungicides in FRAC groups 2, 3, 7, 9 and 11 in Ontario and New York. In the current study, isolates of *S. vesicarium* from Ontario were assessed for sensitivity to two relatively new active ingredients, fluxapyroxad and penflufen, in FRAC 7. A baseline isolate from 1995 was sensitive to both active ingredients based on mycelial growth but insensitive to both based on conidial germination. In a conidial germination assay, 80% of the 45 isolates assessed were insensitive to fluxapyroxad at 100 µg/mL and 94% of 31 isolates were insensitive to

penflufen at 75 µg/mL. In contrast, mycelial growth of all isolates was sensitive to 10 µg/mL fluxapyroxad, but only 1 of 12 isolates (8%) was insensitive to 25 µg/mL penflufen. Assessment of isolates collected since 2012 indicated that insensitivity of *S. vesicarium* mycelium to fluxapyroxad has increased over time, possibly because of cross-reaction with other FRAC 7 active ingredients. The reaction to penflufen is relatively unchanged from the baseline isolate. Studies of *S. vesicarium* insensitivity to other FRAC 3 and FRAC 7 active ingredients are in progress.

45. Enhancing soil health and root rot suppression in canola (*Brassica napus*): an investigation into fungal communities and chemical-physical properties of field soils H. YU, J. CORDERO-ELVIA, S. F. HWANG, R. FREDUA-AGYEMAN, V. MANOLII, AND S. E. STRELKOV *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada*

Root rot, caused by a complex of soilborne pathogens, is an important disease of canola (*Brassica napus*). The health of soil is influenced by its physical and chemical properties, as well as the diversity and activity of its microbial community. In this study, 365 soil samples collected from canola fields in Alberta, Canada, were evaluated for their root rot suppressiveness in greenhouse bioassays. Soil samples exhibiting varying levels of disease suppression, ranging from low to high, were then selected to assess the diversity of microbial communities as well as the chemical and physical properties of the soil. Based on root rot severity, less than 20% of the soil samples were classified as highly suppressive. Correlation analysis indicated that soil texture, clay (< 2 µm) and silt (2-50 µm) content were associated with soil suppressiveness. Soil pH and the level of copper were weakly correlated with root rot severity. Metabarcoding analysis indicated that the fungal genera *Fusarium*, *Acremonium*, *Penicillium* and *Candida* were most abundant across all soil samples. The relative abundance of *Aspergillus*, *Penicillium* and *Arthrinium* was negatively correlated with disease severity, while the abundance of the pathogenic genera *Alternaria* and *Fusarium* was positively correlated with disease severity. The results suggest shifts in the fungal communities associated with suppressive soils.

CSA-Distinguished Agronomist & Genetics and Breeding 1b

46. The rewards of tilting at research dogma P. HUCL *Crop Development Center, Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan S7N 5A8, Canada*

47. Genetic analysis of yield and yield stability traits in spring wheat across diverse Canadian environments A. NEUPANE, M. J. MORRISON, D. G. HUMPHREYS, R. CUTHBERT, C. HIEBERT, S. KUMAR, E. K. BRAUER, S. GRIFFITHS , M. HAWKESFORD, A. RICHE, AND A. J. BURT *(A.N., M.J.M., D.G.H., E.K.B., A.J.B) Ottawa Research and Development Centre (ORDC), Agriculture and Agri-Food Canada (AAFC), Ottawa, ON, Canada; (R.C.) Swift Current RDC, AAFC, Swift Current SK; (C.H.) Morden RDC AAFC, Morden, MB; (S.K.) Brandon RDC, AAFC, Brandon, MB; (S.G.) John Innes Centre, Norwich, UK ; and (M.H., A.R.) Rothamsted Research, Hertfordshire, UK*

The goal of this research project is to improve the understanding of the agronomic traits that support yield and yield stability across diverse growing environments. A subset of 88 lines from a double haploid spring wheat population (AAC Brandon/Pasteur) was grown in yield trials at three Canadian sites, Ottawa, Brandon, and Swift Current from 2019 to 2022. Agronomic data were analyzed to model grain yield and to capture yield stability across multiple environments. Genotypic data from SNP-based array platforms was used with the phenotypic data to detect associated QTL. The linkage map of the population was constructed containing 2350 SNP and a total map length of 4096 cM. Major agronomic traits QTL were detected across multiple environments and located on multiple chromosomes, including plant height on chromosomes 4A, 4B, and 5B, days to maturity on 5B, and 7D, grain yield on 6D, test weight on 3B, 4B and 5A, thousand kernel weight on 3B, 4B and 5A, and protein content on 4B and 7A. Analysis for grain yield stability QTL is in progress. Additional image data was captured and used to model biomass accumulation throughout the growing season at the Ottawa site. This phenomics data will be used with multiple yield components to create yield prediction models and to find associated QTL. This project, part of the International Wheat Yield Partnership, aims to identify yield-related traits and linked markers that can reliably improve yield across diverse environments.

48. Underlying Mechanisms of FHB Susceptibility and Resistance in Wheat: Insights from a Transcriptome-Based Analysis S. SEIFI[†], M. KAVIANI[†], A. NAVABI[§], E. A. LEE, AND H. M. BOOKER *(M.K., A.N.[§] E.A.L., H.M.B.) Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada; and (S.S.) Aurora Cannabis Inc., Comox, British Columbia, Canada*
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Over the last two decades, several QTLs involved in Fusarium head blight (FHB) resistance have been identified and, in a few cases, resolved to the underlying genes. These results have not consistently translated into better FHB-resistant wheat cultivars, nor have they necessarily extended our understanding of how resistance to FHB can be achieved. Despite considerable efforts, FHB remains a serious disease in many wheat-growing regions. To gain insights into the underlying biology, we examined the wheat transcriptome at a key FHB developmental time point—the switch from the biotrophic to the necrotrophic phase—in both highly resistant (AAC Tenacious) and highly susceptible (Wilkin) spring wheat cultivars. Sequestering of deoxynivalenol (DON) does not appear to differentiate the resistant from the susceptible response. Instead, our findings suggest true resistance to FHB requires the plant to downregulate or limit two pathways that are normally associated with disease resistance responses:

programmed cell death (PCD) and the generation/accumulation of reactive oxygen species (ROS). Using a stringent RNA-Seq analysis targeting the transition period of the pathogen from its biotrophic phase to its necrotrophic phase, we show that susceptibility to FHB relies on the pathogen's ability to highjack the PCD response, consistent with other necrotrophs. In contrast, the resistance response to FHB relies on the plant's ability to suppress its PCD response and limit the ROS accumulation/production that is necessary for production of DON by the pathogen.

49. Pathogenicity of *Fusarium graminearum* and *F. Poae* causing Fusarium head blight in barley under controlled conditions R. KHANAL, K. HUDSON, A. FOSTER, X. WANG, L. J. HARRIS, E. BRAUER, AND D. P. OVERY *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Ave, Ottawa, ON K1A 0C6, Canada; (A.F.) Charlottetown Research and Development Centre, Agriculture and Agri-Food Canada, 400 University Avenue, Charlottetown, PE C1A 4N6, Canada; and (X.W.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, Manitoba, Canada R6M 1Y5*

Fusarium head blight (FHB) is one of the most devastating diseases of barley. FHB is caused by a species complex of *Fusaria*, of which *Fusarium graminearum* Schwabe is the species responsible for most FHB epidemics. Field surveys show that two or more *Fusarium* species often co-exist within the same field and *F. poae* is as another dominant species in barley. This study investigated the effect of the interactions between *F. graminearum* and *F. poae* on FHB and mycotoxin accumulation. Two susceptible barley genotypes were spray-inoculated with *Fusarium* conidiospore suspensions and the disease severity and fungal accumulation was evaluated based on symptom and genomic DNA. There was a significant difference in FHB severity between *F. graminearum* and *F. poae* infections, where *F. graminearum* produced severe FHB disease symptoms while *F. poae* did not cause FHB. When heads were co-inoculated with both *Fusarium* species, the resulting FHB severity was unchanged relative to heads inoculated with *F. graminearum* which was reflected in the DNA quantification of the species. The mycotoxin profile of the co-inoculated treatment appeared to be most influenced by *F. graminearum*-related metabolites with a minor influence by *F. poae*-related metabolites. Forty-six features were annotated with metabolite study and which shows *F. graminearum* appears to outcompete *F. poae* in its ability to establish infection in barley and as a result contributes the majority of mycotoxin contamination within this crop.

Session 6: Clubroot disease

50. Clubroot in the Canadian canola crop: two decades into the outbreak S. E. STRELKOV AND S. F. HWANG *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5*

Clubroot is an important soilborne disease of the *Brassicaceae* family caused by the obligate parasite *Plasmodiophora brassicae*. While clubroot has been known to occur in Canada on cruciferous vegetables for over a century, it was not reported on canola (oilseed rape; *Brassica napus*) in the Prairies until 2003. That year, a dozen clubroot-infested canola crops were identified near Edmonton, Alberta. Annual surveys over the past two decades have tracked the continued spread of the disease, with at least 3,984 field infestations confirmed in Alberta by 2022, and dozens of cases in Saskatchewan and Manitoba. While numerous methods have been evaluated to manage clubroot in canola, the control of the disease in western Canada relies heavily on the deployment of resistant cultivars. Unfortunately, the intensive cultivation of clubroot-resistant canola has led to the emergence of "resistance-breaking" pathotypes of *P. brassicae*, which have now been confirmed in at least 425 fields. These changes in the virulence of the pathogen population are reflected in significant shifts in the predominant pathotypes found in Alberta. Prior to the introduction of clubroot resistance in 2009-2010, pathotype 3H (as defined on the Canadian Clubroot Differential set), which is avirulent on all clubroot-resistant canola cultivars, was most common. Since then, various resistance-breaking pathotypes, including 3A and 3D, have become more frequent. Efforts to manage these pathotypes have focused mainly on the identification of resistance, although an integrated approach, which relies on multiple management strategies including longer rotations out of host crops, is probably warranted.

51. Understanding the fitness cost of resistance-breaking capacity in *Plasmodiophora brassicae* Y. AIGU, I. S. STRELKOV, AND S. E. STRELKOV *Department of Agricultural Food and Nutritional Science, University of Alberta, Edmonton, AB T6G2P5, Canada*

Plasmodiophora brassicae causes clubroot, a soilborne disease of canola (*Brassica napus*) managed primarily by planting resistant cultivars. The genetic diversity of pathogen field populations can be high, with these populations often consisting of pathotype mixtures. In Alberta, Canada, resistance-breaking (RB) pathotypes of *P. brassicae* emerged within a few years of the introduction of clubroot-resistant canola. However, a decade after the first RB pathotypes were identified, both RB pathotypes and non-RB pathotypes continue to coexist and spread at similar speeds. The aim of this study was to evaluate the potential fitness cost associated with *P. brassicae* resistance-breaking capacity by characterizing the evolution of the pathogen population structure. Four consecutive cycles of clubroot inoculation were performed on two susceptible and two resistant *Brassica* genotypes using different pathogen populations. The first population was artificially generated by mixing equal proportions of two single spore-isolates (SSIs) representing the non-RB pathotype 3H and RB pathotype 3A. For comparison, these SSIs were also inoculated separately. A second population consisted of a field population of the RB pathotype 5X collected from Alberta. After each infection cycle, clubroot symptom development and resting spore production were quantified. To assess potential changes in these populations during the consecutive infection cycles, a final reverse inoculation was performed, where the cultivars were inverted. Changes in symptom development and spore

production suggest a fitness cost when RB-pathotypes are re-inoculated on resistant hosts following consecutive cycles of infection on susceptible hosts. The genetic structure of the cycled populations will be compared by RAD-seq analysis.

52. Efficient identification of *Plasmodiophora brassicae* pathotypes using molecular tools S. M. VELASCO-CUERVO, H. H. TSO, L. GALINDO-GONZALEZ, S. F. HWANG, AND S. E. STRELKOV *Department of Agricultural, Food & Nutritional Science, University of Alberta, Edmonton, AB T6G 1Y2, Canada; (H.H.T.) Current affiliation: Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada; and (L.G.G.) Molecular Identification Research Laboratory, Canadian Food Inspection Agency, Ottawa, ON K2H 8P9, Canada*

Clubroot (*Plasmodiophora brassicae*) is a threat to canola (*Brassica napus*) production in Canada. The management of this disease relies mainly on the cultivation of clubroot-resistant canola cultivars. However, the selection pressure imposed on *P. brassicae* populations by these resistant hosts has led to the emergence of new, 'resistance-breaking' pathotypes. Currently, pathotype classifications are based on pathogen virulence phenotypes obtained on the Canadian Clubroot Differential set. Molecular tools could facilitate the identification of *P. brassicae* pathotypes, allowing the processing of hundreds of samples in much less time. We developed two PCR-based assays, RNase H2-dependent PCR (rhPCR) and SNaPshot, to distinguish pathotypes based on polymorphisms. With this approach, we could classify 38 single-spore isolates of *P. brassicae* into two distinct pathotype clusters. We are now developing a metabarcoding assay for pathotyping hundreds of samples at once using several polymorphic regions found throughout the genome. We have been using High Fidelity (HiFi) sequencing to construct *de novo* assemblies with better coverage for 10 single-spore isolates and to obtain the pangenome of *P. brassicae* based on Canadian pathotypes. With this approach, we are looking to find more variable genomic regions and polymorphisms that can be used as molecular markers to distinguish specific pathotypes. Finally, we generated two platforms for SNPs analyses (BLAST and Genome Browser), which have facilitated pathotyping and the discovery of barcodes. The identification of *P. brassicae* pathotypes using molecular tools is a promising strategy for the early detection of specific pathotypes in plant and soil samples.

53. The identification of an improved heterologous protein expression system for assessing the function of *Plasmodiophora brassicae* effectors E. R. M. STORFIE, I. STRELKOV, S. F. HWANG, AND S. E. STRELKOV *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada*

On the Prairies of western Canada, canola (*Brassica napus*) production is severely impacted by *Plasmodiophora brassicae*, an obligate biotrophic pathogen that causes clubroot disease. Genome sequencing and transcriptome analyses of *P. brassicae* identified putative effectors that can be deployed by the pathogen to create a more conducive environment during host infection. Unfortunately, *P. brassicae* cannot be cultured *in vitro* and many *in silico* tools provide little information on many effectors, making functional studies laborious and time-consuming. Previous transcriptome analysis of the *P. brassicae* effector repertoire identified two highly expressed putative effectors, SPR01261.1 and SPQ99289.1, predicted to encode a serine carboxypeptidase and an unknown protein with a kinase domain, respectively. Experiments are underway to evaluate various heterologous protein expression systems using these two effectors. Each effector was cloned separately into pDEST17 (T7 promoter and N-terminal hexahistidine) and pMAL-c6T (tac promoter and N-terminal hexahistidine tagged *malE* gene) vectors and transformed into different *Escherichia coli* and *Vibrio natriegens* strains. To increase protein expression and solubility, various induction conditions were tested for each transformed strain including medium, temperature, amount of inducer, and length of induction. To determine if protein folding and solubility could be improved further, the addition of stabilizing and solubilizing agents was assessed using the most promising expression strains. The expression, solubility, and activity of each protein indicated which system was most suitable for expressing *P. brassicae* proteins. An improved heterologous protein expression system for effector characterization will increase the efficiency and ease of protein functional studies in *P. brassicae*.

54. The virulence of *Plasmodiophora brassicae* on canola varieties with 'second-generation' clubroot resistance in Canada K. HOLLMAN, V. P. MANOLII, E. R. M STORFIE, S. F. HWANG, AND S. E. STRELKOV *Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB T6G 2P5, Canada*

Clubroot, caused by *Plasmodiophora brassicae*, is a damaging soilborne disease of canola (*Brassica napus*). In Canada, clubroot is managed mainly by planting resistant varieties. However, new pathotypes of *P. brassicae* virulent on this first-generation of clubroot-resistant hosts have emerged and are becoming increasingly widespread. In response, breeders have released canola varieties with new 'second-generation' resistance. While the nature of this resistance is not in the public domain and may differ among cultivars, it is reportedly distinct from first-generation resistance and conferred by a different resistance gene(s) or stacked resistance genes. The aim of this study was to characterize the virulence of *P. brassicae* on canola varieties with second-generation resistance. Isolates of the pathogen were recovered from second-generation clubroot-resistant canola crops across Alberta, Canada, which showed symptoms of the disease, and were evaluated for their virulence under controlled conditions on seven commercial canola varieties carrying second-generation resistance. Some of these field isolates, which represented a variety of pathotypes, were found to be moderately to highly virulent on several of the host varieties. The isolates are also being evaluated with molecular markers to determine whether they belong to one of two genetically distinct *P. brassicae* populations previously reported in Alberta, or whether they are part of a new, separate population. The results of this study suggest that virulent isolates of *P. brassicae* may be difficult to control solely via the deployment of resistant hosts, and that a more integrated approach to clubroot management is required.

Session 7: Biotic and Abiotic Challenges

55. Sudden apple decline in British Columbia: a potential link between fungal cankers, invasive Sesiidae moths, and abrupt hydraulic failure J. L. MACDONALD, K. D. HANNAM, H. XU, AND D. T. O'GORMAN *Summerland Research and Development Centre, Agriculture and Agri-Food Canada, 4200 Highway 97 Box 5000, Summerland, BC V0H 1Z0, Canada*

Sudden apple decline (SAD) is a poorly understood disorder, resulting in rapid death of apple trees. We investigated the signs and symptoms, biotic and abiotic stressors, fruit quality impacts and internal tree hydraulics of afflicted trees. In 2018, orchard surveys were conducted in seven apple orchards in the Okanagan Valley reporting high tree mortality consistent with SAD. Of 350 trees observed, 28.4% were assessed as declining; necrotic stem lesions were observed on 87.5% of declining trees, and underdeveloped foliage was observed on 27.7% of the declining trees. A survey of a 1-10 year old apple germplasm orchard showed that the probability of trees exhibiting SAD increased with tree age, regardless of parentage. Across orchards, there appeared to be an association between infestation of apple clearwing moth (*Synanthedon myopaeformis*), the size of necrotic stem lesions, and incidence of SAD. Assessment of stem water transport showed a water limiting bottleneck at the graft union, often associated with canker. The trees in decline also had lower midday stem water potential, lower photosynthetic rate, and lower fruit weight and dry matter. Grid (5-m) sampling of soils in four affected orchards showed a possible correlation between SAD-associated tree mortality and a given soil's ability to retain water (e.g., soil depth, coarse fragment content, organic matter content). We propose that impaired water transport across the graft union, due in part to the impacts from fungal canker and associated *S. myopaeformis* infestations, may be a contributing factor to hydraulic failure and the incidence of SAD in this region.

56. Genetic mapping of resistance to Fusarium head blight and DON accumulation in wheat landrace Wat.1190580 S. SINGH, D. MIRANDA, M. A. HENRIQUEZ, Z. YE, C. MCCARTNEY, AND G. S. BRAR *Faculty of Land and Food Systems, The University of British Columbia, 2357 Main Mall, Vancouver, BC V6T 1Z4, Canada; (G.S.B.) Faculty of Land and Food Systems, The University of British Columbia, 2357 Main Mall, Vancouver, BC V6T 1Z4, Canada; (D.M., M.A.H.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100 Morden, MB R6M 1Y5, Canada; and (Z.Y., C.M.) Faculty of Agricultural and Food Sciences, Department of Plant Science, University of Manitoba, 222 Agriculture Building, Winnipeg, MB R3T 2N2, Canada.*

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 our study, we are utilizing a Watkin landrace Wat.1190580 (origin: Iran), with a resistant reaction to FHB and DON accumulation as a male/resistance donor parent to develop three RIL populations: Paragon/Wat.1190580 (F8, n=80), AAC Starbuck/Wat.1190580 (F7, n=111), BW1085/Wat.1190580 (F7, n=101). 'Paragon' is a European cultivar susceptible to FHB. AAC Starbuck and BW1085 are recent hard red spring wheat varieties carrying *Fhb1* and have moderate and intermediate resistance to FHB/DON, respectively. Paragon/Wat.1190580' was screened for FHB incidence, severity, visual rating index (VRI), Fusarium damaged kernels (FDK), and phenological traits- days to anthesis (DTA), and plant height (PHT) at Carman and Morden in 2021 and 2022. The population was genotyped using a high throughput skim sequencing approach. This study will present results on QTL mapping for FHB and DON resistance and results on the epistatic interactions among the novel resistance alleles (contributed by 'Wat.1190580') and *Fhb1.*

57. Microbe-coating fertilizers for sustainable biomass production and yield enhancement: corn and potato case studies M. ANTAR, P. SEGUIN, AND D. L. SMITH *Department of Plant Science, McGill University, Macdonald Campus, 21 111 Lakeshore Road, Sainte-Anne-de-Bellevue, QC H9X 3V9, Canada*

Corn and potato are two high-value economic crops for food security. To maintain a high biomass and yield, farmers generalized to overuse of chemical fertilizers, negatively impacting the ecosystem and soil fertility. For sustainable agriculture, beneficial microbes can associate with plants to increase nutrient availability, playing a key role in establishing plants under field conditions and contributing to plant health and development.A multi-year trial was performed under field conditions on potato and corn to assess the effectiency of five *Bacillus* strains applied as a microbe-coating fertilizer. The study evaluated the field performance of the microbe-coated fertilizer in clay, clay loam and sandy loam soil at alternate seedings dates. The results show that the microbe-coating fertilizer significantly affected potato and corn biomass. Potato yield increased 11-19% in two consecutive years. The growth promotion and yield enhancement may have resulted from the efficiency of the fertilizer in terms of enhanced nutrient availability and uptake. Based on the collected data, in 2018, corn yield and biomass increased considerably in clay soil when seeded early, compared to 2019, when the highest yield and biomass production occurred in clay loam soils when seeded early. Treatment with the microbe-coatings caused consistent increases in yield and biomass production across all soil types in 2020, but the performance was best for clay soil. Corn's response to the microbe-coatings varied from year to year due to the variations in environmental factors. Soil series could also have impacted corn growth and interactions between the microbe-cotings and corn root system.

58. Winter wheat genotype-*Fusarium graminearum* isolate interactions using the detached wheat head bioassay method R. MCCONACHIE, M. SERAJAZARI, N. ALIJANIMAMAGHANI, E. SPARRY, A. SCHAAFSMA, AND H. BOOKER *(R.M., M.S., and H.B.) Ontario Agricultural College, University of*

Guelph, Guelph Campus, 50 Stone Road East, Guelph, ON N1G 2W1, Canada; (N.A., and A.S.) Ontario Agricultural College, University of Guelph, Ridgetown Campus, 120 Main Street East, Ridgetown, ON N0P 2C0, Canada; and (E.S.) C & M Seeds, 6180 5th Line, Palmerston, ON N0G 2P0, Canada

Wheat production in Ontario is limited by Fusarium head blight (FHB) in wheat, caused by *Fusarium graminearum* (*Fg*), which decreases yield and results in grain mycotoxin accumulation. A decrease for FHB resistance in wheat varieties may occur in part due to the emergence of new *Fg* isolates, as the interaction between wheat varieties and *Fg* isolates is highly variable. In addition, the high content of masked mycotoxins in resistant varieties may be reconverted to deoxynivalenol (DON) in the digestive tract of humans and animals. This further degrades resistance capabilities, as low amounts of DON may not equate to safe consumption. To identify specific winter wheat variety × *Fg* isolate interactions, detached spikes from thirty-three Ontario commercial winter wheat varieties were inoculated with 3ADON (3-Acetyl deoxynivalenol), 15ADON (15-Acetyl deoxynivalenol), a mixture of the two isolates, or water at the anthesis stage under a controlled environment. We measured FHB severity 7,10, and 14 days after point inoculation. There were significant differences ($p = <0.001$) between wheat varieties, isolates, and interaction between variety and *Fg* chemotype. The amount of DON, DON-3-glucoside, 3ADON, 15ADON, and 15ADON-3-glucoside were measured for all treatments using high-performance liquid chromatography. The results were then compared with FHB incidence, severity, and index DON levels estimated from grain after harvest from entries at the inoculated FHB nursery at the Elora Research Station. Isolates and their corresponding masked mycotoxin form were positively related. There was a positive relationship between the FHB severity for the field evaluation and the detached head inoculation.

59. Changes in barley seed bacterial endophytes under Fusarium head blight infection W. M. V. C. WEERASINGHE, J. R. TUCKER, A. BADEA, W. G. D. FERNANDO, AND C. WIJEKOON *Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB R3T 2N2, Canada; Morden Research and Development Centre, Agriculture and Agri-Food Canada, Route 100, Unit 100-101, Morden, MB R6M 1Y5, Canada; Canadian Centre for Agri-Food Research in Health and Medicine, 351 Taché Avenue, Winnipeg, Manitoba, R2H 2A6, Canada; and (J.R.T., A.B.) Brandon Research and Development Centre, Agriculture and Agri-Food Canada, 2701 Grand Valley Road, P.O. Box 1000A, Brandon, MB R7A 5Y3, Canada*

Barley is the fourth most cultivated cereal worldwide, mainly used for feed, malting and food. Canada is among the top ten barley-producing countries. The infestation of *Fusarium graminearum* on barley causes Fusarium head blight (FHB), a devastating disease to most cereal crops worldwide. Besides yield loss, the fungus produces mycotoxins making the seeds unsuitable for consumption. Endophytes are known as beneficial microbes in plant defense and productivity. However, limited studies are available on the roles of endophytes in FHB infection. Our study investigates the bacterial endophytes of barley seeds. Seeds were collected separately from four barley genotypes with varying resistance to FHB, grown in clean and FHB-infected plots. They were surface sterilized and directed for Illumina 16s meta-sequencing. Meta-sequencing data revealed compositional differences of potential bacterial endophytes between clean and FHB-infected seeds. The number in total hits and bacterial genera hits in clean seeds were higher than FHB-infected seeds, indicating the difference in bacterial diversity and abundance under the two conditions tested. Among the most abundant bacterial genera, *Streptophyta, Pantoea, Plesiocystis, Pleomorphobacterium* and *Chthonomonas* were common in every barley genotype under both conditions. *Bacteroides* and *Barnesiella* were unique to clean seeds whereas *Pseudomonas* was unique to FHB-infected seeds. Previously published studies indicate that certain *Plesiocystis* spp. improve plant growth and certain species of *Pseudomonas* and *Chthonomonas* are antagonistic. Exploring bacterial endophytes in barley will be an important step to understand their potential role in managing FHB in barley and other cereal crops.

60. Yield, quality, and antioxidant enzyme activities of microgreens in response to different blue: red LED light ratios and growing media R. SALEH AND L. ABBEY *Department of Plant, Food, and Environmental Sciences, Faculty of Agriculture, Dalhousie University, 50 Pictou Road, Truro B2N 5E3, Nova Scotia, Canada*

Microgreens are immature plants grown for their high nutritional values, which can be altered by different LED spectrum and growing media properties. A study was carried out to evaluate the interaction effects between LED light and growing media on yield, phytochemicals and antioxidant activities of kale (Brassica oleracea L. var. acephala) and pak choi (Brasica rapa var chinensis). The microgreens were grown in two different growing media: G1 (20% sawdust+20% perlite) and G2 (30% PittMoss+10% perlite) all containing 30% vermicast and 30% mushroom compost. The LED treatments were blue (B) 80: red (R) 20 (T1); B20:R80 (T2); B60:R40 (T3); B40:R60 (T4); B50:R50 (T5), and white LED as a positive control (PC) at 100 µmol m−2 s−1 light intensity. Kale and Pak choi yield exposed to B20:R80 were significantly increased by 7.2% and 17.4%, respectively in G1 compared to PC.G1. Kale and pak choi protein exposed to B20:R80 was significantly ($P<0.05$) increased by 70% and 87%, respectively in G2 compared to PC.G2. Kale and pak choi phenolics grown in G2 were increased by 51% and 101% under B80:R20, and pak choi and kale flavonoids were increased by 97% and 124% under B40:R60 and B50:R50, respectively compared to PC.G2. The increase in POD and APEX enzymes activities of microgreens grown in G2 under B40:R60 was on the average, 1.4- and 4.2-folds higher than those grown in the PC.G2. We recommend that the application of natural media and precise blue: red LED most likely has a vital role in increasing crop yield and phytonutrients.

Session 8: Emerging/novel tools for plant pathogens diagnostics-2

61. Metagenomics monitoring of plant viruses in Canadian agricultural fruit production systems through honey bee pollination J. S. GRIFFITHS, M. M. GUARNA, S. F. PERNAL, AND M. E. ROTT *(J.S.G.) Vineland research station, Agriculture and Agri-Food Canada, 4902 Victoria Ave N, Vineland Station, ON L0R 2E0, Canada; (M.M.G., S.F.P.) Beaverlodge Research Farm, Agriculture and Agri-Food Canada, 100038 Township Rd 720, Beaverlodge AB T0H 0C0, Canada; and (M.E.R.) Sidney Laboratory, Canadian Food Inspection Agency, 8801 East Saanich Rd, North Saanich BC V8L 1H3, Canada*

Traditional monitoring of plant viruses can be limited to specific assays that only detect individual pathogens. High-throughput sequencing technologies have enabled the identification of multiple plant viruses using a single assay. Metagenomics-based approaches on samples acquired from multiple plants could allow for virus identification at an ecosystem level. Pollen is a unique pathway for the transmission of some plant viruses, which can then spread via pollinators. Commercial honey bee (*Apis mellifera*) pollination is an important aspect of tree fruit and small berry production, worldwide. Honey bees can visit hundreds of flowers and multiple plants in one foraging trip. A metagenomics-based approach was used on samples including bees and pollen from hives located in blueberry, cherry and apple orchards. Twenty-nine unique plant viral species were identified in two blueberry production systems in BC, and a further 5 viruses at one farm in ON. Tomato ringspot virus and Tobacco ringspot virus were common in ON but absent in BC, while blueberry shock virus (BlShV) and Blueberry scorch virus, were identified in BC but not ON. In addition, twenty viruses were detected in apple orchards and 12 viruses were detected from cherry orchards. BlShV Coat Protein (CP) sequences were nearly identical in all samples suggesting low diversity, while prune dwarf virus (PDV) CP sequences were much more variable. Ilarviruses were common in all three types of fruit production systems, with prunus necrotic ringspot virus and PDV being particularly frequent and widespread.

62. In search of a decision support system: A rapid assay to detect a soil's potential to cause *Aphanomyces* root rot S. ALI AND S. CHATTERTON *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 - 1 Ave. South, Lethbridge, AB T1J 4B1, Canada*

Aphanomyces root rot causes severe damage to field peas (*Pisum sativum)* that leads to high yield losses, especially in wet years. Fungicides and/or resistant cultivars are not available.

Understanding the growth dynamics of *Aphanomyces euteiches* in soil after planting a susceptible host could lead to the development of a better decision support system that helps producers make informed field-selection choices. Using quantitative PCR (qPCR), a total of 100 field soils that resulted in varying root rot levels, after a pea bioassay, were tested for pre-plant and post-harvest levels of *A. euteiches* in soils. These two numbers were significantly different for soils containing viable oospores. However, counts from soils that did not cause any disease symptoms remained the same before and after pea growth. To understand oospore germination dynamics in the soil, 5 pea seeds were planted in ~25 ml of soil from 8 fields and changes in quantifiable levels of *A. euteiches* in soils and roots were monitored every other day using qPCR. The earliest detectable surge occurred 7 to 9 days after planting, only from the soils containing viable oospores. The measured DNA levels at this time point, both from roots and soils, showed varying levels of significant correlations with root rot severity. This detection technique is a hybrid between soil bait assays and direct DNA quantification from soils. More soils are being tested to understand how these dynamics can be linked to the risk associated with growing a susceptible crop in any given soil.

63. A Novel Field Assay to Detect DMI Fungicide 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*

Dollar spot, caused by *Clarireedia jacksonii* Salgado and other *Clarireedia* species, is the most common turfgrass disease in North America. The disease is typically managed through multiple fungicide applications during a growing season. A major class of fungicides used to control *C. jacksonii* is the demethylation inhibitors (DMIs). Identification of DMI-resistant *C. jacksonii* populations requires lab facilities to isolate and measure the fungal growth in response to different fungicide concentrations. We developed a selective growth medium containing 0.5 µg/ml propiconazole, antibiotics, and tartaric acid for differentiating between DMI-sensitive or resistant isolates from field samples. This medium was used to evaluate pure cultures of *C. jacksonii* isolates as well as ~2000 leaf blades from plots of inoculated turfgrass. The sensitivity of isolates from pure cultures was always identified accurately, while from leaf blades, accuracy was at 96%. The field assay was tested by end users and researcher at 20 locations across southern Ontario to collect symptomatic leaves on more than 200 plates of the selective medium. *Clarireedia jacksonii* was found at 13 of the sampled locations on antibiotic-amended control plates. At 12 of these 13 locations, colonies grew on the selective medium demonstrating the presence of resistant isolates, which ranged from 5% to 100% on plates tested at each location. This field assay will allow for end-user assessment of *C. jacksonii* DMI sensitivity from field samples saving time, money, and resources. This selective growth assay can be adapted for other fungal pathogens.

64. ER-localized Heat shock protein 70s facilitate Turnip mosaic virus infection in Arabidopsis Z. TANG, S. LYV, C. ZHANG, X. HOU, M. A. BERNARDS, AND A. WANG *Western University of Ontario, 1151 Richmond Street, London, ON N6A 3K7, Canada; (S.L., A.W.) London Research and Development Center, Agriculture and Agri-Food Canada, 1391 Sandford Street, London, ON N5V 4T3, Canada; and (S.L., C.Z., X.H.) College of Horticulture, Nanjing Agricultural University, Nanjing, China*

Turnip mosaic virus (TuMV) is a plant-infecting RNA virus belonging to the family *Potyviridae* and genus *Potyvirus*. It is an agriculturally important virus affecting economically important vegetable, oilseed, forage, and biofuel crops. To develop genetic antiviral strategies, it is essential to identify host factors and understand their functional roles in virus infection, because viruses rely on host cell components to accomplish their life cycle.

ER-localized Heat shock protein 70-12 (HSP70-12) was identified in the Eukaryotic translation initiation factor 4E isoform (eIF(iso)4E) protein complex isolated from TuMV infected *Arabidopsis thaliana* in our previous study. Since eIF(iso)4E is an indispensable host factor for TuMV infection, we hypothesized that ER-localized HSP70s are also recruited by TuMV to facilitate infection.

Our results show that two ER-localized HSP70s: HSP70-11 and HSP70-12, promote TuMV infection and genome replication. *Arabidopsis* HSP70-11 and HSP70-12 knockdown plants are less susceptible to TuMV infection and TuMV genome replication is reduced in protoplasts isolated from these plants. HSP70-11 and HSP70-12 interact with TuMV replicase NIb and co-localize with the TuMV replication complex. Transient overexpression of HSP70-11 or HSP70-12 in *Nicotiana benthamiana* increases TuMV local infection. However, this effect is revoked by removing the ER localization signal from HSP70-11 and HSP70-12. HSP70-11 and HSP70-12 may promote TuMV replication by regulating virus and host protein degradation through their role as protein chaperons because they alter the protein level of their interaction partners. In summary, HSP70-11 and HSP70-12 are host factors facilitating TuMV infection and their role in TuMV infection may depend on their ER localization.

65. Closely-related pathogen classification using Clasnip.com based on gene or genomic sequences J. CHUAN, W. CHEN, L. HALE, AND X. LI
Charlottetown Laboratory, Canadian Food Inspection Agency, 93 Mount Edward Road, Charlottetown, PE C1A 5T1, Canada; (J.C., L.H.) Department of Biology, University of Prince Edward Island, 550 University Avuenue, Charlottetown, PE C1A 4P3, Canada; and (W.C.) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 3701 Carling Ave, Nepean, ON K2H 8S2, Canada

Bioinformatics approaches for pathogen identification have evolved rapidly, but existing methods are time-consuming and complicated for massive screening of pathogens and their non-pathogenic relatives. We developed Clasnip (www.clasnip.com), a web service for efficiently classifying plant pathogens at interspecies and intraspecies levels. The input of Clasnip can be genes or genomic fragments from Sanger or next-generation sequencing platforms. Clasnip outputs a classification summary table, showing sequence identity, and probability. It also generates a multi-locus sequence typing table (MLST) with SNPs details. Currently, Clasnip has curated databases for bacteria ring rot (*Clavibacter sepedonicus*), tomato canker (*C. michiganensis*), soft rot and blackleg (*Dickeya solani, D. dianthicola*, *Pectobacterium parmentieri, P. atrosepticum*, *P. brasiliense*, *P. wasabiae*), zebra chip ('*Candidatus* Liberibacter solanacearum', CLso), and potato virus Y (PVY). Users can also build custom databases of their interest. Databases of PVY, *Clavibacter*, *Dickeya* and *Pectobacterium* are built using whole genome sequences, and Clasnip reached a 100% accuracy for those databases. Besides, Clasnip successfully differentiates CLso using 1-2 single nucleotide polymorphisms (SNPs) on 16S, 16–23 integentic spacer (IGS), and 50S ribosomal protein gene sequences, respectively. Based on the SNP statistics of CLso haplotypes, we proposed a novel standard for haplotyping CLso subgroups. To be classified as a new haplotype, the sequences should contain at least 2 SNPs in the combined region of 16S rDNA and 16–23s IGS (regions, and 2 SNPs in the 50s rplJ/rplL regions. In conclusion, Clasnip (www.clasnip.com) is a powerful bioinformatics tool for pathogen classification and identification.

Symposium 2- CSHS: Controlled Environment Agriculture CSHS

66. Controlled environment cultivation of *Cannabis sativa* Y. ZHEN *School of Environmental Sciences, University of Guelph, 50 Stone Road East, Guelph, Ontario, N1G 2W1, Canada*

It's almost five years since 2018 when *Cannabis sativa* (cannabis) was legalized in Canada for recreational use. Over the past few years, many cannabis cultivation companies were created, merged or bankrupted. New knowledges of cannabis cultivation were generated and accumulated through large scale commercial cultivation and research activities both in commercial cultivation facilities and research institutes. This talk will provide an overview of the current status of Canada's cannabis cultivation industry, a summary of some of the new knowledges generated for controlled environment (CE) cannabis cultivation. The new-knowledge discussion will mainly focus on atmospheric (e.g., light) and rootzone (e.g., nutrient) management for efficiently producing high yield and quality cannabis. It will also discuss future research directions in CE cannabis cultivation.

67. Flowering *Cannabis sativa* under photoperiods longer than 12-h can increase yield and potency A. AHRENS, D. LLEWELLYN, AND Y. ZHENG
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Indoor-grown drug-type cannabis is commonly grown under a 12-h photoperiod during the flowering stage of production. However, we found some cultivars can initiate strong flowering responses under longer photoperiods. Since longer photoperiods inherently provide higher daily light integrals (DLIs), they may increase inflorescence yield. To test this hypothesis, two THC-dominant cannabis cultivars, 'Gorilla Glue' (GG) and 'Incredible Milk' (IM), were grown to commercial maturity under 12-h and 13-h photoperiods under canopy level PPFD of 550 $\mu mol \cdot m^{-2} \cdot s^{-1}$,

resulting in DLIs of 23.8 and 25.7 mol·m^{-2}·d^{-1}, respectively (i.e., ≈ 8% more light in 13-h). There were no delays in flowering initiation, but time to commercial maturity was slightly delayed in the 13-h treatments for both cultivars. The 13-h photoperiod produced larger, more robust plants with substantially more vegetative and floral biomass. Inflorescence yields in 13-h vs. 12-h were 1.50-times and 1.35-times higher in GG and IM, respectively. Incredibly, these increases in yield were 4- to 6-times higher than the increase in DLI. Further, concentrations of major cannabinoids were either higher or not affected in the 13-h vs. 12-h treatments in both cultivars. Indoor cannabis growers are urged to investigate using flowering-stage photoperiods longer than 12-h for their specific cultivars and cultivation environments.

68. Optimization and Scalability of Regenerative *in situ* Electrochemical Hypochlorination for Closed-Loop Hydroponics S. LÉVESQUE, T. GRAHAM, J. PHILLIPS, D. BEJAN, J. LAWSON, AND M. DIXON *(S.L., T.G., J.L., M.D.) Controlled Environment Systems Research Facility, School of Environmental Sciences, University of Guelph, Guelph, Ontario, Canada. N1G 2W1; (J.P.) Senior Design Engineer for the Digital Haptics Lab, School of Fine Art and Music, University of Guelph, Guelph, Ontario, Canada. N1G 2W1; and (D.B.) Environmental Technology Consultant for CESRF, 275 Royalton Common Unit 49, Oakville, Ontario, Canada. L6H 0N2*

Closed-loop hydroponics, where the nutrient solution runoff is collected and reapplied to the crop, is an efficient method for producing crops in controlled environment agriculture (CEA) systems. Although an efficient use of water and fertilizer resources, recirculating the nutrient solution does increase the risk of pathogen proliferation in the overall system. Effective water treatment is a key element in any CEA recirculating hydroponic system. Previous research has demonstrated the use of regenerative *in situ* electrochemical hypochlorination (RisE^{HC}) can inactivate common pathogens such as *Fusarium oxysporum spp.*, without causing phytotoxicity. The next challenge is to scale up the technology and validate efficacy. The presented studies explore the scalability of the RisE^{HC} system and its eventual utility in commercial CEA systems. Computational fluid dynamics (CFD) and response surface analysis were used to determine the optimal design for the electrochemical flow cell presented. A prototype was developed and compared to the previous design for free chlorine evolution, power consumption, and microbial inactivation. The CFD informed design increased microbial inactivation on average by 21.4% in comparison to the previous cell. Furthermore, the prototype design achieved these inactivation rates while the volume of treated solution was increased by 23.2%, and the total area of anodes was reduced by 42.4%. This research demonstrated the scalability of the RisE^{HC} process, through a modular approach, for large-scale CEA.

69. Optimizing environment conditions enhances yield and nutritional quality of hydroponic barley (*Hordeum vulgare* cv. Esma) fodder A. DSOUZA, H. VISNESKIE, T. GRAHAM, M. STASIAK, AND M. DIXON *Controlled Environment Systems Research Facility, School of Environmental Sciences, University of Guelph, 50 Stone Road East, Guelph, N1L 0E4, ON, Canada*

Hydroponic fodder production under a controlled environment (CE) is a promising strategy to increase fresh fodder production Optimizing environmental conditions for CE production has been shown to improve the productivity of several crops. However, no studies exist on optimizing environment conditions for barley (*Hordeum vulgare* L. cv. Esma) fodder. The main aim of this study was to optimize the environment conditions for hydroponic sprouted barley fodder production. Studies were conducted to determine the appropriate temperature and light spectra for seed germination. Of the treatments tested, barley germinated best under red light (600–700 nm) at 25 °C. Next, the effects of light intensity, CO_2 concentration, and temperature on net carbon exchange rate (NCER) were determined. The highest NCER was observed at a photosynthetic photon flux density (PPFD) of 650 µmol m^{-2} s^{-1}, 1800 ppm CO_2, and 17 °C. Finally, the optimized conditions for seed germination and NCER were combined and tested as an environment recipe for barley fodder production. The yield and nutritive quality of 8-day-old hydroponic barley sprouts were compared under optimized and ambient environments (190.5 µmol·m^{-2}·s^{-1} PPFD, 423.5 ppm CO_2, at 23 °C). Optimized conditions increased barley fresh yield by 13.21% and dry yield by 5.5%. Nutritional value, specifically fiber content, increased under the optimized conditions. Overall, the results demonstrate the potential of optimized hydroponic CE production as a promising technique to improve the yield and quality of fodder crops.

70. Central carbon metabolic response of Mexican mint (*Plectranthus amboinicus*) to varying watering regimes Z. WANG, S. CHADA, R. OFOE, AND L. ABBEY *Department of Plant, Food, and Environmental Sciences, Faculty of Agriculture, Dalhousie University, 50 Pictou Road, P.O. Box 550, Bible Hill B2N 5E3, Nova Scotia, Canada*

Water stress is one of the most important threats to the attainment of global food security. A study was performed to investigate the central carbon metabolic (CCM) response of Mexican mint (*Plectranthus amboinicus*) to varying watering regimes. The water treatments were regular watering (RW), drought (DR), flooding (FL), and resumption of regular watering after flooding (DHFL) or after drought (RHDR). The metabolic analysis identified a total of 68 key metabolites of the CCM routes which were significantly ($p < 0.01$) impacted by water stress. Metabolites from the pentose phosphate pathway (PPP) were abundant in all the plants besides the DR plants. The total Calvin cycle metabolites in FL plants, glycolytic metabolites in DR plants, total tricarboxylic acid (TCA) cycle metabolites in DR and DHFL plants, and nucleotide biosynthetic molecules in FL and RH plants were significantly ($p < 0.05$) enhanced compared to RW. The TCA cycle ($r = 0.81$) and PPP ($r = 0.75$) metabolites were positively correlated with total Calvin cycle metabolites ($p < 0.001$). There was a moderately positive relationship between total PPP metabolites and total TCA cycle metabolites ($r = 0.68$; $p < 0.01$) and a moderately negative relationship between total PPP metabolites and total glycolytic metabolites ($r = -0.70$; $p < 0.005$). Overall, the study revealed how Mexican mint responds to various watering regimes and demonstrated that DR stress severely affects plant growth and development.

71. Effect of light quality and extended photoperiod on flower bud induction during transplant production of day-neutral strawberry cultivars V. GRAVEL *Department of Plant Science, McGill University, Ste-Anne-de-Bellevue, QC, Canada*

Session 9: Sustainable Diseases management tools: Bioproducts, cultural practices and prediction modeling-2

72. *Pseudomonas brassicacearum* control of the root rot pathogen *Aphanomyces euteiches* via a novel nitroimidazole antibiotic Z. MORALES MOREIRA, N. R. WANG, J. B. HEDGES, W. ZIWANG, K. S. RYAN, AND C. H. HANEY *(Z.M.M., N.R.W., C.H.H.) Dept. of Microbiology and Immunology, The University of British Columbia, Vancouver, BC, V6T 1Z4, Canada; and (J.B.H., W.Z., K.S.R) Dept. of Chemistry, The University of British Columbia, Vancouver, BC, V6T 1Z1, Canada*

Pseudomonas fluorescens and related species are broadly plant-associated bacteria that can contribute to pathogen control. Root rot diseases are a major problem for crops worldwide. In peas (*Pea sativum*), for example, the *Fusarium-Aphanomyces* root rot complex causes significant losses each year including the largest producer in the world, Canada. In our study, genome-sequenced isolates of *P. fluorescens* were used in a high-throughput phenotyping approach coupled with a comparative genomics pipeline to identify genes involved in the control of the root rot pathogen *Aphanomyces euteiches*. A nitroimidazole biosynthetic operon, previously reported in *Streptomyces*, was identified in one of the strains that exhibited biocontrol activity *in vitro*, *Pseudomonas brassicacearum* DF41. The antibiotic production in DF41 was quantified using liquid chromatography–mass spectrometry (LC-MS). To confirm if the antibiotic was responsible for the control of *Aphanomyces*, a nitroimidazole DF41 mutant was generated. We found that the mutant was no longer able to inhibit the root rot pathogen growth. We are currently testing DF41 wild type and mutant in peas to evaluate the effectiveness of this nitroimidazole *in planta*. Similarly, we are analyzing how the soil oomycete community shifts in the presence of bacteria producing this compound. Our research represents an important step toward the identification of strains and novel mechanisms to control a wide range of important root rot pathogens in a sustainable way.

73. Cereal-pulse rotations and *Fusarium avenaceum* pathogenicity A. ERANTHODI, D. OVERY, L. HARRIS, M. HUBBARD, T. SCHWINGHAMER, N. A. FOROUD, AND S. CHATTERTON *(A.E., T.S., N.A.F., S.C.) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403-1st Avenue South, Lethbridge, AB T1J 4B1; (D.O., L.H.) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6; and (M.H.) Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, 1 Airport Road, Swift Current, SK S9H 3X2.*

Fusarium avenaceum (Fr.) Sacc. is a common pathogen of pulse root rot and cereal head blight. Cereals are rotated with pulses for residual soil nitrogen and moisture benefits for cereal crops. We hypothesize that cereal-pulse rotations can influence *F. avenaceum* pathogenicity. To test natural variation in aggressiveness among isolates collected from different hosts (19 from pea, 16 from wheat, and 7 from lentil), we used seed and soil inoculation methods to infect pea cultivar 'CDC Meadow' and red lentil 'CDC Proclaim', and point inoculation to infect durum wheat cultivar 'Langdon'. Two trials each of soil inoculation of 'CDC Meadow' and point inoculation of 'Langdon' led to higher disease in both species from pea isolates compared to those of wheat. In 'CDC Proclaim', one of two seed inoculation trials resulted in more disease for pea isolates, whereas the other trial did not result in a significant difference between pea and wheat isolates. Relatively lower disease severity was obtained for two trials of 'CDC Proclaim' soil inoculations, and the difference in disease between pea and wheat isolates was not statistically significant. Seed inoculation of 'CDC Meadow' inhibited emergence and disease severity could not be assessed. Currently, we are screening 7 lentil isolates in wheat and pulses. Overall, the pea isolates evaluated were generally more aggressive in wheat and pulses. Whether this supports our hypothesis or not is inconclusive. To get better insights, we will be assessing change in aggressiveness of select isolates after their serial passage through wheat spikes or pulse roots.

74. Effect of diverse crop sequences on Fusarium head blight and leaf spot diseases of wheat in the Canadian Prairies M. A. OVIEDO-LUDENA, L. WANG, K. COLES, M. GRETZINGER, R. MOHR, D. L. MCLAREN, G. FINLAY, M. A. HENRIQUEZ, AND H. R. KUTCHER *Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan S7N 5A8; (K.C., M.G.) Farming Smarter, 211034 AB-512, Lethbridge, Alberta T1J 5N9; (R.M., D.L.M., G.F.) Agriculture and Agri-Food Canada Research Station, 2701 Grand Valley Rd, Brandon, Manitoba R7C 1A1; and (M.A.H.) Agriculture Agri-Food Canada Research station, 101 Rte 100 #100, Morden, Manitoba R6M 1Y5.*

Fusarium head blight (FHB) mitigation requires an integrated disease management approach that includes a diverse crop rotation. In Canada, intensive cereal rotations, the lack of highly resistant cereal varieties, and the limited effectiveness of fungicides make managing the disease difficult. The aim of this study was to determine the effect of multiple host and non-host crops in a planned sequence on FHB severity of bread or durum wheat. To achieve crop diversity, up to nine crops were used in this study with four of the most common field crops in western Canada (wheat, canola, barley, and pea) in a split-block design with three replicates. The study was conduced at three sites with two experiments at each site. The study occurred in experiment 1 in 2018-2020 and experiment 2 in 2020-2022; durum wheat sites were Lethbridge, AB and Saskatoon, SK, while the bread wheat site was Brandon, MB. Generally, the severity of FHB was low in both experiments at all sites; however, there were some effects of crop sequence on FHB incidence or severity and on the frequency of *Fusarium* spp. from wheat kernels in year 3 of each experiment. This

study confirmed that continuous cereal production increased the risk of FHB, greater frequency of multiple *Fusarium* species, and more severe leaf spot diseases. Including a one-year break with legumes or oilseeds was sufficient to increase wheat yield and quality; however, wheat grown on pea stubble had higher frequency of *Fusarium* spp. isolation from wheat kernels and often higher FHB incidence and severity.

75. Suppression of *Botrytis cinerea* Pers. induced bud-rot on greenhouse cultivated cannabis (*Cannabis sativa* L.) via enhanced air circulation and Rootshield-HC (*Trichoderma harzianum* Rifai.) spray applications L. BUIRS, S. LUNG AND Z. K. PUNJA *Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada; and (L.B., S.L.) Pure Sunfarms, 4431 80th Street, Delta, BC V4K 3N3, Canada*

Bud-rot on cannabis inflorescences, caused by the fungus *Botrytis cinerea* Pers., poses a significant threat to yield and quality, particularly during September-November in British Columbia. Infection appears ~day 30 onwards in the ~56-day flowering period, resulting in up to 40% losses in susceptible genotypes. Existing suppression strategies include reducing planting density, increasing air circulation, and applying reduced-risk products during flowering. In this study, we investigated the impact of enhanced air circulation and the application of four biological control/reduced risk products on bud-rot development. Fans were installed 25 cm above two susceptible genotypes – 'Pink Kush' and 'Jet Fuel Gelato' – to provide continuous 7 m/s air circulation, beginning at day 14 of flowering. In three trials conducted in different greenhouse compartments, the fans significantly reduced bud-rot incidence by an average of 81% ($P<0.01$, $P<0.01$, $P<0.05$, respectively). Relative humidity measurements, taken thrice daily one week before harvest using a psychrometer, revealed lower humidity in fan-exposed inflorescences (56.4%) compared to the controls (63.8%) and the ambient environment (59.4%). Spray applications of Rootshield-HC at 10 g/L on days 14, 21, and 28 of flowering in two genotypes – 'Berry Cream Puff' and 'Sugar Cookies' – significantly reduced bud rot by an average of 60.6% across three trials ($P<0.05$, $P<0.01$, $P<0.01$, respectively). In contrast, spraying Regalia Maxx (*Reynoutria sachalinensis* (F. Schmidt) Nakai), Double Nickel-LC (*Bacillus amyloliquefaciens* Fukomoto), and Timorex Gold (tea tree oil) using the same methods did not significantly reduce disease. These results advance the efficacy and economics of bud-rot integrated disease management in cannabis cultivation.

76. Investigating the impact of LED lighting on *Botrytis cinerea* in a controlled environment: A photomorphogenic approach J. P. MOLLIGAN AND V. GRAVEL *Department of Plant Science, McGill University, Macdonald Campus, 21111 Lakeshore Road, Sainte-Anne-de-Bellevue, QC H9X 3V9, Canada*

The ubiquitous hemibiotrophic fungal pathogen *Botrytis cinerea* Pers. is a common pest within controlled environment (CE) plant production settings and utilizes light as an environmental cue to regulate morphogenesis, a key factor influencing propagule dissemination. The effects of wavelength-specific lighting qualities on the morphology of *B. cinerea* have been well-documented; however, the impact of mixed narrow-bandwidth LED emissions on its development remains unclear. The aim of this study was to evaluate mixed narrow-bandwidth emissions of Far-Red:Blue (1:5, 5:1, 1:1) LED diode ratios on the morphogenesis of *B. cinerea in-vitro* within a CE. Our results show that a blue-dominant Far-Red:Blue diode ratio of 1:5 was the most effective treatment in inhibiting the hyphal growth and sporulation of *B. cinerea*, although all LED treatments successfully suppressed development compared to control treatments of high-pressure sodium lighting and complete darkness. Colonies exposed to LED treatments were observed to produced sterile arial hyphae, absent of conidia, with intermittent gaps or breaks in circular banding, indicating a possible disruption in entrainment. Interestingly, when examining the effect of treatments on conidial germination, no difference was found between LED treatments and controls. The optimal photoperiod to inhibit growth and sporulation was found to consist of 16 hours of treatment + 8 hours of darkness. Furthermore, this study demonstrates that incorporating Blue light into a Far-Red:Blue diode ratio of 5:1 was effective in counteracting the conidiation promoting effects reported for Far-Red light. These findings have important implications regarding the asexual proliferation of *B. cinerea* in CE plant production.

77. Spread and impact of *Hop Latent Viroid* on growth and quality of cannabis (*Cannabis sativa* L.) plants Z. K. PUNJA, L. NI, C. SCOTT, J. HOLMES, AND L. BUIRS *Department of Biological Science, Simon Fraser university, 8888 University Drive, Burnaby, BC V5A 1S6, Canada*

Hop Latent Viroid (HpLVd) is a highly infectious RNA molecule that is widespread on *Cannabis sativa*. A survey of HpLVd occurrence in Canadian licenced production facilities in 9 provinces showed presence in 24.6 % out of 14,200 samples tested by RT-PCR. The genomic sequences were 100% homologous to HpLVd strains from hemp in Colorado, USA and hops in China. Infected cannabis mother plants display stunted growth, with smaller leaves and mosaic symptoms on some leaves. Cuttings from affected plants showed reduced rooting; plants in flower showed stunted and reduced growth of inflorescences. Glandular trichomes on flowers were significantly stunted in size, with smaller gland heads and stalks, with 12-30% lower THC, depending on the genotype. HpLVd was successfully transmitted by inoculating cut stem surfaces with sap, was detected in the roots 10-14 days later, followed by movement into young leaves, then older leaves by 4 weeks. Plants in a 12:12 hr photoperiod showed more rapid spread of HpLVd into roots and leaves compared to constant 24 hr. Viroid concentrations were significantly higher in fresh and dried flower tissues compared to the rest of the plant. HpLVd was transmitted through roots and water in a hydroponic growing system. Molecular detection was most consistent in root samples, followed by younger leaves and older leaves. Infected mother plants had varied viroid concentration, from low (latent) to high (active), and by leaf position. Rigorous testing, destroying infected plants, and preventing spread on cut stem surfaces and tools, and preventing root contact, can reduce spread.

Session 10: Plant-soil health and innovation in agronomy-2

78. Improving cropping system performance through rotation diversification with pulse crops K. LIU, A. LASISI, M. ENTZ, F. LARNEY, H. CHAU, M. KHAKBAZAN, Y. M. KIM, S. SHARPE, J. TOWN, N. LUPWAYI, R. LEMKE, S. LIN, M. ST. LUCE, H. ASGEDOM-TEDLA, D. BISWAS, G. PENG, H. KUBOTA, B. TIDEMANN, G. SEMACH, P. LOKURUGE, R. MOHR, M. HUBBARD, G. HERNANDEZ RAMIREZ, K. STANLEY, E. IHESHIULO, S. CURTIS, S. STRYDHORST, AND Y. GAN*(K.L., A.L., S.L., M.S., M.H., Y.G.) Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, #1 Airport road, Swift Current, SK S9H 3X2; (M.E., S.C.) Faculty of Agricultural and Food Sciences, University of Manitoba, MB, 66 Dafoe Road, Winnipeg, MB R3T 2N2; (F.L., H.C., N.L.) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1st Avenue South, Lethbridge, AB T1J 4B1; (M.K., Y.M.K., D.B., R.M.) Brandon Research and Development Centre, Agriculture and Agri-Food Canada, Box 1000a, R.R. #3, Brandon, MB R7A 5Y3; (S.S., J.T., R.L., H.A.-T., G.P.)Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2; (H.K., T.B.) Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, 6000 C and E Trail, Lacombe, AB T4L 1W1;(G.S.) Beaverlodge Research Farm, Agriculture and Agri-Food Canada, 100038 Township Road 720, County of Grande Prairie, Alberta T0H 0C0; (P.L.) Scott Research Farm, Agriculture and Agri-Food Canada, P.O. BOX 10, 7 Highway 374, Main Building Scott, Saskatchewan S0K 4A0I; (G.H.R) University of Alberta, 11223 Saskatchewan Drive NW, Edmonton, AB T6G 2E; (K.S.) Manitoba Crop Alliance, 38 4th Avenue NE, Box 188, Carman, MB R0G 0J0; and (S.S.) Sheri's Ag Consulting Inc., 3401 TwpRd 622 County of Barrhead, AB T0G 1R1*

Adopting a systems approach is essential for developing sustainable cropping systems, since the performance of cropping systems is affected by various biotic, abiotic, and management factors. To develop sustainable cropping systems across the Canadian Prairies, a five-year (2018-2022) crop rotation study was conducted at seven sites, including Beaverlodge, Lacombe, and Lethbridge, AB; Melfort, Scott, and Swift Current, SK; and Carman, MB. Six cropping systems were tested, including: 1) Conventional wheat-based cropping system (Control), 2) Oilseed- or pulse crop -intensified cropping system (Intensified), 3) Diversified cropping system (Diversified), 4) Market-driven cropping system (Market driven), 5) High risk and high reward cropping system (High risk), and 6) Soil-health enhanced cropping system (Soil health). System indicators, such as productivity, soil health, resource use efficiency, pest levels, economic returns, and carbon footprint, were assessed. On average, system yield was 14 and 18% higher in Intensified and Market-Driven systems than in the Control, respectively; however, it was 6, 22, and 24% lower in Diversified, High risk, and Soil Health systems than the control, respectively. We concluded that: 1) the benefits of Diversified systems were not fully realized in the short study period (5 years), and a longer-term study may be necessary to optimize cropping systems, 2) trade-offs exist among system indicators, and producers should consider balancing short-term economic benefits with long-term sustainability, 3) site-specific cropping systems are recommended as no single optimal system can fit all sites, and 4) cropping systems diversified with three or more crop species, including pulse crops, generally perform better overall.

79. Cold plasma seed treatment as a potential agronomic application to increase plant growth, development, and yield in Pea (*Pisum Sativum*) D. N. ABEYSINGHA, R. M. SYAMALADEVI, T. WARKENTIN, AND M. S. THILAKARATHNA *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada; and (T.W.) College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, SK, S7N 5A8, Canada.*

Feeding the world's growing population while maintaining environmental sustainability is becoming a challenge. Cold plasma (CP) is a chemical-free, eco-friendly technology that has the potential to enhance agricultural crop production. Reactive oxygen and nitrogen species in CP can alter some biochemical and molecular processes in seeds which can affect the germination and their further ontogenesis. This study tests the hypothesis that the CP seed treatment can increase root nodulation, root and shoot growth parameters, and seed yield in peas. The CP seed treatment was given using a dielectric barrier discharge plasma unit at atmospheric pressure for 6 minutes. The treated and untreated (control) pea seeds were grown at 30% and 80% field capacities under controlled environmental conditions (n=10). The effects of CP on germination, nodules, and root growth parameters were evaluated at the 50% flowering stage (BBCH 65). Furthermore, shoot and yield parameters were evaluated at the maturity stage. CP seed treatment increased the root parameters (length by 22%; surface area by 27%; volume by 32%) and shoot dry weight (by 14%) and reduced the inactive nodule dry weight (by 61%) compared to the control. Drought stress substantially reduced all the tested parameters; however, the CP treatment could not ameliorate the stress effects. CP treatment did not significantly affect the seed germination and yield parameters; however, pods and seed numbers and weights showed an increasing trend. Future research will focus on evaluating the effect of CP seed treatment on symbiotic nitrogen fixation and seed quality.

80. Corn (*Zea mays* L.) grain yield gains from long-term cover cropping: evidence of increase nitrogen availability possibly due to increased soil organic matter L. L. VAN EERD *School of Environmental Sciences, University of Guelph, Ridgetown Campus, 120 Main St. E., Ridgetown, ON, N0P 2C0, Canada*

Cover crops (CC) are known to enhance soil organic matter (OM) and minimize N losses. Quantifying these enhancements requires long-term research, but there are few long-term trials comparing various CC approaches. At Ridgetown, Ontario, a long-term CC experiment with four replicates and two adjacent sites was established in 2007 and 2008 to evaluate the role of CC [oat (OAT; *Avena sativa* L.), winter cereal rye (RYE; *Secale cereale* L.), radish (RAD; *Raphanus sativus* L. var. *Longipinnatus*), RAD+RYE mix, and control (no-CC)] in a grain/horticulture system.

Consistent with medium-term results (P<0.05), OM was independently verified in 2019 where OM in plots with long-term CC was 3.7 to 3.9% but 3.4% in no-CC plots (P=0.4). By 2020 and 2021 when grain corn was grown with 34 kg N ha^{-1} of fertilizer nitrogen, these summer-planted CC were grown 10 out of 13 years. At V8-V9 corn, optical sensor (SPAD meter) readings (P<0.05) confirmed visual observations of nitrogen deficiency (less green, shorter) in no-CC plots (46.5 and 54.0) in both years, and OAT in 2020 (45.4) and RYE in 2021 (55.5). In 2020, grain yield was 3.8 Mg ha^{-1} greater with RAD than no-CC (11.7 Mg ha^{-1}; P<0.05), with a similar trend in 2021 (P=0.135). In 2020, there was a positive linear relationship of corn yield to soil OM (y=4.03OM-0.72; R^2=0.54; P=0.0001; n= 16). Overall, results provide evidence that CC-mediated increases in soil OM increased corn grain yield, likely due to improved nitrogen availability to corn.

81. Linking plant-level measurements to crop-level outcomes: plant growth regulator effects on lodging in winter wheat K. PILKINGTON, D. HOOKER, B. L. MA, J. NASIELSKI *(K.P., D.H., J.N.) Department of Plant Agriculture, University of Guelph, Guelph, Ontario, N1G 1B6, Canada; and (B.L.M.) Agriculture and Agri-Food Canada, Ottawa Research and Development Centre, Ottawa, ON K1A 0C6, Canada*

Biologists study phenomenon at different levels of biological organization (e.g. molecule, cell). As agronomists, the phenomenon we are primarily interested occur at level of the crop canopy. But we often take plant-level measurements to clarify mechanisms behind crop-level outcomes. But to what extent can these plant-level observations accurately inform our understanding of crop-level outcomes? Here, we present data linking plant-level measurements of lodging resistance to crop-level measurements of lodging in winter wheat (*Triticum aestivum*). Lodging, characterized by the displacement of a crop from its typical upright position, arises when the stem and/or root system fail to withstand the bending forces exerted by wind and rain. Lodging is a common issue in small-grain cereal production in eastern Canada and when it occurs it can reduce grain yield and hamper harvest efficiency. Plant growth regulators (PGRs) are products applied to wheat to reduce lodging risk. While common in Europe, these products are relatively new to eastern Canada. To test the effect of PGRs on yield and lodging in Ontario winter wheat, a strip-split-split plot experiment was imposed for two growing seasons at Winchester, Ontario. Four winter wheat cultivars were grown at two nitrogen fertilizer rates and received one of four PGR treatments including a control. Lodging occurred naturally in both years. Lodging resistance was measured at the plant-level by calculating safety factors for root and stem structures. At the crop-level, lodging was quantified visually using the ADAS lodging index. In the presentation, we discuss the relationship between these measurements.

82. Humic acid improves the growth of wheat seedlings by modulating the expression of genes involved in auxin and cytokinin biosynthesis pathways P. RATHOR, L. Y. GORIM, AND M. S. THILAKARATHNA *Department of Agricultural, Food and Nutritional Science, Agriculture and Forestry, University of Alberta, 116 Street and 85 Ave. Edmonton, AB T6G 2P5, Canada*

Humic acids have been widely used for centuries to enhance plant growth and productivity. However, the mechanisms underlying the growth-promoting effects of humic acids are only partially understood. Several studies reported that the bio-stimulatory effect of humic acids is due to the presence of phytohormone, mostly auxin. However, this topic has been long debated as humic acids are used in very low concentrations and levels of phytohormones in humic acid at these low concentrations may be insufficient to cause a significant improvement in plant growth. Therefore, it is more likely that humic acids may improve plant growth and development by modulating the innate pathways of phytohormone biosynthesis in treated plants. This study demonstrates that humic acid treatment improved the growth of wheat seedlings. Plants treated with humic acid for eight and twelve days at 0.1, 0.2 and 0.4 % (*v/v*) showed a significant increase in root and shoot growth. A gene expression analysis was performed for the genes involved in auxin and cytokinin biosynthesis to understand the mechanism of action. The expression of several genes involved in auxin and cytokinin biosynthesis was up-regulated in humic acid treated plants compared to the control. Furthermore, using the *Arabidopsis* transgenic lines generated by fusing the auxin-responsive *DR5* and cytokinin-responsive *ARR5* promoter to ß-glucuronidase (*GUS*) reporter gene, we showed that bioactive compounds of humic acid stimulate endogenous auxin and cytokinin like activities. These findings demonstrate that humic acid improved plant growth and development by modulating the innate pathways of auxin and cytokinin biosynthesis.

83. Effect of Apex, Top Phos, EXCELIS MAXX and Bio-Stimulants on canola in Northwestern Ontario T. S. SAHOTA *Lakehead University Agricultural Research Station (LUARS), 5790 Little Norway Road Thunder Bay, ON, P7J 1G, Canada*

Field experiments were conducted in RCBD replicated 4 times during 2022-2022 to study the effect of Apex (5 % ammoniacal N, 25 % urea N, 2.9 % Ca, 1.2 % Mg and 8 % S), Top Phos (8-30-0-4.8), EXCELIS MAXX (N Stabilizer) treated urea and Bio-Stimulants (FA STARTER, IRYS, FL GOLD and GENEA) on canola production in northwestern Ontario. Apex, EXCELIS MAXX treated urea and Top Phos were compared with the standard farmers' practice - N (urea + ESN 3:1 ratio on N basis + ammonium sulphate) and P fertilizer (0-45-0). All treatments received 180 kg N ha^{-1}, 20 kg P_2O_5 ha^{-1}, 20 kg K_2O ha^{-1}, 48 kg S ha^{-1}, and 1 kg B ha^{-1}. Averaged over 2020-2022, the results revealed that urea alone and without treatment with EXCELIS MAXX produced the lowest canola seed yield (2.39 Mg ha^{-1}). Treatment of urea with EXCELIS MAXX increased the seed yield by 0.80 Mg ha^{-1}, though non significantly. None of the treatments were statistically better than the standard farmers' practice. N from multiple sources (ammonium sulphate, urea and ESN) gave nearly 1 Mg ha^{-1} higher seed yield than urea alone. Bio-Stimulants didn't improve the canola seed yield; though there was some non-significant/marginal increase (0.15 Mg ha^{-1}) in seed yield by spraying FA STARTER at 2-3 leaf stage.

Session 11: Obligate biotrophic pathogens and soil-borne diseases

84. Understanding the interaction between *Verticillium longisporum* and canola, causing verticillium stripe: the new soil-borne disease creating challenges to the industry D. FERNANDO *Department of Plant Science, University of Manitoba, Winnipeg, MB*

Canola (*Brassica napus* L.) is the number one oilseed crop and the number one cash crop in Canada. *Verticillium longisporum*, is a soil-borne fungal pathogen in canola, which was initially detected in 2014 in Manitoba. This pathogen poses a significant threat to canola production in the Canadian Prairies. It invades canola plants through the root system and establishes itself within the vascular system, resulting in the development of verticillium stripe disease. Since its initial detection in Canada in 2014, *V. longisporum* has now been identified in various provinces including Manitoba, Alberta, Saskatchewan, British Columbia, Ontario, and Quebec. The wide geographic distribution of this pathogen highlights its potential to adversely impact canola crops across multiple regions. The canola-verticillium interactions have been studied in our lab to decipher the common lineages of this pathogen in the prairies, occurrence of the disease in different regions, the most susceptible stages of the canola to the pathogen, resistance in Canadian genotypes, the spatial distribution of the pathogen, the longevity of microsclerotia in soil or in stubble, the genome of *Verticillum longisporum* and their interactions with the stubble-borne blackleg pathogen, *Leptosphaeria maculans*, another devastating disease of canola. In addition to the above, our lab in collaboration with other researchers have initiated studies on genome-wide association studies to identify resistance traits in canola and other relatives, to determine the genetic diversity and population structure of *V. longisporum* lineages prevalent in the prairies, assess the pathogenicity and virulence of different *V. longisporum* lineages on canola cultivars commonly grown in the region, development of molecular markers to better characterize *V. longisporum* populations prevalent in the prairies, identify whether there are genes such as BnCRT1 and BnHVA22, or other susceptibility genes that can be knocked out through CRISPR to understand the host-pathogen interaction better. In addition, we are investigating the impact of *V. longisporum* on the expression of genes involved in plant growth hormones biosynthesis and antioxidant enzymes activity and develop a GFP-tagged *V. longisporum* strain to study invasiveness and infection. Another collaboration is seeking marker development and establishment of qPCR-based screening for verticillium stripe disease in Canola. Once we have identified the genetic polymorphisms underlying resistance QTL, we would develop KASP markers. These KASP markers would be instrumental in introgressing newly identified verticillium stripe resistance alleles into elite Western Canadian breeding material and cultivars. The presentation will highlight the findings and future directions to understand this new host-pathogen interaction in the canola-verticillium playbook.

85. Verticillium wilt early dying status in Manitoba potatoes, 2020-2022 V. BISHT, *M. TENUTA, AND S. GRAHAM Primary Agriculture, Manitoba Agriculture, 65, 3rd Avenue NE, Carman, MB. R0G 0J0, Canada; (M.T.) Department of Soil Science, University of Manitoba, 13 Freedman Crescent, Winnipeg, MB. R3T 2N2, Canada; and (S.G.) J.R. Simplot Co., Highway #1 and Simplot Road, Portage la Prairie, MB. R1N 3A4 Canada*

Potato is a high value and high input crop with significant disease and insect pest risks. Verticillium wilt (VW) disease caused by *V. dahlia* Kleb. (Vd) is an important disease which is endemic in Manitoba. Field surveys for VW early dying were conducted in 2020 to 2022. Fields targeted for summer 2020 and 2021 VW rating were checked for Vd in the fall before. Based on soil tests for Vd propagules using qPCR, fields were termed as high or low inoculum load. The field surveys of 8 fields in 2020, and 26 in 2021 showed a wide variability in Verticillium Severity Index (VSI), which ranged 3.5 to 43.8 in 2020, and 0.6 to 60.6 in 2021, based on rating of stem browning in the cross-section of stems one inch from the soil line. Soil Vd propagule levels in the fall had a good correlation with VW in summer. The VW severity (VSI ranged 4.8 to 19.6) in 2022 was lower than in 2020 and 2021; and could partly be due to the lower heat stress and good soil moisture in 2022. In 2021, 'Russet Burbank' variety had VSI of 60.3 compared to 9.2 for 'Clearwater' variety in the same field. Vd quantification using qPCR could be a good tool to manage VW by using tolerant varieties in fields with high inoculum or history of high VW.

86. Unravelling the life cycle of *Cronartium ribicola,* the causal agent of white pine blister rust B. P DUARTE AND R. C. HAMELIN *Department of Forest and Conservation Sciences, Faculty of Forestry, The University of British Columbia, 2424 Main Mall, Vancouver, BC V6T 1Z4 Canada*

Rust fungi (Pucciniales) are highly complex plant pathogens, producing up to five unique spore types. Heteroecious species, such as *Cronartium ribicola* J.C. Fisch, the causal agent of white pine blister rust utilise these specialised spore types to infect unrelated host species. Basidiospores are responsible for the infection of aecial hosts which are *Pinus* spp. in the *Strobus* subgenus. Aeciospores, and urediniospores, are responsible for the infection of telial hosts within the flowering plant clades *Ribes* and Orobanchaceae. Our objective is to determine how *C. ribicola* spore types maintain host specificity during each stage of the lifecycle forming the foundation of heteroecism. We inoculated two white pine species and one telial host species (*Ribes nigrum* Linn) with each of the three infective spore types (aeciospores, urediniospores, and basidiospores) and used electron and confocal microscopy to determine the outcome of these interactions. We observed that all three spore types can germinate and penetrate *R. nigrum* and pine species via the stomata. However, each spore type exhibited specialized mechanisms for penetrating its compatible host, indicating the use of physical and chemical cues to enter through the stomata. Urediniospores formed appressoria on *R. nigrum* and pine stomata; aeciospores only formed appressoria on *R. nigrum.* The broader range of telial to aecial hosts coupled with fewer restrictions in the formation of appressoria suggests that urediniospores may be crucial in exploring new potential telial hosts. This study provides additional insight into the role of spore types in the life cycle and host interactions of *C. ribicola*.

87. Understanding the causative agents of potato early dying disease in Alberta: a focus on *Verticillium dahliae, V. albo-atrum,* and *Colletotrichum coccodes* A. U. RAHMAN, M. MUNAWAR, M. KONSCHUH, M. TENUTA, M. W. HARDING, AND D. P. YEVTUSHENKO *Department of Biological Sciences, University of Lethbridge, Lethbridge, AB T1K 3M4, Canada; (M.T.) Department of Soil Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada; and (M.W.H.) Alberta Agriculture, Forestry and Rural Economic Development, Crop Diversification Centre South, Brooks, AB T1R 1E6, Canada*

Potato early dying (PED) is a significant issue for potato growers in many parts of the world. PED refers to the premature death of potato plants and is believed to be caused by a combination of soil-borne fungi, including *Verticillium dahliae*, *V. albo-atrum, Colletotrichum coccodes*, *Fusarium* spp., and the nematode *Pratylenchus penetrans*. However, the causal agents of PED in Alberta, Canada, are poorly understood. To address this knowledge gap, we conducted a study to determine the incidence and abundance of *V. dahliae* and *V. albo-atrum* and to assess their relationship with PED severity and yield loss in southern Alberta. Soil samples were collected from 62 potato fields during the fall of 2020 and 2021 and analyzed using quantitative polymerase chain reaction (qPCR) to detect and quantify *V. dahliae* and *V. albo-atrum*. Our results showed that *V. dahliae* was found in both years in 71% and 45% of the fields, respectively. In contrast, traces of *V. albo-atrum* were detected in only one field in 2020. Selected fields were surveyed to assess PED severity in the summer of 2021 and 2022. We found that *C. coccodes* was also present along with *V. dahliae* in 59% and 41% of the plant samples collected in 2021 and 2022, respectively. The potato fields with high inoculum levels of *V. dahliae* in the soil typically showed more PED symptoms and, in some cases, lower yields. However, some low inoculum fields also showed PED symptoms, indicating that additional factors may be involved in the PED complex.

88. Race characterization and strain-level disease diagnosis of the *Puccinia striiformis* f. sp. *tritici* population in western Canada from 2017 to 2022 K. LOU, S. HOLDEN, M. ABBASI, R. BAMRAH, G. S. BRAR, AND H. R. KUTCHER *(K.L., H.R.K.) Department of Plant Science/Crop Development Centre, University of Saskatchewan, 81 Campus Drive Saskatoon, SK S7N 5A8 Canada; and (S.H., M.A, R.B, G.S.B.) Faculty of Land and Food Systems, The University of British Columbia, 2357 Main Mall, Vancouver, BC V6T 1Z4 Canada*

Stripe rust of wheat, caused by *Puccinia striiformis* f.sp. *tritici* (*Pst*) (Eriksson), is a major disease worldwide, and in Canada. *Pst* varies in virulence on wheat cultivars with race-specific R-genes being the main source of genetic resistance. Thus, timely and accurate characterization of the *Pst* population is critical for breeding resistant varieties. A collection of western Canadian *Pst* isolates (n=52) collected from 2017 to 2022 were characterized using a set of 18 yellow rust (*Yr*) single-gene differential lines to determine races. Additionally, a subset of 36 isolates was sequenced using the Mobile And Real-time disEase (MARPLE) diagnostic tool, and compared with publicly available sequence data to identify samples' genetic lineage using a maximum-likelihood approach. Of the 52 isolates characterized, 13 races were identified and matched based on both the nomenclature systems described for Canadian (C-), American and Mexican (PSTv-) *Pst* races. Race C-30/ PSTv-239 (23.5%) and C-39 (23.5%) were the prevalent races, followed by C-43/ PSTv-037 (19.6%), C-17/ PSTv-041 (5.8%), C-38 (5.8%), C-49/ PSTv-031 (5.8%) and PSTv-14 (3.9%). Of the 36 samples sequenced, all were grouped within the North American clade, with no new strain identified. The results suggest that the current races of *Pst* in western Canada are likely to have migrated from the USA, and some races may be of local origin. It is unlikely that a foreign incursion into the *Pst* population from other continents has occurred. Virulence was not detected on *Yr5*, *Yr15*, or *YrSP* indicating that they are effective against the *Pst* population in western Canada.

89. Soil microbiome and calcium content in relation to the risk of cavity spot on carrots U. ILYAS, M. N. RAIZADA, M. KALISCHUK, L. J. DU TOIT, AND M. R. MCDONALD *Department of Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1, Canada; and (L.D.T.) Department of Plant Pathology, Washington State University, WA 98195, United States of America*

Cavity spot is an economically important disease of carrots caused by several soilborne species of *Pythium* Pringsheim. The disease appears as superficial lesions on carrot roots and symptomatic carrots are unmarketable. Currently, disease management is limited to fungicide application at seeding and avoiding fields with a history of cavity spot. There are no diagnostic tools to identify fields with high-risk for cavity spot. It is hypothesized that the soil microbiome and some soil properties, in addition to the amount of inoculum, influenced disease development. Bulk muck soil (organic matter 40–80%) was collected from six fields in 2021 and 12 fields in 2022 at the Holland Marsh, soon after seeding, for microbiome and soil nutrient analysis. The fields were grouped as low or high-risk, based on cavity spot severity rating in the growers' fields by the local integrated pest management program. Metagenomic analysis of 2021 samples showed greater relative abundance of the following taxa in low-risk soils compared to high-risk soils: the fungi *Fusarium, Mortierella*, *Penicillium*, and *Tetracladium*; the bacteria *Bauldia* and *Rhizobium,* and the oomycetes *Albugo* and *Phytophthora.* The 2022 soil samples also were sent to Harvest Genomics for DNA sequencing. Soil nutrient analysis of both years showed low-risk soils had greater pH ~7, organic matter ~63 % and calcium content ~83 % compared to high-risk soils with pH ~6, organic matter ~72 %, and calcium content ~66 %. This information will help to identify fields with greater risk of cavity spot, enabling growers to avoid high-risk fields.

Session 12: Biovigilance approach for Emerging and novel phytopathogens

90. Challenges and possible solutions for moving towards sustainable crop protection: How can biovigilance help to structure the transition? O. CARISSE, H. VAN DER HEYDEN, AND M. L. FALL *Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu Research and Development Centre, 430 Gouin Boulevard, Saint-Jean-sur-Richelieu, QC, J3B 3E6*

Achieving the 2030 targets for biodiversity conservation, adaptation to climate change, and sustainable agricultural systems will require, among other things, a radical change in our plant protection approaches. The current range of management tools provides an essential basis for future progress but is not sufficient to trigger a transition towards sustainability. One way of meeting these challenges is to move away from conventional production (protection) systems reliant on fossil fuels towards agroecological alternatives that store carbon, maintain ecologically balanced systems, improve food security, and preserve biodiversity. The transition to sustainable agriculture must be gradual since it implies changes in mentality for all stakeholders, including scientists. In this context, our role as researchers is crucial, as more attention needs to be paid to understanding farming systems, the effects of environmental pressures, pathways to sustainability, promising initiatives, and obstacles to change. Many researchers propose agroecology as a path towards sustainable agroecosystems. The fundamentals of agroecology are well known and have been for many years, but its implementation is progressing slowly. This presentation aims to stimulate discussion on how best to facilitate the transition to more sustainable agriculture, how to structure change (biovigilance), and how to integrate innovation and clean technologies into control programs

91. Fungal diversity, surveillance and incidence forecasting of crop-associated phytopathogens using metabarcoding of aerial spore and suction traps É. D. TREMBLAY, B. B. GOULET, É. LORD, S. SAMSON, M. LIU, B. M. T. BRUNET, AND J. -P. PARENT *(É.D.T., B.B.G., M.L., B.M.T.B.) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, K1A 0C6, Canada; and (É.L., S.S., J.-P.P.) Saint-Jean-sur-Richelieu Research and Development Centre, Agriculture and Agri-Food Canada, 430 Gouin Boulevard, Saint-Jean-sur-Richelieu, QC, J3B 3E6, Canada*

Phytopathogens present a risk to the health of crops, seeds, timber and other economically important plant-derived commodities. Occasionally introduced through international trade, some plant pathogens and pests can threaten the biodiversity associated with native plants' and beneficial microorganisms'. The rate of these introductions is accelerating as climate change creates more permissive conditions in areas previously protected by inhospitable conditions. Increased presence and the emergence of new phytopathogens in agricultural environments may also lead to more restrictive international trade regulations and therefore a rapid response needs to be established to mitigate the consequences. Metabarcoding is a powerful high-throughput sequencing (HTS) approach to scrutinize the distribution and incidence of phytopathogens and locate emerging species' hotspots. The diversity of environmental fungi and oomycetes in agricultural fields from the provinces of Quebec and Ontario was assessed using samples collected with aerial spore and suction traps. An artificial intelligence-based model using a Graph Neural Network (GNN) is being developed to forecast phytopathogen incidence based on weather factors, climate change and geographical locations. Preliminary results will be presented. Application of metabarcoding and artificial intelligence-based modeling methods as a pre-screening tool could be instrumental to improve phytopathogen risk readiness and response at a larger scale than highly-specific but low-throughput and time-consuming classical methods, and to increase our understanding of pest incidence and transmission across space and time.

92. Finding a needle in a haystack using NGS and associated bioinformatics Toolkit X. LI, J. CHUAN, W. CHEN, AND L. R. HALE *(X.L., J.C.) Canadian Food Inspection Agency, Charlottetown Laboratory, PE, C1A5T1; (C.J., L.R.H.) Biology Department of University of Prince Edward Island, PE, C1A4P3; and (W.C.) Agriculture and AgriFood Canada, Ottawa Laboratory, On, K1A0C6*

Emerging and re-emerging plant diseases pose an enormous threat to agricultural production and global food security. Early detection and identification of outbreaks using advanced high-throughput sequencing (HTS) technology and bioinformatics tools are playing increasingly important roles. To date, a few web-based taxonomic application, including Microbial Species Identifier (MiSI), Microbial Genomes Atlas (MiGA) and Genome Taxonomy Database (GTDB) are available for microbial identification using genome sequence data. However, none of these online systems are efficient in time and computing resources for differentiation at interspecies and intraspecies levels of plant pathogens. At CFIA, the Clasnip platform (www.clasnip.com) and PolyChrome (PC) system are developed for the early detection and identification of bacterial ring rot, zebra chip and soft rot of potato, as well as potato wart disease. The Clasnip is a web-based platform to quickly classify pathogens and their closely-relatives based on SNPs and/or whole-genome sequences. The PolyChrome system, is comprisied of two command-line pipelines (PC Classifier (PCC) and PC Detector (PCD)), an integrated state-of-the-art bioinformatics software and a high-quality genomic reference database. The analysis system allows for timely and accurate detection and identification of high-risk pathogens at the species/subspecies levels, such as bacterial ring rot caused by Clavibacter sepedonicus, and bacterial brown rot caused by Ralstonia solanacearum race 3 biovar 2. In this presentation, PCD was used to detect DNA fragments resembling to potato wart in metagenomics datasets. The PCC and PCD system has demonstrated great potential in the detection and identification of plant pathogenic bacteria, viruses and fungus, including potato wart.

93. Naturally occurring propiconazole-tolerant fungal isolates in the phyllosphere of *Agrostis stolonifera* E. MCNAB AND T. HSIANG *Environmental Sciences, University of Guelph, 50 Stone Road East, Guelph, Ontario, N1G 2W1, Canada.*

Agrostis stolonifera L. is a commonly used amenity turfgrass and can experience frequent fungicide applications because of intensive management. The frequent use of fungicides has given rise to problems with fungicide resistance in several major turfgrass pathogens. However, there are other organisms in this environment, which may be naturally tolerant of particular fungicides and of which little is known. The purpose of this work was to examine the identity and diversity of these organisms during two growing seasons by sampling asymptomatic leaf blades of *A. stolonifera* from research plots which were only established one or two years before the sampling and had no or very little exposure to fungicides. Over 2400 asympomatic leaf samples were obtained from March through October in two years, and were plated on media amended with propiconazole and antibiotics. The ~2200 isolates were categorized into 21 morphotypes, and ITS sequencing placed these into 19 different fungal species. The five species that showed the greatest representation were as follows: *Microdochium bolleyii* Sprague (23%), *Rhizoctonia solani* Kuhn (11%), *Papiliotrema flavescens* Saito (9%), *Cryptococcus aspenensis* Ferreira (9%), and *Mucor nidicola* Madden et al. (8%). Why these species are naturally tolerant of propiconazole remains to be explored, as well as whether the types of genes and mutations that confer this tolerance are the same as the ones that produce acquired resistance in targeted fungal pathogens.

94. Screening of grain and oilseed using a combination of long read sequencing and qPCR assays for bio-surveillance of phytopathogens J. B. PEPIN, E. GIROUX, AND G. J. BILODEAU *Ottawa Laboratory Fallowfield, Canadian Food Inspection Agency, 3851 Fallowfield Road, Ottawa, ON K2H 8P9, Canada*

The grain and seed export markets could require disease testing in order to certify shipments free of specific pathogens. Our lab has been developing rapid new methods for screening grain and oilseed. These methods include the use of long-read sequencing on material collected from soybean, wheat and canola seed washes, and the development of a qPCR assay to identify target organism such as some challenging groups within the *Colletotrichum truncatum* species complex. Anthracnose cause by the fungi *C. truncatum* is a major pathogen affecting lentil and soybean seed production. As Canada is the world leading producer of lentil seeds and one of the world's largest producers of soybean, rapid identification is essential in mitigating the spread of this pathogen. In response, we are developing a qPCR specific for *C. truncatum* on lentil and soybeans seeds. Through long-read sequencing with the MinION device, we have successfully identified pathogenic bacterial species by 16s rRNA sequencing and whole-genome sequencing, including correctly identifying all bacterial species in a microbial community DNA standard. We have also been able to identify several fungal pathogens down to the genus level through both whole-genome sequencing and amplicon sequencing of rDNA regions. However, for many fungi, species level identification has proven challenging as species within some genera, such as *Colletotrichum* have highly conserved rDNA regions. Thus, for fungal identification we plan on continuing to implement whole-genome sequencing with an improved bioinformatics pipeline allowing us to extract regions of interest in combination with amplicon sequencing of several highly variable genes.

95. Assessing the variability of *Sclerotinia sclerotiorum* isolates collected from different host crops across Canada B. CALDER, M. W. HARDING, A. DICKSON, S. CHATTERTON, AND D. YEVTUSHENKO *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1st Ave S., Lethbridge, AB T1J 4B1; (M.W.H.) Alberta Ministry of Agriculture and Forestry, 301 Horticultural Station Rd., Brooks, AB T1R 1E6; (A.D.) Syngenta Canada Inc., 946863 Twp Rd 14, Plattsville, ON N0J 1S0; and (D.Y.) University of Lethbridge, 4401 University Dr W, Lethbridge, AB T1K 3M4*

Sclerotinia sclerotiorum (Lib.) de Bary causes white mould in dry beans and sclerotinia stem rot in canola, both economically damaging diseases. Fungicides are routinely applied to manage the diseases, but the sensitivity of *S. sclerotiorum* isolates to these fungicides has not been fully evaluated in Canada. Although *S. sclerotiorum* has been extensively studied for many years, recent studies suggested that there is greater genetic variability in pathogen populations than previously thought. Therefore, the objectives of this study were to determine the variability of aggressiveness of *S. sclerotiorum* isolates on dry beans and canola, and characterize their sensitivities to fungicides, using a pan-Canadian population. More than three hundred isolates were collected from field crops in Alberta, British Columbia, Saskatchewan, Manitoba, and Ontario, from these, two hundred isolates were selected from unique field locations. Mycelium compatibility grouping (MCG) was conducted to identify basic diversity among the isolates, and 14 MCGs have been identified to date, although testing is ongoing. The isolates were assessed for aggressiveness on two dry bean and two canola lines using a detached leaf assay. There were clear differences among isolates, and statistical analyses are underway to determine the effect of host and geographic origin on aggressiveness ranking. Fungicide resistance testing against the most commonly used fungicide active ingredients is being conducted as part of a joint initiative with Syngenta Canada Inc. The knowledge generated from these studies will provide new insights into the diversity and fungicide resistance in *S. sclerotiorum* populations and is the first step in developing a genomics-enhanced biovigilance approach to disease management.

Session 13: Genetics, biotechnology, and breeding-2

96. Unravelling resistance mechanisms: Dual RNA sequencing of soybean and soybean Cyst Nematode (SCN) S. TORABI AND M. ESKANDARI *Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada*

Soybean cyst nematode (SCN), caused by *Heterodera glycines* Ichinohe, is a devastating disease that poses a serious threat to soybean production worldwide. A comprehensive understanding of the interplay between soybean and SCN is urgently needed to develop effective strategies to cope

with this devastating nematode disease. In this study, we utilized dual RNA sequencing to investigate how SCN invasion modulates soybean gene expression and simultaneously examined SCN reactions across multiple soybeans lines with varying levels of resistance. We monitored the transcriptome landscape of the three most common SCN-resistant Plant Introduction (PI) soybean lines, PI 437654 (aka. Hartwig), PI 548402 (aka Peking), and PI 88788, along with the SCN-susceptible line Lee-74, against the SCN HG type 1.2.5.7. Our goal was to unravel the resistance mechanisms and identify SCN virulence genes involved in resistance breakdown. Our bioinformatic analysis, pathway analyses, and intra- and inter-genotype analysis revealed the involvement of the phenylpropanoid pathway, MAPK signaling pathway, plant hormone signal transduction, and secondary metabolite pathways in the resistance mechanisms. However, we found that the key defence mechanism of PI 437654, which exhibits strong resistance (Female index, FI=0%), involves the expression of several genes that strengthen the cell wall, oxidative enzymes, and ROS scavengers as well as Ca+2 sensors governing the salicylic acid biosynthesis process. Furthermore, our use of different hosts with varying levels of immunity and a susceptible line provided insights into SCN pathogenesis and how *H. glycine* overcomes different layers of host immunity by modulating its virulence genes.

97. Insights from the first FHB-resistant wheat cultivar AAC Tenacious R. DHARIWAL, D. G. P. FUNDORA, M. A. HENRIQUEZ, W. ZHANG, P. NICHOLSON, AND H. S. RANDHAWA. *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1st Avenue South, Lethbridge, AB T1J 4B1, Canada; (M.A.H.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB R6M 1Y5, Canada; (W.Z.) Aquatic and Crop Resources Development, National Research Council of Canada, Saskatoon, SK S7N 0W9, Canada; and (P.N.) Department of Crop Genetics, John Innes Centre, Norwich Research Park, Norwich, NR4 7UH, United Kingdom*

Fusarium head blight (FHB), predominantly caused by mycotoxin-producing *Fusarium graminearum* (*Fg*), is a devastating wheat disease. Resistant cultivars offer the most effective approach to managing FHB. Recently, we identified and mapped two major FHB resistance QTL, *QFhb.lrdc-2D.1* and *QFhb.lrdc-2D.2*, respectively on short and long arms of chromosome 2D of Canadian wheat cultivar AAC Tenacious. The favourable allele at *QFhb.lrdc-2D.1* and *QFhb.lrdc-2D.2* are descended from Canadian wheat cultivar Marquis and the highly Fusarium-resistant Chinese wheat breeding line Ning 7840, respectively. In this study, we identified that resistance at *QFhb.lrdc-2D.1* results from the fine-tuning of 'booting time' to 'heading time'. Furthermore, we found that AAC Tenacious derived photoperiod sensitive allele at *Ppd-D1* acts as a resistance allele at *QFhb.lrdc-2D.1* which increases the ratio of 'booting time' to 'heading time'. Conversely, *QFhb.lrdc-2D.2* is a true FHB resistance QTL from AAC Tenacious and had not negatively associated with any other trait. To fine-map these QTL, we constructed a large genetic mapping population and also conducted Bulked Segregant RNA-Seq analysis on resistant and susceptible bulks following *Fg* inoculation. The results of this study will be discussed.

98. Cannabis landraces and exotic germplasm as a great source for resistance breeding against powdery mildew disease S. SEIFI, J. CELEDON, T. O'BRIEN, AND G. BAUTE

Cannabis sativa L. (cannabis) indoor cultivation is severely threatened by the ascomycete pathogen *Golovinomyces cichoracearum*, the causal agent of the powdery mildew (PM) disease. PM can be controlled by different means including the application of approved IPM products, altering cultural conditions and more importantly, breeding for genetic resistance. Conventional breeding activities in the legacy market during the past decades have been mainly focused on higher potency and yield. This trend, coupled with the liberal use of pesticides to control pest and pathogens, has resulted in the loss of disease resistance (R) genes in the genetic pool of the available cannabis cultivars. Landraces and exotic genotypes of cannabis, on the other hand, offer a great source of resistance alleles, particularly for economically important pathogenic fungi like PM. Here we present our latest findings on the interaction of different agronomic traits and PM disease resistance in a diversity panel comprising of more than a hundred of cannabis landraces and exotic genotypes. Our results indicate that genetic resistance to PM is independent of major agronomic traits. Moreover, novel effective resistance mechanisms against PM were identified and studied at the cellular level.

99. Understanding Potato Greening through 'omics approaches K. DOUGHERTY, T. F. MITTERBOECK, M. LAGUE, M. ZAIDI, B. BIZIMUNGU, AND B. FOFANA *(K.D., T.F.M., M.L., B.B.) Agriculture and Agri-Food Canada, Fredericton, New Brunswick, Canada E3B 4Z7; and (M.Z.) Agriculture and Agri-Food Canada, Charlottetown, Prince Edward Island, Canada C1A 4N6*

Potato 'greening' occurs when tubers are exposed to light, and results from a de novo synthesis of chlorophyll and a simultaneous formation of steroidal glycoalkaloids, which are toxic to humans and animals. Potato is one of the four crops that supply 50% of the world's food energy needs and the largest vegetable crop in Canada, however this greening causes substantial loss of products. Currently, there are no potato cultivars that are resistant to light–induced greening available on the market. The goal of this study is to understand the genetic components and molecular mechanisms of light-induced greening, and to use this knowledge for developing gene-editing tools aimed to generate cultivars resistant to greening. From a core germplasm collection of mutant diploid potato clones, those found to be tolerant to light-induced greening were selected. These non-greening clones, along with a greening control, underwent transcriptomic sequencing after light exposure and their whole genome sequenced. Here, we will show our findings on the transcriptomic expression and genomic variations that differentiate the non-greening from greening clones and how this information contributed to the development of gene-editing tools targeting commercially significant potato varieties. Deploying the non-greening trait into popular potato cultivars would be of high interest to the industry and stakeholders both for tuber appearance, quality, safety, marketability, and food waste reduction.

100. An insight into sainfoin breeding in western Canada: challenges and achievements H. POUDEL, S. BHATTARAI, S. SINGER, B. BILIGETU, AND S. ACHARYA *Lethbridge Research and Development Center, Agriculture and Agri-Food Canada, 5401 1st Ave S, Lethbridge, AB, T1J 4B1, Canada; (S.B.) SARDA Ag Research, 510 Main St SW, Falher, AB, Canada, T0H 1M0, Canada; and (B.B.) Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8, Canada*

There has been a renewed interest in sainfoin (*Onobrychis viciifolia* scop.) among western Canadian forage and beef-cattle producers over the last decade. A major trigger for this growing appeal has been the availability of new sainfoin cultivars (Mountainview and Glenview) with improved compatibility with alfalfa. Such mixed stands have resulted in reduction of alfalfa frothy bloat in grazing animals. While the development of new sainfoin cultivars was considered a paradigm shift in forage breeding for western Canada, this alone did not ensure its adoption by producers. Concerns and questions persisted such as 1) whether sainfoin could grow together with alfalfa and persist as a perennial crop, 2) if the presence of sainfoin in a mixed stand with alfalfa would be enough to make for a bloat safe pasture, 3) if the aboveground biomass yield of sainfoin would be comparable to that of alfalfa for a profitable return of investment, and 4) whether the animals would prefer to graze sainfoin equally to alfalfa. We synthesized the answers to these questions based on our published papers, unpublished in-house research data, and long-term research experience in sainfoin breeding. In addition to historical sainfoin breeding activities, we also highlight current progress on the compatibility issue of sainfoin with grass species in western Canada and prospects of sainfoin as a sustainable livestock feed.

101. Evaluating 'AAC Trueman' Alfalfa in Saskatchewan Y. PAPADOPOULOS, B. HOUSTON, AND C. KAYTER *Agriculture and Agri-Food Canada, 58 River Road, PO Box 550, Truro, NS, B2N 5E3, Canada; (B.H.) Agriculture and Agri-Food Canada, 300-12th Avenue, Regina, SK, S4P 0M3, Canada; and (C.K.) Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, 107 Science Place, Saskatoon, SK, S7N 0X2, Canada*

We are exploring the adaptability of a new alfalfa variety, 'AAC Trueman' in Saskatchewan with sites successfully seeded in three soil zones: Brown (Swift Current), Dark Brown (Outlook); and Black Soil Zone (Melfort). The large plot trial at the Outlook site was seeded in 2020 while the other plots were seeded in 2021. Outlook large plots are irrigated. Soil moisture was monitored to achieve moisture treatment levels: (a) excess moisture, (b) normal irrigation and (c) dryland conditions. The plots at Swift Current and Melfort are not irrigated but have topographic variation which provides a range of soil moisture levels. Forage yields in 2022 were highest at Outlook (2 cuts) and ranged from 9287 to 15,410 kg/ha for the season. Forage yields (1 cut) at Melfort ranged from 5688 to 7229 kg/ha while Swift Current ranged from 1413 to 7500 kg/ha. Small plots were also seeded near Outlook in 2021 to evaluate ST1 Timothy as a potential forage mix with AAC Trueman in higher soil moisture sites. Forage production, forage quality and winter hardiness were evaluated in 2022. This growing season had very good alfalfa production; although ST1 Timothy production was lower likely due to poor establishment related to windy conditions during seeding. Flooding tolerance of AAC Trueman, ST1 Timothy and check varieties were tested in the AAFC Swift Current Salinity Testing facility. The test was completed in June 2022 and initial results showed that all varieties performed well during the 5 week flooding period.

Session 14: Long-term studies: Soil and plant

102. Changes in pea yield and root rot levels in field trials naturally-infested with *Aphanomyces euteiches* in Alberta and Saskatchewan S. CHATTERTON, R. BOWNESS DAVIDSON, M.W. HARDING, M. HUBBARD, L. SHAW, S. SHIRTLIFFE, AND S. BANNIZA *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada (AAFC), 5403 1st Ave S, Lethbridge, AB T1K 6M5, Canada; (R.B.D) Lakeland College, 6000 C&E Trail, Lacombe AB T4L 1W1, Canada; (M.W.H) Alberta Agriculture and Irrigation, Crop Diversification Centre South, 301 Horticulture Station Road E., Brooks, AB T1R 1E6, Canada; (M.H.) Swift Current Research and Development Centre, AAFC, 1 Airport Rd., Swift Current, SK S9H 3X2, Canada; (L.S) South East Research Farm, Box 129, Redvers, SK S0C 2H0, Canada; and (S.S., S.B) Department of Plant Sciences, University of Saskatchewan, 51 Campus Dr., Saskatoon, SK S7N 5A8, Canada*

Aphanomyces root rot, caused by *Aphanomyces euteiches* Drechs., was first detected in pea (*Pisum sativum* L.) fields in Saskatchewan and Alberta in 2012 and 2013, respectively, and has caused significant crop loss in both provinces. Extending the cropping interval between susceptible crops and avoiding infested fields are the only root rot management recommendations. Field trials to determine the effects of seed treatments and other inputs were conducted at various locations in Alberta and Saskatchewan from 2015 to 2022. Trials were located in producers' fields that had high levels of natural inoculum of *A. euteiches* and *Fusarium* spp. Some seed treatment products provided early season suppression of root rots at some locations in some years, but did not result in significant yield differences. Average yields across all treatments varied from 0 to >4,000 kg/ha at different locations, regardless of disease pressure, emphasizing the seasonal and regional variability of root rot severity, and difficulties assessing impacts of root rots on pea yields. At some locations yields improved slightly as the length of time out of peas increased, but root rot severity remained unchanged. In 2018 and 2019, *A. euteiches* and *Fusarium* spp. biomass in the roots were quantified using droplet digital PCR at 2 time points. At all locations, *A. euteiches* levels peaked in roots in early June, but was replaced by *Fusarium* spp. by flowering (July). Results highlight the long-term impact of *A. euteiches* on yield loss, and the lack of effective management options for this destructive pathogen.

103. Survey and management of plant parasitic nematodes in Ontario ginseng S. M. WESTERVELD, M. J. FILOTAS, AND F. SHI *Ontario Ministry of Agriculture, Food and Rural Affairs, Simcoe Resource Centre, 1283 Blueline Road, Simcoe ON N3Y 4K3, Canada; and (F.S.) Ontario Ginseng Growers Association, 1283 Blueline Road, Simcoe ON N3Y 4K3, Canada*

American ginseng (*Panax quinquefolius* L.) is the most valuable field-grown horticultural crop in Ontario. Although considerable damage to ginseng has been attributed to root lesion nematodes (RLN: *Pratylenchus* spp.), there have been few studies on their extent, life cycle or

management on ginseng itself. A survey of soil populations of plant parasitic nematodes was conducted on 23 commercial ginseng farms in Ontario in 2011. Fields were tested before any treatment, after nematode-suppressive cover crops (if using), first- and third-year gardens (1 or 3 years after fumigation). Management trials were established in 2016 on two commercial farms with moderate populations of RLN to compare application in fall after seeding and/or spring near germination of a new nematicide, fluopyram, against the industry standard fumigant metam-sodium and an untreated control. Pre-treatment populations of RLN were moderate, lower in fields after cover crops, and mostly absent in both first and third-year gardens. In contrast, populations of root knot nematode (*Meloidogyne* spp.) for which ginseng is a known host, were high in pre-treatment fields, unaffected by cover crops, slightly lower in first year gardens and highest in the third year. Fall applications of fluopyram at or after seeding significantly reduced RLN damage and was comparable to fumigation. Results from this study support the conclusion that ginseng is not a suitable host of RLN, but significant damage can occur during germination before populations begin to decline. Nematode management is needed before germination to be effective. Fluopyram is a viable management option for RLN in ginseng.

104. Climate change and crops health in the Caribbean: Threats and challenges N. BENKEBLIA-*Department of Life Sciences, The University of the West Indies, Mona Campus, Kingston 7, Jamaica*;*The Biotechnology Centre, The University of the West Indies, Mona Campus, Kingston 7, Jamaica*

The Caribbean, as many other regions of the world, are facing an increased vulnerability because of climate change, threatening this agriculture and food security. Therefore, research work should focus on identifying how climate change might increase pest and diseases threats and the development of resistant varieties to maintain good crop production and to increase shelf-life. As the 'International Year of Fruits and Vegetables' was celebrated, the main goal was aiming in promoting sustainable agriculture by focusing on plant health, food production and food security. Numerous studies have shown that climate change is having devastating effects on plant health due to an increase in pests and diseases of crops, and global warming in the region is establishing a favourable environment for invasive species, like the giant African snails which is destroying crops by their growing appetite alone. Nowadays, prevention of plant pests before they reach the region and control current plant pests and diseases before they cause any more damage.

105. Survival of *Plasmodiophora brassicae* over time in trials on the Canadian Prairies B. D. GOSSEN, D. FROESE, M. WIGNESS, AND M. R. MCDONALD. *Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada; (D.F.) Manitoba Agriculture, P.O. Box 1149 65-3rd Avenue NE, Carman MB R0G 0J0, Canada; and (M.R.M.) University of Guelph, 50 Stone Road East, Guelph, ON NIG 2W1, Canada.*

Plasmodiophora brassicae Wor., which causes clubroot of brassica crops, can persist in soil for many years as resting spores, and high spore concentrations are associated with rapid breakdown of clubroot resistance. Replicated field trials were initiated at five sites across the Canadian Prairie in 2018 or 2019 to assess changes in spore concentration over time in response to environmental conditions and selected treatments. The soil at three sites was pH neutral to slightly alkaline and acidic (pH ~ 5.5) at two sites. All of the sites included the application of lime to a target pH of 7.5 and a ryegrass cover crop, but other treatments were site-specific. Five soil cores per plot (15-cm depth) were collected, bulked, air-dried and spore concentration was assessed using ddPCR. The trials were sampled each year until 2022. Application of hydrated lime initially had a larger impact on pH relative to standard lime, but its effect on pH dropped off more quickly over time, as expected. Resting spore concentration was highly variable, which resulted in an inconsistent treatment response over time, both within and among sites. Neither liming nor a grass cover crop consistently reduced spore. One pattern, however, was consistent; spore concentration declined substantially over time at all sites, irrespective of treatment. However, spore concentration remained high enough to produce severe symptoms in a susceptible crop at four of five sites. The exception was a site where initial spore numbers were substantially lower than at the other sites.

106. Pea-brassica intercropping does not ameliorate root rot in pea, but sometimes provides yield benefits M. HUBBARD, L. SHAW, R. BOWNESS DAVIDSON, S. SHIRTLIFFE, S. CHALMERS, A. ABDELMAGID, R.L. CONNER, AND S. CHATTERTON *Swift Current Research and Development Centre, Agriculture and Agri-Food Canada (AAFC), 1 Airport Rd., Swift Current, SK S9H 3X2, Canada; (L.S.) South East Research Farm, Box 129, Redvers, SK S0C 2H0, Canada; (R.B.D.) Lakeland College, 6000 C&E Trail, Lacombe AB T4L 1W1, Canada; (S.S.) Department of Plant Sciences, University of Saskatchewan, 51 Campus Dr., Saskatoon, SK S7N 5A8, Canada; (S.C.) Westman Agricultural Diversification Organization, Manitoba Agriculture, 139 Main St., Melita MB, ROM 1L0, Canada; (A.A., R.C.) Morden Research and Development Centre, AAFC, Unit 101 Route 100, Morden, MB R6M 1Y5, Canada; and (S.C.) Lethbridge Research and Development Centre, AAFC, 5403 1st Ave S, Lethbridge, AB T1K 6M5, Canada.*

Root rot is a serious constraint on the agricultural production of field pea (*Pisum sativum* L.) on the Canadian prairies. This disease is caused by a complex of soil-borne pathogens, including *Aphanomyces eutieches* Drechs., *Fusarium* species, *Rhizoctonia solani* and *Pythium* species. The only effective means of managing root rot in pea are avoiding planting pea or lentil at least six to eight years or not planting either of these crops in fields known to harbour high inoculum levels of the root rot pathogens. Growing a brassica crop as an intercrop with pea could, in theory, be expected to reduce the risk of root rot via "biofumigation" due to the release of glucosinolates as brassica tissue decomposes. Glucosinolates, in turn, break down into isothiocyanates, which can negatively impact soil microorganisms, including plant pathogens. In order to test the effectiveness of pea-brassica intercropping as a root rot management strategy, small-plot field trials were conducted from 2018 to 2022 in Alberta, Saskatchewan and Manitoba. Brassica species included canola, brown, yellow and hybrid mustard, and camelina. The severity of root rot was not reduced in pea. However, in some site-years, yield benefits (land equivalency ratios (LERs) greater than 1.0) were observed. While intercropping with brassicas should not be relied upon to ameliorate root rot in pea, it could still be worthwhile as an agronomic practice.

POSTER SESSION 1

Climate change and biodiversity

P1. Estimating greenhouse gas emissions and carbon footprint for different cropping systems on the Canadian Prairies S. LIN, K. LIU, AND R. LEMKE *(S.L., K.L.) Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, #1 Airport road, Swift Current, SK S9H 3X2; and (R.L.) Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2*

Diversifying crop rotations can effectively sequester carbon (C) and reduce greenhouse gas emissions (GHGe). However, most studies investigated (GHGe) and soil organic carbon changes (dSOC) separately, resulting in a lack of integrated assessments of both. To address this gap, we applied the Holos and Campbell models to estimate the impacts of different crop rotation systems on GHGe and dSOC, respectively, based on a 4-yr (2018-2021) cropping system study in three ecozones (Melfort, Scott, and Swift Current) of Saskatchewan, Canada. We tested six rotation systems, including the conventional wheat-based cropping system (Control), oilseed or pulse intensified cropping system (Intensified), diversified cropping system (Diversified), market-driven cropping system (Market Driven), high risk and potential high reward cropping system (High Risk), and soil-health enhanced cropping system (Soil Health). On average, GHGe were highest in the Market Driven system and lowest in the Soil Health system, with nitrogen synthetic fertilizer being a significant contributing factor. All rotation systems increased SOC at all sites except Melfort. Based on the carbon footprint estimated from GHGe and SOC, we predicted net C losses at Melfort but net C sequestrations at Scott and Swift Current. Although the differences in dSOC and C footprint among different cropping systems were not significant, Soil Health consistently showed a larger SOC increase and the highest C sequestration compared to other systems. Our findings suggest that Soil Health is a promising crop management practice that can simultaneously reduce GHGe and increase SOC stock, thus improving soil quality and mitigating GHG emissions.

P2. Western Canadian spring wheat (*Triticum aestivum*) yield may be enhanced by the use of cultivar mixtures in contrasting conditions J. TOERPER, K. SEMAGN, M. IQBAL, H. RANDHAWA, B. BERES, PIERRE J. HUCL, L. GORIM, AND D. SPANER *(J.T., K.S., M.I., L.G., D.S.) Department of Agricultural, Food and Nutritional Science, University of Alberta, 116 St. & 85 Ave., Edmonton, AB, T6G 2R3, Canada; (H.R., B.B.) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403-1st Avenue South, Lethbridge, AB, T1J 4B1, Canada; and (P.J.H.) Crop Development Centre and Dep. of Plant Sciences, Univ. of Saskatchewan, 51 Campus Drive, Saskatoon, SK, S7N 5A8, Canada.*

Canadian wheat (*Triticum aestivum*) production may be susceptible to climate change if production strategies remain constant. One potential way to enhance yield stability is with cultivar mixtures; such a practice may promote resilience in the face of climate change. The aim of this study is to evaluate the yield and yield stability of mixtures in conventional and organic production systems at six sites across Alberta and Saskatchewan from 2016-2017 and 2021-2022. Canada Western Red Spring (CWRS) and Canada Prairie Spring Red (CPSR) wheat classes were used. Five cultivars from each class were grown in pure stands (100) and in two (50:50) and three (33:33:33) way mixtures for 25 combinations. Yield, yield stability, phenotypic correlation, heritability, and specific mixing ability parameters were measured. In CWRS wheat, the mixtures Carberry:Glenn, Go Early:Glenn:CDC Titanium, and Glenn:CDC Titanium had the highest specific mixing ability (SMA) >0. In CPRS wheat Forefront:AAC:Penhold, AAC Foray:Forefront, and AAC Foray:Forefront:AAC Penhold had the highest SMA >0. While both CWRS and CPSR classes had SMA >0 the results were not significant. CPSR yield stability was greatest for Forefront:AAC Penhold and AAC Foray:AAC Penhold:AAC Tenacious. CWRS yield stability was greatest for Glenn:CDC Titanium:Lillian and CDC Titanium:Lillian. The environment and genotype had a significant effect on yield ($p < 0.001$) for both wheat classes. These results indicate that cultivar mixtures may outyield and be more stable than pure stands. Prairie wheat production under climate change may benefit by identifying the most stable and highest yielding cultivar mixtures.

P3. Selection of heat and drought stress tolerance in a diverse bread wheat panel J. S. SANGHA, H. RANDHAWA, R. D. CUTHBERT, R. DHALIWAL, W. WANG *(J.S.S., R.D.C., W.W.) Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, 1 Airport Road, Swift Current, SK S9H 3X2, Canada; and (H.R., R.D.) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1st Ave South, Lethbridge, AB T1J 4B1, Canada*

Extreme weather events, such as heat and drought, could negatively impact the crop growth and production. Development of new drought resilient cultivars may help to address the impact of heat and drought on wheat production, and help to and meet the increasing demand of food for the growing world's population. A field based study was completed in 2022 under two environments (Swift Current, SK and Lethbridge AB) to determine heat and drought stress response in a global collection of 403 diverse bread wheat lines. Mean grain yield for both locations showed significant genotypic variation ($p<0.0001$) ranging from 206 to 899 g/plot, but no differences were observed between environments. Among various spectral indices collected at the grain-fill stage, significant but moderate correlations were observed between grain yield and red normalized difference vegetation index (RNDVI=0.51), green normalized difference vegetation index (GNDVI=0.51), and vegetation index (VI=0.51) and). Negative but low correlations were observed between grain yield and water index (WI=-0.21), and four other normalized water indices (NWI-1 to NWI-4). The number of seeds per spike also correlated positively with grain yield (r=0.32). These results helped to shortlist a smaller number of candidate wheat lines for further characterization of heat and drought stress response in multilocation field trials.

P4. Identification of phoma-like fungi isolated from medicinal plants (Apiaceae) Y. HIROOKA, S. KATO AND T. SATO. *Department of Clinical Plant Science, Hosei University, 3-7-2 Kajino-cho, Koganei, Tokyo, 184-8584, Japan; and (T.S.) Research Center for Medicinal Plant Resources, NIBIOHN, 1-2 Hachimandai, Tsukuba, Ibaraki, 305-0843 Japan*

Phoma-like fungi are cosmopolitan and plant pathogens commonly found in nature. Identification of these fungi to species rank is, however, not easy because of their simple morphological characters, wide host ranges and endophytic lifestyles. Six diseases of medicinal plants belonging to

the family Apiaceae caused by the phoma-like fungi were recently observed in Japan. Their symptoms are as follows: root rot of *Bupleurum falcatum* L. and *Angelica acutiloba* (Sieb. & Zucc.) Kitagawa; damping-off of *A. keiskei* (Miq.) Koidz.; and leaf spot of *A. acutiloba*, *A. dahurica* (Hoffm.) Benth. & Hook.f. ex Franch. & Sav. and *B. falcatum*. In this study, isolates taken from the symptomatic parts of these medicinal plants were identified. Although the morphology of each isolate was quite similar, subtle morphological characteristics, hosts, symptoms, and multi-locus phylogenetic results of the isolates indicated that they represent at least five undescribed species of the genus *Didymella*, which have phoma-like morphologies. Morphology of mature conidia may provide taxonomically-informative characters for differentiating these species.

P5. Characterization of the endophytic mycobiota in cultivated and wild barley species: insights into potential contributions to host adaptation and stress Tolerance W. CHEN, R. KHANAL, E. TREMBLAY, AND M LIU. Ottawa *Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Ave., Ottawa, ON, K1A 0C6.*

Modern barley (*Hordeum vulgare*) was cultivated from its wild ancestor (*H. spontaneum*), dating back to ~ 8,000 BC in the Middle East. Cultivated and wild barley species differ significantly in physiological and phytomorphological attributes, with the latter exhibiting greater resistance to various abiotic and biotic stresses, such as pests, salinity, and drought. Studies have shown that endophytic fungi have the ability to facilitate symbiotic association, enhance nutrient acquisition, and induce host defence systems; therefore, contributing to the host's overall well-being and adaptation to diverse habitats. We hypothesized that the endophytic mycobiota of the wild barley species differs from that of the cultivated barley cultivars, with some beneficial fungal taxa that can improve the host's resistance to various environmental stresses. To this end, we characterized the endophytic mycobiota of the 52 seed and/or stem samples of cultivated barley and eight wild barley species using metabarcoding of the Internal Transcribed Spacer (ITS) 2 region. Ascomycota (97.9 ± 11.2% in abundance) was the dominant phylum in all samples. The most abundant genera were *Alternaria, Cladosporium, Fusarium, Nigrospora*, and *Penicillium* in the endophytic mycobiota of barley seeds, and *Alternaria*, *Cladosporium, Claviceps, Epichloë,* and *Epicoccum* in barley stems. Surprisingly, we did not find significant differences in the endophytic mycobiota diversity and composition between wild and cultivated barley species. Our preliminary results suggest that further studies with expanded sampling coverage may be necessary to reveal potential differences in the endophytic mycobiota that could contribute to barley adaptation and stress tolerance.

P6. Soil-borne oomycete communities are shaped by tillage and crop rotation regimes in long-term soybean, corn, and wheat cropping systems A. C. GAHAGAN, Y. SHI, D. RADFORD, M. J. MORRISON, E. GREGORICH, AND S. ARIS-BROSOU, W. CHEN *(A.C.G., Y.S., D.R., M.M., E.G., W.C.)Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling ave., Ottawa, ON K1A 0C6, Canada; and (A.C.G., S.A.B., W.C.) Department of Biology, University of Ottawa, Ottawa, 60 Marie Curie Prv., Ottawa, ON K1N 6N5, Canada*

Soil-borne oomycete pathogens cause significant losses in the agricultural sector, but how these communities respond to tillage and crop rotation regimes is not well understood. To address this question, we used an amplicon sequencing approach at the Internal Transcribed Spacer 1 (ITS1) region to characterize the post-harvest soil-borne oomycete communities over three years. The soil samples were collected from a split-plot experiment field with tillage as the main plot factor (conventional tillage [CT] vs. no-till [NT]) and rotation as the subplot factor (monocultures of soybean, corn, or wheat, and corn-soybean-wheat rotation). Tillage and rotation did not show significant impact on soil moisture content likely due to the fall sampling time as the soil had compacted throughout the growing season. We recovered 292 Amplicon Sequence Variants (ASVs) representing 34 species, predominantly in *Globisporangium* (85.1% in abundance, 203 ASV) and *Pythium* (10.4%, 51 ASV). NT decreased diversity and community compositional structure heterogeneity, while the crop rotation only affected the community structure under CT. Oomycete species diversity may be driven by host availability, preceding crop residue, and the natural soil suppressiveness. Crop yield and soybean seedling vitality were used to evaluate soil health. NT significantly promoted corn yield, while rotation promoted wheat yield. CT soils from soybean or corn resulted in the lowest seedling vitality under controlled environments. The interaction effects between tillage and rotation emphasized the complexity of oomycete management in agricultural soils, possibly through modulating the general suppressiveness of soils.

P7. Fungal endophyte diversity in barley infected with Fusarium head blight C. WIJEKOON, D. EMBRADOR, Z. QUILL, J. R. TUCKER, AND A. BADEA *Morden Research and Development Centre, Agriculture and Agri-Food Canada, Route 100, Unit 100-101, Morden, MB R6M 1Y5, Canada; Canadian Centre for Agri-Food Research in Health and Medicine, 351 Taché Avenue, Winnipeg, Manitoba, R2H 2A6, Canada; and (J.R.T., A.B.) Brandon Research and Development Centre, Agriculture and Agri-Food Canada, 2701 Grand Valley Road, P.O. Box 1000A, Brandon, MB R7A 5Y3, Canada.*

Fusarium head blight (FHB) caused by *Fusarium graminearum* is a devastating disease that affects the grains of barley (*Hordeum vulgare* L.). Grains infected with FHB contain mycotoxins such as deoxynivalenol that is known to induce health related problems in humans and animals. In our study, we compared the fungal endophytes identified in barley genotypes (AAC Synergy, GB132013, CDC Bold, and Kutahya) with different response to FHB, that were grown for 2 years (2021 and 2022) in FHB artificially infected (FHB-infected) and non-infected (clean) field trials. Each year, the samples from both trials were collected at 3 different plant growth stages (8-leaf, mid dough and mature). The roots, stems, spikes, and grains from each genotype were surface sterilized, and tissue samples were taken for culturing to isolate fungal endophytes and meta-sequencing. Metagenomics internal transcribed spacer (ITS) sequencing was performed, and the analysis showed that the FHB-infected barley and clean barley displayed diverse fungal endophytes that varied in abundance between each tissue and genotype. However, certain endophytes such as *Alternaria* spp., *Bipolaris* spp. and *Metschnikowia* spp. were abundant and overlapped among the FHB-infected and clean barley samples. Meanwhile, *Alternaira* spp. were most abundant in the spike tissues of the FHB-infected and clean 2021 stage #2 samples, particularly in the CDC Bold and GB132013 genotypes,. Understanding and identifying the interactions and roles of these fungal endophytes that are most abundant in each genotype and stages may be advantageous for future applications in barley breeding, biocontrol, biotechnology, and other areas of science.

P8. Development and evaluation of a target enrichment bait set for phylogenetic analysis of oomycetes H. D. T. NGUYEN, W. MCCORMICK, J. EYRES, Q. EGGERTSON, S. HAMBLETON, AND J. R. DETTMAN *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, K1A 0C6, Canada*

Target enrichment involves using specific molecular baits to capture desired genomic regions, followed by next generation sequencing. A molecular bait set, based on 426 oomycete-specific genes and three barcoding genes, was designed, developed, and tested on 27 oomycete live and herbarium samples, including 4 samples of true fungi and 3 plant samples as controls. The results show that the method effectively recovers 61% of genes on average and it works specifically on oomycetes. Sequencing approximately 100,000 paired-end reads per sample was considered optimal for recovering genes while maintaining low sequencing costs. Multi-gene phylogenetic analysis, using the data generated, showed the expected relationships between major oomycete groups. This is the first report of an oomycete-specific target enrichment method that has broad potential applications for evolutionary and taxonomic studies.

Genetics, biotechnology, and breeding

P9. Identification of Resistance QTL for Bacterial Brown Spot and Common Bacterial Blight in Common Bean C. R. CORREA, E. MORNEAU, O. WALLY, C. GILLARD, AND R. J. LARSEN *(C.R.C., C.G., R.J.L.) Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada; and (E.M., O.W., R.J.L.) Harrow Research and Development Centre – Agriculture and Agri-Food Canada, Harrow, ON, Canada.*

Common bean (*Phaseolus vulgaris* L.) is the most important legume crop for direct human consumption, providing a vital source of dietary protein, fiber, and essential micronutrients. Bacterial blights, including bacterial brown spot (BBS) and common bacterial blight (CBB), are a recurring production constraint in Ontario, causing yield losses of 20-45% in severe outbreaks. Significant progress has been made on improving CBB resistance levels in small-seeded market classes such as navy and pinto beans, but large-seeded classes, such as kidney beans, are still highly susceptible to bacterial diseases. Thus, the objective of this research is to identify quantitative trait loci (QTL) associated with resistance to BBS and CBB in large-seeded common bean lines to be used in marker-assisted selection. Three populations of 125 recombinant inbred lines were genotyped and screened for BBS and CBB severity, and a restricted two stage multi-locus genome-wide association study (RTM-GWAS) was performed to detect single nucleotide polymorphisms potentially linked to resistance genes. Disease severity varied among genotypes, and ratings for CBB were significantly higher than for BBS. The RTM-GWAS revealed 26 and 23 major QTL for BBS and CBB, respectively. The identified QTL are potential targets for marker assisted breeding in common bean and for further studies aiming to explore the effects of the underlying resistance genes.

P10. High-throughput phenotyping in maize *(Zea mays L.)* to estimate black layer A. L. HORNBY, J. SULIK, AND E. A. LEE *Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON N1G 2W1, Canada; (J.S.) Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON N1G 2W1, Canada; and (E.A.L.) Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON N1G 2W1, Canada*

Black layer (BL), characterized by the formation of an abscission zone between the developing kernel and the plant, is the indicator of physiological maturity in maize. Traditional phenotyping methods for BL include destructive sampling or using proxy traits (i.e., grain moisture and flowering time) which are resource-intensive and unreliable, making this trait difficult to measure and one that is not routinely phenotyped in breeding programs. BL is triggered when photosynthate levels in the leaves fall below a threshold. Because of BL's connection to leaf photosynthetic activity, it is a candidate trait to follow using remote sensing (RS) technologies. Previous research in our lab using hyperspectral measurements demonstrated that the reflectance curve changes during the grain filling period (GFP) and identified several promising vegetative indices to follow these changes. To further examine the potential of using RS to determine BL, 5 commercial maize hybrids were grown at 2 locations for 2 years using a 4-rep randomized complete block design. Using an unmanned aerial vehicle integrated 5-band camera, multi-spectral images were acquired weekly during the growing season for each location-year. Flowering and BL dates, and days of green canopy during the GFP were determined for each plot. Two indices, the normalized red-green index (NGRDI) and the plant senescence reflectance index (PSRI) exhibited a consistent feature which was able to estimate timing of BL within 1-2 days. These indices provide an alternative tool to replace the resource intensive ground-based phenotyping methods allowing breeders to accurately phenotype this trait in a rapid, cost-effective manner.

P11. The identification, mapping, and effectiveness of the wheat leaf rust resistance gene *Lr46* in Canadian wheat B. D. MCCALLUM, M. K. LEWARNE, C. A. MCCARTNEY, F. E. BOKORE, R. E. KNOX, R. D. CUTHBERT, AND C. W. HIEBERT *(B.D.M., C.W.H.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, Route 100, Unit 100-101, Morden, MB, Canada, R6M 1Y5; (M.K.L.) Manitoba Crop Alliance; (C.A.M.) Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada, R3T 2N2; and (F.E.B, R.E.K., R.D.C.)Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, Swift Current, SK, Canada*

The wheat leaf rust and multi-pest resistance gene *Lr46* was discovered in 1998 and conditions resistance to stripe rust (*Yr29*), stem rust and powdery mildew. It imparts a partial level of adult plant resistance that has not been overcome by genetic changes in the pathogen population over wide use throughout the world. It had previously not been identified in Canadian wheat cultivars. Through genetic mapping of leaf rust resistance in the wheat line BW278 a QTL was identified for an adult plant resistance gene on chromosome 1B in the expected location of *Lr46*. BW278 inherited *Lr46* from AC Domain which was a popular wheat cultivar in Canada due to its rust resistance, good agronomics and pre-harvest sprouting resistance. Due to these traits AC Domain was used extensively as a parent in the development of Canadian wheat cultivars, and

therefore *Lr46* may be present in some of these cultivars including the widely grown cultivar Carberry. *Lr46* was also mapped in a cross between Carberry and Thatcher. It consistently reduced leaf rust severity and acted in an additive manner with other resistance genes, including *Lr34* which is also a slow rusting adult plant resistance gene present in many Canadian wheat cultivars. The combination of these two genes along with other resistance genes holds the promise for durable multi-pest disease resistance in Canadian wheat.

P12. Progress in breeding winter wheat with increased resistance to Fusarium head blight (FHB) and deoxynivalenol (DON) level L. TAMBURIC-ILINCIC, S. ROSA, AND A. NEUPANE *Ridgetown Campus, University of Guelph, 120 Main St E., Ridgetown, ON, NOP 2CO, Canada; (S.R.) Centre de recherche sur les grains (CÉROM), 740 Chemin Trudeau, Saint-Mathieu-de-Beloeil, QC, J3G 0E2, Canada; and (A.N.) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, Ontario, K1A 0C6, Canada*

Fusarium graminearum (Schwabe) (FG) is the principal cause of Fusarium head blight (FHB), one of the most serious diseases of wheat. Deoxynivalenol (DON) is the most important mycotoxin produced by FG. Winter wheat is mainly grown in Eastern Canada. Development of wheat resistant to FHB, without significant yield and quality penalties, is important. Conventional breeding, doubled haploid method, and marker-assisted selection are used in our program. By using 'Sumai 3' sources of resistance, we found that breeding lines grouped in the 3B QTL class had the lowest FHB index, DON content and FDK level and did not have a significantly lower yield or protein content compared to the lines grouped in other QTL classes. We identified QTL for FHB resistance on chromosomes 2D, 4B, 4D and 7A, in a population 'Vienna' x '25R47', and on chromosomes 2D, 4A, and 4B in 'Maxine x 'FTHP Redeemer' population. The most effective QTL associated with FHB resistance coincided with plant height QTL. Genotyping and QTL analysis for populations 'Triumph' x '25R51' and 'Superior' x 'D8006W' were performed using Illumina Infinium 90K SNP BeadChip platform and results will be discussed. All wheat commercially grown in Ontario is entered in the Performance Trial and tested for FHB resistance in the nurseries spray inoculated with FG. 'Marker', 'UGRC Ring', 'UGRC C2-5' and 'UGRC GL164' are soft red winter wheats developed by our breeding program and moderately resistant or moderately susceptible to FHB/DON level (www.gocereals.ca). The cultivars had competitive yield in Performance trials grown in Ontario/ Quebec.

P13. Evaluation of resistance to *Verticillium longisporum* in *Brassica* genotypes Y. WANG, S. E. STRELKOV, R. FREDUA-AGYEMAN, AND S. F. HWANG *Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB T6G2P5, Canada*

Verticillium stripe, caused by *Verticillium longisporum*, is an emerging disease of the Canadian canola (*Brassica napus*) crop. Symptoms of Verticillium stripe include half stem senescence, shredding and the appearance of black microsclerotia on the stem. Following its initial identification in Manitoba in 2014, the pathogen has been commonly reported across western Canada. Infection by *V. longisporum* can cause yield losses of up to 50%, which is a cause for concern since most canola varieties in Canada are susceptible to this pathogen. The objective of this study was to phenotype a collection of 206 *Brassica* genotypes for their reactions to *V. longisporum*, and to use genome-wide association mapping to identify single nucleotide polymorphism (SNP) markers for resistance. The host collection, which included 110 rutabagas (*B. napus* ssp. *rapifera*) and 96 other *Brassica* genotypes, was screened for resistance under greenhouse conditions and genotyped using a 15K *Brassica* SNP array. General linear models (GLM) and mixed linear models (MLM) were used to evaluate the markers. Several *B. rapa* and *B. oleracea* genotypes developed low area under the disease progress curve (AUDPC) values and could be linked to filtered SNP markers, indicating that these genotypes may serve as important sources of *V. longisporum* resistance. The markers identified in this study will be valuable for marker-assisted selection in the development of Verticillium stripe-resistant canola in the future.

P14. Response of *Lens ervoides* leaves to agroinfiltration with *Colletotrichum lentis* effector ClToxB C. KOLB, M. BAGA, R. CHIBBAR, AND S. BANNIZA. *Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8; and (S. B.) Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8*

Anthracnose, caused by *Colletotrichum lentis* Damm, has developed into one of the most damaging diseases of cultivated lentil (*Lens culinaris* Medik.) in western Canada. There are currently no high levels of resistance to the highly virulent *C. lentis* race 0. *Lens ervoides* Grande is a wild relative of *L. culinaris* that has been used as a source of resistance to both races of lentil anthracnose. *Colletotrichum lentis* secretes toxic effector proteins that manipulate host cell physiology and promote infection. ClToxB is a host-specific effector secreted by *C. lentis* that likely induces cell death during the pathogen's switch from biotrophy to necrotrophy. The mechanism of ClToxB is likely contributing to quantitative differences in virulence between *C. lentis* races 0 and 1. To test this hypothesis, ClToxB was expressed as a soluble GST-tagged protein in *E. coli* SHuffle and purified. The purified protein was agroinfiltrated into *L. ervoides* susceptible (LR-66-524) and resistant (LR-66-528) RILs. Disease symptoms were monitored post-agroinfiltration to characterize the interaction between ClToxB and host plant cells. Preliminary results have found that infiltration of purified ClToxB into *L. ervoides* leaf tissue results in necrosis of plant tissues, which supports the hypothesis that the protein is an effector playing a role in altering host cell physiology to facilitate infection. Further studies are underway to confirm this interaction.

P15. Genetics of common bunt resistance in a spring wheat (*Triticum aestivum* L.) population Carberry x Thatcher F. E. BOKORE, R. E. KNOX, S. BERRAIES, R. D. CUTHBERT, Y. RUAN, AND B. MEYER. *Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, 1 Airport Road, P.O. Box 1030, Swift Current, Saskatchewan S9H 3X2, Canada*

The threat by common bunt *(Tilletia tritici*) to wheat production in Canada has been reduced by using resistant cultivars and chemical seed treatments. This study strived to determine chromosomal regions associated with reduced common bunt infection in a doubled haploid population of 297 lines developed from the cross of a bunt resistant cultivar Carberry and intermediately resistant variety Thatcher. The lines, parents and checks were inoculated before sowing by dusting with a mixture of predominant bunt isolates, L16 (*T. lavis*) and T19 (*T. tritici*) and rated for bunt incidence in a specialized disease nursery near Swift Current, SK in 2018, 2019 and 2021. The population was genotyped with the Illumina iSelect 90K SNP markers, linkage map constructed using JoinMap 5 and QTL analysis performed using MapQTL 6. Carberry derived QTL were detected on chromosomes 1A, 1B, 2D, 3D, 4A and 6D, and Thatcher derived QTL on 2A, 3A, 3D and 4B. The QTL on 1B, 2D and 4A from Carberry, and the QTL on 3D from Thatcher are important as they significantly reduced disease incidence in at least two environments. All the QTL except 1B were previously reported in Canadian germplasm. The 1B QTL was reported in Carberry. Progeny lines with combined resistance from both Carberry and Thatcher could be used as future parents to develop wheat varieties with improved common bunt resistance. SNP markers associated with the most consistent QTL will be converted to KASP markers to facilitate marker assisted breeding.

P16. Using QR Barcoding To Improve the Efficiency of the Guelph Wheat Program's Winter Wheat Breeding Pipeline Z. ZHANG, M. PAVONE, KAITLYN LEW, M. KAVIANI, M. SERAJAZARI, AND H. BOOKER *(Z.Z., M.P., K.L., M.K., M.S., H.B.) Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada*

The University of Guelph Wheat Breeding Program uses QR barcode technology to accurately track the parentage and molecular marker data of wheat breeding lines throughout the breeding pipeline. Each parent plant is tagged with a QR code which tracks information on allelic discrimination of DNA molecular markers such as Fhb1, Yr15, Yr5, Lr34, PpdD1, and PpdA1. By scanning the QR code of the parents during the crossing process, a new lot number is created for each F1 cross, enabling accurate tracking of the cross back to its parental plants. This allows breeders to trace desirable traits, such as resistance to Fusarium Head Blight (FHB), from one generation to the next. The F_2 generation is planted in the field with 2400 seeds per unique cross combination, and the selected plants are tagged with unique QR codes. The F3 and F4 generations are screened using molecular markers to reduce population size and identify desirable genotypes. The F5 generation is planted in the field as a progeny row, and 1/3 of the rows are selected based on visible agronomic traits such as plant structure and disease resistance. In the Preliminary Yield Trial (F6) and Advanced Yield Trial (F7+), each entry is subsampled for assessment of flour quality. The breeder then selects lines for Ontario variety registration trials based on agronomic traits, yield, kernel/flour quality, FHB index, and DON rating. Through utilizing QR code technology, our breeding program accurately tracks each entry's pedigree, molecular marker data, and agronomic data from when the cross was first made all the way to commercialization, leading to a more efficient and effective breeding process.

P17. Genetic mapping of aggressiveness in *Fusarium graminearum*, the cause of Fusarium head blight in durum wheat Y. ZHANG, C. POZNIAK, G. S. BRAR, AND E. SARI. *Faculty of Land and Food Systems, The University of British Columbia, 2357 Main Mall, Vancouver, BC V6T 1Z4, Canada; (C.P.) Crop Development Centre, University of Saskatchewan, College of Agriculture and Bioresources, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada; and (E.S.) Department of Microbiology and Plant Pathology, University of California Riverside, Boyce Hall 1463, Riverside, CA 92521, USA*

Fusarium graminearum, the predominant causal agent of Fusarium head blight (FHB) in cereal crops, impacts the Canadian wheat industry through reduced yield and seed contamination with mycotoxins. According to the type of mycotoxins produced by *F. graminearum*, the strains can be classified into 3-acetyl-deoxynivalenol (3ADON) and 15-acetyl-deoxynivalenol (15ADON) chemotypes. A highly virulent population producing 3ADON is becoming more prevalent in North America, compared to the historically dominant population producing 15ADON. It indicates the increasing risk of FHB to more western part of the wheat growing region in Canada. Decoding the genetic determinants of aggressiveness and evolution among field populations by identifying effective QTL markers is necessary for studying the wheat-*Fusarium* interactions. This project aims to map QTL conferring aggressiveness (Fg-QTL) in *F. graminearum* using a bi-parental population developed from Nit-5 (derived from the 15ADON isolate PH-1) and SK-17-97 (a 3ADON isolate with a high level of aggressiveness). A high-density genetic map of the bi-parental population and their phenotypic data of aggressiveness toward durum wheat was linked to reveal aggressiveness loci and the magnitude of Fg-QTL's expression in the population. The pan-genome analysis of a Nested Association Mapping Population of *F. graminearum* (FgNAM), reflecting phenotypic variations among the field populations, will be combined with the transcriptome analysis of the bi-parental population to narrow down the Fg-QTL interval and the list of candidate genes. This study will provide a better understanding of the virulence mechanism in *F. graminearum* and the genetic basis of aggressiveness variations among field populations in North America.

P18. Genetic mapping of stem rust resistance derived from accession 'PC11' in a six-row, spring barley population using 50k SNP Infinium iSelect assay J. R. TUCKER, T. G. FETCH, C. W. HIEBERT, M. M. U. A. LITON, AND A. BADEA *(J.R.T., T.G.F., M.M.U.A.L., A.B.) Agriculture and Agri-Food Canada, Brandon Research and Development Centre, P.O. Box 1000A, R.R. 3, Brandon, MB R7A 5Y3, Canada; and (C.W.H.) Agriculture and Agri-Food Canada, Morden Research and Development Centre, 101 Rte 100 #100, Morden, MB R6M 1Y5, Canada*

Stem rust, caused by *Puccinia graminis* f. sp. *tritici* (*Pgt*) is a significant disease of barley and wheat crops worldwide, which can result in massive yield losses. While it can be controlled by fungicides, deployment of resistant cultivars is the most durable, economic, and environmentally-responsible means of disease management. A single major gene (*Rpg1*) located on the short arm of barley chromosome 7H has been deployed in the majority of western Canadian barley cultivars, which has effectively controlled epidemics for decades. However, new virulent *Pgt* races have been recently reported in North America that are able to overcome the *Rpg1*-based resistance. In this study, a

doubled-haploid, bi-parental (PC11 x Steptoe) population of 226 lines was genotyped with an Illumina 50k single-nucleotide polymorphism (SNP) iSelect chip, and was evaluated over three years in a stem nursery at Brandon, MB using virulent *Pgt* race 'QCCJB'. A linkage map of 1558 cM was constructed containing 10,827 SNPs and inclusive composite interval mapping was used to identify quantitative trait loci (QTL) for reaction type and percent coverage. As a result, significant QTLs were detected on chromosomes 2H, 5H and 6H. Functional annotations of nearby genes will be discussed. The flanked SNP markers could be applied in marker-assisted breeding to improve stem rust resistance in barley.

P19. Single-cell sequencing of *Plasmodiophora brassicae* demonstrates the genetic diversity present in a single clubbed root A. SEDAGHATKISH, H. DJAMBAZIAN, A. HARUTYUNYA, B. D. GOSSEN, I RAGOUSSIS, AND M. R. MCDONALD *University of Guelph, 50 Stone Road East, Guelph, ON NIG 2W1, Canada; (H.D., A.H., I.R.) Department of Human Genetics, McGill University, Montreal, QB, N1G 2W1, Canada; and (B.D.G.) Saskatoon Research and Development Centre*, *Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*

Plasmodiophora brassicae is an obligate Chromid plant pathogen that causes clubroot of brassica crops (*Brassica napus* L.). There are many pathotypes of *P. brassicae*, which are differentiated by their virulence on specific differential host cultivars and lines. Single-cell sequencing of resting spores from a single clubbed root was conducted using 10x Genomics and de novo genome assembly was performed using SPAdes genome assembler. Python api vireoSNP was used to both cluster the reads and produce plots for the cell assignment probability, the mean allelic ratio, and the ELBO plots. Assessment of the sequences from 500 single spores showed that there were at least seven distinct genotypes present, with one genotype much more prevalent than the other six. These genotypes were genetically very different from one another, differing in hundreds or thousands of SNPs. The presence of multiple genetically-distinct genotypes in a single club strongly supports the hypothesis that balancing selection occurs in field populations. Under balancing selection, entire genotypes are carried forward in the population at low frequency. This likely occurs because infection by many individual spores can occur in a single host plant and contributes to the development of the clubbed root. The results of the current study demonstrate that many genotypes are present within a single club, and that the pathogen population is genetically (and likely pathogenically) very diverse. This diversity, in turn, explains how the pathogen population can shift rapidly when single-gene host resistance is deployed, since a range of pathotypes is already present in the population.

P20. Paired-NLR immune receptors confer resistance to wheat stripe rust V. KLYMIUK, K. WIEBE, H. S. CHAWLA, J. ENS, AND C. J. POZNIAK *Crop Development Centre and Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada*

Nucleotide-binding domain leucine-rich repeat-containing (NLR) receptors play an important role in plant innate immunity. Most resistance genes cloned to date encode single NLR proteins. However, in some cases, a pair of NLRs is required to provide resistance – a sensor NLR (sNLR) to detect the presence of the pathogen and a helper NLR (hNLR) that transmits the signal to downstream cascades. We have identified and functionally validated a novel wheat NLR pair, which confers *Yr84*-mediated resistance to stripe (yellow) rust disease. This was achieved through a combination of bulk-segregant analysis sequencing (BSA-Seq), fine mapping, PacBio genome sequencing and EMS-mutagenesis. These NLRs are physically linked on chromosome arm 1BS but are structurally divergent and do not represent a gene duplication. An expression study showed that the putative sNLR is constitutively expressed, while the hNLR is upregulated in the presence of the pathogen. Interestingly, we did not detect any integrated domains within either of the NLRs in this pair, although such domains have been suggested to be essential in sNLRs for pathogen effector recognition. Currently, we are examining the molecular features and interactions of *Yr84* NLRs to decipher the molecular function of paired NLRs in plants, which remains poorly understood at molecular level. Results are expected to contribute to our understanding of the incomplete dominance function of *Yr84*-mediated resistance to wheat stripe rust.

P21. Understanding naturally occurring avrLm2 and avrLm7 *L. maculans* isolates and their mutations and genetic diversity in Canada L. ZHAO, S. KANNANGARA, A. ALUKUMBURA, N. W. GAMAGE, S. WALKOWIAK, AND W. G. D. FERNANDO *Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB R3T 2N2, Canada; Canadian Grain Commission, 196 Innovation Dr., Winnipeg, Manitoba, R3T 6C5*

Blackleg disease caused by the fungal pathogen *L. maculans* is the most important disease of canola (*Brassica napus*) in Canada. Qualitative resistance, which is mediated by single major genes (R-gene), is fundamental in fighting against the blackleg pathogen. However, R-gene breakdown was observed in grower fields (e.g. Rlm3 in Canada), but the reasons behind this breakdown have not been investigated thoroughly. Canola varieties carrying an R-gene of either *Rlm2* or *Rlm7* are new to Canada and was available to growers since 2022. However, these new genes could breakdown (like *Rlm3*) over time and use. If the breakdown process for the two genes can be studied from their initial introduction to Canada, it could provide valuable information in understanding R-gene breakdown. Therefore, we studied the initial mutation patterns of virulent genes (*avrLm2* and *avrLm7*) in *L. maculans* before the introduction of the two new R-genes. We found that most of our collected avrLm2 isolates showed a similar mutation pattern compared to a previous study (three mutation sites were found), indicting few mutations have happened without *Rlm2* selection pressure. However, one *avrLm2* isolate showed a severely mutated pattern and the RIP-like mutation (TpG to TpA or CpA to TpA) takes a large proportion (26 out of 39 mutations). Interestingly, in *avrLm7*, 34 out of 64 total mutations were found to be RIP-like mutations from five isolates. The relatively large proportion of RIP-like mutations might be an indication to an opportunity towards R-gene breakdown mechanisms, and these naturally occurring mutations can function as a starting point to understand *B. napusL. maculans* interactions.

P22. Chain cross, a better breeding method to achieve polygene resistance to northern corn leaf blight X. ZHU, A.Z. KEBEDE, J. WU, and T. WODEMARIAM *Agriculture and Agri-Food Canada, Ottawa Research and Development Centre, Ottawa ON, K1A 0C6*

The purpose of this study is to find a better method for resistance breeding to northern corn leaf blight (NCLB) by analysis back cross (BC), double cross (DC), and chain cross (CC) used since 2005. All methods involved high yield line(s) and dominant gene *Ht*(S) and/or polygene (PG) sources.

CC started from single cross, followed by designed DC, quad-, and Octo- crosses. This analysis included eleven BC families, four DC families, four CC families with 4 genotypes, and one CC family with 7 PG genotypes. Developing resistant populations needed 5, 3, 4 and 6 seasons, inbred selection needed 4, 6, 5 and 3 seasons for BC, DC, 4- and 7- genotypic CC, respectively. Inoculations and irrigation were used to create NCLB epidemic condition. Smaller disease rating (DR) (1 = no disease, and 7 = 100% leaf area diseased), sensitive reactions, silk days, and other plant, ear, kernel traits were used for selections. Total of 236, 148, and 238 lines from BC, DC, and CC crossed with different testers, in which 14.8%, 38.5%, and 68.5% for lines, and 11.0%, 10.7%, and 31.7% for lines × tester crosses with DR ≤ 2 (≤ 1% leaf area diseased), respectively. CC lines with DR ≤ 2 along could make resistant crosses similar as BC and DC line crossed with another resistant line. It proved that CC was a better method to develop PG resistance lines. CC method also successfully selected lines with multi-resistances to eyespot and common rust from the 7- genotypic population.

P23. Identification of Fusarium head blight resistance markers in a genome-wide association study of CIMMYT spring synthetic hexaploid derived wheat lines M. SERAJAZARI, D. TORKAMANEH, E. GORDON, E. LEE, K. P. PAULS, HELEN BOOKER, AND A. NAVABI† *(M.S., E.G., E.L., K.P.P., H.B., A.N.†) Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada N1G 2W1; and (D.T.) Département de Phytologie, Université Laval, Québec City, Québec, Canada G1V 0A6. Institut de Biologie Intégrative et des Systèmes (IBIS), Université Laval, Québec City, Québec, Canada G1V 0A6*

Fusarium head blight (FHB), one of the most destructive wheat diseases worldwide, can dramatically reduce grain yield and quality due to mycotoxin contamination. Wheat resistance to FHB is quantitatively inherited and many low-effect quantitative trait loci have been mapped in the wheat genome. Synthetic hexaploid wheat, derived from *Aegilops tauschii* and *Triticum turgidum*, represents a novel source of FHB resistance that can be transferred into common wheat. In this study, a panel of 194 spring Synthetic Hexaploid Derived Wheat (SHDW) lines from the International Maize and Wheat Improvement Center were evaluated for FHB response under field conditions over three years (2017-2019). Significant phenotypic variation was found for disease incidence, severity, index, number of Fusarium-damaged kernels, and deoxynivalenol content. Genotyping of the SHDW panel using a 90K single nucleotide polymorphism chip array revealed 31K polymorphic SNPs with a minor allele frequency (MAF > 5%), which were used for a genome-wide association study of FHB resistance. A total of 52 significant marker-trait associations for FHB resistance were identified. A survey of genes associated with the markers identified 395 candidate genes that may be involved in FHB resistance. Collectively, our results strongly support the view that the utilization of synthetic hexaploid wheat in wheat breeding would enhance diversity and introduce new sources of resistance against FHB into the common wheat gene pool. Further, validated SNP markers associated with FHB resistance may facilitate the screening of wheat populations for FHB resistance.

P24. Immunity to stripe rust in wheat: A case study of a hypersensitive-response (HR)- independent resistance to *Puccinia striiformis* f. sp. *tritici* in Avocet-Yr15 H. SEIFI, M. SERAJAZARI, M. KAVIANI, P. PAULS, H. BOOKER, AND A. NAVABI

Stripe (yellow) rust, caused by the biotrophic fungal pathogen *Puccinia striiformis* f. sp. *tritici* (Pst), is emerging as a serious threat to wheat (*Triticum aestivum* L.) production in many regions of North America. Genetic resistance to stripe rust is typically conditioned by the products of resistance genes that detect pathogen-associated molecular patterns and initiate a cascade of signalling events, culminating in the generation of reactive oxygen species (ROS) and a hypersensitive response (HR) that eventually suppress the pathogen. Complete resistance with no symptoms (immunity response) has also been observed, but less frequently, in certain Pst-wheat interactions. However, such HR-independent resistance responses to Pst have not been well studied. Here we report that the Pst-resistant near isogenic line Avocet-*Yr15* (carrying the *Yr15* resistance gene) exhibited an immunity response to an isolate of Pst collected in Elora, Ontario, while the Avocet-S line (lacking *Yr15*) was highly susceptible to the same isolate. Histochemical assays of defence-associated ROS generation and HR were negative during the early stages of the interaction between Pst and the resistant Avocet-*Yr15*. Microscopic analysis indicated that the pathogen was not able to penetrate the stomata of Avocet-*Yr15*. Moreover, RNA-sequencing of the immunity response of Avocet-*Yr15* to Pst highlighted the activation of a global antioxidative- stress response consisting of genes involved in the maintenance of cell viability, redox homoeostasis and photosynthesis. These results provide insights into the molecular mechanisms controlling the immunity response to stripe rust of wheat.

P25. Using QR Barcoding To Improve the Efficiency of the Guelph Wheat Program's Winter Wheat Breeding Pipeline Z. ZHANG, M. PAVONE, K. LEW, M. KAVIANI, M. SERAJAZARI, AND H.BOOKER *(Z.Z., M.P., K.L., M.K., M.S., H.B.) Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada*

The University of Guelph Wheat Breeding Program uses QR barcode technology to accurately track the parentage and molecular marker data of wheat breeding lines throughout the breeding pipeline. Each parent plant is tagged with a QR code which tracks information on allelic discrimination of DNA molecular markers such as Fhb1, Yr15, Yr5, Lr34, PpdD1, and PpdA1. By scanning the QR code of the parents during the crossing process, a new lot number is created for each F1 cross, enabling accurate tracking of the cross back to its parental plants. This allows breeders to trace desirable traits, such as resistance to Fusarium Head Blight (FHB), from one generation to the next. The F_2 generation is planted in the field with 2400 seeds per unique cross combination, and the selected plants are tagged with unique QR codes. The F3 and F4 generations are screened using molecular markers to reduce population size and identify desirable genotypes. The F5 generation is planted in the field as a progeny row, and 1/3 of the rows are selected based on visible agronomic traits such as plant structure and disease resistance. In the Preliminary Yield Trial (F6) and Advanced Yield Trial (F7+), each entry is subsampled for assessment of flour quality. The breeder then selects lines for Ontario variety registration trials based on agronomic traits, yield, kernel/flour quality, FHB index, and DON rating. Through

utilizing QR code technology, our breeding program accurately tracks each entry's pedigree, molecular marker data, and agronomic data from when the cross was first made all the way to commercialization, leading to a more efficient and effective breeding process.

Obligate biotrophic pathogens and soil-borne diseases

P26. Effect of environment on survival of resting spores of *Plasmodiophora brassicae* K. HOLY, B. D. GOSSEN, AND M. R. MCDONALD. *Department of Plant Agriculture, University of Guelph, 50 Stone Road E, Guelph, ON N1G 2W1, Canada; and (B.D.G.) Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*

Clubroot, caused by *Plasmodiophora brassicae* (Woronin), is an important disease of Brassicaceae crops worldwide. Resting spores of *P. brassicae* can remain viable in soil for many years. Studies under controlled conditions have shown that repeated freeze-thaw cycles can reduce resting spore viability by up to 85%, but this factor has not been examined under field conditions. Also, resting spores can spread through surface water runoff and flooding, but their longevity in liquid suspensions is unknown. In a field trial at the Ontario Crops Research Centre – Bradford during the winter of 2022–2023, clubs were buried at 10 cm depth, which would be typical for clubbed roots, or placed on the soil surface to mimic tilled soil conditions to assess the effect of natural freeze-thaw cycles. The control was maintained in a freezer at -20°C. Spore viability was assessed in April 2023 based on reaction to Evans Blue (a vital stain) and confirmed in a bioassay. Spore viability was reduced to 91% in frozen (control) and in buried clubs, and to 56% in clubs at the soil surface. To assess spore survival in water, suspensions of 1 x 10^7 spores/mL were subjected to three temperatures (21°, 4° or -20°C) for 1, 3, 7 or 14 days. After 14 days, viability was reduced to 66% at 4° and 21°C and to 52% at -20°C. These studies confirmed that freeze-thaw cycles reduce the viability of clubs on soil surface and demonstrated that freezing and holding spores in suspension also reduced spore viability.

P27. Improved isolation of *Plasmodiophora brassicae* single-spores by laser microdissection B. KIRK, S. OH, A. BOTERO-RAMÍREZ, S. F. HWANG, AND S. E. STRELKOV *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada*

The isolation of single-spores of the soilborne obligate parasite (*Plasmodiophora brassicae*) (clubroot of crucifers) is critical for generating genetically homogeneous pathogen collections for use in research and host resistance screening. This process, however, is time-consuming, given the small size (3-4 µm diam.) of the resting spores and inability to culture *P. brassicae* on axenic medium. Most methods rely on visual identification of a single-spore under the microscope, which is then inoculated onto a susceptible host; the resulting infection rates are low, so the process must be repeated many times to obtain few isolates. In this study, a PALM MicroBeam Laser Microdissection System (Zeiss) was evaluated to improve the efficiency and precision of single-spore isolation. A 10 µL aliquot of a resting spore suspension (1×10^4 mL^{-1}) obtained from frozen root galls was pipetted onto a Zeiss membrane slide and allowed to dry for 10 min. The membrane slide was then placed in the PALM MicroBeam, and individual resting spores were excised with a focused laser beam and catapulted into individual Zeiss AdhesiveCap PCR tubes. The tubes were centrifuged and the isolated spores were used to inoculate 7-day old *B. rapa var. pekinensis* cultivar *Granaat* seedlings by incubating in darkness for 24-72 h. Subsequently, inoculated seedlings were transplanted into potting mix and grown for six weeks to allow root gall development and the generation of daughter resting spores. While the protocol is still being optimized for efficiency, it promises to serve as a much-improved method for *P. brassicae* single-spore isolation.

P28. Virulence of *Puccinia coronata* var. *avenae* f.sp. *avenae* (crown rust) on oats from Manitoba, Ontario and Quebec in 2022 J. G. MENZIES, S. DECEUNINCK, AND Z. POPOVIC *Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB, R6M 1Y5, Canada*

Puccinia coronata var. *avenae* f. sp. *avenae* (Urban & Marková) (PCA), the causal agent of crown rust, is considered the most widespread and destructive pathogen of oats worldwide. The disease poses a significant economic threat to oats in Saskatchewan, Manitoba, Ontario and Quebec, Canada. Control of this disease in Canada is largely through the development of resistant oat varieties, based on knowledge of the virulence spectrum of the Canadian PCA populations. Collections of PCA isolates were made from wild oats, commercial oat fields and research plots in Canada in 2022, followed by the development of single pustule isolates (spi) for virulence assessment on a host differential set consisting of 24 lines, each with a single gene for crown rust resistance. Two hundred nine spi from Manitoba, and 25 spi from Eastern Canada (Ontario and Quebec) were individually inoculated onto the differential host set to determine virulence to the different resistance genes. Manitoba spi were virulent to all 24 resistance genes, with less than 5% of the spi being virulent to resistance genes *Pc96*, *Pc97*, and *Pc98*. Spi from eastern Canada did not exhibit virulence to resistance genes *Pc50*, *Pc96*, *Pc98*, and *Pc101*. Virulence to resistance genes *Pc38*, *Pc39*, *Pc48*, *Pc51*, *Pc52*, *Pc56*, and *Pc68* was observed at >85% in spi from Manitoba and Eastern Canada. Spi from Manitoba had a greater frequency of virulence to *Pc45* and *Pc91*, but lower frequency to *Pc54* compared to spi from Eastern Canada.

P29. Detection of powdery scab of potatoes and evaluation of fungicides for disease suppression M. S. SHAFIQUE, M. KONSCHUH, J. FOSTER, M. HARDING, AND D. P. YEVTUSHENKO *Department of Biological Sciences, University of Lethbridge, Lethbridge, AB T1K 3M4, Alberta, Canada; (J.F.)*

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Powdery scab is an emerging potato disease caused by the fungal-like pathogen *Spongospora subterranea* f. sp. *subterranea*. The visible symptoms include root galls and tuber blemishing on potatoes. Study of pathogen population levels in soils and its impact on potato production is necessary to manage this disease. Currently, no effective treatments are available to control *S. subterranea* in Alberta. Our research focused on the detection of the pathogen(s) involved in powdery scab of potatoes and evaluating a potential chemical treatment to control this disease in the province. Different fungicides were applied in-furrow at planting in the seed potato field with a known history of powdery scab, using a small-plot replicated design. Soil samples were collected from experimental plots before treatments. Disease assessment was done by taking total and marketable yield. Lesions from powdery scab suspected tubers were subjected to further morphological and molecular analyses. The results of our study will improve the diagnostics of powdery scab and will provide a possible solution to reduce the impact of this disease in potato fields of Alberta.

P30. Resistance to clubroot in brassica vegetables in relation to pathotype in the Holland Marsh, Ontario S. C. DRURY, B. D. GOSSEN, AND M. R. MCDONALD *Department of Plant Agriculture, University of Guelph, 50 Stone Road E, Guelph, ON N1G 2W1, Canada; and (B.D.G.) Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*

Clubroot, caused by the Chromist pathogen *Plasmodiophora brassicae* (Woronin), can cause substantial yield loss in susceptible cultivars of Brassica vegetables. Host resistance can protect yield, but host reaction varies in response to the dominant pathotype of *P. brassicae* present at a site. The Williams differential system uses four differential hosts, two cabbages and two rutabagas, to characterize 16 pathotypes. Recently, a new differential system was developed by Smilde et al. (2012) specifically for *Brassica oleraceae* L. that identified four pathotypes: Pb:0 to Pb:3, based on the differential reaction of three cultivars of *B. oleraceae*. Field trials were conducted in 2018, 2019 and 2020 on a high organic matter soil in Ontario that was naturally infested with Williams pathotype 2 to assess clubroot reaction in cabbage, broccoli, cauliflower, and napa cabbage in comparison to a highly susceptible Shanghai pak choi culivar. Also, controlled environment studies were conducted by inoculating many of the same cultivars as in the field trials with resting spores (5 mL of 1 x 10^7 spores) of *P. brassicae* pathotypes 2 or 6. Cabbage cultivar 'Bronco' was susceptible and cabbage cvs. 'Bejo 2962' and 'Tekila' were resistant in all studies. Cabbage 'Lodero' and broccoli 'Emerald Jewel' were resistant to pathotype 6 but susceptible to pathotype 2, and were susceptible in the field trials. Evaluation of the reaction of 'Lodero' (susceptible) and cabbage 'Kilaton' (resistant) indicated that the pathotype in the field plots (pathotype 2 in Williams system) is Pb:3 in the *B. oleraceae* system.

P31. The effect of nitrogen on root architecture traits and clubroot development in *Brassica* genotypes D. ROTARIU, R. FREDUA-AGYEMAN, Y. AIGU, S. E. STRELKOV, AND S. F. HWANG *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada*

Clubroot disease, caused by the obligate soilborne parasite *Plasmodiophora brassicae*, is a serious threat to Canadian canola (*Brassica napus*) production. Additionally, canola requires a high nitrogen input, which can lead to the over-application of chemical fertilizers. Studies have shown that high nitrogen availability can increase the severity of infections by obligate parasites, suggesting a need for canola with lower nitrogen requirements. A possible approach to mitigating the impact of clubroot and the high nitrogen requirements of canola comes from breeding for beneficial root architecture traits. The aim of this project is to evaluate the effects of different nitrogen concentrations and *Brassica* root system architecture on clubroot development. In the first phase of this study, 10 fertilizer (Hoagland's No. 2 Basal Salt Mixture) concentrations (relative to the recommended full-strength dose of 1.6 g L^{-1}) were assessed for their impact on the root system architecture of four *Brassica* genotypes in a hydroponic system. The roots were scanned after three weeks of growth, and 36 root architectural traits were measured including primary root length, branching, diameter, angle, and total surface area. Based on an analysis of these results and reports from the literature, a subset of key root architecture traits will be selected and used to test the effects of nitrogen and root architecture on the response of 12 *Brassica* genotypes to inoculation with two important pathotypes of *P. brassicae*. This study may help to identify clubroot-resistant *Brassica* germplasm adapted to low-nitrogen conditions, contributing to more sustainable management of clubroot of canola.

P32. Canola cultivar mixtures for the management of *Plasmodiophora brassicae* A. BRINKMAN, A. BOTERO-RAMÍREZ, S. F. HWANG, AND S. E. STRELKOV *Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB T6G2P5, Canada*

Clubroot (*Plasmodiophora brassicae*) is a major soilborne disease of canola (*Brassica napus*) in western Canada. While numerous clubroot-resistant canola cultivars are available to growers, their widespread cultivation has resulted in the emergence and spread of novel, 'resistance-breaking' pathotypes of *P. brassicae*. This highlights the need for an integrated approach to clubroot management that relies on multiple control strategies. Accordingly, the aim of this study is to evaluate the use of cultivar mixtures as a potential clubroot management tool. The canola cultivars 'Westar' (universally susceptible) and 'P501L' (clubroot-resistant) were grown as mixtures in various combinations (0%, 10%, 25%, 50%, 75%, and 100% susceptible) in a 1:10 soil: potting medium mix inoculated with pathotypes 3H and 5X of *P. brassicae* at three different concentrations (1×10^3, 1×10^4, and 1×10^5 resting spores gram $soil^{-1}$). While pathotype 3H can be controlled by all clubroot-resistant canola cultivars on the market, pathotype 5X can overcome the resistance in many varieties including 'P501L'. Plants were rated for clubroot symptom

severity seven weeks after inoculation, and pathogen inoculum concentration in the soil mix was measured by quantitative PCR analysis. The pathotype designation(s) of isolates recovered from the potting mix will also be assessed on the Canadian Clubroot Differential set. While the experiments are still ongoing, we hypothesize that inclusion of cultivar mixtures may slow pathotype shifts and reduce clubroot development on resistant hosts.

P33. Virulence of *Puccinia striiformis* (stripe rust) in Canada from 2020 to 2022 B. WEI, R. GOURLIE, AND R. ABOUKHADDOUR *Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB, Canada T1J 4B1; and (B.W.) Department of Agriculture, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada T6G 2P5*

Stripe rust of wheat, caused by *Puccinia striiformis* f. sp. *tritici* (*Pst*), is one of the most important cereal diseases worldwide. Since 2000, the disease has become a threat due to the emergence of new virulent races of pathogen. In addition to wheat, stripe rust can infect barley and other grasses. In this study, 45 different stripe rust isolates were collected from wheat, barley, and foxtail barley in Canada (Alberta, Quebec, and PEI) between 2020 to 2022, and were tested for their virulence. *Pst* isolates were evaluated for their virulence on wheat and barley differential set using a spore/talc mixture inoculation method, and the infection type was scored by rating the symptoms on a scale 0 to 9 on the second leaves. The experiment was repeated twice independently and the results revealed that most tested *Yr* genes (*Yr6*, *Yr7*, *Yr8*, *Yr9*, *Yr10*, *Yr17*, *Yr18*, *Yr24*, *Yr27*, *Yr32*, *Yr43*, *Yr44*, *YrTr1*, and *YrExp2*) were defeated by the majority of tested isolates, while *Yr1*, *Yr5*, *Yr15*, *YrSP*, and *Yr76* remained undefeated. The isolates collected from barley and foxtail barley were virulent on barley differential 'Heils Franken' and wheat differentials *Yr6*, *Yr7*, *Yr8*, and *Yr17*, but were avirulent on all other differential lines. There is a need to expand the wheat differential set as most of the *Yr* genes have been defeated by most of *Pst* isolates. Understanding the pathogen population on barley and other hosts will provide more useful insight into the overall virulence evolution of stripe rust populations in Canada.

P34. Two new records of grass rust species in British Columbia: morphological and molecular characterization M. ABBASI, S. HAMBLETON, M. LIU, AND G. S. BRAR *Faculty of Land and Food Systems, The University of British Columbia, 2357 Main Mall, Vancouver, BC V6T 1Z4, Canada; and (S.H., M.L.) Biodiversity and BioResources, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada*

This study reports the identification of two new incidences of grass rust species; *Puccinia gibberosa* Lagerh. and *Puccinia bromina* Erikss., in western Canada (British Columbia). Morphological and molecular analyses were used to identify these rusts. *Puccinia gibberosa* found on ornamental Blue oat grass (*Helictotrichon sempervirens* (Vill.) Pilg.) in Vancouver, BC produced only uredinia, usually between the veins singly or in rows on the upper side of the leaves of infected plants. This is the first report of rust caused by *P. gibberosa* on Blue oat grass in Canada. *Puccinia bromina* found on Soft brome (*Bromus hordeaceus* L.) in Vancouver, BC produces uredinia mostly on the adaxial leaf surface and telia mostly on abaxial or on sheaths of infected plants. Distinctive morphological characteristics were observed for each rust collection, including spore size and shape, number of germ pores, and type of infection structures. Additionally, rDNA sequencing of the internal transcribed spacer two (ITS2) and partial large subunit ribosomal (28S) DNA provided molecular evidence to support the morphological identifications. For *P. bromina,* the ITS2 sequence matches published data for some specimens collected in Europe and Western Asia but differs from data for others and for collections from North America. The discovery of the new geographic locations of these two rust species expands our knowledge of rust diversity in Western Canada and highlights the importance of using both morphological and molecular methods for accurate identification of plant pathogens. This study also underscores the importance of ongoing surveillance and monitoring for emerging plant diseases.

P35. Development of a hydroponic system to phenotype *Plasmodiophora brassicae* virulence and clubroot resistance R. SALIH, A. BROCHU, C. LABBÉ, S. E. STRELKOV, C. FRANKE, R. BÉLANGER, AND E.PÉREZ-LÓPEZ *Department of Plant Sciences, Faculté des sciences de l'agriculture et de l'alimentation (FSAA); Centre de Recherche et D'innovation sur les Végétaux (CRIV); Institute de Biologie Intégrative et des Systèmes (IBIS), Université Laval, Quebec City, QC G1V 0A6, Canada; (S.E.S.) Department of Agricultural, Food and Nutritional Science, University of Alberta, 410 Agriculture/Forestry Centre, Edmonton, AB T6G 2P5, Canada; and (C.F.) R&D Pathology Research, Nutrien Ag Solutions, Saskatoon, SK S7N 4L8, Canada*

Clubroot, caused by the obligate parasite *Plasmodiophora brassicae*, is one of the most devastating diseases affecting the canola (*Brassica napus*) industry worldwide. Currently, the use of clubroot-resistant cultivars is the most effective strategy to reduce the spread and the economic losses of the disease. However, virulent *P. brassicae* isolates have been able to overcome the resistance and the options to manage the disease are becoming limited. Another challenge for the industry has been the classification of *P. brassicae* isolates based on their ability to infect certain plant genotypes. Although several differential classification sets have been developed, their implementation can be laborious and expensive, with potentially variable results due to user-associated bias. In this study, we have developed a hydroponic bioassay using well-characterized *P. brassicae* single-spore isolates representative of the virulence widespread in Canada and field isolates from Alberta, Québec and Saskatchewan. This has been combined with the use of canola inbred homozygous lines demonstrating clubroot resistance profiles available to growers in Canada. To evaluate *B. napus-P. brassicae* interactions, the test relied on host dry weight, root area, and macronutrient acquisition. According to the results, this bioassay offers a reliable, less expensive, and reproducible option to evaluate *P. brassicae* virulence and to identify what canola resistance profile would be effective against the tested isolates. This bioassay will contribute to breeding new clubroot-resistant canola cultivars and the identification of *P. brassicae* avirulence genes that could trigger host resistance and which have been elusive to this day.

P36. AlphaFold-Based Refinement of the Clubroot Pathogen Effector Repertory M. A. JAVED, L.B. GÓMEZ-LUCIANO, AND E. PÉREZ-LÓPEZ *Département de phytologie, Centre de recherche et d'innovation sur les végétaux (CRIV), Faculté des sciences de l'agriculture et de l'alimentation, Université Laval, 2480 Bd Hochelaga, Québec City. QC G1V 0A6, Canada; and Institute de Biologie Intégrative et des Systèmes, Université Laval, 1030 Av. de la Médecine Québec City, QC G1V 0A6, Canada*

Plasmodiophora brassicae is a devastating pathogen that causes clubroot disease in cruciferous crops and results in annual economic losses of over one billion dollars worldwide. To elucidate the virulence mechanism of the clubroot pathogen in the susceptible host, it is crucial to understand the function and evolution of *P. brassicae* effectors. The clubroot pathogen is well-known for not sharing effector sequence homology with known proteins or functional motifs even with evolutionary-related pathogens. To overcome this challenge, we used computational structure prediction tools such as AlphaFold2 to predict the fold of *P. brassicae* predicted effectors and unveil ancestral fold similarities based on predicted structures. We identified effector candidates structurally similar to evolutionary-related phytopathogens members of Rhizaria supergroup, especially *Spongospora subterranea*, oomycetes, and plant-like protist algae, irrespective of low sequence similarity. Additionally, some effector candidates had similar folds to proteins of three *Brassica* spp. hosts, offering future targets to study virulence mechanisms and co-evolution during plant-pathogen interaction. Our study refined the neglected effector repertory into nine general families, including one family completely uncharacterized based on sequence and structural features called *P. brassicae* uncharacterized effectors (PbUEs). The refined effector repertory of the clubroot pathogen is rich in proteins with carbohydrate-binding motifs, kinases, hydrolases, and ankyrin repeats, which require functional validation to determine their role in pathogen infection. Our analysis allowed us to predict the presence of sequence-unrelated but structurally similar effectors, enabling us to identify core and novel folds to enhance clubroot effectors prediction, resolve effector virulence mechanisms with unknown functions, and understand the evolution of this unique pathogen.

P37. Effect of *Plasmodiophora brassicae* inoculation on the root and rhizosphere microbiomes of clubroot-susceptible and resistant canola J. CORDERO-ELVIA, L. GALINDO-GONZALEZ, R. FREDUA-AGYEMAN, S. F. HWANG, AND S. E. STRELKOV *(J.C.-E., R.F.-A., S.F.H., S.E.S.) Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada; and (L.G.-G) Ottawa Plant Laboratory, Science Branch, Canadian Food Inspection Agency, 3851 Fallowfield Road, Ottawa, ON K2H 8P9, Canada*

Clubroot is a soilborne disease of canola (*Brassica napus*) and other crucifers caused by the obligate parasite *Plasmodiophora brassicae*. In western Canada, clubroot is usually managed by planting resistant cultivars, but the emergence of resistance-breaking pathotypes of *P. brassicae* represents a major threat to sustainable canola production. The rhizosphere and root microbiomes contain beneficial microorganisms that can improve plant health, yet have not been examined in the context of clubroot of canola. In this study, we evaluated the effect of two *P. brassicae* inoculants with different virulence on the root and rhizosphere microbiomes of clubroot-resistant and clubroot-susceptible canola. The experiment was conducted under greenhouse conditions with treatments arranged in a completely randomized design. Rhizosphere and root samples were collected at 7, 21 and 35 days after inoculation (dai) and analyzed for fungal and bacterial abundance and diversity by high-throughput sequencing. Two *P. brassicae* field isolates (termed A and B) were inoculated separately. Although both were classified as pathotype 3A, isolate A caused a higher disease severity index (DSI = 50%) in the resistant canola genotype compared with isolate B (DSI = 28%). Metabarcoding analysis indicated a shift in the bacterial and fungal communities in response to inoculation with either field isolate. Root endophytic bacterial and fungal communities responded to changes in inoculation, inoculant type, and time and canola genotype. In contrast, fungal communities associated with the rhizosphere exhibited significant differences between sampling times, while bacterial communities associated with the rhizosphere exhibited low variability.

P38. Repeated freeze thaw cycles reduce viability of resting spores of *Plasmodiophora brassicae* J. ROBSON, B. D. GOSSEN, AND M. R. MCDONALD *Department of Plant Agriculture, University of Guelph, 50 Stone Road E, Guelph, ON N1G 2W1, Canada; and (B.D.G.) Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*

Plasmodiophora brassicae (Woronin), is an obligate Chromist pathogen that causes clubroot of Brassica crops. It produces long-lived resting spores that are released into the soil as infected roots decay. Repeated thawing and refreezing of clubs was observed to reduce the effectiveness of inoculum in laboratory studies. Clubs from canola harvested in 2022 were subjected to thaw / freeze cycles (24 h at 22° C, 48 h at -20° C) in a study with continuously frozen clubs (0 cycles) and 2, 4, 6, 8 and 10 thaw/freeze cycles. Resting spores were extracted from the clubs and viability was estimated using Evans blue staining and a bioassay. Clubroot-susceptible Shanghai pak choy was inoculated with 5 mL of 1 x 10^5 or 1 x 10^6 resting spores per mL in a replicated study. Clubroot severity was assessed 6 weeks after inoculation. Resting spores from frozen clubs and clubs with two thaw/freeze cycles were over 90% viable based on Evan's blue staining. Viability dropped to 79, 42, 29 and 27% after 4, 6, 8 and 10 cycles, respectively. The bioassay with 10^6 resting spores had a disease severity index (DSI) of 80, 25, 17, 11 and 0 for 0, 2, 4, 6 and 8 cycles, respectively. Inoculation with 10^5 spores showed a similar trend. Researchers often freeze clubbed roots to store inoculum for months or years, but repeated thawing and freezing reduced the viability of resting spores and subsequent infection. The effect on clubbed roots in a field is likely similar.

P39. Uncovering the history of recombination and population structure in western Canadian stripe rust populations through mating type alleles S. HOLDEN, G. BAKKEREN, J. HUBENSKY, R. BAMRAH, M. ABBASI, D. QUTOB, M. DE GRAAF, S. H. KIM, H. R. KUTCHER, B. D. MCCALLUM, H. S. RANDHAWA, M. IQBAL, K. ULOTH, R. BURLAKOTI, AND G. S. BRAR *(S.H., J.H., R.B., M.A., G.S.B.) Faculty of Land and Food Systems, The University of*

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Wheat stripe rust (causal agent *Puccinia striiformis* f. sp. *tritici.* Eriksson) is a globally important pathogen of wheat. As a dikaryotic obligate biotroph: genetic and genomic work with the species is difficult. There has been speculation that *Pst* isolates recombine sexually or somatically to produce novel lineages, such as the epidemic-causing 'Warrior' lineage in 2011, but there has been no comprehensive effort to assess mating type frequency or recombination in known *Pst* lineages. In Canada previous work in Brar et al. (2018) identifies at least four present linages: *PstS0*, *PstS1* and *PstS1-related*, and PstPr, the last two of which exhibit signs of recent sexual recombination such as high telia production.

To investigate the history of these lineages we analysed NGS data from 57 Canadian field isolates and 319 publicly available global datasets and reconstructed the homeodomain-binding mating type alleles (*Pst-b-HD*) in each, as well as a conventional phylogenetic comparison using exon-derived SNPs. We identify 9 different mating type alleles across the global population, and show that the modern Canadian population is predominantly *PstS1-related* lineage, which is the product of a hybridisation event between the older *PstS1* lineage and an unknown isolate with a single shared mating type allele (ie. haplotype) between them. We show that the *PstPr* isolate is likely an unsuccessful foreign incursion from a recently recombinant lineage, and highlight the benefits of modern genomics approaches for identifying pathogen lineages from field samples, as well as underscore the necessity for monitoring the field population of this rapidly evolving pathogen.

P40. Exploring the molecular diversity and phylogenetic relationships of selected *Phragmidium* species in Iran M. EBINGHAUS, M. ABBASI, M.C. AIME, AND G. S. BRAR *Faculty of Land and Food Systems, The University of British Columbia, 2357 Main Mall, Vancouver, BC V6T 1Z4, Canada; (M.E.) Centro de Investigación y Extensión Forestal Andino Patagónico, U9200 Esquel, Argentina; and (M.C.A.) Department of Botany and Plant Pathology, Purdue University, West Lafayette, IN, USA*

In Iran, 17 species of the fungal genus *Phragmidium* are known causing rust on Roseaceae. Here, we analysed seven of them for the first time using ITS, LSU and partially CO3 sequence data. Among those species, *Phr. iranicum*, *Phr. bulbosum*, and *Phr. aff. violaceum* parasitize on *Rubus*, while *Phr. rosae-lacerantis*, *Phr. tranzschelianum*, *Phr. tuberculatum* infect *Rosa* and *Phr. asiae-mediae* is found on *Geum*. Our analyses confirm that *Phragmidium* on *Rubus* likely evolved only once, unlike the Rose rusts. We identified *Phragmidium iranicum* as a distinct species, while *Phr. bulbosum* and *Phr. rubi-idaei* are forming a complex with *Phr. acuminatum*, despite showing distinctly different teliospore morphologies. Our specimen resembling *Phr. violaceum* may represent a new taxon within this complex. *Phragmidium asiae-mediae* on *Geum kokanikum* is an unusual species with respect to its host relationship as neither genetic distance nor morphological differences to the *Rosa* rust *Phr. xinjiangensis* ined., was found. It may be the first species within the genus *Phragmidium* to infect two different host genera if it is conspecific with this rust fungus. The Rose rusts *Phragmidium rosae-lacerantis* and *Phr. tranzschelianum* appeared phylogenetically indistinct from *Phr. tuberculatum*, but only the conserved CO3 gene marker could be used for the former two species and based on recognizable morphological differences, we assume that they are distinct species. Our study of Iranian species of *Phragmidium* contributes to ongoing research aiming to understand the diversity and evolution of this divergent group of rust fungi but also highlights the taxonomic challenges we currently still face.

Disease Management of Horticultural Crops

P41. Efficacy of greenhouse disinfectant products against Tomato brown rugose fruit virus G. MARCHAND, A. THIBODEAU, AND J. GRIFFITHS *(G.M., A.T.) Harrow Research and Development Centre, Agriculture and Agri-Food Canada (AAFC), 2585 County Road 20, Harrow, ON N0R 1G0, Canada; and (J.G.) Vineland Research Station, AAFC, 4902 Victoria Avenue North, Vineland Station, ON L0R 2E0*

Since its discovery in Jordan in 2014, the *Tomato brown rugose first virus* (ToBRFV) has spread to most areas of the world producing greenhouse tomato. Its impact on worldwide production has been significant, reducing crop yield and production cycles. Like other viruses belonging to the genus *Tobamovirus*, it is mechanically spread and persistent on surfaces in the greenhouse environment. Following crop removal, proper greenhouse disinfection is critical to avoid the infection of future crops. A limited number of disinfectant products are registered for use in the greenhouse crop production areas in Canada. Data on their efficacy against Tobamoviruses is not always available, and formulations and label rates and use patterns may vary from those allowed in other jurisdictions or tested in different studies. Over the course of three trials, the efficacy of three products (Virkon Greenhouse, Virocid, and household bleach) was evaluated. Inoculum of ToBRFV was exposed to disinfectant solutions (prepared according to their labels) for varying periods of time (0, 1, 10, 30, 60, 120 minutes) before inoculating two leaves of '81v9' tobacco plants. Negative controls included a mock inoculation with phosphate buffered saline. Phytotoxicity and the presence of hypersensitive lesions were assessed 14 days afterwards. Results of these bioassays validate that extended contact time is required to inactivate ToBRFV below the

threshold required for infectivity on tobacco, and this contact time varied between products and trials. Bioassays provide a useful indicator of the presence of infectious viral particles, in contrast with molecular (PCR) or serological (ELISA) methods.

P42. RNA interference against fungal pathogens protects horticultural and crop plants S. J. KOEPPE AND M. L. KALISCHUK *Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON N1G 2W1, Canada*

RNA interference (RNAi) is a cross-kingdom mechanism that is triggered by double-stranded RNA (dsRNA) to elicit post-transcriptional gene silencing (PTGS) which allows for crop protection. The RNA-induced silencing complex (RISC) is a versatile, sequence-specific innate immunity mechanism of the RNAi pathway that delivers disease protection in plants and horticultural crops. Exogenous application of dsRNA complementary to a pathogen/pest can provide systemic resistance for the host crop in the form of spray-induced gene silencing (SIGS). Plant fungal pathogens cause several major devastating diseases worldwide, yet the potential for SIGS as a control method to improve crop quality and yield remains poorly understood. The β-tubulin gene plays an integral role in the formation of tubulin fibres during chromosome separation in cell division. As it is a target of site-specific systemic fungicides, the β-tubulin sequence was used to explore RNAi in controlling *Fusarium* species and other pathogens in horticultural berries, grapes, and other crop plants. Platforms for *in vitro* and *in vivo* assays were developed to demonstrate that RNAi can be used as an effective tool to control these fungal pathogens. Depending on assay conditions, the onset of plant disease symptoms or signs was delayed or totally prevented. The *in vitro* assays delayed or completely inhibited pathogen growth and spread. *In vivo* experiments showed delayed disease symptom incidence and severity following pathogen inoculation. SIGS appears to be a specific and environmentally friendly option for crop protection of fungal pathogens and further refinement of its application methods will improve efficiency of field applications.

P43. Comparison of physiological characteristics of single nucleotide sequence genotypes of Erwinia amylovora isolates from Korean apple and pear trees S. H. KIM, Y. I. KIM, S- J LEE AND M. NAM *Department of Microbiology, Dankook University, Cheonan, Chungnam 31116, Republic of Korea; (S-J.L.) Animal and Plant Quarantine Agency, Gimcheon 39660, Republic of Korea; and (M.N.) genomicbase Incorporated, Namyangju 12248, Republic of Korea*

Erwinia amylovora is a serious bacterial pathogen that causes fire blight on a variety of Rosaceae plants. Since fire blight broke out in Korea in 2015, it has spread to many regions. Whole-genome sequencing and genome-wide SNPs were performed on 82 *E. amylovora* isolates from multiple regions. The presence of various genome-wide SNPs was found in *E. amylovora* isolates and 10 representative isolates of the SNP type were selected for further analysis. This study was conducted to compare the physiological properties of representative isolates of these SNP types. Cellulose, cellobiose, pectin, protein, and xylan degradation abilities were not different among the 10 SNP isolates. However, some isolates showed different growth rates at different temperatures and pH. Among the 10 isolates of the SNP type, few isolates differed in utilization of the 20 different substrates in the API 20N kit. All 10 isolates of the SNP type were streptomycin sensitive. However, there was little difference in the degree of susceptibility to antibiotics among the 10 isolates. The formation ability of biofilm on microplate was also differed among the 10 isolates. We anticipate that genome-wide SNP analysis and information on physiological traits can be used as new epidemiological methods to study how fire blight spreads in a given geographic area.

P44. *In vitro* screening of different salts for their capacity to induce plant defense mechanisms V. SOLTANIBAND, A. BARRADA, M. DELISLE-HOUDE, M. DORAIS, R.J. TWEDDELL, AND D. MICHAUD *Département de phytologie, Université Laval, Québec, 2425, rue de l'Agriculture, QC G1V 0A6, Canada.*

Various salts including sodium, potassium, and aluminum-based salts, were shown to control plant diseases caused by fungi or bacteria. The prophylactic effect of salts was generally attributed to their antimicrobial properties. In this study, we aimed to evaluate the effects of salts such as sodium benzoate, sodium bicarbonate, sodium carbonate, sodium metabisulfite, potassium sorbate, and aluminum chloride on plant defense activation in the model species *Arabidopsis thaliana*. We used a transgenic reporter line expressing *β*-glucuronidase (GUS) under the control of a pathogen-inducible promoter, the promoter of pathogenesis-related protein PR1, as an experimental system. Potassium bicarbonate and benzothiadiazole (BTH; Actigard™) were used as positive controls for the study. Our results revealed that sodium benzoate (at both 0.1 M and 0.01 M), sodium bicarbonate (at 0.01 M), and sodium metabisulfite (at 0.001 M) significantly induced GUS expression in Arabidopsis seedlings compared to positive and negative controls. These findings suggest that some salts show the potential to stimulate plant defense mechanisms. Further research will be welcome to determine the efficacy of these salts in controlling pathogens *in vivo* through the activation of defense mechanisms.

P45. Effect of essential oils from different Nordic plant species on mycelial growth of *Alternaria solani*, *Sclerotinia sclerotiorum*, and *Phytophthora capsici* A. ROY-LEMIEUX, M. DELISLE-HOUDE AND R. J. TWEDDELL *Département de phytologie, Université Laval, 2425 rue de l'Agriculture, Québec, QC G1V 0A6, Canada*

Several studies reported the antifungal activity of essential oils (EOs) obtained from various plant species such as oregano (*Origanum vulgare* L.), common thyme (*Thymus vulgaris* L.), rosemary (*Rosmarinus officinalis* L.), and clove [*Syzygium aromaticum* (L.) Merr. & Perry]. In this study, the volatile part (vapors) of EOs from five Nordic plant species including Labrador tea (*Ledum groenlandicum* Retzius), sweet gale (*Myrica gale* L.), black spruce [*Picea mariana* (Mill.) Britton, Sterns & Poggenburgh], jack pine (*Pinus banksiana* Lamb.), and balsam poplar (*Populus balsamifera* L.) were investigated for their effect on the growth of *Alternaria solani* Sorauer, *Sclerotinia sclerotiorum* (Lib.) de Bary, and *Phytophthora capsici* Leonian. Fungi (*A. solani*, *S. sclerotiorum*) or oomycete (*P. capsici*) were grown on agar in petri dish placed in an airtight glass chamber with a sterile filter paper soaked with one of the EOs tested for 96 hours and 288 hours, respectively. The radial growth of the fungi/oomycete was then measured. Based on radial growth, the EOs can be ranked (from the strongest inhibiting effect to the weakest inhibiting effect) as follows: Labrador tea, black spruce, jack pine, sweet gale, balsam poplar. Labrador tea EO showed strong inhibition of mycelial growth suggesting that it could eventually find application as antifungal/anti-oomycete agent.

P46. Suppressive effects of black soldier fly frass on Fusarium wilt disease in tomato plants: insights into soil microbial communities G. ARABZADEH, M. DELISLE-HOUDE, M. DORAIS, M.-H. DESCHAMPS, N. DEROME, G. W. VANDENBERG, AND R. J. TWEDDELL *(G.A., M.-H.D., G.W.V.) Département des sciences animales, 2425 rue de l'Agriculture, Université Laval, Québec, QC G1V 0A6, Canada; (M.D.H., M.D., R.J.T.) Département de phytologie, 2425 rue de l'Agriculture, Université Laval, Québec, QC G1V 0A6, Canada; and (N.D.) Département de biologie, 1045 avenue de la Médecine, Université Laval, Québec, QC G1V 0A6, Canada*

Tomato (*Solanum lycopersicum* L.), one of the most important horticultural crops in Canada, is susceptible to several diseases including Fusarium wilt caused by *Fusarium oxysporum* f. sp. *lycopersici*. Recent *in vitro* bioassays revealed the presence of antagonistic microorganisms against *F. oxysporum* in black soldier fly (BSF) larval frass. In this study, tomato plants were grown in soil amended with pasteurized (70°C; 1 h) or not BSF larval frass derived from two diets [Gainesville (GV) and fruit/vegetable/bakery/brewery (FVBB)] and inoculated with *F. oxysporum* f. sp. *lycopersici*. Fusarium wilt severity was measured each week for 49 days of growth in greenhouse, and the area under the disease progress curve (AUDPC) was calculated. The results showed that GV frass strongly reduced disease severity while FVBB frass slightly reduced disease severity. Pasteurization affected the repressive effect of both GV and FVBB frass. GV frass-treated plants had higher shoot weight and stem length. Soil pH, P and K contents demonstrated a positive correlation with plant growth parameters and negative correlation with disease severity. In the bacterial communities, the abundance of order Actinomycetales and Gemmatales showed a negative correlation with AUDPC. In the fungal communities, family Nectriaceae showed a positive correlation with AUDPC. The study suggests that BSF larval frass, especially GV frass, has a potential to control Fusarium wilt disease in tomato plants. Additionally, the study provides valuable insights into the relationship between soil microbial communities, plant growth, and disease severity.

P47. Spread and impact of *Hop Latent Viroid* on growth and quality of cannabis (*Cannabis sativa* L.) plants Z. K. PUNJA, L. NI, C. SCOTT, J. HOLMES, AND L. BUIRS *Department of Biological Science, Simon Fraser university, 8888 University Drive, Burnaby, BC V5A 1S6, Canada*

Hop Latent Viroid (HpLVd) is a highly infectious RNA molecule that is widespread on *Cannabis sativa*. A survey of HpLVd occurrence in Canadian licenced production facilities in 9 provinces showed presence in 24.6 % out of 14,200 samples tested by RT-PCR. The genomic sequences were 100% homologous to HpLVd strains from hemp in Colorado, USA and hops in China. Infected cannabis mother plants display stunted growth, with smaller leaves and mosaic symptoms on some leaves. Cuttings from affected plants showed reduced rooting; plants in flower showed stunted and reduced growth of inflorescences. Glandular trichomes on flowers were significantly stunted in size, with smaller gland heads and stalks, with 12-30% lower THC, depending on the genotype. HpLVd was successfully transmitted by inoculating cut stem surfaces with sap, was detected in the roots 10-14 days later, followed by movement into young leaves, then older leaves by 4 weeks. Plants in a 12:12 hr photoperiod showed more rapid spread of HpLVd into roots and leaves compared to constant 24 hr. Viroid concentrations were significantly higher in fresh and dried flower tissues compared to the rest of the plant. HpLVd was transmitted through roots and water in a hydroponic growing system. Molecular detection was most consistent in root samples, followed by younger leaves and older leaves. Infected mother plants had varied viroid concentration, from low (latent) to high (active), and by leaf position. Rigorous testing, destroying infected plants, and preventing spread on cut stem surfaces and tools, and preventing root contact, can reduce spread.

P48. Seasonal variation of the antibacterial activity of ethanolic leaf extracts from different maple tree species against *Clavibacter michiganensis* V. TREMBLAY, M. DELISLE-HOUDE, M. FILION AND R. J. TWEDDELL *Département de phytologie, Université Laval, 2425 rue de l'Agriculture, Québec, QC G1V 0A6, Canada; and (M.F.) Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu Research and Development Center, 430 boulevard Gouin, Saint-Jean-sur-Richelieu, QC J3B 7B5, Canada*

Recent work revealed the presence of antibacterial compounds in sugar maple (*Acer saccharum* Marsh.) and silver maple (*Acer saccharinum* L.) leaves. In this study, ethanolic extracts prepared from leaves of sugar maple, silver maple and red maple (*Acer rubrum* L.), harvested monthly between May and October, were tested *in vitro* for antibacterial activity against *Clavibacter michiganensis* (Davis *et al.*) Li *et al.*, the causal agent of bacterial canker of tomato (*Solanum lycopersicum* L.). Antibacterial activity was determined according to minimal inhibitory concentrations (MICs) and minimal bactericidal concentrations (MBCs). Extract yields were determined, as well as polyphenols contents using the Folin-Ciocalteu method. Sugar maple leaf extracts showed the strongest antibacterial activity out of the three species tested with a MIC value of 1.56 mg/mL and a

MBC value of 12.5 mg/mL. Antibacterial activities and polyphenols contents were very similar regardless of sampling time, but higher yields were generally observed in extracts obtained from leaves harvested in July and August. The antibacterial activity of maple leaf extracts against *C. michiganensis* shows potential to be used to control bacterial canker in tomato.

P49. TEN-TG : A TILLING and Genome resource for Fusarium head blight (FHB) improvement M. A. HENRIQUEZ, C. J. POZNIAK, S. WALKOWIAK, K. T. NILSEN, S. SURA, S. KUMAR, AND P. WALKER *(M.A.H., S.S., P.W) Morden Research and Development Centre, Agriculture and Agri-Food Canada, Unit 101 Route 100, Morden, MB, R6M 1Y5, Canada; (C.J.P.) Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK, S7N 5A8, Canada; (S.W.) Grain Research Laboratory, Canadian Grain Commission, 196 Innovation Drive, Winnipeg, MB, R3T 6C5, Canada; and (K.T.N., S.K.) Brandon Research and Development Centre, Agriculture and Agri-Food Canada, 2701 Grand Valley Road, Brandon, MB, R7A 5Y3, Canada*

Fusarium head blight (FHB) is the most serious fungal disease affecting wheat and other small grain cereals in Canada. FHB reduces grain yield, result in grade loss and end-use quality in cereals compromising its marketability, particularly because of the production of harmful mycotoxins. Over the past decade, significant progress has been made in improving FHB resistance and disease management, but it has proven much more difficult than other diseases. In fact, only a registered single bread wheat cultivar AAC Tenacious is rated as resistant in Canada. We developed a Targeting Induced Local Lesions In Genomes (TILLING) population of AAC Tenacious, that in field trials showed variation for a range of useful agronomic traits (for example, semi-dwarf stature with levels of FHB resistance equal to AAC Tenacious). Importantly, we have identified lines that are highly susceptible to FHB, allowing us for the first time, to use genomic strategies to isolate with precision those genes which confer the superior resistance in 'AAC Tenacious'. By sequencing the genome of AAC Tenacious and comparing that to the sequence of the susceptible TILLING mutants, we can identify the mutated alleles associates with the susceptible phenotype. The germplasm, genotypic and phenotypic data of the TILLING population, will be available to all wheat research programs.

P50. Sugar maple (*Acer saccharum*) leaf extracts: a potential new tool for the management of *Clavibacter michiganensis* in tomato V. TREMBLAY, M. DELISLE-HOUDE, M. FILION, AND R. J. TWEDDELL *Département de phytologie, Université Laval, 2425 rue de l'Agriculture, Québec, QC G1V 0A6, Canada; and (M.F.) Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu Research and Development Center, 430 boulevard Gouin, Saint-Jean-sur-Richelieu, QC J3B 7B5, Canada*

Clavibacter michiganensis (Davis *et al.*) Li *et al.*, the causal agent of bacterial canker of tomato (*Solanum lycopersicum* L.), is a seed-borne pathogen causing important worldwide losses. Currently, very few phytosanitary products other than copper-based pesticides are available to efficiently manage diseases caused by phytopathogenic bacteria, including *C. michiganensis*. In this study, ethanolic sugar maple (*Acer saccharum* Marsh.) leaf extracts were tested as seed and foliar treatments to control *C. michiganensis*. Seed and foliar treatments were conducted *in vitro* and *in planta* on tomato plants cultivated in greenhouse conditions, respectively. Seed treatments strongly decreased *C. michiganensis* seed contamination, without affecting seed germination. Foliar treatments limited the development of bacterial canker symptoms, for both primary and secondary infections. Sugar maple leaf extracts show an interesting potential to control *C. michiganensis* in tomato. Based on the promising results obtained under control conditions, the efficacy of the extracts to control bacterial canker of tomato under field conditions will be investigated in future work.

P55. Identification and pathogenicity of fungal pathogens associated with root rot of canola (*Brassica napus*) H. YU**,** K. F. CHANG, S. F. HWANG, R. FREDUA-AGYEMAN AND S. E. STRELKOV *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada*

Root rot is an important disease of canola (*Brassica napus*) that can result in severe yield losses under conducive conditions. Symptomatic canola roots were collected during field surveys conducted in 2021 and 2022 and cultured on potato dextrose agar to recover the associated fungi. *Fusarium* species were isolated most frequently from the tested root samples, occurring at an average incidence of >80%. Other fungal pathogens, including *Leptosphaeria maculans*, *Alternaria* spp., *Clonostachys rosea*, *Trichoderma paraviridescens*, and *Plenodomus biglobosus* (*Leptosphaeria biglobosa*), were also recovered but less frequently. Molecular identification and pathogenicity testing indicated that multiple *Fusarium* spp. are involved in root rot development, with *F. avenaceum*, *F. redolens*, *F. solani*, and *F. oxysporum* found to be most prevalent. Root rot severity caused by inoculation with *Fusarium* isolates representing these species ranged from 1.2 to 3.5 on a 5-point scale, with 60% of the isolates causing disease severities >2.0 and 20% of the isolates causing severities >3.0; seedling emergence was reduced by 9% to 91% after inoculation. Several isolates of *C. rosea* and *P. biglobosus* also caused disease severities of ~2.0 and ~3.5, respectively, and a reduction in emergence of >20%. The results indicate that *Fusarium* spp. are the primary cause of canola root rot, causing severe disease and reductions in emergence. Nonetheless, other fungal pathogens also contribute to root rot development, causing moderate to severe disease.

POSTER SESSION 2

Emerging/novel tools for plant pathogens diagnostics

P51. Development of a droplet digital-PCR assay for the detection of Grapevine Pinot gris virus infecting grapevines B. M. VEMULAPATI, T. WANG, AND S. POOJARI *Cool Climate Oenology and Viticulture Institute, Brock University, St. Catharines, Ontario, L2S 3A1, Canada.*

Grapevine Pinot gris virus (GPGV), a member of the trichovirus (Betaflexiviridae) genus, was first identified in vineyards in Trentino, Italy. The virus has been reported in 58 countries. Vines infected with symptomatic strain of GPGV show chlorotic mottling, deformation, stunted growth, low-quality fruit and abnormal branching. GPGV spreads via exchange of infected propagation material and grafting. Accurate detection of viruses from plants having mixed infections, low-titers or phloem-limited conditions can be a challenging task. Droplet digital polymerase chain reaction (ddPCR) is based on water-oil emulsion droplet and can be used to measure the absolute copy number of nucleic acid targets with high sensitivity and without the need for external standards. Here, we developed a reverse transcription ddPCR (RT-ddPCR) method for the detection of GPGV from infected grapevine samples. The ddPCR assays were performed on a Bio-Rad QX200 AutoDG system using an EvaGreen assay. GPGV movement protein (MP) gene was used as the target for GPGV detection from test samples. A two-step gradient RT-PCR was standardized to determine the optimal conditions for ddPCR. Serial dilution of plasmid DNA containing GPGV-MP gene was used for the absolute quantification of the detection limit for optimum 'call' values and 10^{-4} to 10^{-8} dilution was found to be ideal. The dd-PCR assay could detect <10 GPGV copies uL-1. The assay exhibited high specificity for GPGV and showed no cross-reactivity with grapevine leafroll-associated virus-3, the other major grapevine virus prevalent in the vineyards of Ontario. This ddPCR assay showed a higher sensitivity compared to the end-point RT-PCR for GPGV detection and could be potentially used in regulatory and certification programs.

P52. Measuring quantitative resistance to blackleg based on pathogen growth kinetics in canola L. MCGREGOR AND G. PENG. *Saskatoon Research & Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2*

Quantitative resistance (QR) is important for management of blackleg [*Leptosphaeria maculans* (Desmaz.) Ces. & De Not.] of canola (*Brassica napus* L.) in western Canada where the pressure of disease tends to be lower than in Europe or Australia. QR identification has mostly relied on extensive field trials, which is time consuming and can often give variable results under different field conditions. In this study, canola varieties (54) with susceptible, resistant and moderately resistant ratings in multi-year plot trials were measured for QR in relation to *L. maculans* growth kinetics in canola stems using droplet-digital PCR (ddPCR) that quantifies the amount of fungal DNA. In a greenhouse, the cotyledon or petiole was prick inoculated with *L. maculans* isolates capable of evading R genes in these varieties. Fourteen of the varieties with a range of resistance were inoculated similarly under field conditions (2019-2022). Petiole inoculation caused higher incidence and severity of stem infection than cotyledon inoculation under greenhouse and field conditions. ddPCR readings of *L. maculans* DNA in stem tissues resulting from petiole/cotyledon inoculation was correlated with resistance levels observed in multi-year field trials for these 54 varieties (R =0.534-0.550; P <0.003), as well as with the resistance efficacy of selected varieties in inoculated field trials (R =0.613-0.710; P <0.019). ddPCR data were also correlated for petiole and cotyledon inoculations (R =0.7035; P =0.0002). These results showed that growth kinetics of *L. maculans* during stem colonization measured with ddPCR can be used as an indicator of QR against blackleg.

P53. Identification and detection of a virulence factor in *Plasmodiophora brassicae* A. SEDAGHATKISH, B. D. GOSSEN, AND M. R. MCDONALD. *University of Guelph, 50 Stone Road East, Guelph, ON NIG 2W1, Canada; and (B.D.G.) Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada*

Plasmodiophora brassicae (Wor.), the causal agent of clubroot, is an important pathogen of brassica crops worldwide. Clubroot management based on a single resistance gene is not durable when deployed on a large scale because new, highly-virulent pathotypes emerge quickly. An inexpensive, rapid, and consistent method is needed for differentiation of pathotypes, which is currently based on the reaction of differential lines, an approach that is slow, resource-intensive, and often variable. In the current study, a virulence factor in *P. brassicae* was identified based on 43 whole-genome sequences from around the world in GenBank. The gene for this factor was not present in the initial cohort of pathotypes present in Canada, but was present in pathotypes that were virulent on the first-generation of clubroot-resistant canola (*Brassica napus* L.). Three KASP markers were designed to detect the virulent pathotypes and validated by two different laboratories. The putative structure, domains, and gene ontogeny of the protein product of this gene were assessed using on-line software resources. Structural analysis of the putative protein product indicated that it was likely localized intracellularly, with involvement in cellular processes and catalytic activity. This represents a step towards the molecular identification of pathotypes in *P. brassicae*.

Biotic and Abiotic Challenges

P54. Effect of heat stress and auxin application at flowering on grain yield of Wheat (*Triticum aestivum* L.) and specific QTL associated with grain yield under heat stress and non-stress conditions D. N. ABEYSINGHA, D. M. REINECKE, M. IQBAL, AND J. A. OZGA *Plant Biosystems Group, Department of Agricultural, Food, and Nutritional Science, University of Alberta, Edmonton, AB, Canada T6G 2P5, Canada*

The wheat reproductive phase is sensitive to heat stress (HS), resulting in poor grain set and weight. Genetic modifications and proper agronomic practices can be used to ameliorate the negative effects of HS. This study tests the hypotheses that: 1) auxin application can reduce the negative

impact of short-term pre-anthesis HS and, 2) variation in HS response and grain yield parameters among a wheat RIL population ('Attila' × 'CDC Go') will allow for the identification of quantitative trait loci (QTL) associated with HS responses. A single foliar application of an auxin (4-Cl-IAA, 1µM) or control solution at the pre-anthesis (BBCH 41-45) stage was followed by a short-term HS treatment (35°C for 6 hrs for 6 days) under controlled environmental conditions and grain yield parameters were assessed at maturity. Out of 163 recombinant inbred lines (RILs), 45% were categorized as heat-resistant, 20.5% as moderately heat-susceptible, and 7.6% as highly heat-susceptible. Auxin treatment maintained some grain yield traits under HS and/or control conditions in a small number of RILs (5). Inclusive composite interval QTL mapping identified 73 QTLs (non-stress, 37; HS, 36) on 14 of the 21 chromosomes that individually explained 1.6 to 47.5% phenotypic variation. Eight QTL clusters associated with two or more grain yield traits were identified on chromosomes 5A, 4B, 2B, 2D, and 1B. This study suggests that a one-time foliar auxin application can increase wheat yield in some genotypes, and it identified QTL hotspots in the wheat genome that can potentially be used in future breeding programs.

P56. Resistance gene expression and antioxidant enzymes in wheat genotypes affected by *Bipolaris sorokiniana* and *Heterodera filipjevi* M. MONAZZAH, M. NASR-ESFAHANI, F. QALAVAND, AND M. MOTAMEDI *(M.M.) Department of comparative biomedicine and food science, School of agricultural sciences and veterinary medicine, University of Padua, Agripolis, 16-35020, Legnaro, Italy; (M.N.E.) Plant Protection Research Department, Isfahan Agricultural and Natural Resources Research and Education Center (AREEO), P.O. Box. 81785199, Isfahan, Iran; (F.Q.) Plant Pathology Department, University of Lorestan, P.O. Box. 465, Lorestan, Iran; and (M.M.) Department of Agricultural-Biotechnology, Sabzevar Branch, Islamic Azad University, P.O. Box. 1477893855, Sabzevar, Iran*

Bipolaris sorokiniana, and *Heterodera filipjevi,* are important wheat diseases that lead to yield losses worldwide. Identifying novel resistant sources helps us combat these devastating diseases. In this study, we studied the role of *Cre3* gene and antioxidant enzymes in the immune responses of wheat genotypes to *H. filipjevi* and *B. sorokiniana*. Therefore, real-time PCR analysis using *Cre3* gene marker, a resistant gene to cereal cyst nematodes, was conducted on leaves and roots, along with changes in activity of antioxidant enzymes, peroxidase and catalase. Enzyme activity assay was performed on roots attacked by nematode and in leaves infected with Bipolaris. Wheat accessions including "Bam" (resistant), "Parsi" (moderately-resistant), "Azar2", "Ohadi", "Homa" (highly-susceptible) were previously screened against both stresses under greenhouse and field conditions. Results showed that *Cre3* expression against cyst nematodes was significantly higher in resistant cultivars compared to susceptible cultivars. *Cre3* was used in marker-assisted selection programs to identify genotypes carrying resistant genes to cyst nematodes. Interestingly, *Cre3* were also up-regulated in both tissues of resistant cultivars to *B. sorokiniana*. Therefore, *Cre3* in wheat similarly modulates-immunity against *B. sorokiniana* and might be one of the central components of the induced immune system in wheat. The activity of antioxidant enzymes also indicated the highest increase in resistant genotypes upon both stresses that subsequently neutralize oxidative stress in tissues and decrease damage. Further studies on these resistance components may help us gain insight into the molecular basis of resistance and shed new light on the interaction and overlap between different forms of stress.

P57. Quantification of wheat infection by ToxA and ToxB producing isolates of *Pyrenophora tritici-repentis* M. LARIBI, X. MA, R. ABOUKHADDOUR, I. S. STRELKOV, S. F. HWANG, AND S. E. STRELKOV *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada*

Tan spot is an important foliar disease of wheat caused by the fungus *Pyrenophora tritici-repentis* (Ptr). Isolates of the fungus can differentially produce three necrotrophic effectors (NE), termed ToxA, ToxB and ToxC. ToxA-producing isolates ($ToxA^+$) are predominant in Canada, while ToxB-producers ($ToxB^+$) are very rare, despite the fact that many Canadian wheat genotypes are sensitive to $ToxB^+$. The objective of this study was to determine whether $ToxA^+$ isolates could outcompete $ToxB^+$ isolates, potentially explaining the scarcity of the latter. The hexaploid wheat genotype 'Katepwa', which is sensitive to both ToxA and ToxB, was inoculated with three $ToxA^+$ isolates and three $ToxB^+$ isolates either alone or in different combinations. Infected leaves were collected 24 - 120 h post-inoculation (HPI) and the infected leaf area (ILA) was measured. Analysis of variance indicated a significant effect of isolate, HPI, and HPI-isolate interaction on ILA. With few exceptions, all isolates caused more severe symptoms when they were inoculated together vs. on their own. Quantitative PCR analysis targeting the *chitin synthase 4* gene (as a measure of total fungal biomass) and the *ToxA* or *ToxB* genes (to monitor $ToxA^+$ and $ToxB^+$ isolates, respectively) also indicated an increase in total *in planta* fungal biomass with co-inoculation in most cases. However, the relative abundance of $ToxA^+$ and $ToxB^+$ isolates after co-inoculation varied depending on the specific isolates involved, with an increase in $ToxB^+$ isolates often detected. This suggests that $ToxA^+$ isolates do not outcompete $ToxB^+$ isolates, at least with respect to colonization of susceptible host tissue.

P58. The effect of fungicides, cultivars and seeding rates on stripe rust level, yield and quality of winter wheat L. TAMBURIC-ILINCIC *Ridgetown Campus, University of Guelph, 120 Main St E., Ridgetown, ON, NOP 2CO*

Experimental plots of were planted in October 2016 and 2017 at Ridgetown, and in 2017 at Tupperville, Ontario. The treatments included three seeding rates (400, 500 and 600 seeds/m^2), four cultivars ('UGRC Ring', 'Venture', 'OAC Flight', 'Gallus') and three fungicide regimes: control, QUILT, STRATEGO and PROSARO applied at flag leaf stage (ZGS 39). Heading dates were recorded as Julian days (JD) and plant height in cm. Stripe rust (*Puccinia striiformis* f. sp. *tritici* Erikss.) severity was estimated by visually rating the plots on a 0-9 scale. Grain was harvested and reported at T/ha, test weight was recorded in kg/hL and thousand kernel weights (TKW) in grams. All data were analyzed using SAS (9.4). Environments-E,

cultivars-C, fungicides-F and seeding rate-SR, had a significant influence on yield. E, C and SR had a significant influence on plant height, while E and C had a significant influence on stripe rust ratings, test weight, TKW and heading date. Level of stripe rust was low in winter wheat in 2017 and 2018, but cultivars 'Venture' and 'OAC Flight' were the most susceptible to stripe rust. All fungicides increased the yield compared to the control, but the highest increase was after Prosaro application. The highest yield was of cultivar 'UGRC Ring' (7.7 t/ha, 5.4 t/ha and 9.2 t/ha at Ridgetown in 2017, 2018 and at Tupperville in 2018, respectively). The lowest yield was of cultivar 'Gallus' at Ridgetown (4.8 and 4.2 t/ha in 2017 and 2018, respectively) and 'OAC Flight' (7.1 t/ha) at Tupperville in 2018. We concluded that application of fungicides increased the yield of winter wheat even when stripe rust, and other leaf diseases, levels were low.

P59. Effect of biostimulants on baby leaf lettuce and Batavia lettuce exposed to abiotic stress under two different growing systems J. CLEMENT, M. DELISLE-HOUDE, T. A. T. NGUYEN, M. DORAIS, AND R. J. TWEDDELL *Département de phytologie, Université Laval, 2425 rue de l'Agriculture, Québec, QC G1V 0A6, Canada*

Plant biostimulants are considered as potential tools for the modulation of plant physiological processes to stimulate growth, mitigate stress-induced limitations, and increase yield. Several studies reported the positive impacts of biostimulants on plants subjected to abiotic stress. However, these studies have generally focused on the effects of biostimulants on plants exposed to different levels of a specific stress in one particular growing system. In this study, ten biostimulants were tested under two different growing systems for their effect on lettuce (*Lactuca sativa*) exposed to varying levels of salinity stress or water stress. Baby leaf lettuce (cv. Garrison) and Batavia lettuce (cv. Salanova® Red Batavia) treated with biostimulants (seed treatment or drenching) were respectively exposed to a salinity stress (0, 40, 80 and 120 mM NaCl L^{-1}) and a water stress (-0.5, -2, -4 and -6 kPa) during growth under organic or conventional management in a greenhouse. The germination rate of seeds (baby leaf lettuce) and the shoot dry biomass of plants (baby leaf and Batavia lettuce) were evaluated. The results showed that lettuce response to biostimulants was influenced by the growing system used and the type or level of stress applied. The effects of the tested biostimulants varied from strongly beneficial to strongly detrimental.

P60. Overexpression of *BnNAC19* in *Brassica napus* enhances resistance to *Leptosphaeria maculans*, the blackleg pathogen of canola Z. ZOU AND W. G. D. FERNANDO *Department of Biology, Wilfrid Laurier University, Waterloo, ON N2L 3C5, Canada*; *and (Z.Z., W.G.D.F.) Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada*

Leptosphaeria maculans is a fungal pathogen that causes blackleg disease in canola (*Brassica napus*), resulting in significant yield and economic loss in Canada. Plant *NAC (NAM, ATAF1/2, CUC2)* transcription factors play critical roles in plant development and in response to biotic or abiotic stress. In this study, we identified and characterized a *BnNAC19* gene from *Brassica napus*. The overexpression of *BnNAC19* contributed to the improvement of seedling resistance in transgenic canola plants against *L. maculans*. The growth and production of *L. maculans* pycnidiosopres and mycelium were inhibited in the overexpressed *BnNAC19* transgenic canola plants. In addition, the *BnNAC19* overexpressing canola transgenic line showed increased disease resistance in adult plant, which was determined by the quantitative resistance. Both increased seedling and adult plant resistance in overexpressed *BnNAC19* canola transgenic plants indicate that *BnNAC19* gene plays a positive effect against *L. maculans*. Expression of upstream (*BnMYC2:* helix-loop-helix transcription factor) and downstream (*BnVSP1*: vegetative storage protein 1) genes were investigated as well as salicylic acid and jasmonic acid signaled plant defense genes in response to *L. maculans* infection. The enhanced disease resistance by up-regulated *BnNAC19* expression can provide another option as a genetic modification or quantitative resistance to protect canola plants.

Biovigilance approach for Emerging and novel phytopathogens

P61. A more inclusive biovigilance approach to pest management: Case study of the strawberry blossom weevil and implications for plant disease monitoring strategies J. L. MACDONALD, M. FRANKLIN, AND S. HANN *Summerland Research and Development Centre, Agriculture and Agri-Food Canada, 4200 Highway 97 Box 5000, Summerland, BC V0H 1Z0, Canada; (M.F.) Agassiz Research and Development Centre, Agriculture and Agri-Food Canada, 6947 Highway 7 Box 1000, Agassiz, BC V0M 1A2; and (S.H.) Fredericton Research and Development Centre, Agriculture and Agri-Food Canada, 850 Lincoln Road, Fredericton, NB, E3B 4Z7*

Biovigilance is an ecosystems-based approach to understand and reduce the negative effects of climate change, pest movements and changes in behaviour, and new crops and farming practices on plant health. Anticipating and understanding how pests, their natural enemies, and environmental conditions will evolve allows for adapting agricultural practices to cope with changing conditions, and results in increased agroecosystem resilience and crop health. This approach relies on a continuum of science-based activities to ensure that mitigation strategies are efficient and do not create new problems. These steps start with awareness and detection, particularly when invasive species are involved, then build towards understanding, mitigating, and anticipating unintended consequences of mitigation effots. Biovigilance requires a holistic, de-silo'd approach in order to be successful. Monitoring and understanding the effects of insects, disease, and reactionary management practices beyond our agro-ecosystems, into the broader landscape is fundamental. A pilot project based in in British Columbia is working to apply a biovigilance approach to the establishment and management of the newly established insect pest, *Anthonomus rubi* (strawberry blossom weevil), and involves

a diverse group of stakeholders to collectively address the issues surrounding it. This effort and organization should be replicated with emerging disease and disease vectors in the future.

Controlled Environment Agriculture (CEA)

P62. Impact of ultraviolet-C treatments on powdery mildew of fruiting crops grown in a fully controlled environment G. MARCHAND, J. LANOUE, H. DEN BAK, M. D. SCHADE, AND Q. DIGWEED *Harrow Research and Development Centre (Harrow RDC), Agriculture and Agri-Food Canada, 2585 County Road 20, Harrow, ON N0R 1G0, Canada*

Controlled environment agriculture (CEA) involves growing plants in fully enclosed systems. There is growing interest in CEA production of food crops, notably to provide fresh and nutritious food to remote and Northern communities. Plant pests and pathogens pose a particular challenge in CEA, as there are no pesticide products registered for use in this production system in Canada, thus their control requires alternative methods. Ultraviolet radiation has shown potential as a physical method to control foliar plant diseases caused by fungal plant pathogens, such as powdery mildews. A custom CEA container system, designed after those already deployed in Gjoa Haven (Nunavut), was designed and built at the Harrow RDC and outfitted with light fixtures emitting in the ultraviolet-C (UV-C) range and a shutter system, allowing precise control of the exposure time and resulting dose of radiation. During a first trial (February to April 2023), a target dose of 50 uJ cm^{-2} was applied three times a week to tomato, cucumber and strawberry crops in hydroponic growing systems, following inoculation with powdery mildew. UV-C treatments had a statistically significant impact on disease incidence and severity in tomato and cucumber, while inoculation on strawberry was not successful. Tomato and strawberry plants did not exhibit visual signs of phytotoxicity, but cucumbers showed a reduced leaf area and curling heads. Future trials will aim to refine the dosage and application schedule of UV-C treatments, and provide a basis for recommendations for their use to control powdery mildew in CEA systems.

P63. Effects of salt stress on total lipid values, fatty acid profiles, omega-3, omega-6 and omega-9, in the brown algea *Sargassum boveanum* on Bushehr coast M. AKBARI, R. RAZAVIZADEH, R. SAMADPOUR, M. MONAZZAH, H. SOBHANIAN, GH. BAKHSHIKHANIKI, A. MARYAMABADI, AND G.H. MOHEBBI *(R.R., H.S., Gh.B.) Department of Biology, Payame Noor University, Lashkarak Road, 19395-4697, Tehran, Iran; (M.M., R.S.) Department of comparative biomedicine and food science, School of agricultural sciences and veterinary medicine, University of Padua, Agripolis, Viale dell'Università, 16–35020, Legnaro (PD), Italy; and (A.M., G.H.M.) The Persian Gulf Marine Biotechnology Research Center, The Persian Gulf Biomedical Sciences Research Institute, Bushehr University of Medical Sciences, Moalem Street, Setade Namaze Jome, 3631, Bushehr, Iran*

Some algae are rich sources of various beneficial fatty acids. The present study was performed to investigate the effect of different concentrations of sodium chloride on total lipid content, fatty acid profile, and omega-3, 6, and 9 amounts in the alga *Sargassum boveanum*. Algae samples were collected from the shores of Bushehr Province and kept in three aquariums for 30 days in three control groups and treatments of 1 and 2 g / l sodium chloride. Then their lipid extraction was performed using Bligh and dyer method (1959). The factors of acid value (AV), peroxide value (PV), and refractive index (RI) of lipids were determined according to ISO standard methods for numbers 660 (2009), 3960 (2017), and 6320 (2017), respectively. The methylation of the samples was performed according to the standard method of 66-2-AOCS-Ce, and the analysis of fatty acids was performed by gas chromatography equipped with a flame ionization detector (GC-FID). The amount of fat in the treatment of one gram/liter of salt increased compared to the control group and then showed a decreasing trend in the treatment of two grams per liter. GC-FID analysis showed 17 types of fatty acids in each group, palmitic acid and seronic acid showed the highest levels in all three groups. A slight increase in salinity caused a change in the amount of omega-fatty acids. The findings of this study can be extended to achieve targeted mechanisms and conditions of salinity stress that increase specific fatty acids.

P64. The first and volatile secondary metabolites of the *Sargassum boveanum* algae from the Persian Gulf, Iran T. KHALIFEH, GH. MOHEBBI, M. MONAZZAH, R. SAMADPOUR, A. VAZIRIZADEH, AND A.H. DARABI *The Persian Gulf Marine Biotechnology Research Center, The Persian Gulf Biomedical Sciences Research Institute, Bushehr University of Medical Sciences, Moalem Street, Setade Namaze Jome, 3631, Bushehr, Iran (M.M., R.S.) Department of comparative biomedicine and food science, School of agricultural sciences and veterinary medicine, University of Padua, Agripolis, Viale dell'Università, 16–35020, Legnaro (PD), Italy; (A.V.) Department of Marine Biotechnology, The Persian Gulf Research and Studies Center, The Persian Gulf University, Moalem Square, Parastar street, 7513974515, Bushehr, Iran; and (A.H.D.) The Persian Gulf Tropical Medicine Research Center, The Persian Gulf Biomedical Sciences Research Institute, Bushehr University of Medical Sciences, Moalem Street, 7514633341, Bushehr, Iran.*

Algae are increasingly being consumed as nutraceuticals cause of biologically active compounds. Some nutraceutical effects of *Sargassum boveanum* brown algae to produce more nutritious foods were investigated. The total lipid and protein contents, fatty acid, amino acid profiles, and volatile secondary metabolites, were analysed by the Bligh and Dyer, Kjeldahl, GC-FID, HPLC-UV, and GC-MS methods, respectively. The total lipid content of the algal sample extracted with n-hexane solvent was 2.62 ± 0.06% of dry weight. Among the 16 saturated fatty acids (SFA; 97.23%), and 2 unsaturated fatty acids (UFA; 2.77%), palmitic acid, caproic acid, and myristic acid had the highest levels. The ω-6 and ω-9 values were 1.463 and 1.304%, respectively. The total protein content of the sample was 12.0 ±0.11%. Among the 17 amino acids in the algal sample, the highest level was lysine, followed by glycine and aspartic acid. The total percentages of essential (EAA), semi-essential (SEAA), and non-essential

(NEAA) amino acids were 48.1, 24.6, and 27.5%, respectively. The ratios of EAA/NEAA and SEAA/NEAA were 1.75 and 0.92, respectively. The GC-MS analysis of *S. boveanum* extract indicated 25 volatile chemical composition (**S1**-**S25**) with different functional groups, such as quinoline, indole, pyrimidine isoquinoline, pyrrole alkaloids, phenolic compounds, glycosides, carbohydrates, and carotenoids. *Sargassum boveanum* is high in protein content and abundant in amino acids, mainly essential amino acids, and various valuable fatty acids, including medium-chain fatty acids. Different types of alkaloids, phenolic, steroidal, and terpenoid compounds have been considered as potentially functional foods with bioactive metabolites or dietary supplements.

Plant-Soil health and Innovations in Agronomy

P65. Identifying superior photosynthetic traits in canola *Brassica napus* gene pool F. GUERRERO-ZURITA, K. GIL, H., AND L. GORIM. *Department of Agriculture, Food, and Nutritional Sciences, University of Alberta, Agriculture/Forestry Centre, Edmonton, AB T6G 2P5, Canada*

Canola is the second major source of high-quality vegetable oil in the world. Improvements in canola have predominantly emerged from breeding and manipulation of both plant morphology and management are at saturation. This study focuses on the assessment of photosynthetic efficiency as a strategy to improve crop performance. In the present study, a *Brassica napus* gene pool of 170 accessions (two checks included) encompassing seven parental lines were grown at West-240 and St. Albert University of Alberta Research Stations in 2021 and 2022, respectively using an incomplete randomized block design. Accessions were tested for photosynthetic efficiency using both chlorophyll fluorescence and gas exchange parameters. Principal component analysis showed that for both years (2021 was a drought year compared to 2022) the quantum yield of photosystem II (ΦII) was driven by the ability of the leaf to thermoregulate its own temperature through stomatal regulation, whereas the maximum quantum efficiency of photosystem II (Fv´/Fm´) influences the CO_2 assimilation rate. Moreover, the crosses whose accessions got a higher response in most of the parameters than the checks are *B. napus* (winter variety) x *B. rapa* (accessions 5CA1627.1533-A2090, 5CA1627.1537-A2090, 5CA1627.1563-A2090, and 5CA1627.1573-A2090), and [*B. napus* (winter variety) x *B. napus* (spring variety)] x *B. napus* (rutabaga) (accessions 1CA2160.017-A2069, 1RA1751.287-A2088, 1RA2054.102-A2008, 1CA2165.063-A2069, 1CA2582.010-A2040, 1CA2591.004-A2040, and 1CA2639.008-A2040. This study will provide both canola breeders and crop producers with new photosynthetic and physiological information and accessions with outstanding sunlight harvesting capacity to improve canola yield in future efforts.

P66. Agronomic performance of inter-seeded legume-cereal Cover crops mixtures in silage corn in boreal climate S. J. R. BUKHARI, S. AHMAD, Y. KATANDA, L. GALAGADERA, AND M. CHEEMA *(S.J.B., S.A., Y.K., L.G., M.C.) School of Science and the Environment, Memorial University of Newfoundland, Corner Brook, NL, A2H 5G4, Canada*

Cover crop (CC) mixtures are increasingly gaining the attention among farmers and researchers due to their multi-functionality (e.g., supplementary forage, erosion control, weed suppression, soil health, and nitrogen supply). A field trial was conducted in Pynn's Brook, NL, to assess biomass production and weed suppression potential of grass-legume CC mixture in boreal climate. Fourteen CC mixtures were inter-seeded in silage corn at V4-V6 stage (July 5th, 2022) at 50% of recommended sole-crop seeding rates. The experimental treatments included 2 and 3 species, two CC mixtures treatments were; red clover+ annual ryegrass (RCAR), red clover+ cereal rye (RC+CR), red clover+ triticale (RC+TR), berseem clover+ annual ryegrass (BC+AR), berseem clover+ cereal rye (BC+CR), berseem clover+ triticale (BC+TR), hairy vetch+ annual ryegrass (HV+AR), hairy vetch+ cereal rye (HV+CR), hairy vetch+ triticale (HV+TR), bird's foot trefoil+ annual ryegrass (BT+AR), bird's foot trefoil+ cereal rye (BT+CR), bird's foot trefoil+ triticale (BT+TR) and three species treatments (BT+BC+CR) and (BT+BC+TR). The experimental design was randomized complete block design with four replicates. CC biomass sampling was done at the time of silage corn harvest (late October 2022). All CCs treatments were successfully established, except for BT, which did not germinate. There were no significant differences in CC biomass, which ranged between 0.16 Mg ha^{-1}(BT+CR) and 3.50 Mg ha^{-1} (HV+AR). All CC mixtures reduced weed biomass by over 86% compared to no cover crops (control). Our findings indicate that inter-seeded CCs have the potential for establishment and weed suppression in silage corn systems in podzolic soils of west NL.

P67. Six Years of On-Farm Research – Manitoba Crop Alliance's Experience A. AMMETER AND M. LEWARNE *Manitoba Crop Alliance, 38 Fourth Ave NE, Carman MB, R0G 0J0*

Manitoba Crop Alliance's (MCA) Research on the Farm trial program conducts scientific research with farmer members, on their fields, using their equipment, and results are directly relevant to the individual farmer's operation. Protocols are simple, easy to implement and are used to determine whether a practice is effective through assessment of economic, agronomic, and environmental parameters. On-farm research is also beneficial to the industry, as involving farmers in the scientific method allows results to accumulate over a wide range of environments. MCA has been conducting on-farm trials since 2017. To date, 17 protocols (206 individual trials sites) covering five crop types (wheat, barley, corn, sunflower, flax) have been completed. MCA continues to engage with farmers to determine what management practices should be tested on-farm.

P68. Anaerobic soil disinfestation: phytotoxic effects and volatile fatty acid profiles S. ZIEDI, M. DELISLE-HOUDE, AND R. J. TWEDDELL. *Département de phytologie, Université Laval, 425 rue de l'Agriculture, Québec, QC G1V 0A6, Canada*

Anaerobic soil disinfestation (ASD) is an environmentally friendly method to control soil-borne plant pathogens and weeds. Volatile fatty acids (VFAs) produced during ASD are suspected to be involved in the mechanisms by which ASD suppresses plant soil-borne pathogens and weeds. The current work aims to study (*i*) the phytotoxic effect of ASD on weeds [Curly dock (*Rumex crispus* L.) and Powell's amaranth (*Amaranthus powellii* S. Watson)], (*ii*) the post-ASD phytotoxic effect on crops [oat (*Avena sativa* L.), forage turnip (*Brassica rapa* L.), and forage pea (*Pisum sativum* L.)] and (*iii*) determine the VFA profiles produced during ASD. ASD was performed for four weeks in airtight glass containers where water saturated soil (containing weed seeds) was amended with either apple (*Malus domestica* Borkh.) pomace, molasses, brewers' spent grain, or raspberry (*Rubus idaeus* L.) residues as carbon sources. The concentrations of VFAs (acetic acid, butyric acid, isobutyric acid, and propionic acid) in the soil solutions as well as the viability of weed seeds were subsequently determined using respectively HPLC analysis and triphenyltetrazolium chloride assay. Thereafter, crop seeds were planted in each ASD-treated soil previously transferred to multi- cell trays to determine the post-ASD phytotoxic effect on the germination rate of seeds. The ASD carried out with molasses as carbon source caused the most important post-ASD phytotoxic effect on crop seeds and killed 100% of weed seeds. The highest concentration of total VFAs was observed in soil amended with molasses; acetic acid and butyric acid were the VFAs detected at the higher concentrations.

P69. Evaluating 'AAC Trueman' Alfalfa in Saskatchewan Y. PAPADOPOULOS, B. HOUSTON, AND C. KAYTER *Agriculture and Agri-Food Canada, 58 River Road, PO Box 550, Truro, NS, B2N 5E3, Canada; (B.H.) Agriculture and Agri-Food Canada, 300-12th Avenue, Regina, SK, S4P 0M3, Canada; and (C.K.) Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, 107 Science Place, Saskatoon, SK, S7N 0X2, Canada*

We are exploring the adaptability of a new alfalfa variety, 'AAC Trueman' in Saskatchewan with sites successfully seeded in three soil zones: Brown (Swift Current), Dark Brown (Outlook); and Black Soil Zone (Melfort). The large plot trial at the Outlook site was seeded in 2020 while the other plots were seeded in 2021. Outlook large plots are irrigated. Soil moisture was monitored to achieve moisture treatment levels: (a) excess moisture, (b) normal irrigation and (c) dryland conditions. The plots at Swift Current and Melfort are not irrigated but have topographic variation which provides a range of soil moisture levels. Forage yields in 2022 were highest at Outlook (2 cuts) and ranged from 9287 to 15,410 kg/ha for the season. Forage yields (1 cut) at Melfort ranged from 5688 to 7229 kg/ha while Swift Current ranged from 1413 to 7500 kg/ha. Small plots were also seeded near Outlook in 2021 to evaluate ST1 Timothy as a potential forage mix with AAC Trueman in higher soil moisture sites. Forage production, forage quality and winter hardiness were evaluated in 2022. This growing season had very good alfalfa production; although ST1 Timothy production was lower likely due to poor establishment related to windy conditions during seeding. Flooding tolerance of AAC Trueman, ST1 Timothy and check varieties were tested in the AAFC Swift Current Salinity Testing facility. The test was completed in June 2022 and initial results showed that all varieties performed well during the 5 week flooding period.

P70. Critical sulfur concentrations for canola production B. L. MA AND D. L. SMITH *Agriculture and Agri-Food Canada, Ottawa Research and Development Centre, Ottawa, ON, K1A 0C6. D.L.S. Macdonald Campus of McGill University, Ste Anne de Bellevue, QC, H9X 3V9*

Critical plant sulfur (S) concentration (Sc) and nitrogen (N) to S ratio (N:S) at early growth stages of canola (*Brassica napus* L.) are important indicators for diagnosing S deficiencies. A field study was conducted for three growing seasons (2019-2021) in sandy and clay soils at two sites in eastern Canada, to determine Sc and N:S ratio across various growth stages. At each site-year, a factorial experiment consisting of four levels of N and four levels of S combinations were tested in a randomized complete block design with four replications. Sulfur application increased Sc at each growth stage, and the increase trend was stronger at the mature stage, but decreased the tissue N:S ratio. Both tissue Sc and N:S ratio varied with growth stage, environmental conditions and soil types, and declined with plant aging. Critical whole-plant Sc ranged from 0.44% at 4-leaf to 0.31% at early flowering stage). Visual signs of plant S deficiency seems to be the best way to identify S problem in the field, and tissue Sc and tissue N:S ratios can confirm deficiencies. If tissue Sc is below 0.35% and N:S ratio is above 9.6 at rosette stage, the plants are likely deficient in S.

P71. Impact of agricultural practices on microbial communities in soils from organic and conventional potato production systems O. I. MOLINA, M. GORZELAK, P. NEUBERGER, H. WILSON, M. A. HENRIQUEZ, AND S. SAGER *(O.I.M., M.A.H., S.S.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB R6M 1Y5, Canada; (M.G., P.N.) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1 Avenue South Lethbridge, AB T1J 4B1, Canada; and (H.W.) Brandon Research and Development Centre, Agriculture and Agri-Food Canada, 2701 Grand Valley Road, Brandon, MB R7C 1A1, Canada*

Agricultural practices in organic and conventional potato production systems can have significant effects on soil microbial communities. Organic potato production has increased in Manitoba during the last decade, where compost application and crop rotations with green manure and cover crops are used for nutrient management. However, little is known about the impact of these practices on the soil microbial communities compared to those under conventional management systems. In this study, we examined how organic and conventional farming systems influenced the alpha-diversity, beta-diversity, and taxonomic abundances of fungal and bacterial communities, and total and active soil organic carbon. Soil samples were collected from twelve potato fields (six organic and six conventional) in southern Manitoba. Preliminary results suggested that organic and conventional cropping systems have an effect on fungal and bacterial communities. Fields under organic management, with compost applications and crop rotations with hemp and cover crops, had greater total organic carbon and active carbon compared to those under conventional management. The findings from this study will enhance our knowledge of how agricultural practices influence soil conditions and its microbial communities.

P72. Liming remediates soil acidity and improves crop yields and profitability- A meta-analysis R. O. ENESI, M. DYCK, AND L. GORIM *(R.O.E., M.D., L.G) Department of Renewable Resource Department, University of Alberta, Edmonton, Alberta, T6G 2E3, Canada*

The significant increase in soil degradation globally has negatively impacted agricultural sustainability and soil health. A major driver of soil degradation is acidification (i.e., low soil pH <5) and liming has been used as a strategy in remediating soil acidification. Various studies have extensively looked at liming effect on crop production and soil processes at field scale, but studies designed to understand the effect of liming under different management practices on crop yields, soil pH and economic profitability are rarely reported. In this meta-analysis, we analyzed 247 data points from 29 literatures to understand the efficacy of liming across different crop type and agricultural practice. We examined the profitability of yield change due to liming for different crop types after one time lime application. The results showed that liming significantly increased crop yields and soil pH. Changes in soil pH increased with higher lime rates and yield increases were proportional to the magnitude of increases in soil pH. The effect of liming was significantly higher under no-tillage than conventional tillage systems. Liming increased crop yields in fertilized compared to unfertilized trials. The profitability of liming differed with crop type and liming rates, with liming being more profitable at lower rates. Overall, the results shows that liming can decrease soil acidity and improve crop yields. Furthermore, liming rates should be tailored to specific crops and soil types to achieve maximum economic profitability.

P73. On-farm assessment and literature review of the effect of liming and lime sources on crop production in the Prairies J. CHIRCHIR, L. GORIM, AND M. DYCK. *Department of Agricultural, Food, and Nutritional Science, University of Alberta, Edmonton, T6G 1C9, Canada, Alberta; and (M.D.) Department of Renewable Resources, University of Alberta, Edmonton, T6G 2E3, Canada, Alberta*

Low soil pH, caused by nitrogen fertilization and other soil processes, is a prevalent problem in Northern and Central Alberta. It decreases the availability of calcium and magnesium for plant uptake, and increases the solubility of aluminum ions, resulting in reduced root development, nutrient absorption, and crop yields. Numerous studies have been conducted on liming in the Prairies, however, limited research exists on crop responses to liming and their sensitivity to soil acidity. Our study compares data from published literature in the Prairies and from on-farm trials in Alberta to assess the impact of liming on crop production. Results from this study show that crops respond differently to lime application. In the literature reviewed, the largest yield responses (15%) were observed with canola, within the first year of study, but average values for over 2 years of study, show that barley has higher yield responses to liming over time. Preliminary results from the on-farm trials are comparable with previous studies, except for oats that exhibited negative yield responses to liming. From the literature studied, barley and canola recorded the highest yield response (55%) to agricultural lime compared to other lime sources. Future research will focus on checking the effect of different lime sources on crop production in the Prairies. This study seeks to provide insight into the status and benefits of liming in the Prairies and inform future research directions.

Sustainable Diseases management tools: Bioproducts, cultural practices and prediction modeling

P74. The combination of pelletized limestone and calcium cyanamide for reducing clubroot of canola Z. YU, S. F. HWANG, AND S. E. STRELKOV *Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB, T6 G2P5*

Clubroot, caused by *Plasmodiophora brassicae*, is a serious soilborne disease of canola (*Brassica napus*). In this study, a pelletized limestone product (98G) and granular calcium cyanamide (Perlka) were evaluated for their efficacy in reducing clubroot on two canola hybrids '45M35' (susceptible) and 'CS2000' (moderately resistant) in the greenhouse and at three field sites in 2022. The treatments included untreated controls (UTCs), 98G applied at 5 and 10 t ha^{-1}, and Perlka at 0.5 t ha^{-1} combined with 5 or 10 t ha^{-1} of 98G. In the greenhouse, treatments were evaluated at low (1×10^5 spores g^{-1} soil) or high (1×10^7 spores g^{-1}) *P. brassicae* spore concentrations (SCs). The combination of Perlka and 98G resulted in significant reductions in clubroot disease severity index (DSI) relative to the UTCs, regardless of hybrid or SC, while the lowest DSI was obtained with a combination of 0.5 t ha^{-1} Perka and 10 t ha^{-1} 98G. In applications of 98G alone, however, only the 10 t ha^{-1} rate significantly reduced DSI at low SC or on 'CS2000' at high SC. Similarly, in the field, significantly lower DSIs relative to the UTCs were observed at all three sites in plots treated with combinations of Perlka and 98G, while 98G applied at 10 t ha^{-1} reduced DSI significantly on '45M35' at two sites and on 'CS2000' at one site. The results indicate that the combined application of 98G and Perlka may represent an effective component of an integrated clubroot management strategy in canola.

P75. Agriculture and Agri-Food Canada's Pest Management Centre: 20 years of successes in disease management C. KORA, B. AHN AND J. F. DUBUC. *Agriculture and Agri-Food Canada, Pest Management Centre, 960 Carling Avenue. Ottawa, ON, K1A 0C6, Canada; and (J.F.D.) Agriculture and Agri-Food Canada, Pest Management Centre, 430, Gouin Blvd. St-Jean-sur-Richelieu, QC, J3B 3E6, Canada;*

Since 2003, the Minor Use Pesticides (MUP) and Pesticide Risk Reduction (PRR) Programs of Agriculture and Agri-Food Canada's Pest Management Centre (PMC) have been working

together to improve access to new pesticide uses and reduced risk pest management alternatives for Canadian growers. Every year, targeted pest issues and grower needs are identified and prioritized through stakeholder consultations. With its staff across Canada, the MUP team generates regulatory data for submission to Health Canada's Pest Management Regulatory Agency to support registration of new pesticide uses. Also, collaboration with the US IR-4 Project helps to support simultaneous access to new pesticide uses for growers and reduce trade barriers between the two countries. Since 2003, the MUP team has conducted over 600 plant pathology projects, involving trials with over 160 crops, addressing about 260 diseases and more than 140 pesticide products, including biopesticides. The PRR team delivers non-conventional pest management solutions including biological products, cultural and mechanical practices, as well as decision support tools to facilitate development and implementation of integrated approaches to pest management. Over the past two decades, the PRR team supported full registration of 18 biofungicide products, 10 new biopesticide uses, and enabled development of various management tools for multiple diseases through over 75 research projects addressing pathology issues. The poster highlights examples of successful disease management solutions delivered to growers over the last 20 years.

P76. Impact of crop diversification on the bacterial dynamics of a Sudden Death Syndrome (SDS) suppressive soils of Soybean R. MALLA, K.E. DUNFIELD, A. WRAGG, L.A. PHILLIPS, M. TOSI, D. OBREGON, AND O. S. WALLY *(R.M., K.E.D., M.T., D.O.) School of Environmental Sciences, OAC, University of Guelph, 50 Stone Rd E, Guelph, ON N1G 2W1, Canada; and (A.W., L.A.P, O.S.W.) Harrow Research and Development Centre, Agriculture and Agri-Food Canada, 2585 County Road 20, Harrow, ON N0R 1G0, Canada*

Sudden Death Syndrome (SDS) of Soybean caused by *Fusarium virguliforme* (*Fv*) is among the most devastating diseases that infect soybeans in North America, causing farm gate losses in excess of 1B USD annually. A field in Essex Ontario with a history of SDS was under soy monoculture for 15 years for variety testing, and in recent years lower disease levels were observed despite favorable environmental conditions and pathogen levels. Nearby fields with SDS infestations under traditional rotations however, showed little disease suppression. Growth room bioassays showed a biotic influence leading to disease suppression. Crop diversification can shift soil microbial composition, but little is known about how monoculture-induced microbial shifts lead to suppression or how rotation breaks that suppression. This study aimed to understand the dynamics of bacterial communities in soybean monoculture and soybean-corn rotations and understand the drivers leading to the development of soil suppressiveness against SDS. Soil samples were taken at two time points (spring and fall) during the growing season in suppressive (Essex) and conducive (Chatham) sites with monoculture and rotation treatments, and bacterial community dynamics were evaluated using amplicon sequencing. Overall bacterial diversity was evaluated using ordination approaches followed by PERMANOVA. Soil type, time of sampling and crop sequence clearly altered bacterial communities. Higher species richness and diversity was promoted in soy-monoculture compared to soy-corn rotations in the suppressive soils. The study suggests that bacterial communities are involved in the development of disease suppressive soils and the project is working on identifying specific biotic drivers of suppression.

P78. Endophyte *Beauveria bassiana* suppresses clubroot in cabbage under controlled environment conditions K. RUIGROK, J. ROBSON, B. D. GOSSEN, AND M. R. MCDONALD *Department of Plant Agriculture, University of Guelph, 50 Stone Road E, Guelph, ON N1G 2W1, Canada; and (B.D.G.) Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*

Clubroot, caused by the soil borne Chromist *Plasmodiophora brassicae* (Woronin), causes characteristic distorted roots or 'clubs' and can result in total yield loss on susceptible Brassica crops. The fungus *Beauveria bassiana* (Balsamo) Vuillemin is an entomopathogen and commercial formulations are registered for management of several insects pests. This fungus also colonizes plants as an endophyte and beneficial effects, including disease resistance, have been reported. A trial was conducted to assess disease suppression of clubroot. Cabbage cv. Bronco (clubroot-susceptible) was seeded in plug trays in LA4 soilless mix. At the cotyledon stage, *Beauveria* products BioCeres (10 mL / L) or Botanigard (8 mL / L) were applied as a drench at 500 mL per tray. Early application was selected to maximize root colonization before challenge with *P. brassicae*. Seedlings were transplanted 6 weeks after seeding and inoculated with 5 mL of resting spore suspension at 1 x10^5, 10^6 or 10^7 spores per mL. There were controls with no *B. bassiana* and others with no *P. brassicae*. Clubroot severity was assessed 6 weeks after inoculation with *P. brassicae*. With no *B. bassiana*, the disease severity index (DSI) for clubroot was 23, 58 and 87 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 on plants with the same concentrations of *P. brassicae*. There was no clubroot in the non-inoculated control. Treatment with *B. bassiana* could be useful for cabbage growers and future research on canola is warranted.

P79. Characterization of the mycovirome of *Botrytis cinerea* to identify potential biocontrol agents for gray mould disease S. C. DRURY, P. MOFFETT AND M. L. FALL *(S.C.D., M.L.F.) 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 (S.C.D., P.M.) Centre SÈVE, Département de Biologie, Université de Sherbrooke, 2500 Boulevard de l'Université, Sherbrooke, QC J1K 2R1, Canada*

Species of *Botrytis* Pers. are necrotrophic fungal pathogens that infect many important crops, including vegetables, small fruits, and ornamental plants. Fungicides are the primary management strategy, but resistance to fungicides is rising among many species of *Botrytis.* Harnessing mycoviruses that cause reduced virulence (hypovirulence) in *Botrytis* as biocontrol agents is a promising alternative management strategy. Over 100 mycoviruses have been identified in *Botrytis* to date, including several hypovirulence-inducing mycoviruses. This research aimed to further characterize the mycovirome of *B. cinerea* Pers. and identify mycoviruses, including ones with extracellular activity, that are good candidates as

biocontrol agents. Isolates of *B. cinerea* were collected from fruits and vegetables in Quebec. Fitness and pathogenicity criteria, including production of sclerotia, conidiation, radial growth, and morphotype, were evaluated. Double-stranded RNA (dsRNA) extraction was conducted on low-performing isolates, and the Illumina MiSeq platform was used for sequencing. The DIAMOND-MEGAN workflow and a Snakemake-based viral metagenomics pipeline were used to analyze the results. Consensus viruses detected with both pipelines were considered to be positive detections. Mycoviruses were found in 42 of 45 isolates. Most mycoviruses had positive-strand RNA and dsRNA genomes, and a small number had negative-strand RNA and single-stranded DNA (ssDNA) genomes. Hypovirulence-inducing mycoviruses, including Botrytis cinerea mitovirus 1, Botrytis cinerea endornavirus 1, and Botrytis cinerea hypovirus 1 were identified. In addition, promising ssDNA mycoviruses in the *Genomoviridae* family that may be infective extracellularly were detected. Further studies will be conducted on selected mycoviruses to determine the mechanisms that cause adverse phenotypes in *Botrytis*.

P80. More than one needle in a haystack — searching for *Epichloe* fungal endophytes in Canadian grasses M. LIU, P. SHOUKOUHI, W. CHEN, R. KHANAL, É. D. TREMBLAY, R. OTFINOWSKI, AND M. G. BAKKER *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, K.W. Neatby Building, 960 Carling Avenue, Ottawa, ON K1A 0C6 Canada; (R.O.) Department of Biology, University of Winnipeg, 515 Portage Avenue, Winnipeg, MB R3B 2E9 Canada; and (M.G.B.) Department of Microbiology, University of Manitoba, 45 Chancellors Cir, Winnipeg, MB R3T 2N2*

Fungi in the genus *Epichloe* (Fr.) Tul. & C. Tul. (Clavicipitaceae) have endophytic symbiotic relationships with cool-season grasses (Poaceae). The alkaloids produced by the fungus inside the grass can deter insects and are associated with drought resistance of host plants. These functions have been investigated for protecting grasses or cereal crops in many countries. In Canada, studies on *Epichloe* or other grass endophytes are lacking and vouchered germplasm is scarce. With the aim to explore these promising natural resources for sustainable agriculture, we validated the presence of fungal endophytes in the seeds and stems of cultivated barley, wild barley, and selected grasses through a meta-barcoding approach. Among the 96 samples are 19 lines of cultivated barley and wild barley seeds obtained from the Plant Germplasm Resource Centre (PGRC, Saskatchewan), 16 lines from the Agriculture and Agri-Food Canada barley breeding program, 15 wild barley specimens from the Canada National Collection of Vascular Plants (DAO), and miscellaneous grasses (potential hosts of *Epichloe*) collected from the Riding Mountain National Park (Manitoba) and Ottawa areas. *Epichloe* spp. were detected in 20 samples, including seeds or/and stems of *Achnatherum richardsonii* (Link) Barkworth, *Bromus* sp., *Elymus trachycaulus* (Link) Gould ex Shinners, *Glyceria striata* (Lam.) Hitchc., *Lolium arundinaceum* (Schreb.) Darbysh, *Hordeum bogdanii* Wilensky, and *H. roshevitzii* Bowden. In addition, we found species in *Alternaria*, *Fusarium*, *Penicillium*, and *Cladosporium*, etc. are common in the samples. However, the roles of these fungi, whether beneficial, pathogenic, or weak-pathogenic, in relation to their respective host plant need to be investigated.

P81. Evaluation of *Epicoccum nigrum* for suppression of *Monilinia vaccinii-corymbosi* in highbush blueberry production E. KITURA, Z. K. PUNJA, AND D. HENDERSON *Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada; and (D.H.) Institute for Sustainable Horticulture, 20901 Langley Bypass, Langley, BC V3A 8G9, Canada*

Monilinia vaccinii-corymbosi, the causal agent of mummy berry disease of highbush blueberry (*Vaccinium corymbosum*), is a significant pathogen which can reduce yields by up to 80% under certain conditions. In British Columbia (BC), highbush blueberry production has expanded from an annual $200 million industry to $7 billion in just over a decade, with 600 farms producing 86,000 tons of berries, accounting for 96% of Canada's overall production. *Epicoccum nigrum* is a naturally occurring, endophytic fungal species shown to be effective against *Monilinia* sp. in *Prunus* sp. (stone fruits) crops, but efficacy studies in highbush blueberry have not been conducted. Isolates of *E. nigrum* were obtained from surface-sterilized ripe healthy berries collected from an organic farm in the Fraser Valley of BC and grown on potato dextrose agar at 25˚C for 7 days. Morphological identification of *E. nigrum* and *M. vaccinii-corymbosi* from blueberry fruit was confirmed by PCR using ITS1 and ITS4 primers. A dual culture antagonism test and percentage inhibition of radial growth was conducted, which showed significant suppression of *M. vaccinii-corymbosi* by *E. nigrum*. This research will investigate the effect of *E. nigrum* as an antagonist against *M. vaccinii-corymbosi* in highbush blueberry, and provide efficacy data that could pave the way for the registration of a novel biological control product. Additional trials will investigate whether this novel endophytic biological control species can be incorporated into an integrated management plan to suppress plant pathogens, potentially providing a sustainable alternative to broad-spectrum chemical fungicides in highbush blueberry.

P82. Development of novel wheat-rust assay system for characterizing the mode of action of commercial fungicides and formulations on rust disease management M. LI, S. FORMBY, L. LIU, G. S. BRAR, A. ROZEK, AND G. BAKKEREN *Faculty of Land and Food Systems, The University of British Columbia, 2357 Main Mall, Vancouver, BC V6T 1Z4, Canada; (S.F.) Simon Fraser University, 8888 University Dr, Burnaby BC V5A 1S6, Canada; (A.R.) Terramera Inc. 199 W 6th Avenue, Vancouver BC V5Y1K3, Canada; and (L.L., G.B.) Agriculture and Agri-Food Canada, 4200 Highway #97 Summerland, BC V0H 1Z0, Canada*

Among the significantly different virulence, aggressiveness, and adaptation from worldwide pathogen populations, the quarantine measures of wheat rust fail to prevent the disease from entering Canada due to the arrival of new and potentially mutated rust spores blown in from Mexico via the US by common airflows known as the Puccinia pathways. In addition, rust fungi regularly evolve new strains that are highly virulent towards the current resistant wheat varieties available to farmers. Over the last decade, a complementary measure to control the occurrence and severity of rust diseases is fungicide application estimated as an average cost of over $17.25/acre annually in wheat field of Canadian Prairies. Even though

fungicides are targeted to fungal pathogens, they have also been reported to trigger some effects on the host plant. Therefore, our collaboration between industrial technology and wheat-rust research has developed an improved diagnostic system of plant genetics and formulation treatment that allows for dramatic reductions in the dose of synthetic fungicides required for wheat leaf rust control. Moreover, the comparative transcriptomic analysis among formulation-treated urediniospores, as well as on whole infected wheat plants has point towards the potential mode of actions (molecular mechanisms) of those commercial compounds and been used to identify biomarkers for diagnosing gene expression patterns and mimicking virulence-reducing and defense-enhancing effects in both fungus and host. Soon, this new system will generate significant cost savings and increase the options available to farmers, as well as reduce negative environmental impacts of synthetic fungicides while improving crop yield and quality.

P83. Reduction of clubroot with application of lime and / or boron on muck soil S. G. CHESNEY, B. D. GOSSEN AND M. R. MCDONALD *University of Guelph, 50 Stone Road East, Guelph, ON NIG 2W1, Canada; and (B.D.G.) Saskatoon Research and Development Centre*, *Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK Z7N 0X2, Canada*

Soil amendment with lime or boron can reduce clubroot (*Plasmodiophora brassicae* Wor.) severity. However, the effect of added lime has not been studied in muck (very high organic matter) soils. A study was conducted to assess the effect of lime and boron on clubroot severity on canola (*Brassica napus* L.) on muck soil at the Ontario Crops Research Station-Bradford. One field trial was conducted in 2021 and two in 2022. All studies were arranged in a RCBD with four replicates. Lime was applied as hydrated lime (calcium hydroxide), selected for its rapid effect on soil pH, except for one field trial treated with standard lime (calcium carbonate) applied the previous fall and supplemented with hydrated lime in spring to achieve the pH targets. The target pH in each study was 7.0 and 7.5, with a base pH ~ 6.4. Boron was applied as Solubor, at 16 kg B ha^{-1}. After application and incorporation of treatments, the trials were seeded with a clubroot susceptible canola cultivar and assessed for clubroot severity 6 weeks later. In addition, controlled environment studies using soil-less mix were conducted and repeated. Lime reduced clubroot severity in both sites in 2022 and there was a negative correlation between achieved pH and clubroot in all trials; achieving a pH ≥ 7.0 was essential to reduction in clubroot severity. Boron at 16 kg ha^{-1} produced a small reduction in clubroot severity in some of the trials, and there was no interaction between lime and boron.

P84. Soilless cultivation of raspberry: A two-year case study on fire blight with the cultivars Prelude, Killarney, and Tulameen M. DELISLE-HOUDE, F. DEMERS, V. TREMBLAY, S. TELLIER, AND R. J. TWEDDELL *Département de phytologie, Université Laval, 2425 rue de l'Agriculture, Québec, QC G1V 0A6, Canada; (F.D.) Club les productions Écolo-Max inc., 1036, chemin Saint-Joseph, Lévis, QC G7A 2N7, Canada; and (S.T.) Ministère de l'Agriculture, des Pêcheries et de l'Alimentation du Québec, Direction régionale Capitale-Nationale et Chaudière-Appalaches, 1685 boulevard Wilfrid-Hamel, Québec, QC G1N 3Y7, Canada*

In Québec province, cultivation of raspberry (*Rubus idaeus* L.) has changed a lot in the last decade with increasing of popularity of soilless growing systems. Fire blight (*Erwinia amylovora*), a destructive disease in some Rosaceae, is poorly studied in raspberry and still less in the new growing systems. In other horticultural crops such as apple (*Malus domestica* Borkh.), management of fire blight is based on predictive models where the protection against blossom infection is a key point. In this study, weather data (cumulative daily precipitations, daily temperatures, wetness), blooming patterns, and fire blight incidence were collected for two years (2021-2022) in a soilless red raspberry (cultivars: Prelude, Killarney, Tulameen) growing system to highlight some key points leading to the development of the disease. This study showed that the three cultivars were very susceptible to fire blight in a soilless growing system regardless of weather conditions and that time and intensity of bloom (blooming patterns) varied a lot between cultivars. Blooming peaks, precipitations, and consecutive days with high average daily wetness appeared as the main parameters leading to an important increase of disease incidence. The results of this study could help to develop a predictive model in raspberry to determine the best times to applied phytosanitary products to control fire blight.

P85. An overview of the Prairie Crop Disease Monitoring Network, 2018-2023 T. K. TURKINGTON, R. WEISS, M. VANKOSKY, J. OTANI, M. FERNANDEZ, AND E. SVENDSEN *(T.K.T) Lacombe Research and Development Centre, Agriculture and Agri-Food Canada (AAFC), 6000 C&E Trail Lacombe, AB T4L 1W1, Canada; (R.W., M.V., E.S.) Saskatoon Research and Development Centre, AAFC, 107 Science Place, Saskatoon, SK S7N 0X2, Canada; and (J.O.) Beaverlodge Research Farm, AAFC, Beaverlodge, AB T0H 0C0, Canada; and (M.F.) Swift Current Research and Development Centre, AAFC, Swift Current No. 137, SK S0N 2Y0, Canada*

The Prairie Crop Disease Monitoring Network (PCDMN) was established from 2018-2023, using the successful Prairie Pest Monitoring Network (PPMN) as a template. Objectives of the PCDMN were to 1) establish a network as part of an overall disease monitoring initiative for Alberta, Saskatchewan and Manitoba; 2) to develop surveillance protocols for key field crop diseases; 3) to issue weekly forecasts for Prairie cereal rust risk from the USA; 4) to facilitate the development of GIS mapping capacity for disease surveillance results; and 5) to assist with training and resources related to disease identification, scouting and management. The PCDMN Twitter feed was established in spring 2019, while the PCDMN blog was initiated in June, 2020. The blog has sections and posts related to cereal rust risk, disease scouting cards that illustrate typical symptoms and key management strategies, and recommended disease scouting, survey and biosecurity protocols. During the summers of 2019-2022, 8-10 cereal rust risk reports were released on a weekly basis from mid-May to early-mid July. Disease scouting cards were developed for key diseases of canola, wheat, barley and pulses, especially those where timely scouting is needed in relation to risk assessment and fungicide need. Five disease

monitoring protocols were also developed for: canola – blackleg and sclerotinia stem rot; wheat – end-of-season leaf spot assessment; barley – end-of-season leaf spot assessment; and field pea – Ascochyta/Mycosphaerella assessment.

Other

P86. Investigating the nectar associated microbiota of stone fruit crops V. VENUGOPAL, C. SHUM, M. RAIZADA, AND J. SUBRAMANIAN *Department of Plant Agriculture, Ontario Agricultural College, University of Guelph, Guelph, Ontario, N1G 2W1*

Several microorganisms that are essential for plant health and growth have evolved alongside plants. In contrast to using a single beneficial species, the plant microbial communities said to increase the effectiveness, reliability, and consistency of the plant growth and overall well-being. Therefore, the objective of this study was to extensively characterize the nectar microbiome of six major Prunus species with two varieties in each species (peach, Japanese plum, European plum, sweet cherry, sour cherry, and apricot). Bacterial16s rRNA amplicon sequencing using the high-throughput Illumina Miseq, targeting V4 variable region were used to analyse the bacterial communities associated with these *Prunus* spp. Our results indicated that, different *Prunus* spp., shared unique bacterial assemblage. Interestingly, Actinobacteria was the most abundant phylum, followed by Proteobacteria and Firmicutes. To our knowledge this is the first report of such microbiome study in the nectar of *Prunus* spp. These results could facilitate to understand the interaction of endophytic bacteriota with the *Prunus* genome and could support to identify the endophytes among the stone fruit crops and their relationship with various biotic and abiotic resistance.

P87. Do Haskap varieties keep their promises in northern Québec? J. LAJEUNESSE, M. BELLEMARE, P.LAFONTAINE, A. -A. COUTURE , J. BRIÈRE, AND P. -O. MARTEL *(J.L., M.B.) Research Farm, Quebec Research and Development Centre, Agriculture and Agri-Food Canada, 1468 Saint-Cyrille St., Normandin, QC G8M 4B8, Canada; (P.L., A.-A.C., J.B.) Carrefour industriel et expérimental de Lanaudière, 801A rang Bas L'Assomption Nord, L'Assomption, QC J5W 2H1, Canada; and (P.-O.M.) Direction régionale du Saguenay-Lac-Saint-Jean, Ministère de l'Agriculture, des Pêcheries et de l'Alimentation du Québec,801 chemin du Pont Taché Nord, Alma, QC G8B 5B7, Canada.*

Haskap (*Lonicera caerulea*) is an extremely hardy plant with early ripening fruits. To reduce production costs, the introduction of high-yielding cultivars suitable for mechanized harvesting under our conditions is essential for growers, but there is a lack of information on the productivity and characteristics of new varieties. In 2020, fourteen (14) varieties, including two controls (Berry blue and Indigo Gem), were planted under plastic mulch with an irrigation system in three replications at Normandin. In 2021, yields ranged from 4.5 g to 89.7 g of fruit per plant. Boreal Beauty and Boreal Blizzard had the highest yields (89.7 g plant^{-1} and 80.4 g plant^{-1}, respectively), while Blue Banana had the lowest yield (4.5 g plant^{-1}). In 2022, fresh fruit yields ranged from 22.8 g plant^{-1} to 382.1 g plant^{-1}. Again, Blue Banana had the lowest yields and Kapu (Solo) (382.1 g plant^{-1}) had the highest yields with Boreal Beauty (376.9 g plant^{-1}). A plant with an erect growth habit is more suitable for mechanical harvesting. The cultivars Vicky (Zojka) and Indigo Gem had a spreading growth habit, while the other 12 cultivars tested had an erect growth habit. At this point, several varieties show promise. However, blue banana yields have been disappointing in the two years of evaluation. The plants of the tested varieties are not mature and more data on agronomic performance and plant development are needed to determine which of these varieties have the best yield potential and desired characteristics for the target market.

P88. Integrating bio-strip tillage into overwintering cover crop mixtures prior to grain corn (*Zea mays* L.) F. YASMIN, J. NASIELSKI, K. SCHNEIDER, AND L. L. VAN EERD *School of Environmental Sciences, University of Guelph Ridgetown Campus 120 Main Street East, Ridgetown, ON, N0P 2C0, Canada; (J.N., K.S.) Department of Plant Agriculture, University of Guelph 50 Stone Road East, Guelph, ON, N1G 2W1, Canada.*

Bio-strip tillage is alternate strips of overwintering and winter-terminated cover crops (CCs) to improve seedbed conditions at corn planting. In a soybean-winter wheat-CC-corn rotation at four site-years in Ontario, the efficacy of bio-strip tillage on corn yield was tested (alpha=0.05) in a split-plot design experiment with four replications. Main-plot treatments were a control (noCC), RYE (*Secale cereale* L.), hairy vetch (HV; *Vicia villosa*, Roth), RYE/HV biculture and polyculture (RYE/HV/kale (*Brassica oleracea* L. var. *acephala*)/sunflower (*Helianthus annuus* L.)). Split-plot treatments were no-till, fall-strip-till, bio-strip-radish and bio-strip-mix of 4 winter-terminated species. Overwintering CCs and bio-strips were planted in early August. Compared to the no-till treatment (i.e., overwintering CC), both bio-strip tillage treatments consistently produced greater fall CC biomass at freeze-up (265.0±28 to 2835±178 kg ha^{-1} depending on the site-year). The polyculture CC treatment had the greatest fall biomass (315.0±24 to 3050±297 kg ha^{-1} at New Liskeard and Ridgetown, respectively). In the following spring, the CC with the greatest amount of biomass varied across site-years. At Ridgetown, corn grain yield was 1.5 Mg ha^{-1} greater with HV but 1.4 Mg ha^{-1} lower with RYE than the noCC control (12.4±0.24 Mg ha^{-1}). At New Liskeard, the biculture decreased yield by 1.68 Mg ha^{-1} than noCC but other CC treatments were intermediary. At Winchester, CCs did not impact corn grain yield in either year. The lack of tillage system effect and no interaction with CC (except one site-year, suggests that any of the tested tillage systems can be adapted with appropriate CC species.

P89. Vapors of essential oils from five Nordic plant species: insecticidal and acaricidal activity A. ROY-LEMIEUX, M. DELISLE-HOUDE, AND R. J. TWEDDELL *Département de phytologie, Université Laval, 2425 rue de l'Agriculture, Québec, QC G1V 0A6, Canada*

Mites and aphids cause significant economic losses in horticultural crops. Several studies reported the efficacy of plant essential oils (EOs) to control pests in horticultural crops. The present study investigated the insecticidal/acaricidal activity of the volatile components (vapors) of EOs from five Nordic plant species, namely Labrador tea (*Ledum groenlandicum* Retzius), sweet gale (*Myrica gale* L.), black spruce [*Picea mariana*

(Mill.) Britton, Sterns & Poggenburgh], jack pine (*Pinus banksiana* Lamb.), and balsam poplar (*Populus balsamifera* L.), against spider mite (*Tetranychus urticae*) and aphid (*Rhopalosiphum padi*). Spider mites/aphids were placed in a hermetic glass chamber and exposed to vapors of each EO. After an exposition period of 6 hours (aphids) or 24 hours (spider mites), the mortality rates of spider mites/aphids were determined. All EOs tested caused high mortality rates of both spider mites and aphids at the highest concentrations tested. The study revealed the insecticidal and acaricidal activity of EOs of Labrador tea, sweet gale, black spruce, jack pine, and balsam poplar. In future works, it would be interesting to investigate the toxicity of these EOs against other common pests of horticultural crops.

P90. Phytotoxic activity of essential oils from different Nordic plant species A. ROY-LEMIEUX, M. DELISLE-HOUDE AND R. J. TWEDDELL *Département de phytologie, Université Laval, 2425 rue de l'Agriculture, Québec, QC G1V 0A6, Canada*

Essential oils (EOs) of several plants such as lemon-scented gum [*Corymbia citriodora* (Hook.) K.D. Hill & L.A.S. Johnson], common thyme (*Thymus vulgaris* L.), and mint (*Mentha* spp.) are well known for their phytotoxicity. This study investigated the phytotoxic activity against Powell's amaranth (*Amaranthus powellii* S. Watson) and rye (*Secale cereale* L.) of EOs from five Nordic plant species, namely Labrador tea (*Ledum groenlandicum* Retzius), sweet gale (*Myrica gale* L.), black spruce [*Picea mariana* (Mill.) Britton, Sterns & Poggenburgh], jack pine (*Pinus banksiana* Lamb.), and balsam poplar (*Populus balsamifera* L.). Seeds of Powell's amaranth or rye were placed in an airtight glass chamber and exposed to vapors of either balsam poplar, black spruce, jack pine, Labrador tea or sweet gale EO for 120 hours. The hypocotyl elongation (length) was then measured with a ruler. The experiment was conducted as a completely randomised design with six replicates. Results showed that vapors of all tested EOs strongly inhibit seed hypocotyl elongation for both Powell's amaranth and rye. Vapors of Labrador tea EO completely inhibited hypocotyl elongation. Based on hypocotyl elongation, vapors of all tested EOs were shown phytotoxic.

P91. Effects of insecticide and tolerant alfalfa cultivars on potato leafhopper (*Empoasca fabae*) populations and forage yields in Quebec X. SHI, P. SEGUIN, J. SAGUEZ, H. MARTEL, AND A. CLAESSENS *(X.S., P.S.) McGill University, Sainte-Anne-de-Bellevue, QC, Canada, H9X 3V9; (J.S.) Centre de Recherche sur les Grains, Saint-Mathieu-de-Beloeil, QC, Canada, J3G 0E2; (H.M.) Ministère de l'Agriculture, des Pêcheries et de l'Alimentation du Québec, Sherbrooke, QC, Canada, G1R 4X6; and (A.C.) Quebec Research and Development Centre, Agriculture and Agri-Food Canada, Québec, QC, Canada, G1V 2M2*

The potato leafhopper [PLH, *Empoasca fabae* (Harris), Hemiptera: Cicadellidae], which affects several crops including alfalfa (*Medicago sativa* L.), is a recurrent problem in several regions in the province of Quebec. The objective is to evaluate alfalfa management tools in order to reduce yield losses caused by this pest. An experiment was conducted at two sites over three field seasons to evaluate the impact of insecticide applications and the use of PLH-tolerant cultivars on forage yield and PLH populations. When PLH populations reached the economic threshold, insecticide was applied at both sites. Foliar insecticide applications in the seeding year reduced PLH populations but generally failed to increase alfalfa yields compared to untreated alfalfa. However, at one site, three applications conducted in the seeding year resulted in increased first-cut alfalfa yields in the post-seeding year compared to untreated alfalfa, even if PLH populations were low. Differences in alfalfa yields between PLH-tolerant and PLH-susceptible cultivars were minimal in the seeding and post-seeding years regardless of the PLH population levels. However, at one site, two PLH-tolerant cultivars produced lower alfalfa yields compared to other cultivars in the post-seeding year. Preliminary results suggest that foliar insecticide applications and harvesting could be more effective ways to reduce PLH populations than the use of PLH-tolerant cultivars. However, more data will be required to confirm these results and determine the impact of these management tools on alfalfa yields.

P92. Characterizing the growth, harvest parameters, disease and arthropod susceptibility of *Vitis vinifera* cultivars in Quebec, Canada A. HÉBERT-HACHÉ AND C. PROVOST *Centre de recherche agroalimentaire de Mirabel,9850 Rue de Belle Rivière, Mirabel, QC J7N 2X8*

The production of the European grapevine, *Vitis vinifera,* comes with challenges such as high disease susceptibility and poor cold hardiness, and little information is available on its growth in Quebec's climate. This project aimed to characterize the agronomic properties of the main *V. vinifera* cultivars in five viticultural regions of Quebec. The study was carried out in ten commercial vineyards over two years (May 2021 to May 2023). In both years, phenological development occurred over a short window, approximately mid-May to early October. The vines were in the late stages of cold acclimation by the time cold protection strategies (e.g., geotextiles) were deployed. Primary bud survival was site-specific and not related to cultivar, ranging from 2% to 98%. Pest (e.g., leafhoppers, Japanese beetles) and disease (black rot, powdery and downy mildew,) susceptibility was similar among cultivars and severity was associated with site management. Harvest parameters were variable among sites and between years. Yields of Chardonnay, for example, varied from 2.69 ± 1.09 kg/vine (mean ± standard deviation, n = 6) in 2021 to 1.09 ± 1.43 kg/vine (n = 5) in 2022. Berry composition at harvest indicated low maturity levels (< 20 Brix, > 10 g tartaric acid/L), particularly for the colder sites and the Riesling cultivar. From this study, cultivar suitability to Quebec viticultural areas can be determined. Gaining a better understanding of the *V. vinifera* behaviour in Quebec will help the industry's sustainability by assisting in the decision-making process when establishing new vineyards.

P93. Evolution and diversity of *ToxA* across multiple fungal speciplant disease M. HAFEZ, M. TELFER, R. GOURLIE, M. A. CARMONA, F. J. SAUTUA, C. S. MOFFAT, P. M. MOOLHUIJZEN, P. T. SEE, M. MCDONALD, AND R. ABOUKHADDOUR *Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre, Lethbridge, AB, Canada; (M.A.C., F.J.S.) Cátedra de Fitopatología, Facultad de Agronomía, Universidad de Buenos Aires, Buenos Aires, Argentina; (C.S.M., P.M.M., P.T.S.) Centre for Crop and Disease Management, School of Molecular and Life Sciences, Curtin University, Australia; and (M.M.) University of Birmingham, Edgbaston, Birmingham, United Kingdom*

ToxA is a proteinaceous effector produced by fungal plant pathogens that induces necrosis. It is one of the most studied effectors, and its encoding gene, *ToxA*, was first identified in the tan spot pathogen and later in several species in the leaf spot complex. In this study, we examined the genetic diversity of *ToxA* in a large collection of *Pyrenophora tritici-repentis* (Ptr) isolates (422) from different regions, including North and South America, Europe, North Africa, Asia, and the Fertile Crescent. The generated sequences of *ToxA* ORF in this study and in addition to other sequences released from various species were analysed for polymorphisms and mutation types. We revealed the presence of 27 different *ToxA* haplotypes across multiple species worldwide and constructed a haplotype network using PopART to show their genetic and evolutionary relationships. We collaborated with other scientists working on the *ToxA* gene and other effectors and released a revised nomenclature to resolve confusion in the literature. Furthermore, we discovered four additional haplotypes of *ToxA* in Ptr, which is a significant finding since only one haplotype had been reported in this species over the past 30 years. We observed that the spetoria nodorum pathogen had the highest gene diversity with a higher ratio of nonsynonymous mutations. In contrast, the gene in tan spot and spot blotch pathogens were less diverse and had a higher ratio of synonymous mutations. Exploring *ToxA* in these important cereal pathogens may reveal unknown aspects of their evolution.

P94. Toward the identification of a novel necrotrophic effector secreted by *Pyrenophora tritici-repentis* M. HAFEZ AND R. ABOUKHADDOUR
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Three necrotrophic effectors have been identified worldwide in the tan spot pathogen, *Pyrenophora tritici-repentis* (Ptr). ToxA is a necrosis-inducing effector, and ToxB and ToxC are two different chlorosis inducing effectors. In our lab a number of Ptr isolates were confirmed to cause necrosis on ToxA-sensitive wheat genotypes, yet these isolates lacked the *ToxA* gene. The aim of this work was to identify the unknown necrotic effector in one of these isolates (SW21-5), which is a ToxC-producer recovered from durum wheat in Canada. A combination of protein purification methods (i.e. size exclusion and ion-exchange) have been used to fractionate the secreted proteins into several fractions based on the size and/or net charges. Protein fractions were then used to infiltrate differential wheat genotypes, then rated for necrosis symptoms. The necrosis-inducing effector in SW21-5 ranged in size between 3 to 30 KDa with a net positive charge. Denaturing with heat resulted in disappearance of necrosis, confirming the proteinaceous nature of this effector. The fraction that induced necrosis was subjected to protein identification using Mass Spectrometry (LC-MS/MS), and a total of 326 proteins have been identified. Functional annotation of identified proteins has been done against the database for the SW21-5 complete genome sequence. Out of 326 total identified proteins, 21 were found to be predicted effectors with no function annotation, among these, five are unique to SW21-5 and might contain the novel necrotic effector. In order to identify the novel effector from SW21-5 Ptr isolate, these 5 predicted effector proteins will be heterologously expressed and then used to infiltrate differential wheat genotypes.

P95. Functional characterization of a barley thaumatin-like protein using CRISPR-Cas9 C. KAYE, I. IQBAL, R. TRIPATHI, W. Y. CHEN, J. SINGH, M. SINGH, R. KAUR, Z. ZHOU, P. KANDPAL, AND J. SINGH *Department of Plant Science, McGill University, Macdonald Campus, 21 111 Lakeshore Road, Sainte-Anne-de-Bellevue, QC H9X 3V9, Canada*

Thaumatin-like protein 8 (TLP8), a protein expressed in barley (*Hordeum vulgare*), has been identified as a candidate for the enhancement of malting cultivars. TP8 has been shown to bind (1, 3, 1, 4)-β-D-glucan and may be involved in its breakdown during germination, but this interaction has not yet been fully characterized. The glucanase activity of a recombinant TLP8 protein purified from *e. coli* will be evaluated using a glucanase assay. As well, the function of the *HvTLP8* gene will be investigated using CRISPR-Cas9. Knockout plants will be created to evaluate if TLP8 expression correlates with the breakdown of (1, 3, 1, 4)-β-D-glucan in the grain during germination. The gene encoding hygromycin phosphotransferase (hpt) expressed under the cauliflower mosaic virus promoter (35S) will be used as a selectable marker for the identification of transgenic tissues. In this study, we aim to gain insight into the function of TLP8 in germinating barley grain.

P96. Disease resistance in *Hordeum vulgare* sbsp. *spontaneum* accessions and in lines derived from interspecific crosses with wild Hordeum species M. JABOOBI, M. AMOUZOUNE, H. HIDDAR, A. AMRI, AND S. REHMAN; (M.J., M.A., H.H., A.A., S.R.) *International Center for Agricultural Research in the Dry Areas, ICARDA-Al-Irfane, Rabat, Morocco; (M.A.) Université Ibn Tofail, Faculté des Sciences, Kenitra, Morocco; (H.H.) Microbiology and Molecular Biology Laboratory, Faculty of Sciences, Mohammed V University Rabat, Morocco; and (S.R.) Field Crop Development Center, The Olds College, Lacombe, Alberta, Canada*

Barley (*Hordeum vulgare L.*) ranks fourth among the most important cereal crops worldwide and it is produced for food, feed, and malting purposes. Foliar diseases, mainly powdery mildew (PM), net blotch (NB), scald (SC), yellow and leaf rusts, and barley yellow dwarf virus (BYDV), cause significant reductions in yield and quality all over the barley growing areas. Crop wild relatives, exclusively, *Hordeum vulgare* ssp. *spontaneum* and *H. bulbosum*, are important genetic resources needed to develop new adapted varieties. In this study a total of 117 accessions of *H. spontaneum* from different origins and 145 lines derived from crosses between barley and *H. bulbosum* supplied by NordGen were evaluated for field reactions to four major diseases. In addition, a set of 45 lines derived from interspecific crosses with *H. spontaneum* and *H. bulbosum* along with 10 checks were evaluated for agronomic traits and yield performance under four different environmental conditions and for quality attributes. The results showed that 37.7%, 71.6%, 15.1%, and 79.5% of *H. spontaneum* accessions were resistant to moderately resistant to net form net blotch, scald, leaf rust and powdery mildew, respectively, while the respective percentages in case of *H. bulbosum* derivatives were 31%, 20.4%, 17.9% and 70.6%. Only three accessions of *H. spontaneum* showed high resistance levels to the four diseases while 23 other accessions and

16 *Bulbosum* derived lines showed resistance to a combination of two to four diseases. Pre-breeding efforts need to be strengthened further by evaluating more wild barley accessions, their crossing with the best available parents and selection of elite germplasm to be made available to barley breeding programs for the development of new adapted and high yielding varieties.

P97. Uncovering genetic population structure of *Puccinia coronata* f. sp. *avenae* in Canada and identifying novel sources of resistance in oat B. YADAV, K. NILSON, AND G. BRAR *(B.Y., G.B.) Faculty of Land and Food Systems, The University of British Columbia – Vancouver Campus, BC; and (K.N.) Agriculture and Agri-Food Canada - Brandon, MB*

Oat crown rust (*Puccinia coronata* f. sp. *avenae*) is a destructive fungal disease that causes significant yield losses in oat crops in Canada. The genomic diversity of the pathogen population is crucial for understanding its adaptation and evolution to new hosts and environments. In this study, we aimed to detect the genomic diversity of the *Puccinia coronata* f. sp. *avenae* (*Pca*) population in Canada using high-throughput sequencing data. We obtained genomic data from 83 *Pca* isolates collected from various locations across Canada. We genotyped all isolates using Illumina NovaSeq 6000 sequencing (target depth 10X) and used bioinformatics pipelines to process the sequencing data, including quality control, mapping, and variant calling. We then performed population genetic analysis to evaluate the level of genetic diversity and population structure within the pathogen population. Our preliminary results showed that the *Pca* population in Canada is highly diverse, with a high level of genetic variation among isolates. Our preliminary results suggest a clear structure in the population, with different geographic regions i.e., Eastern Prairie region and Eastern Canada, exhibiting distinct patterns of genetic differentiation with time. To strengthen our findings, we are working with various statistical tools and validations. We also focusing on several candidate genes associated with virulence, which may play a role in the adaptation of the pathogen population to different environments. In conclusion, our study provides new insights into the genomic diversity of the *Puccinia coronata* f. sp. *avenae* population in Canada, which will be valuable for understanding the evolution and adaptation of the pathogen population to new hosts and environments. This scientific research will support the development of effective strategies for controlling oat crown rust in Canada.

P98. Genes in soybean contributing to quantitative resistance against *Sclerotinia sclerotiorum* L. BUCHWALDT, A. DAVIES, F. FU, M. BUCHWALDT, J. DURKIN, ELROY COBER *(L.B., A.D., F.F., M.B., J.D.) Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science place, Saskatoon, SK, S7V 0x2, Canada; and (E.C.) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, K1A 0C6, Canada*

The acreage planted to soybean (*Glycine max* L.) continues to increase in western Canada, and with this comes a risk of yield loss caused by the fungal pathogen *Sclerotinia sclerotiorum* (Lib. de Bary). The objectives were to develop a method for phenotyping of soybean lines for quantitative resistance to sclerotinia, to identify lines with a combination of resistance and early maturity for breeding of new varieties, and subsequently to identify genes contributing to the resistant trait. Initially 341 varieties and breeding lines were phenotyped in the field for resistance by inoculating stems of flowering plants with mycelium of *S. sclerotiorum* (isolate MB51) grown on PDA. Disease severity was rated as lesion length and percent wilted plants 14 days after inoculation. Lines with quantitative resistance and 82-96 days to maturity were 38777 (Japan), Zarja (Bulgaria), Wielnska Brunatna (Hungary), B/34 (Germany) and No. 128/49 (USA). A sub-set of 192 lines with the most consistent sclerotinia phenotypes in replicated test were genotyped with a 50,000 SNP array (Illumina). Sclerotinia phenotypes and SNP genotypes were combined in a genome wide association study which resulted in identification of 565 SNPs on chromosomes 5, 6, 9, 10, 11, 13 and 19 each explaining 22-25% of the sclerotinia trait; 175 SNPs occurred in genes including 40 known defense genes such as *SYNTAXIN OF PLANTS* (SYP121), *HEVEIN* (PR4), *DEFENSIN* (PDF2.1), *MLO12*, *ETHYLENE-RESPONSE-FACTOR1* (EIN3), *CHITINASE*, *WRKY6* and several genes with TIR-NBS-LRR domains. SNPs in these genes can be utilized for selection of sclerotinia resistant progenies in a breeding program.

P99. Mining PGRC genebank wheat accessions for resistance to stripe rust J. S. GILL, E. M. C. ACODE, N. KUMAR, H. R. KUTCHER, AND G. S. BRAR *Faculty of Land and Food Systems, The University of British Columbia, 2357 Main Mall, Vancouver, BC V6T 1Z4, Canada; and (E.M.C.A, H.R.C.) Crop Development Centre/Department of Plant Science, University of Saskatchewan, 51 Campus Dr., Saskatoon, SK S7N 5A8, Canada*

Stripe rust of wheat is caused by *Puccinia striiformis* Westend f. sp. *tritici* Eriks (*Pst*) and is one of the five priority-one diseases in Canada. Host resistance and growing resistant varieties is one of the most effective management strategies. Resistance to stripe rust in wheat is classified into adult-plant resistance (APR) or all-stage or seedling resistance (ASR) depending on the growth stage of the plant when resistance is active. Our study utilized the top 84 Plant Gene Resource of Canada (PGRC) wheat accessions expressing some level of APR to stripe rust in preliminary research. Our aim was to determine whether the top 84 accessions only have APR or if the resistance conferred by them is ASR. The accessions were screened with three Pst races: C-PST-1 (isolate W034), C-PST-5 (isolate W057), and C-PST-33 (isolate W034). The race C-PST-1 is the most common in western Canada and the other two races has wider virulence spectrum (i.e. virulent on most *Yr* genes). Seedling screening demonstrated variation in phenotypic expression of the studied wheat accessions. Of all the entries, 28 expressed ASR to C-PST-1, 56 to C-PST-5, and 46 to C-PST-33. Some accessions that may carry novel unknown APR could be subjected to genetic mapping of resistance.

P100. Rapid domestication of *Rubus arcticus* for controlled environment agriculture S. M. CLARK, A. TODD, T. ORR, D. CRAM, D. KONKIN, AND AMR FERRIE *National Research Council of Canada, 110 Gymnasium Place, Saskatoon, SK, S7N 0W9, Canada*

Food security in northern and remote regions within Canada is a well-documented issue which disproportionately impacts Indigenous communities. Controlled environment agriculture (CEA) can provide a source of food sovereignty and also be part of a larger effort to address food security problems. Some communities are exploring this option but significant issues exist regarding both the variety of plants that can be grown economically and the energy requirements involved. We have initiated a number of projects to better understand the challenges communities face including expanding the available options of berry producing species. *Rubus arcticus* is an herbaceous ground cover raspberry species that is found across Canada and northern Europe. This species, known for its nutritious berries, has potential as a CEA crop but has not been adapted for this purpose. Gene editing can provide a method to rapidly domesticate orphan species to improve agronomic traits and increase productivity. We have sequenced the genome of *R. arcticus* with Oxford Nanopore and PacBio technology, generated Hi-C chromosome contact data and conducted RNA sequencing of a number of tissues to generate resources for candidate gene identification. Gene editing methods have been developed and validated while targeting the phytoene desaturase gene. Work is now ongoing to improve the flowering characteristics of this species and create self-compatible flowers, with a number of candidate genes being evaluated. The rapid domestication of *R. arcticus* will expand the plant species options available to communities exploring a CEA approach to promoting food sovereignty.

P101. Early detection of abiotic-stressed crop health using electrical signals G. WEN AND B. L. MA. *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa ON K1A 0C6 Canada*

Drought and high temperature are major constraints on crop production. Quantification of physiological and morphological responses is generally used to identify the health gradient of crops under unfavorable environments. However, traditional measurements of these responses are time-consuming and laborious, sometimes requiring destructive sampling. In this study, we developed an electrical sensor-based signal platform and examine its feasibility for early quantifying plant root morphological and leaf photosynthetic features without damaging the plants. A series of water- and temperature-controlling experiments were conducted using canola and oat as model crops. Results showed that plant photosynthetic capacity and root architectural traits were significantly varied by 10- or 15-day heat and drought treatment. The stressed environment decreased grain yield by 30-80% depending on the extent of stress and species. Results of Pearson's correlation analysis showed that signal measurement explained at least 33%, 55%, and 73% of canola root traits in 1, 5, and 10-min, respectively, but 3-5% lower for oat root quantification due to the complex and complete underground root structure caused by high plant density (25 oat plants per pot vs. 1 canola plant per pot). For both crops, over 65% of photosynthetic traits, such as photosynthesis and respiration rates were stimulated within 30 min. Furthermore, 1-h signal measurement could explain over 80% of yield variation and 85% above-ground biomass accumulation based on random forest prediction. Our study indicated that electrical signal measurement is a promising method to quickly identify stress-induced crop health status, enabling plant breeders to select stress-tolerant traits, and allowing crop growers to take preventive measures when needed.