Canadian Society of Agronomy
La Société Canadienne d'Agronomie

THE CANADIAN PHYTOPATHOLOGICAL SOCIETY
LA SOCIÉTÉ CANADIENNE DE PHYTOPATHOLOGIE

CANADIAN SOCIETY FOR HORTICULTURAL SCIENCE
LA SOCIÉTÉ CANADIENNE DE SCIENCE HORTICOLE

TRI-SOCIETY
VIRTUAL CONFERENCE
JULY 5-9, 2021

INNOVATION IN PLANT SCIENCE AND AGRICULTURAL RESILIENCE

Message from the Chair

Dr. Guillaume J. Bilodeau, Chair of the Virtual Organizing Committee

Dear colleagues, on behalf of the Virtual Organizing Committee, I am honored and delighted to welcome you to this virtual Tri-Society Conference with the Canadian Phytopathological Society (CPS), the Canadian Society of Agronomy (CSA) and the Canadian Society for Horticultural Science (CSHS).

This meeting will bring together researchers in plant science with a around the theme on "Innovation in Plant Science and Agricultural Resilience". There will be scientific programming daily from 11 AM to 5 PM EST (8 AM–2 PM PST). Scientific sessions will consist of pre-recorded videos followed by interactive discussions with the presenters. Videos from the meeting will be available on-demand for registrants from July 9th to July 23rd. Our program features talks from keynote speakers and societies awardees on the topics of genetics, biotechnology, and breeding; genomic applications for crop improvement; plant, soil health and the microbiome; climate change; innovations in agronomy and innovations for pre- and post-harvest quality. We will have virtual meeting rooms which will offer opportunities for you 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 for best flash presentations, oral and poster sessions. We will also have rooms with planned student activities, including advice on career progression, fun games and contests. I want to thank all the meeting committees and chairs and our sponsors who have helped keep the costs of this conference down. We could not have a successful conference without you. We received 170 abstracts and will see over 300 attendees. Your participation makes this event a success, thank you! I wish you a great week with this 5 day conference followed with two workshops the following week. Have a good meeting!

Scientific Program Schedule Monday, July 5

Start times	Abst no	Monday July 5	Minutes
10:00		**Introduction to the day and invited keynote speaker by Guillaume Bilodeau**	3-5
	1	**Session 1. Charles Brummer:** Crop improvement for an uncertain future.	25
10:30		**Live QA1 on Zoom**	15
		Session 2. Student oral competition: Genetics, Biotechnology, and Breeding	
	2	Abstract withdrawn	
10:45	3	Longfei Wu - Identification of quantitative trait loci associated with partial resistance to Fusarium root rot and wilt caused by Fusarium graminearum in field pea	12
	4	Momna Farzand - Mapping quantitative trait loci associated with stripe rust resistance from Canadian wheat cultivar AAC Innova.	12
	5	Sherry Sun - Delineating the SAR pathway in common hexaploid wheat	12
	6	Varinder Sidhu - Interactions between light quality and plant hormones signaling to control flower bud induction in day-neutral strawberry.	12
	7	Mohsen Yoosefzadeh Najafabadi - Using Hyperspectral Wide Association Study (HWAS) and Machine Learning-Mediated Genome Wide Association Study (GWAS) for Identifying Yield QTL in Soybean from Reflectance Bands and Yield Component Traits	12
	8	Amanda Seto - Unravelling RNA helicases in Ustilago maydis and their role during teliospore dormancy and germination	12
12:00		**Live QA2 on Zoom**	20
12:20		**Networking**	50
		Session 3. Student oral competition: Genetics, Biotechnology, and Breeding	
1:00	9	Monique Lariviere - Natural antisense transcripts and stress response in Ustilago maydis	12
	10	Matthew Wengler - Good things come to those who bait: using fungal effector proteins to identify host targets	12
	11	Rasanie Padmathilake. Does trophic switch of Leptosphaeria maculans happen under both incompatible and compatible interactions with canola (Brassica napus)?	
	12	Venessa Clemis - IdentifiIdentification and characterization of novel powdery mildew resistance genes in flax	12
	13	J. Duncan Giebelhaus - Gibberellin regulation of protein accumulation in developing pea (Pisum sativum L.) seeds	12
	14	Heather Tso - A single base extension assay for pathotyping clubroot [Plasmodiophora brassicae] of canola	12
2:00		**Live QA3 on Zoom**	15
		Session 4. Student oral competition: Innovations for Pre- and Post-harvest Quality	
2:15	15	Amadou Sidibé - Preharvest UV treatment a potential ecological approach for the control of Xanthomonas campestris pv. vitians induces key genes associated with homeostasis, growth, and defense in lettuce	12
	16	Karthika Sriskantharajah - Pre-harvest spray hexanal enhances the post-harvest quality of Honeycris apples by regulating membrane degradation-associated genes.	12
	17	Victoria Rodriguez Morrison - Cannabis inflorescence yield and cannabinoid concentration are not improved with long-term exposure to UV radiation	12
	18	Portiaa McGonigal - Compost amendments affect plant performance and crop quality without affecting disease severity in a long-established crown gall-diseased vineyard	12
	19	Niluni Wijesundara - Can herbal essential oils use to treat strep throat?: antibacterial activity of carvacrol against Streptococcus pyogenes	12
	20	Tharindu Lakshan Suraweera - Plant-Derived Dietary Flavonoids Protect Cultured Human Lung Epithelial Cells from Chemical-induced DNA Damage.	12
3:30		**Live QA4 on Zoom**	20
3:50		**Networking**	60

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Invited speakers and society award winners
Student 12 min oral presentations in a competition
Student 5 min poster flash-talks in a competition
Regular 12 min oral presentations
Live questions and answer session via Zoom

Concurrent sessions that begin after the first networking			
Start times	**Abst no**	**Session 5. Genetics, biotechnology, and breeding**	
12:55	**21**	Maya Subedi - Genetic stability analysis of stem solidness and grain yield in spring wheat	12
	22	Mohammad Sayari - Role of NOX genes in Verticillium dahliae pathogenicity	12
	23	Zhongwei Zou - Functional characterisation of minor genes of Brassica napus in response to blackleg disease	12
	24	Jyoti Saini Sharma - Characterizing The Common Wheat Accession KU168-2 For The Stem Rust Resistance	12
	25	Mamadou Lamine Fall - Temporal dynamics of the virome composition and transcriptional response of three grapevine cultivars	12
	26	Shuanglong Huang - A deep dive into the game of hide and seek in the Brassica napus-Leptosphaeria maculans pathosystem: combined transcriptome and proteome analysis	12
	27	Leonardo Miguel Galindo González - Using molecular biology and omics to manage clubroot of canola	12
	28	Nick Wytinck - Clathrin Mediated Endocytosis is Involved in the Uptake of Exogenous double-stranded RNA in the White Mold Phytopathogen Sclerotinia sclerotiorum	12
2:31		**Live QA5 on Zoom**	24

Scientific Program Schedule Tuesday, July 6

Start times	Abst no	Tuesday July 6	Minutes
10:00		**Introduction to the day and invited keynote speaker by Lone Buchwaldt**	3-5
	29	**Session 6. Sean Walkowiack: Genomics: Changing how we improve crops.**	25
10:30		**Live QA6 on Zoom**	10
		Student oral competition: Genomic Applications for Crop Improvement	
10:40	30	Christopher Manchur - Bye-bye fungicides, hello RNAi: Understanding the uptake of RNAi-based controls and application of RNAi in controlling obligate biotrophic oomycetes	12
	31	Erika Dort - Improving biosurveillance in the genomics era: using large-scale genome comparisons with machine learning to predict fungal phytopathogenic lifestyles	12
	32	Jonathan Reich - Comparison of qPCR, Illumina amplicon sequencing, and Oxford Nanopore MinION sequencing for the detection and quantification of airborne plant pathogens	12
	33	Mackenzie Hladun - Continuing the vital search for Fusarium head blight resistance	12
	34	Cunchun Yang - The regulation of intrinsic signaling in Brassica napus defending against Leptosphaeria maculans	12
	35	Hu Wang - Genetic responses of alfalfa (Medicago sativa L.) populations to long-term grazing	12
	36	Claudia Escobar-Gil - Transcriptomic profiling of the host-pathogen interaction in tan spot of wheat	12
12:04		**Live QA7 on Zoom**	21
12:25		**Networking**	30
		Session 8. Student oral competition: Plant and Soil Health	
12:55	37	Ji Cui - Comparison of inoculation techniques for Verticillium longisporum on canola	12
	38	Kyle Biscaglia-Horvath - Disease Dynamics of Root Rot Complex in Field Pea	12
	39	Claudio Ignacio Fernandez - Cucumber powdery mildew detection using non-georeferenced multispectral images	12
	40	Piratheepa Jegatheeswaran - Understanding the effects of landscape structure on the abundance of cabbage seedpod weevil and lygus bugs, and associated crop damage	12
	41	Jessica Prosser - Role of Tomato ringspot virus in Tree Fruit Decline in the Niagara Region.	12
	42	Kenneth Eteme Anku - Potential use of vegetative indices to detect and estimate disease severities of Monilinia and Botrytis blight on wild blueberry fields	12
	43	Sanjib Sapkota - Metalaxyl sensitivity of Phytophthora spp. associated with red raspberry in British Columbia	12
2:19		**Live QA8 on Zoom**	21
		Session 9. Student poster flash-talks: Genetics, Biotechnology, and Breeding	
2:40	44	Bohan Wei - Novel mutations in the CYP51 gene in a global collection of Pyrenophora tritici-repentis (tan spot of wheat)	5
	45	James Tucker - Modern breeding strategies assist development of disease-resistant, two-row malting barley adapted for production in western Canada.	5
	46	Kallum McDonald - Creating a Genetic Screening Platform from Arabidopsis for Breeding Canola with Increased Seed Protein.	5
	47	Sachithrani Kannangara - CRISPER/Cas9 mediated gene editing to create a Leptosphaeria maculans isolate carrying a single avirulent gene - AvrLepR1	5

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	48	Arindam Sikdar - Genomic methylation levels appear adverse effect on total phenolic content between in vitro and greenhouse grown lingonberry (Vaccinium vitis-idaea)	5
	49	Rasanie Padmathilake - Is less virulent Leptosphaeria biglobosa robust enough to protect canola from highly virulent L. maculans?	5
	50	Daniel Gladish - Evaluation of plant-pollinator ecosystem health and rapid detection of plant and bee pathogens by high-throughput sequencing of European honey bee (Apis mellifera)	5
	51	No flash talk, but see poster	
	52	Cindy Yu - Polyphenols-rich apples exhibit anti-diabetic properties in vitro.	5
3:25		**Live QA9 on Zoom**	30
3:52		**Networking**	60
4:52		**Student activity - 3 minute talks**	60

Concurrent sessions that begin after the first networking			
Start times	**Abst no**	**Session 10. Pathogen Challenges and Genomic Applications**	
12:55	**53**	Thomas Jeanne - Use of high throughput sequencing for the identification of plant pathogens	12
	54	Melanie Kalischuk - Molecular diagnostics for bronze leaf disease affecting Canadian poplar and aspen trees	12
	55	Miao Liu - The 168-year taxonomy of Claviceps in the light of variations: From three morphological species to four sections based on multigene phylogenies	12
	56	Lone Buchwaldt - Characterization of genomic and pathogenic diversity in Sclerotinia sclerotiorum population needed for development of resistant canola	12
	57	Maria Antonia Henriquez - Physiological and RNASeq analysis of the wheat cultivar AAC Tenacious under F. graminearum infection	12
	58	Naz Islam - Levels of mycotoxins in barley grains as infected by Fusarium head blight species in Manitoba, Canada from 2017 to 2020	12
	59	Holly Bartholomew - A double agent: The mycotoxin patulin serves multiple roles during host-fungal-nonhost interactions	12
	60	Huimin Xu - Modernization of Canadian Potato Post Entry Quarantine program by introducing molecular and genomic diagnostic methods for detecting virus and viroid pathogens in imported potato germplasm	12
2:31		**Live QA10 on Zoom**	24

Scientific Program Schedule Wednesday, July 7

Start times	Abst no	Wednesday July 7	Minutes
10:00		**Introduction to the day and invited keynote speakers by Dilantha Fernando**	3-5
	61	**Session 11. Bernard Glick: Soil bacteria and plant growth.**	25
10:30		**Live QA11 on Zoom**	10
10:40	62	**Session 12. Carolee Bull: The second century of phytobiome research.**	25
11:05		**Live QA12 on Zoom**	**10**
		Session 13. Student oral competition: Plant and Soil Health, and the Microbiome	
11:15	63	Arshani Alukumbura - Does application of Trichoderma gamsii T6085 for control of Fusarium head blight alter the microbiome of wheat?	12
	64	Edward McNab - Creeping bentgrass microbiome: traditional culturing and sequencing results compared to metagenomic techniques.	12
	65	Harini Aiyer - Cover crops differentially affect root disease susceptibility by changing the soil microbiome	12
	66	Ibraheem Olamide Olasupo - Impacts of ditch-buried garlic straw fortified with chemical fertilizer on soil microbial biomass, bacterial community and yield of a tunnel-grown chili	12
	67	A.C. GAHAGAN - How oomycete community structure responds to crop rotation and tillage	12
	68	Louis-Olivier Larouche - Identification of exotic forest pests by metabarcoding from a unique trap	12
	69	Palaniappan Ramanathan - Characterization of wireworm populations in the floodplains of Lac Saint-Pierre.	12
12:39		**Live QA13 on Zoom**	23
1:00		Networking	60
1:00		**Session 14. Student activity - Carolee Bull: How to write a research statement and cover letter**	Concurrent
		Session 14. Student oral competition: Plant and Soil Health	
2:00	70	Andrea Botero-Ramirez - Effect of clubroot (Plasmodiophora brassicae) on yield of canola (Brassica napus)	12
	71	Emilee Storfie - Fungal pathogen emergence: an Ustilago maydis x Sporisorium reilianum model	12
	72	Gursahib Singh - The chemotypes 3ADON, 15ADON, NIV, and NX-2 of Fusarium graminearum vary in aggressiveness on wheat.	12
	73	Allison Bailey - Impact of long-term nitrogen fertilization on soil organic carbon, total soil nitrogen and future production in continuous corn (Zea mays L.) in Ontario	12
	74	Anuradha Jayathissa - Fusarium graminearum infection of differentially resistant barley cultivars reflect growth and deoxynivalenol production during malting	12
	75	Kerin Hudson - Pathogenicity of Fusarium graminearum and F. poae Causing Fusarium Head Blight on Barley Under Controlled Conditions	12
	76	Sachithrani Kannangara - Fusarium Head Blight species diversity and deoxynivalenol (DON) levels in Western Canadian producer wheat fields	12
	77	Keisha Hollman - The virulence of Plasmodiophora brassicae on canola with '2nd generation' clubroot resistance	12
3:36		**Live QA14 on Zoom**	20
3:56		**Networking**	60

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Regular 12 min oral presentations
Live questions and answer session via Zoom

Concurrent sessions that begin after the first networking

Start times	Abst no	**Session 15. Plant and Soil health**	
2:00	**78**	Malinda Thilakarathna - Trends in symbiotic nitrogen fixation over 100 years of soybean breeding	12
	79	Jennifer Owens - Altering nitrogen management to improve winter wheat yields and nitrogen efficiency in the Northern Great Plains	12
	80	Mumtaz Cheema - Effect of wood ash, sludge, and biochar on heavy metals mobility in plant-soil system of annual ryegrass and kale	12
	81	Dahu Chen - Effect of biofumigation and fumigation on population density of root-lesion nematodes, Verticillium dahliae and potato yield in New Brunswick	12
	82	Muhammad Nadeem - Potential role of root neutral lipids in mediating forage soybean acclimation to cultivation on acidic soil in boreal climate	12
	83	Gurbir Singh Dhillon - Adapting precision planters for pulse crop production in southern Alberta	12
	84	Jiangying Tu - Cell-wall reinforcement contributes to clubroot resistance	12
	85	Lawrence Kawchuk - Elimination of zebra chip in Canada	12
3:36		**Live QA15 on Zoom**	24

Scientific Program Schedule Thursday, July 8

Start times	Abst no	Thursday July 8	Minutes
10:00		**Introduction to the day by Valerie Gravel**	3-5
	86	**Andre Levesque:** CPS Career Recognition Award. Riding the wave of digitization – towards a better understanding of the role and impact of fungi and oomycetes.	15
	87	**Francois Tardif:** CSA Best paper award. Widespread Herbicide Resistance in Pigweed Species in Ontario Carrot Production is Due to Multiple Photosystem II Mutations	15
	88	**Yun Kong:** Response of growth, yield and quality of edible-podded snow peas to supplemental light-emitting diode lighting during winter greenhouse production	15
	89	**Vara Prasad:** Innovations in sustainable agricultural intensification to address climate change, food security, nutrition and resilience.	25
11:25		**Live QA16 on Zoom**	15
		Session 17. Student oral competition: Plant Health and Resilience	
11:40	90	Ariana Forand - Building a better cell wall- How structural modifications in pectin impact the role of the cell wall as a barrier to both abiotic and biotic stress	12
	91	Will Short - The role of drought stress on the acquisition of freezing tolerance in asparagus (Asparagus officinalis L.) under controlled conditions	12
	92	Seth Lundell - Effects of two bacterial inoculants on the physiology and transcription of osmoprotectant related genes in four generations of alfalfa breeding lines	12
	93	Dilrukshi Kaushalya Dias Kombala Liyanage - Understanding the genetic basis for nitrogen fixation in early maturity soybean under the drought stress	12
	94	Loveleen Kaur Dhillon - Breeding for improved nitrogen fixation in pea	12
	95	Sara M. Stricker - Fungicide sensitivity of Stemphylium vesicarium in Ontario	12
	96	Melissa Moher - Photoperiodic response of in vitro Cannabis sativa plants	12
1:04		**Live QA17 on Zoom**	21
1:25		**Networking**	25
		Session 18. Student oral competition: Plant Health and Innovations in Agronomy	
1:50	97	Taurai Matengu - Weather-based models for forecasting and managing Fusarium head blight risk in western Canadian cereal production	12
	98	Zhiyu Yu - Greenhouse and Field Evaluation of Amisulbrom for Clubroot Management	12
	99	Sijan Pandit - Development of a consistent greenhouse inoculation method for Fusarium avenaceum for screening germplasm of Pisum sativum	12
	100	Sarah Drury - Growing wheat and liming to manage clubroot	12
	101	Xiangyue Kong - Estimating fresh weight of pea shoot using measurable morphological traits	12
	102	Maram Istaitieh - Genetic Study of Germination and Seed Shattering in Euphorbia lagascae Spreng in Response to Different Seed Treatments	12
	103	Cesaree Morier-Gxoyiya - Validation of prediction models for sclerotinia stem rot (Sclerotinia sclerotiorum) in soybean (Glycine max) in Quebec	12

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3:14		**Live QA18 on Zoom**	21
		Session 19. Student poster flash-talks: Biotic and Abiotic Challenges	
3:35	**104**	Someshwar Latchman - Characterization and developing effective screening methods of bacterial blight of highbush blueberry in the Lower Mainland of British Columbia	5
	105	Christopher Morrison - Comparing extraction methods to quantify Aphanomyces euteiches inoculum levels in field soils	5
	106	Jiaxu Wu - Effects of low temperature stress on physiological and biochemical processes of silage-corn genotypes	5
	107	Ji Cui - Yield Losses in Canola Caused by Verticillium longisporum	5
	108	Yixiao Wang - Impact of blackleg (Leptosphaeria maculans) on canola yield	5
	109	Marla Roth - Evaluation of the pH sensitivity of Plasmodiophora brassicae strains	5
4:05		**Live QA19 on Zoom**	15
4:20		**Networking**	60

Concurrent sessions that begin after the first networking

Start times	Abst no	**Session 20. Climate change and biodiversity**	
1:50	**110**	Justine Cornelsen - Impact of Changing Climate on the Canadian Prairies on Pest Threats, Canola Yields and Quality	12
	111	Guoqi Wen - Machine learning-based canola yield prediction and site-specific nitrogen recommendation	12
	112	Ian Epp - The Role of Canola in Carbon Sequestration in Western Canada soils	12
	113	Samir C. Debnath - Wild berries for northern agriculture - selection, propagation, conservation and production	12
	114	Kui Liu - Assessing the yield and stability of cropping systems in the major ecozones on the Canadian Prairies	12
	115	Nityananda Khanal - Is plant growth regulator application reliable option for forage seed crop management in the Peace River Region of Canada?	12
3:02		**Live QA20 on Zoom**	20

Scientific Program Schedule Friday, July 9

Start times	Abst no	Friday July 9	Minutes
10:00		**Introduction to the day by Andrew Burt**	3-5
	117	**Session 22. Rattan Lal:** Managing soil Organic matter for global food and climate security	25
10:30		**Live QA21 on Zoom**	10
10:40	118	**Andrew Hammermeister:** Organic as a platform for ecological innovation in agriculture.	25
11:05		**Live QA22 on Zoom**	10
		Session 23. Student oral competition: Innovations in Agronomy and Crop Management	
11:15	119	Maria Alejandra Oviedo-Ludena - Effect of cereal and non-cereal crop sequences on Fusarium head blight severity across the Canadian prairies	12
	120	Kaitlyn Sjonnesen - Assessing the phenotypic response to phosphorus in a winter wheat (Triticum aestivum L.) diversity panel field screened in Ontario, Canada.	12
	121	Amy Mangin - Canopy management: the balance between lodging risk and nitrogen use in western Canadian spring wheat production	12
	122	Audrey-Kim Minville - Grass cover crops during vineyard establishment in southern Quebec: Their effects on weed control and soil aggregate stability to water.	12
	123	Bilal Javed - Wood ash and paper sludge: Potential liming and nutrient sources for podzolic soils	12
	124	Kaitlyn Nielsen - Agronomic analysis of sainfoin (Onobrychis viciifolia Scop.) and grass mixtures for forage production in western Canada	12
	125	Therese Audrey Nzwinda M. - The Effects of Nitrogen Fertilizer Stabilizers on the Growth, Yield, and Feed quality of Silage Corn in a Boreal Climate.	12
	126	David MacTaggart - Estimating the plant characteristics of cicer milkvetch (Astragalus cicer L.) using a remote sensing approach	12
12:49		**Live QA23 on Zoom**	21
1:10		**Networking**	60
1:10		**Panel discussion for early career scientists**	concu-rrent
		Session 24. Student poster flash-talks: Progress in Plant Health	
2:10	127	Patrick Le Heiget - Effects of fertility management on the phenological development of dual-purpose intermediate wheat-grass and impact on grain yield and forage quality characteristics.	5
	128	Kaitlyn Nielsen - Nutritive value of sainfoin (Onobrychis viciifolia Scop.) and grass mixtures for forage production in western Canada	5
	129	Muhammad Faran - Potential of dairy digestate as a biofertilizer: Effects on growth, yield and phytochemical profile of lettuce in hydroponics	5
	130	Christine Dervaric - Alternative products for management of Cercospora leaf spot (Cercospora beticola Sacc.) of sugarbeet (Beta vulgaris L. spp. vulgaris).	5
	131	Alex Cornel - Assessing fungicide efficacy for improved management of the wild blueberry foliar disease complex in eastern Canada	5
2:35		**Live QA24 on Zoom**	15

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		Session 25. Student poster flash-talks: Plant Health and Resilience	
2:50	**132**	Awa Barro - In vitro screening of different forest tree species residues for their antifungal/antibacterial activity against strawberry pathogens	5
	133	Chunxiao Yang - Effect of Brassica napus seedling age at time of inoculation on fusarium wilt severity	5
	134	Fang (Amy) Shi - The effect of plant age on the susceptibility of American ginseng (Panax quinquefolius L.) to replant disease	5
	135	Devdutt Kamath - Seed germination responses to low-intensity monochromatic light spectra for 14 ornamental plant genotypes	5
	136	Mathieu Bouchard-Rochette - Efficacy of Bacillus pumilus and Bacillus subtilis to control gray mold on tomato and cucumber plants grown in greenhouse.	5
	137	Portiaa McGonigal - Screening for potential biological control agents against Allorhizobium vitis, the causal agent of crown gall disease of grapevine	5
	138	Romaric Armel, MOUAFO-TCHINDA - Competition between Plasmopara viticola clade aestivalis and clade riparia: who can win the aggressiveness battle	5
3:25		**Live QA25 on Zoom**	20
3:45		**Announcement of winners and closing remarks**	20
4:15		**Networking**	60

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 formed in 1929. The CPS' purpose is 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 and include 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 including 'award for outstanding research', a career recognition award, an '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 2021-2022 the Board consists of:

President	Lone Buchwaldt
President Elect	Sheau-Fang Huang
Vice President	Gary Peng
Past President	Barry Saville
Secretary	Tom Fetch
Treasurer	Kenneth Conn
Membership Secretary	Vikram Bisht
CJPP Editor in Chief	Steven Strelkov
Senior Director at Large	Syama Chatterton
Junior Director at Large	Wen Chen

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

To promote communication among plant pathologists CPS members have the opportunity to meet nationally once a year, and the regional societies also meet annually. The CPS collaborates with the American Phytopathological Society and the British Society of Plant Pathology primarily by amalgamation of annual meetings and exchange of speakers. In 2019, the CPS celebrated its' 90th anniversary during the Plant Canada meeting in Guelph with participation seven Canadian scientific societies.

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

CSA Executive Members (2020-2021)

President	Andrew Burt
Executive Director	Nancy Zubriski
Past President	Sheri Strydhorst
President-Elect	Mumtaz Cheema
Secretary-Treasurer	Douglas Cattani
Western Directors	Laurel Thompson Gurcharn Singh Brar
Eastern Directors	Jamie Larsen Kathleen Glover
Student Representative	Amy Mangin
Industry Representative	Logan Skori
Canadian Journal of Plant Science Representative	Ben Thomas

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

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

Canadian Society for Horticultural Science

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 (2021-2022)

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 CSHS secretary (bourlaye.fofana@canada.ca) if you are interested in joining the CSHS executive board or if you are interested in 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. Although most of their plans had to be postponed because of the current situation, they are looking forward to resuming their outreach activities.


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McGill University


Vice-President
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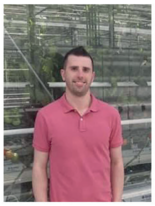
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Dalhousie University


Student representative
Claudio Ignacio Fernandez
University of New Brunswick

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, Claudio Ignacio Fernandez (ci.fe@unb.ca).

Becoming a member of the CSHS

Numerous benefits are offered to CSHS members including:

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

In addition, for students, benefits also include:

- Eligibility for the Awards for oral and poster presentation
- Eligibility for Travel Awards to annual conference
- Community & Extension Funding, which supports students 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

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Acknowledgement

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Wen Chen	CPS, Chair
Tom Forge	
Hai Nguyen	Co-Chair

Workshops immediately after the conference

Andrew Burt
Edel Pérez-López

Workshops in the fall/winter of 2021

Guus Bakkeren
Andrea Botero Ramírez
Dilantha Fernando
Tom Forge
James Menzies
Gary Peng
José Ramon Úrbez Torres
Mike Rott
Amy Fang Shi
Sean Westerveld

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Session moderators as of June 9

Kanak Bala	CPS, Chair
Harini Aiyer	CPS
Kenneth Anku	CSHS
Guus Bakkeren	CPS
Autumn Barnes	CPS
Harvinder Bennypaul	CPS
Gurcharn Singh Brar	CSA/CPS
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Amy Fang Shi	CPS
Vincent Fetterley	CPS
Dilantha Fernando	CPS
Shuanglong Huang	CPS
Naz Islam	CPS
Melanie Kalischuk	CPS
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Keiko Nabetani	CPS
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SeedWorld Group

Shawn Brook	SWG, President
Aiden Brook	SWG, Business Development Manager
Laura Burtnyk	SWG, Project Coordinator
Kristine Langlois	SWG, Project Coordinator

Workshops Immediately After The Conference

Title	Equity, Diversity and Inclusion (EDI) in Agronomy Research
Description	There are many researchers in Canadian agronomy and other agriculture-related research areas who originates outside of this country such as Latin America, Africa and Asia. Many individuals have experienced systemic barriers that have hindered their full inclusion and equity both in Academia and Industry. It is particularly difficult for early career researchers to fight these 'old habits' as that are deeply rooted in people's perception and research institutions customs. In this workshop we will have a group of panelists who will share their experiences in navigating and succeeding in equity, diversity and inclusion. They will help us find the best practices when it comes to eliminating barriers of various kinds.
Date	July 12, 2021
Duration	2 hours including 30 minutes for discussion with panelists
No. of participants	50 – the workshop is full!
Organizer	Dr. Edel Pérez-López, Université Laval, Montréal, QC

Title	Tips for successful publishing in peer reviewed journals
Description	As researchers, the quantity and quality of our peer-reviewed publications is an important metric in almost all of our career choices. But especially when we're at the start of our careers, preparing and submitting a manuscript for publication is a daunting task. This workshop is designed for graduate students and early career scientists to learn tips and tools to improve your chances of being published.
Date	July 13, 2021
Duration	2 hours including 30 minutes for discussion with panelists
No. of participants	50 - the workshop is full!
Organizer	Dr. Andrew Burt, AAFC, Ottawa Research and Development Centre, ON

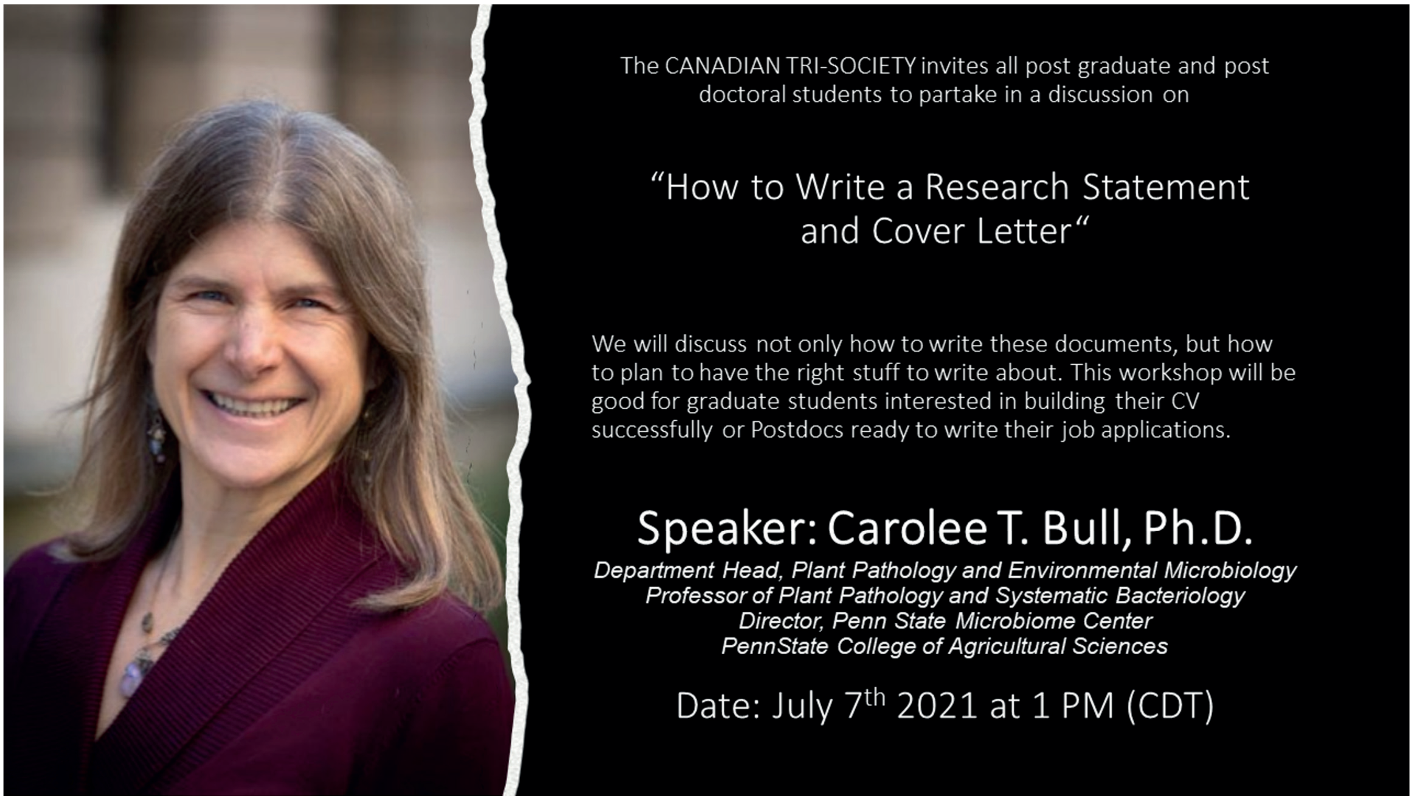
Contests

Engaging 3-minute talks by students

Date: Tuesday July 6 at 4:50 – 5:50 pm CDT
The Student Social Committee will create an engaging event by selecting the best 3-minute talks submitted by students.
Summarize any entertaining topic in three minutes or less to win a prize, or come watch the fun and help choose a winner. Only graduate or undergraduate students can submit a video: https://forms.gle/SJQjYNmWePRq8L1x6. The topic could be about your life, your research, or an interesting experience you have had. Make it entertaining! Winners will be selected by the audience; $75 for first, $50 for second, and $25 for third place.

How to write a research statement and cover letter

Date: Wednesday July 7 at 1:00 -2:00 PM CDT.



The CANADIAN TRI-SOCIETY invites all post graduate and post doctoral students to partake in a discussion on

"How to Write a Research Statement and Cover Letter"

We will discuss not only how to write these documents, but how to plan to have the right stuff to write about. This workshop will be good for graduate students interested in building their CV successfully or Postdocs ready to write their job applications.

Speaker: Carolee T. Bull, Ph.D.
Department Head, Plant Pathology and Environmental Microbiology
Professor of Plant Pathology and Systematic Bacteriology
Director, Penn State Microbiome Center
PennState College of Agricultural Sciences

Date: July 7th 2021 at 1 PM (CDT)

Panel discussion for early career scientists

Date: Friday July 9 at 1:10 -2:10 PM CDT.
The Student Social Committee has gathered panelists from the industry, academia, government, and private sectors. This is primarily for graduate students, post docs and early career professionals. Come ask questions to the panelists, about how to start a career in plant pathology, horticulture, and agronomy; or submit questions anonymously the following Google form: https://forms.gle/LP5JL7fHkzdMYPNm8

Career Panel Members:

Stephanie Bach
Stephanie is the Director of Projects & Operational Training at Dynaleo Inc, a leading-edge designer and manufacturer of cannabis confectionery in Canada. She also runs her own consulting company offering full-suite hydroponic and aquaponics consultation services. Since obtaining her 2011 MSc in Plant Agriculture from the University of Guelph, Stephanie has worked building a unique skill set with experience in agriculture & agri-food, indoor vertical farming, aquaponics, hydroponics, and aquaculture. Stephanie was a recognized by Global Edmonton as the June 2018 Woman of Vision, and was named as one of the 2018 Top 10 under 40 by Greenhouse Canada.

Marisol Berti
Dr. Marisol Berti is a professor at the Department of Plant Sciences, North Dakota State University. Previously to NDSU, she worked for 14 years at the Department of Agronomy at the Universidad de Concepcion (UDEC), in Chile, her home country. She has had experience in research, teaching, extension, and administration during her 27-years in academia. Her research experience includes forages, cover crops, and bioenergy crops production research. She has been involved in several scientific organizations such as the Association for the Advancement of Industrial Crops, C6- Forage and Grazinglands Division of the Crop Science Society of America, and Midwest Forage Association. She is also editor-in-chief of the Industrial Crops and Products Journal and serves as reviewer for over 20 other journals.

Diane Edwards
As a researcher at ABI Environmental Services, Dr. Edwards identifies aquatic and terrestrial invertebrates, currently specializing in spiders from prairie habitats, and quantifies insect diversity using biosurvey techniques. Dr. Edwards is also an instructor of plant sciences at Ambrose University in Alberta. Additionally she is the current Treasurer of CSHS and Plant Canada.
Diane Edwards' education specialized in the greenhouse production of horticultural crops. Diane and her family moved to Calgary, AB in 2009 where she worked as a sessional lecturer at the University of Calgary and Ambrose University and as a contractor. In 2014, Diane and her husband started ABI Environmental Services Ltd where they do a wide variety of work from aquatic invertebrate identification and biological surveys, designing courses in plants and invertebrates, workshops and museum displays. Diane has been a board member of Plant Canada, Canadian Society of Horticultural Science, the U of C Community Garden and the Varsity Community Garden.

George Lazarovits
Dr. Lazarovits is director of research at A&L Biologicals in Ontario and is also a research director at the Agroecology Research Services Center, which develops farming practices that reduce growers' input costs. Dr. Lazarovits has served on NSERC Review Committees and played a key role in obtaining funding of the Biocontrol Network.

Andrew McKenzie-Gopsill
Dr. McKenzie-Gopsill is a research scientist at Agriculture Agri-food Canada, PEI. His speciality is herbicide resistant management for potato, weed diversity for sustainable agriculture, and physiological consequences of crop-weed interactions. Dr. McKenzie-Gopsill is an early career scientist and can answer questions about the AAFC hiring process.

Sheri Strydhorst
Dr. Strydhorst is an Agronomy Research Specialist with Alberta Wheat and Barley Commissions and supports the wheat and barley commission agronomy research and extension programs. Part of her work includes assisting scientists to refine research proposals to ensure they accurately address farmer's production challenges and produce results that are meaningful at the farm level. Additionally, she conducts extension activities throughout Alberta with a focus on central and northern Alberta. Her goal is to improve the profitability of farming using science.


Panel Discussion for Early Career Scientists

July 9, 2021
1:10 PM CDT

Where to find a job?

How to ace an interview?

Graduate students, post doc researchers, and early career scientists are welcome to ask our diverse panel job-related questions.

Fun for All

The Student Social Committee has also worked to bring some contests to the virtual conference which will run throughout the week. There is a live Leaderboard where you can satisfy your competitive spirit, and see your points increase for participating in the different contests and other conference activities. The contests are for all registrants to participate in. They are accessible through the 'Contests' tab. You can submit a photo, write a photo caption or create poetry, and also play along by 'liking' these contributions.

Score points on the Leaderboard

• Request and attend a one-on-one virtual meeting with another attendee	300 points
• Participate in a contest	100 points
• Attend a session	50 points
• Visit the lounge during a networking session	50 points
• View the profile of another attendee	50 points

Take-a-nature-selfie contest

Take a break and go outside! It could be in your back yard, in the field, or in the forest. Get creative! Submit your photo until July 8th at midnight using the contests tab. Winners will be selected by the most "likes" on the website. The photo with the most likes will receive 300 points on the leaderboard.

Caption-that-photo contest

Each day there will be a new "Photo of the Day" in the Contests tab. It's up to you to create a clever, funny, or sarcastic caption for it. Submit your caption through the contests tab. Winners will be selected by the most "likes" on the website. The top caption each day will receive 200 points on the Leader Board.

Write-science-poetry contest

Pathology, Agronomy, and Horticulture meet the literary arts. Submit your Sonnet, limerick, or haiku until July 8th at midnight using the contests tab. We would love to hear rhymes from you. Winners will be selected by the most "likes" on the website. The poem with the most likes will receive 400 points on the leaderboard.

Vote in the Canadian Phytopathological Society photo contest

The Canadian Phytopathological Society is hosting a photo contest which was open to everyone until June 27, 2021. Photos were submitted in the five categories: Field, Lab, Microscope, People, and Art. Winners from each category will be selected using a voting platform during the Tri-Society Virtual Conference. For each category the first place is $75 and the second place is $45.

Keynote Speakers

Dr. E. Charles Brummer

Dr. E. Charles Brummer is the Director of the Plant Breeding Center and a Professor in the Department of Plant Sciences at the University of California, Davis. His research includes cultivar improvement of alfalfa, tall fescue, spinach, hemp, and zinnia. His lab conducts research on improving breeding methodologies for outcrossing crops, on applying genetic markers to practical plant improvement programs, and on using genomics to understand the genetic control of important traits. He teaches Advanced Plant Breeding and leads the Student Collaborative Organic Plant-breeding and Education program, which includes several student-led breeding projects on tomato, pepper, common bean, lima bean, wheat, and zinnia. Prior to moving to Davis in 2014, he was Senior Vice President at the Noble Foundation in Ardmore, OK, Director of the Institute for Plant Breeding, Genetics, and Genomics at the University of Georgia, Professor at Iowa State University. His research has been funded by national competitive grants from USDA-NIFA and DOE, by smaller local and national granting programs and commodity groups, and by contracts with various plant breeding companies. He has published over 160 refereed journal papers and presented numerous invited talks nationally and internationally. He was President of the Crop Science Society of America (CSSA) in 2017 and served as Editor-in-Chief of CSSA from 2010-2016. He is a Fellow of CSSA and of the American Association for the Advancement of Science.

Dr. Sean Walkaviak

Dr. Sean Walkowiak is a Research Scientist and Program Manager for Microbiology at the Canadian Grain Commission's Grain Research Laboratory, since 2019. Sean is also an Adjunct Professor in the Department of Plant Science at the University of Manitoba, since 2021. Dr. Sean Walkowiak's graduate research on plant pathogen genomics was conducted with Agriculture and Agri-Food Canada at the Central Experimental Farm in Ottawa under Dr. Gopal Subramaniam. After completing his Ph.D in 2016, Sean was a Research Officer at the University of Saskatchewan where he conducted applied genomics research as part of the durum and elite bread wheat breeding program under Dr. Curtis Pozniak. Sean's research, particularly on the wheat genomics and its application for crop improvement, has recently been highlighted in top-ranked journals including Nature, Nature Genetics, Science, and PNAS.

Dr. Bernard Glick

Following a B.Sc. in Chemistry in 1969 at the City College of New York, I obtained a Ph.D. in Biochemistry at the University of Waterloo in 1974. After four years as a postdoc in Molecular Biology at the University of Toronto and one year as a Research Associate in Microbiology at the National Research Council in Ottawa, I joined "Bio Logicals" Canada's first biotechnology company in Toronto where I spent three years as the Group Leader of the Molecular Genetics and Biochemistry Group. In 1982, I joined the Biology Department at the University of Waterloo where I was tasked with establishing a program in Molecular Biotechnology. I was Chair of Biology at Waterloo from 2002-2008 and officially retired in 2018. Since that time, I have been a Distinguished Professor Emeritus. During my career I have published 372 scientific manuscript and chapters, authored or coauthored four books including "Molecular Biotechnology" published by the American Society for Microbiology with the 6th edition currently in press, and "Beneficial Plant-Bacterial Interactions" published by Springer with 2nd edition coming out in 2020. The work from our lab has been cited more than 51,000 times (according to Google Scholar). I have trained 56 graduate students, 18 postdocs and 36 visiting scientists. Over the years, I have been a visiting Professor at 18 different universities in 14 countries, offering courses in Molecular Biotechnology at 11 of these universities. While I have worked in several different scientific fields during my career, over the last ~30 years, the focus of our group has been directed towards understanding and elaborating the mechanisms used by plant growth-promoting bacteria to stimulate plant growth. In retirement, I continue to collaborate and publish with scientists from seven different countries.

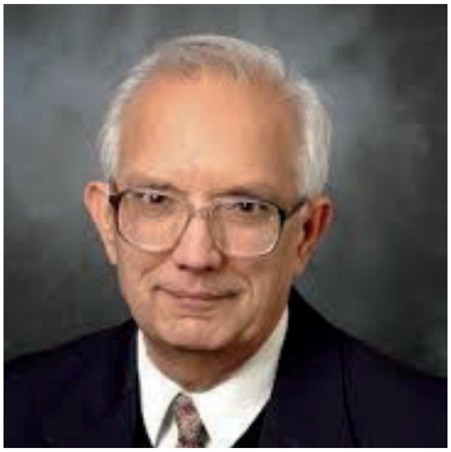
Keynote Speakers

Dr. Carolee Bull

Dr. Carolee T. Bull is Professor and Head of the Department of Plant Pathology and Environmental Microbiology at Penn State and the Director of the Penn State Microbiome Center. Dr. Bull served 20 years as a Phytobacteriologist with the USDA/ARS in Salinas, CA prior to joining Penn State in 2015. Bull's research focuses on Translational Taxonomy to manage bacterial diseases of plants and mushrooms. Bull is the Project Director for an SCRI project using multiple approaches including diagnostic metagenomics to develop management strategies for of seedborne diseases of cucurbit, beet, and chard food and seed crops. Dr. Bull served as the convener of the Committee on the Taxonomy of Plant Pathogenic Bacteria for the International Society of Plant Pathology and serves on the Judicial Committee of the International Committee on the Systematics of Prokaryotes. Bull provides bacterial taxonomy lectures and mentorship workshops for classes, universities, and scientific societies world-wide. Bull received the highest award for service to the US in Agriculture for her mentorship of underrepresented students in agricultural science in 2013 and is a Fellow of the American Phytopathological Society in 2020.

Dr. Vara Prasad

Dr. P.V. Vara Prasad is a University Distinguished Professor, R.O. Kruse Endowed Professor in Agriculture, and Director of the Sustainable Intensification Innovation Lab at Kansas State University. His research focuses on understanding responses of crops to changing environments; developing best management strategies to improve yields; providing food and nutritional security to smallholder farmers; and improving livelihoods of people. He is passionate about research, education, outreach, building social capital and enhancing human and institutional capacity around the world. He has active programs in multiple countries in Asia and Africa. He has published 285 peer-reviewed journal articles and book chapters; trained 160 students and research scholars from 25 countries; and gave more than 100 invited talks in 40 different countries. He received more than 120 million US dollars in grant funding and donations. He is an elected fellow of American Society of Agronomy; Crop Science Society of America; and American Association for the Advancement of Science. At present he serves on the International Commission on Sustainable Agricultural Intensification. He is the current President of the Crop Science Society of America (2021). He obtained his B.S. and MS from Andhra Pradesh Agricultural University (India) and Ph.D. from the University of Reading (U.K.).



Dr. Rattan Lal

Dr. Rattan Lal, Ph.D., is a Distinguished University Professor of Soil Science and Director of the CFAES Carbon Management and Sequestration Center at The Ohio State University, as well as an Adjunct Professor of University of Iceland and the Indian Agricultural Research Institute (IARI), India. He received a B.S. from Punjab Agricultural University, Ludhiana, India (1963); M.S. from Indian Agricultural Research Institute, New Delhi, India (1965); and Ph.D. from the Ohio State University, Columbus, Ohio (1968). He served as Sr. Research Fellow with the University of Sydney, Australia (1968-69), Soil Physicist at IITA, Ibadan, Nigeria (1970-87), and Professor of Soil Science at OSU (1987 to date). His research interests include soil carbon sequestration for food and climate security, conservation agriculture, soil health, principles and practices of soil erosion control, soil structure and carbon dynamics, eco-intensification of agroecosystems, soil restoration, the fate of soil carbon transported by soil erosion, and sustainable management of world soils. Prof. Lal is Editor-In-Chief of Advances in Soil Science and of the Encyclopedia of Soil Sciences. He was the Speaker for Summer 2019 commencement, and TEDx speaker for the Ohio State University in 2021. He has authored/co-authored over 1000 refereed journal articles and more than 550 book chapters, has written and edited/co-edited more than 100 books. Prof. Lal has cumulative citation index of 120,000 and h-index of 164. He was included in the Thomson Reuters list of (2014-2016), and he is among Researchers in Agriculture (2014-2020), as well as ranked #111 globally and #1 in Agriculture and Agronomy among the top 2% of scientists by Ioannidis et al. (2019, 2020). He has received an Honoris Causa degree from nine universities in Europe (Norway, Moldova, Germany, Spain), USA, South America (Chile) and Asia (India); the Medal of Honor from UIMP, Santander, Spain (2018); the Distinguished Service Medal of IUSS (2018); and is fellow of the five professional societies. Dr. Lal has mentored 112 graduate students, 54 postdoctoral researchers and 181 visiting scholars from around the world. He was President of the World Association of Soil and Water Conservation (1987-1990), International Soil and Tillage Research Organization (1988-1991), Soil Science Society of America (2006-2008), and the International Union of Soil Sciences (2017-2018). He holds a Chair in Soil Science and Goodwill Ambassador for Sustainability Issues for the Inter-American Institute for Cooperation on Agriculture (IICA), Costa Rica, and member of the 2021 United Nations Food Security Summit Science Committee and Action Tracks 1 and 3 Commitees. Dr. Lal is laureate of the GCHERA World Agriculture Prize (2018), Glinka World Soil Prize (2018), Japan Prize (2019), U.S. Awasthi IFFCO Prize of India (2019), Arrell Global Food Innovation Award of Canada (2020), World Food Prize (2020), and Padma Shri Award (2021) of the Government of India.

Dr. Andrew Hammermeister

Dr. Andrew Hammermeister is the Director of the Organic Agriculture Centre of Canada (OACC) and Associate Professor in the Faculty of Agriculture at Dalhousie University, Nova Scotia, Canada. He has a B.Sc. in Agriculture specializing in Soil Science from the University of Saskatchewan, M.Sc. in Land Reclamation and Ph.D. in Applied Ecology from the University of Alberta. Andrew has worked with the OACC since 2002, collaborating in research on grain, vegetable and fruit cropping systems, exploring soil fertility and weed management. Most recently he has been studying, small bush fruits such as haskap, landscape biodiversity, and applications of smart technologies to organic agriculture. Andrew is the Science Director for the Organic Science Cluster, the coordinated national initiative for organic agricultural research in Canada where he leads national organic research priority setting, coordination, and impact assessment. He sits on the national organic standards review committee and several other organic sector committees.

Award Winners

CPS Career Recognition Award for 2021 – Dr. André Lévesque

The awards committee recommends that Dr. André Lévesque is awarded the inaugural CPS Career Recognition Award. Dr. André Lévesque is highly deserving of this award based on the impact his career of more than 25 years has had on research and service to the plant pathology community. André retired from his position with CFIA in November 2020. There is no doubt that Dr. Lévesque has made significant contributions on the use of genomics and molecular tools in the study of plant pathogens for early detection and biosystematics, and during his distinguished career he had considerable outreach and involvement with the broader community, including leadership roles and education. Dr. Lévesque's nomination was supported by numerous signatories of highly-regarded plant pathologists from across Canada and are a testament to his wide-ranging impact on the scientific community. Dr. Lévesque's impact on plant pathology research and the community in Canada are too many to summarize in a short brief, but highlights of his career include seminal work on the phylogeny and genomics of Pythium species; recommendation of the nuclear Internal Transcribed Spacer (ITS) as a universal DNA barcoding marker for fungi; building capacity for Canada to address risks of accidental or deliberate introduction of plant pathogens; leadership in the International DNA Barcode Initiative; and development of DNA multi-arrays for diagnostics that are still widely in use. He published 125 peer-reviewed scientific papers, 10 book chapters and 200 conference proceeding over his research career. He received over 100 invitations to important scientific events as presenter or keynote speaker, including to many prestigious international events. These achievements clearly indicate that Dr. Lévesque has contributed to plant pathology research in Canada. Dr. Lévesque's contribution to the plant pathology community include providing many guest lectures at Canadian universities, supervision of numerous highly qualified personnel (graduate students, post-doctoral fellows and technicians) that are now active contributors to plant pathology themselves, and active involvement in many scientific societies and advisory committees. He has influenced policy in the Canadian government in relation to serious plant pest invasions, and development and implementation of the Canadian Agriculture partnership program and the Federal Science and Technology Infrastructure Initiative. He has disseminated information in numerous media articles, government news bulletins, and television and radio interviews. In the words of the group of 30+ plant pathologists that nominated Dr. André Lévesque for this award: "André is an exemplary role model for many of us - his career and all his achievements have influenced and will continue to influence our research for decades to come. As a researcher, Dr. Lévesque is admired; as a mentor he is loved by his mentees; and as a person, he is appreciated by us all."

The CSA 2020 Best Paper Award – Dr. François Tardif

Dr Tardif's paper, 'Widespread herbicide resistance in pigweed species in Ontario carrot production is due to multiple photosystem II mutations', published in the Canadian Journal of Plant Science (CJPS), was selected for the Canadian Science Publishing and CSA 2020 Best Paper Award. The article provided a unique opportunity to assess the range of herbicide resistance in horticulture production and it's broader potential implication for pigweed management in a multitude of cropping systems. The work is relevant not only to the readership of CJPS, but also farmers and other stakeholders. Notably, it is the first report of double mutation in psbA in any weed species and the first report of Ala251Val and Phe273Val in pigweed species.

François Tardif is a weed scientist and professor at the University of Guelph. He teaches at the bachelor's and diploma level, trains graduate students and conducts research on herbicide activity, weed biology and integrated weed management.

François studied agronomy at Laval University, Quebec City, and obtained his bachelor's degree in 1985. Having worked on the provincial weed survey in 1982 and 1983, he decided to pursue a career in weed science. Thus, he began his master's and doctoral studies, under the direction of Dr. Gilles Leroux at the Department of Plant Science at Laval University focusing his research on the control and physiology of quackgrass.

Dr. Tardif received his PhD in January 1991 and later worked in Australia at the University of Adelaide under the supervision of Professor Stephen Powles, aiming to understand the physiology of herbicide cross-resistance in annual ryegrass. He joined the University of Guelph in 1996 and is conducting most of his research on understanding and managing herbicide resistance as well as the management of invasive plants such as giant hogweed and wild parsnip. Dr. Tardif has taught multiple classes on various aspects of agronomy and weed science and supervised or co-supervised 30 graduate students.

The CSHS 2020 Most Cited Paper Award – Dr. Yun Kong

Dr Kong's paper, entitled "Response of growth, yield, and quality of edible-podded snow peas to supplemental LED lighting during winter greenhouse production", published in the Canadian Journal of Plant Science (CJPS), was the recipient of the CSHS 2020 Most Cited Paper Award.

Dr. Yun Kong is a postdoctoral research associate working in Dr. Youbin Zheng's lab at the University of Guelph. He has many years' experience in horticulture, especially in greenhouse production. His research interests include environmental physiology of greenhouse plants and greenhouse environment adjustment technologies. In the past decade, his research has been focused on the interaction between light environment and horticultural plants.

In the recent five years, he has published 21 peer-reviewed scientific journal articles.

Dr. Kong obtained his master's and doctoral degrees in Agri-biological, Environment and Energy Engineering from the China Agricultural University, focussing on greenhouse horticulture. He then pursued his research career internationally having worked in the United States and Israel before joining Dr. Zheng's lab in 2014.

Abstracts Click on abstract thumbnail to see the poster.

Session 1. Invited keynote speaker

1. Crop improvement for an uncertain future

E. C. BRUMMER. *Plant Breeding Center, Plant Sciences Department, University of California, Davis, One Shields Ave., Davis, CA 95616, USA.*

The world faces a raft of challenges and many of them impinge directly on agricultural production: climate variability, population growth, soil deterioration, water limitation, and urban expansion, to name five. The increase in crop productivity over the past several decades has been substantial, but can it continue? Plant breeding programs have always looked for and adopted new tools to make genetic gains larger and faster. Today, the array of technologies that could improve the delivery of better cultivars is large and growing. From genomics-assisted selection to high-throughput phenotyping, from precisely edited genes to advanced analytical methods and superior experimental designs, the opportunity for continued improvement seems likely. At the same time, we see a continual streamlining of crop production with ever greater emphasis on ever fewer major crops. Paradoxically, as the well-known benefits of crop rotation and other time-tested management considerations are pushed aside, new issues needing genetic solutions arise, for example, resistance to new diseases and insect pests formerly controlled by rotation. I will argue that the impressive advances in crop breeding and genetics can have a larger positive impact on developing a healthier food system and minimizing negative externalities of agricultural production if concurrent reimagining of farming systems creates an agricultural landscape that by its very design prevents the emergence of problems requiring new defensive breeding.

Session 2. Student oral competition: Genetics, Biotechnology, and Breeding

2. Genome-wide association study of soybean germplasm derived from Canadian x Chinese crosses to mine for unique seed-yield alleles

C. JAGODA ARACHCHIGE AND I. RAJCAN. *Department of Plant Agriculture, Crop Science Bldg., University of Guelph, 50 Stone Road East, Guelph, ON N1G 2W1, Canada.*

Abstract withdrawn

3. Identification of quantitative trait loci associated with partial resistance to Fusarium root rot and wilt caused by *Fusarium graminearum* in field pea

L. F. WU, R. FREDUA-AGYEMAN, S. F. HWANG AND S. E. STRELKOV. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, ABT6G 2P5, Canada.*

Fusarium root rot, caused by a complex of *Fusarium* spp., is a major disease affecting field pea production. While the development of genetic resistance represents one of the most promising approaches for root rot management, no sources of complete resistance have been identified. The aim of this study was to detect quantitative trait loci (QTL) conferring partial resistance to root rot and wilting caused by *Fusarium graminearum*, a major component of this pathogen complex. An F_8 recombinant inbred line (RIL) population consisting of 129 individuals derived from the cross 'Reward' (root rot susceptible) × '00-2067' (root rot tolerant) was inoculated with *F. graminearum* under various greenhouse conditions. Plants were assessed for root rot and wilt severity in the fourth week after inoculation. The F_8 population was genotyped using 13.2K single nucleotide polymorphisms (SNPs) and 212 simple sequence repeat (SSR) markers evenly distributed on seven pea chromosomes. A significant genotypic effect (P<0.05) and high heritability (92.1%) indicated that a high proportion of the genetic variance was transmitted to the progeny. Seven QTL for root rot severity were detected on Linkage Group (LG) I, III, IV and V, including four stable QTL identified in more than one environment. The two largest stable QTL, *Fg-Ps3.1* and *Fg-Ps3.2*, were located on LG III and explained 6.56-12.75% and 8.18-13.24% of the phenotypic variance, respectively. The flanking markers may contribute to marker-assisted selection in breeding programs for partial resistance to *F. graminearum*.

4. Mapping quantitative trait loci associated with stripe rust resistance from Canadian wheat cultivar AAC Innova.

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Stripe rust, caused by *Puccinia striiformis* Westend. f.sp. *tritici* Erikss., is one of the most devastating diseases of wheat *(Triticum aestivum L.)* globally. Exploring and utilising new sources of resistance is essential for breeding resistant wheat cultivars. The Canadian spring wheat cultivar 'AAC Innova' possesses an effective level of stripe rust resistance under field conditions, although the genetic resistance is unknown. To dissect the genetics of resistance in 'AAC Innova', a doubled haploid (DH) mapping population of 291 lines was developed from hybrids of 'AAC Innova' and the susceptible Canadian wheat cultivar 'AAC Proclaim'. This population was tested for stripe rust severity in disease nurseries at Creston, British Columbia (in 2016 and 2020) and Lethbridge, Alberta (in 2016, 2017 and 2020), and genotyped using the wheat 90K Infinium iSelect SNP assay. A high-density genetic map was constructed and consisted of 7,112 SNPs markers with an average marker interval of 2.31 cM. Composite interval mapping (CIM) identified one major *(QYr.lrdc-2A)* and 10 minor effect QTLs *(QYr.lrdc-2B.1, QYr.lrdc-2B.2, QYr.lrdc-2B.3, QYr.lrdc-2B.4, QYr.lrdc-2D, QYr.lrdc-3B, QYr.lrdc-5A, QYr.lrdc-5B, QYr.lrdc-5D* and *QYr.lrdc-7D)*. *QYr.lrdc-2A* mapped to chromosome arm 2AL and explained up to 33.0% of the phenotypic variance and was detected across all environments. Other QTLs were inconsistent and explained less than 10% of the phenotypic variance. 'AAC Innova' contributed stripe rust resistance alleles for most of the QTLs except for *QYr.lrdc-2D, QYr.lrdc-5A* and *QYr.lrdc-7D,* which were derived from the susceptible parent 'AAC Proclaim'. These QTLs and the flanking markers identified in this study can be used for developing stripe rust resistant cultivars.

5. Delineating the SAR pathway in common hexaploid wheat

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In response to biotic stressors, plants mobilize metabolic compounds in defense. Local threats can quickly lead to a robust, whole-plant immune response, or systemic acquired resistance (SAR). A L-lysine catabolic pathway was recently characterized in Arabidopsis, where the metabolites Pipecolic acid (Pip) and *N*-hydroxylated pipecolic acid (NHP), produced by the reductase SAR-Deficient 4 (AtSARD4) and Flavin-monooxygenase 1 (AtFMO1), respectively, are crucial for proper SAR establishment. While recent studies implicate NHP in pathogen defense across angiosperms, the functional characterization of *SARD4* and *FMO1,* and their participation in SAR in common hexaploid wheat (*Triticum aestivum*), is lacking. Here, we employed a reverse-genetics approach to identify functional orthologs of *AtSARD4* and *AtFMO1* in wheat. Gene and protein homology searches and transcriptome analyses yielded 48 *TaFMO1* and 3 *TaSARD4* candidates. Representatives were selected and two *TaFMO1* candidates were successfully expressed in a SAR-deficient Arabidopsis *fmo1* deletion mutant. These transgenic *TaFMO1* Arabidopsis lines revealed a potential partial recovery in SAR to oomycete *Hyaloperonospora arabidopsidis*, indicating possible functional complementation. Similarly, *TaSARD4*-expressing transgenic Δsard4 Arabidopsis lines are being generated. Preliminary trials of wheat supplemented with 1mM Pip and 10mM NHP significantly enhanced wheat resistance to two fungal pathogens: *Blumeria graminis* f.sp. *tritici* (powdery mildew) and *Puccinia triticina* (wheat leaf rust). Evaluating levels of Pip and NHP in the transgenic Arabidopsis lines and in wheat when challenged by pathogens is in-progress using HPLC-MS. We are exploiting the vast knowledge emanating from Arabidopsis research to draw parallels with wheat, as to improve disease resistance in a major crop plant.

6. Interactions between light quality and plant hormones signaling to control flower bud induction in day-neutral strawberry

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Light quality is the key factor that regulates flowering time, phenological growth and consequently, strawberry fruit production. Mechanism that directs flowering time under different light quality is poorly understood in day-neutral strawberry cultivars, despite their rising popularity. In the present study, we determined how light quality controls flower bud induction during transplant production for ‘Albion’ strawberry. We determined the transcriptional levels of flowering related genes, FLOWERING LOCUS T (FvFT1) and TERMINAL FLOWER1 (FvTFL1) as well as the quantification of the plant hormones Gibberellins, Auxins and Cytokinin in crown tissue. Our results affirm that transplants grown under far-red (760nm) and blue (450nm) light emitting diodes at a dominant blue ratio (1:5) exhibited significant increase in flower bud induction compared to ratios of 5:1 and 1:1 in *Fragaria vesca* and *Fragaria ananassa*. This dominant blue ratio-induced growth is accompanied by significant increase in concentrations of flowering stimulators Gibberellins (GA1 and GA7) and Cytokinin (kinetin) in both species. Auxin concentrations was higher for *F. vesca* in response to dominant blue light, but an equal ratio (1:1) resulted in the highest concentration in *F. ananassa*. From these results, it can be suggested that light quality controls flower bud induction by its effect on gibberellins and cytokinin. Expression of flowering related genes were significantly higher in dominant blue light 1 week after treatment (WAT), followed by dominant far-red (6-WAT). Also, a dominant blue ratio activates the expression of both FvFT1 and FvTFL1 gene at an earlier stage, although flowering seemed to occur independently of FvTFL1.

7. Using Hyperspectral-Wide Association Study (HWAS) and machine learning-mediated Genome-Wide Association Study (GWAS) for identifying yield QTL in soybean from reflectance bands and yield component traits

M. YOOSEFZADEH-NAJAFABADI AND M. ESKANDARI. *Department of Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1, Canada.*

Soybean [*Glycine max* (L.) Merr.] is known as a major strategic crop with low historical genetic gain for seed yield. To increase the genetic gain of soybean yield, a better understanding of the genetic architectures of its related traits such as hyperspectral reflectance and yield component traits may be useful. While recent advances in high throughput phenotyping and genotyping techniques have equipped breeders to generate large reliable datasets, using appropriate tools for analyzing big data is a bottleneck, especially in public breeding programs. In this study, we used two conventional genome-wide association study (GWAS) methods along with support vector regression (SVR) and random forest (RF), as two machine learning-mediated GWAS methods, to evaluate the associations between yield and its components as well as hyperspectral reflectance bands in a diverse soybean population. We have also proposed *hyperspectral-wide association study* (HWAS) as a new procedure for studying the association between hyperspectral reflectance bands and yield. Using HWAS, we identified five hyperspectral reflectance bands with significant importance values suitable for association analyses. The results demonstrate the outperformance of SVR-mediated GWAS over conventional GWAS methods through the identification of admissible yield-related QTL using yield component traits and selected hyperspectral reflectance bands. In this presentation, the results of this study will be discussed in more detail, and we hope the information will be beneficial to soybean breeders for developing high-yield cultivars with improved genetic gains.

8. Unravelling RNA helicases in *Ustilago maydis* and their role during teliospore dormancy and germination

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The emergence of fungal diseases is a major threat to sustainable crop production. Fungal pathogens can persist in the environment by forming resistant spores. As such, spore dormancy, dispersal, and germination are integral to the spread of fungal diseases. We use *Ustilago maydis* D.C. Corda as a model to study molecular aspects of teliospore germination. Teliospores are thick-walled, dormant, diploid cells that germinate and complete meiosis to initiate new rounds of infection. Early fungal spore studies indicated that all the necessary components required for germination, including preformed messenger RNAs (mRNAs), are stored in the spore during dormancy. We hypothesize that some stored mRNAs are stabilized in the dormant teliospore through double-stranded RNA (dsRNA) formation and are unwound by RNA helicases during germination to be made available for translation. RNA helicases are highly conserved enzymes that are capable of forming RNA clamps, unwinding RNA-RNA duplexes, and displacing proteins. We identified all RNA helicases in *U. maydis* and determined, by RNA seq, that five RNA helicases had elevated transcript levels in dormant teliospores and that these levels decreased during germination. Deletion strains were created, and their phenotypes were assessed to gain insight into the function of two RNA helicases. The information gained from this study enhances our understanding of fungal spore germination, which may lead to the development of novel disease control measures.

Session 3. Student oral competition: Genetics, Biotechnology and Breeding

9. Natural antisense transcripts and stress response in *Ustilago maydis*

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The climate is changing at an accelerated rate, raising concern about global food security. While advances are being made to increase crop yields, the threat of evolving pathogens must also be considered. Fungal pathogens and their host plants are evolving together, but as the climate changes, fungal pathogens are adapting at an accelerated rate compared to their hosts. We hypothesize that RNA-mediated mechanisms enhance fungal adaptation to stress. We are using the model fungal pathogen *Ustilago maydis* to investigate the role that natural antisense transcripts (NATs) play in modulating the stress response. NATs are a subset of non-coding RNAs which have regions of their sequence complementary to an mRNA. An RNA-seq comparison of three smut fungi revealed that 349 of the 2617 NATs found in *U. maydis* are conserved among all three smut species. The conservation of NATs among these smut species suggests that they have important functional roles. Genes complementary to these conserved NATs were investigated to identify those with previously documented roles in stress response. Among these genes, the levels of complementary NATs were assessed by reverse transcription-PCR, using RNA isolated from haploid *U. maydis* cells exposed to various stresses. Seven NATs with altered expression levels were identified and will be further characterized. Future experiments will assess whether expression of these NATs alters complementary mRNA stability, stress responses, or pathogenesis by the fungus. Identifying and describing these RNA-mediated responses to environmental stress may provide new tools for combating the increasing prevalence and severity of fungal diseases.

10. Good things come to those who bait: using fungal effector proteins to identify host targets

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Of the foliar diseases that threaten lentil production, anthracnose (caused by the hemibiotrophic *Colletotrichum lentis*) poses the greatest threat. A wild relative of lentil, *Lens ervoides*, is a source of superior resistance to the virulent race currently dominating the pathogen population in Canada. A combination of transcriptome and proteome analyses and the genome assembly of the pathogen has revealed an extensive catalogue of candidate secreted effector proteins (CSEPs) employed by *C. lentis* to mediate infection. Among 38 CSEPs evaluated for gene expression during the necrotrophic phase, only five showed expression at that stage and not in mycelium. Using a bait-and-capture approach, we aim to identify *L. ervoides* host proteins targeted by these CSEPs. Three CSEPs were successfully expressed as glutathione-S-transferase (GST)-tagged fusion proteins in *Escherichia coli*. Unfortunately, heterologous expression resulted in the aggregation of each fusion protein into insoluble inclusion bodies. Modifications of culture conditions (e.g., length and temperature of incubation period and concentration of inducer) did not enhance solubility. The successful solubilization of each natively folded fusion protein was mediated by incubating the insoluble pellet with 10% sarcosyl following a published method developed for GST-tagged fusion proteins. Purification of the solubilized proteins requires further optimization to improve yield. Once established, the proteome of *L. ervoides* will be screened for interacting host proteins. The identification of protein isoforms targeted by *C. lentis* CSEPs could be used to introgress resistance from *L. ervoides* into *L. culinaris* germplasm while removing undesirable traits from the wild species.

11. Does trophic switch of *Leptosphaeria maculans* happen under both incompatible and compatible interactions with canola (*Brassica napus*)?

K. R. E. PADMATHILAKE, Z. ZOU AND W. G. D. FERNANDO. *Department of Plant Science, University of Manitoba, Winnipeg, MB R3T2N2, Canada.*

Canola *(Brassica napus)* is a 29.6-billion-dollar crop in Canada. *Leptosphaeria maculans* causes blackleg, is one of the most economically significant diseases of canola. Since the breakdown of resistance in *B. napus* genotype grown in Canada, it is pivotal to introduce new resistant genotypes. This study focused to evaluate the potential of *B. napus* genotype, '01-23-2-1' which carries *Rlm7* to be the next candidate gene to be introduced. 01-23-2-1 line was inoculated with *L. maculans* isolate (UMAvr7) carrying an avirulence gene AvrLm7, and the CRISPR/Cas9 knockout *AvrLm7* mutant (umavr7) of the same isolate to make incompatible and compatible interactions, respectively. The susceptible Westar was used as the control targeting key time points in these interactions and analyzed by dual RNA-seq. L. maculans is a hemibiotrophic fungus which starts its life cycle as a biotroph and turns into a necrotroph later. Out of phytohormone composition, salicylic acid (SA), jasmonic acid (JA), and ethylene (ET) play vital roles in plant-pathogen interactions and trophic switch of the pathogen. Genes related to host SA metabolism, phytohormone considered against biotrophs, upregulated early stage of the incompatible interaction compared to the compatible interactions. In contrast, genes of JA and ET metabolism, which are considered to be high against necrotrophs, were significantly higher in later stages of compatible interactions. However, the genes of JA and ET metabolism were several times lower at later time points in incompatible interaction suggesting the *L. maculans* incompatible interaction remain under control at 7- and 11- dpi and the pathogen remains more as a biotroph without switching into necrotrophic stage.

12. Identification and characterization of novel powdery mildew resistance genes in flax

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Powdery mildew (PM), caused by *Podosphaera lini,* is a common fungal disease that can lead to reduced flax seed quality and yield. Currently however, the causative resistant genes are not well known and characterized. The objective of this study is to identify the flax genomic regions associated with PM resistance for a detailed identification and characterization of PM resistance genes. A recombinant inbred line (RIL) flax population derived from a cross between Linda (moderately resistant) and Norman (susceptible) was used for PM phenotyping, genotyping and a Genome Wide Association (GWAS) mapping. PM phenotypic data showed a normal distribution, indicating a quantitative inheritance of the PM resistance trait and the GWAS identified significant SNPs in three genomic regions on chromosomes 1, 9, and 14. These data, along with the progress achieved in the candidate genes characterization, will be presented and discussed.

13. Gibberellin regulation of protein accumulation in developing pea (*Pisum sativum* L.) seeds

J. D. GIEBELHAUS, J. A. OZGA AND D. M. REINECKE. *Plant BioSystems Division, Department of Agricultural, Food, and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada.*

Many field pea varieties have a mutation in the *PsGA3ox1* gene which causes a decrease in bioactive gibberellins (GAs), a plant hormone that regulates growth and development. This mutation in field pea leads to lower GA levels, producing shorter stemmed plants useful for cultivation; however, its effects on seed composition are not well understood. This study tests the hypothesis that part of GAs effect on seed development is through modulation of protein accumulation in the developing seeds. Using GA overproducing and isogenic null control lines, changes in seed tissue free amino acid and total nitrogen content were determined to identify potential GA-induced effects on processes that affect protein accumulation during seed development. Cotyledon nitrogen content per seed and estimated protein content were elevated in the GA-overproducing line during development and at maturity compared to the null line, suggesting that seed storage protein accumulation is influenced by GA. Developmental variation in the profiles of key free amino acids involved in seed nitrogen transport and storage in seed coat, endosperm, and cotyledon seed tissues indicate that GA could potentially regulate amino acid transport and metabolism dynamics within developing seeds. These modifications, in turn, could influence the rate of storage protein synthesis in the cotyledons with possible implications on final seed protein content. The knowledge gained on GA regulation of storage protein production during seed development can be used to improve protein content in conventional field pea varieties, which could address issues faced by global agriculture and the plant-protein industry.

14. A single base extension assay for pathotyping clubroot [*Plasmodiophora brassicae*] of canola

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Clubroot, caused by the soilborne pathogen *Plasmodiophora brassicae*, is one of the most detrimental diseases of canola (*Brassica napus*) in Canada. Several host differential sets have been developed for pathotype identification, including the Canadian Clubroot Differential (CCD) set. However, pathotyping based on the reaction of host differentials is time-consuming, labor-intensive, and requires biosecure greenhouse facilities. To facilitate rapid pathotype identification, a highly specific assay was developed to detect clusters corresponding to *P. brassicae* pathotypes 3H and 5X. This assay is based on SNaPshot, a single base extension (SBE) reaction. Primers are designed upstream of the discriminating polymorphic base and extended by one base with fluorescently labeled dideoxynucleotides (ddNTPs) when the respective template is in the mix. A conventional polymerase chain reaction (PCR) primer pair was designed to produce the 304 base pair amplicon to be used as template for the SBE reaction, and a SNaPshot primer was designed for pathotyping. The SNaPshot primer was optimized on individual templates from single-spore isolates providing the expected base resolution, and then assessed for its limit of detection in template proportions of 10:90, 20:80, 30:70, 40:60, and 50:50. Additional testing was carried out on DNA extracted from canola root galls collected from the field to evaluate the sensitivity of the assay against field isolates. The assay was able to detect a 10% relative allelic proportion in a 10:90 template mixture with both single-spore isolates and field isolates. The application of this technique appears promising for large-scale SNP pathotyping to produce highly sensitive results.

Abstracts

Session 4. Student oral competition: Innovations for Pre- and Post-harvest Quality

15. Preharvest UV treatment a potential ecological approach for the control of *Xanthomonas campestris* pv. *vitians induces* key genes associated with homeostasis, growth, and defense in lettuce

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Lettuce (*Lactuca sativa* L.) is one of the most widely consumed leafy vegetables in the world. Its susceptibility to bacterial leaf spot (BLS) caused by *Xanthomonas campestris* pv. *vitians* (*Xcv*) can result in 100% yield losses. Despite the excessive and repeated use of pesticides, control of this disease remains difficult. Consumers, concerned about human-health and environmental protection, denounce the presence of residues on horticultural products and the abusive use of pesticides in agriculture. The search for new and effective biological approaches is need to improve the control of BLS. In the present study, a series of independent trials were conducted to evaluate the repeated use of a hormetic dose of 0.4 kJ/m^2 of UV-C radiation to control *Xcv* and to assess the impact of this treatment on lettuce yield. This study showed a 30-50% reduction in lettuce susceptibility to BLS as a function of the number of cycles of UV-C treatment without negative effects on agronomic characteristics and with an increase in total mineral concentrations, shelf life, and dry mass. Data revealed differential expression of genes associated with homeostasis, growth, and defense. We conclude that UV-C hormesis, under the conditions described in the present study, is an effective eustress that will not interfere with normal growth or the ability of plants to defend themselves against other potential stressors. The knowledge gained from this work could promote pre-harvest UV-C hormesis as an environmentally friendly approach in the implementation of an integrated pest management program.

16. Pre-harvest spray hexanal enhances the post-harvest quality of 'Honeycrisp' apples by regulating membrane degradation-associated genes

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'Honeycrisp' (*Malus domestica* Borkh.), a premium apple cultivar, is highly susceptible to bitter pit during post-harvest storage. Hexanal has been shown to enhance the shelf life of many temperate and tropical fruits. Here we report the effects of hexanal on post-harvest shelf life, including bitter pit disorder in 'Honeycrisp.' 'Honeycrisp' trees grown in a commercial orchard in the Niagara region were sprayed with hexanal and compared against harvista™ and non-treated control. Apples were harvested at the commercial harvest day and stored at 2.5 °C for four months. Both hexanal and harvista™ treated fruits showed lower ethylene production and decreased physiological loss in weight compared to control. Further, hexanal treatment significantly reduced the occurrence (8-14%), severity (7-10%) and progression (8-19%) of bitter pit compared to the harvista™ and control, respectively. Hexanal also decreased the phospholipase-D (PLD) enzyme activity throughout the storage compared to the other two treatments. qRT-PCR was conducted to study the expression profiles of four PLD and six calcium/calmodulin-related genes potentially involved in membrane degradation and cellular calcium modulation on post-harvest quality. Hexanal significantly decreased the expression of *MdPLDa1, MdCNGC14-like and MdCAM4* throughout the storage compared to other treatments. These findings indicate that a delay in the membrane degradation process caused by hexanal modulates the expression of the above genes and thus enhances the post-harvest quality of 'Honeycrisp.'

17. Cannabis inflorescence yield and cannabinoid concentration are not improved with long-term exposure to UV radiation

V. RODRIGUEZ-MORRISON, D. LLEWELLYN AND Y. ZHENG. *School of Environmental Sciences, University of Guelph, Guelph, ON N1G 2W1, Canada.*

It is commonly believed that exposing *Cannabis sativa L.* (cannabis) plants to ultraviolet (UV) radiation can enhance Δ^9-tetrahydrocannabinol (Δ^9-THC) concentrations in female inflorescences. However, a lack of published scientific studies has left knowledge-gaps in the effects of UV on cannabis. In this study we investigated the effects of UV exposure level on photosynthesis, growth, inflorescence yield, and secondary metabolite composition of two indoor-grown cannabis cultivars: 'Low Tide' (LT) and 'Breaking Wave' (BW). After growing vegetatively for 2 weeks under a canopy-level photosynthetic photon flux density (PPFD) of ≈225 $\mu mol \cdot m^{-2} \cdot s^{-1}$ in an 18-h light/6-h dark photoperiod, plants were grown for 9 weeks in a 12-h light/12-h dark "flowering" photoperiod under a canopy-level PPFD of ≈400 $\mu mol \cdot m^{-2} \cdot s^{-1}$ and 3.5 $h \cdot d^{-1}$ of supplemental UV radiation with UV photon flux densities (UV-PFD) ranging from 0.01 to 0.8 $\mu mol \cdot m^{-2} \cdot s^{-1}$ provided by light-emitting diodes (LEDs) with a peak wavelength of 287 nm. The severity of UV-induced morphology and physiology symptoms worsened as UV exposure level increased. Dry inflorescence yield decreased with increasing UV exposure level in LT, but not in BW. In LT, total equivalent Δ^9-THC and total equivalent cannabidiol (CBD) concentrations decreased with increasing UV exposure level, whereas there were no UV treatment effects on total equivalent concentrations of individual cannabinoids in BW. The potential for using UV to enhance cannabis quality must still be confirmed before it can be used as a production tool for modern, indoor-grown cannabis cultivars.

18. Compost amendments affect plant performance and crop quality without affecting disease severity in a long-established crown gall-diseased vineyard.

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Crown gall disease of grapevine has severe detrimental effects on grapevine performance and crop quality. The disease is induced by the soil-dwelling bacterium *Allorhizobium vitis,* which can be introduced into vineyard soil via infected planting material. Soil-borne *A. vitis* infections are enhanced by the presence of plant-parasitic nematodes because they induce root wounds through which the bacterium can enter the vine and establish systemic infection. Compost application has previously reduced pathogenic nematode populations in soil. Therefore, we hypothesized that compost amendments would reduce the severity of *A. vitis* infection by reducing soil nematode populations. In this study, three composts were applied in-row in a long-established vineyard infested with both plant-parasitic nematodes and *A. vitis* in the spring of 2019 and 2020. Bulk soil was collected in the spring and fall of both years to quantify *A. vitis* per gram of soil. Visual ratings of disease severity, plant performance, and crop quality measurements were also taken throughout 2019 and 2020. There were no significant differences in the concentration of *A. vitis* in bulk soil, nor in visual ratings of disease severity between treatments. Average berry weights (g; $p = 0.023$), berry titratable acidity (g/L; $p = 0.040$), and leaf greenness ($p = 0.033$) were affected by the application of compost treatments after two years. Our data indicate that berry tartness and sourness, berry weights, and overall plant vigour increased following compost application. Increased plant vigour may be detrimental as it can reduce grape production and make vines more susceptible to disease.

19. Can herbal essential oils use to treat strep throat?: antibacterial activity of carvacrol against *Streptococcus pyogenes*

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Herbal plants and spices have biologically active compounds with several therapeutic and pharmacological applications. Identify the specific phytochemicals as natural antimicrobial agents has renewed interest due to the current paucity of antimicrobial development. The present study aimed to assess the antibacterial activity of carvacrol, naturally present in essential oils of herbs such as oregano and thyme, against *Streptococcus pyogenes*. Carvacrol was evaluated for the growth inhibition, bactericidal effect and time-to-kill, against four strains of *S. pyogenes*. Cytoplasmic leakage of carvacrol-treated bacteria supernatants were assessed by agarose gel electrophoresis and lactose dehydrogenase (LDH) activity. Ultrastructureal changes were observed by transmission microscopy (TEM). Changes in cell membrane potential and permiability were assessed using Flow cytometry (FCM). A protoplast-model was used to confirm the membrane target of carvacrol. All the tested strains were susceptible to carvacrol with the minimum inhibitory concentration (MIC) of 125 µg/mL and minimum bacterial concentration (MBC) of 250 µg/mL. Time-to-kill was only 5 min for carvacrol at MBC when compared to 24 hr for Penicillin G at its respective MBC. Dose-dependent leakage of nucleic acids, LDH activity, morphological damages, cell permeability increasement and decrease in membrane potential were observed in carvacrol-treated bacteria. Protoplast experiments confirmed the membrane damage mechanism of carvacrol. However, carvacrol doesnot exhibited the cytotoxicity towards to human tonsil epithelial cells. Carvacrol exhibited growth inhibition and bactericidal properties against *S. pyogenes* through disruption of the bacterial membrane. Therefore, carvacrol has the potential to develop safe and efficacious natural health products for *S. pyogenes* infections.

20. Plant-derived dietary flavonoids protect cultured human lung epithelial cells from chemical-induced DNA damage

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Fruits and vegetables are dietary sources of flavonoids, a group of polyphenols that are known to exert anti-cancer properties via multiple cellular mechanisms. Even though there are advancements in early detection of cancer, surgery, chemotherapy, and radiotherapy to manage various cancers, five-year survivability is lesser than 15%, and chemotherapy-associated side effects are significant. Therefore, cancer prevention through dietary modifications has been received growing interest. Hence, this study focuses on investigating the effects of selected flavonoids in reducing 4-[(acetoxymethyl)nitrosamino]-1-(3-pyridyl)-1-butanone (NNKAc)-induced DNA damage in cultured human bronchial epithelial cells (BEAS-2B). To identify effective flavonoids, the dose-dependent response of selected compounds against NNKAc-induced reactive oxygen species (ROS) was conducted using 2’,7’-dichlorofluorescin diacetate (DCFDA) assay. The most effective tested compounds of carcinogen-induced ROS generation were assessed for cytotoxicity using the MTS assay. The ability to reduce carcinogen-induced DNA damage of selected flavonoids was conducted using gamma-H2AX immunofluorescence and DNA fragmentation assays. Luteolin, chrysin, quercetin, genistein, cyanidin, and isorhamnetin reduced significantly ($p<0.05$) the carcinogen-induced ROS generation in BEAS-2B cells. Furthermore, quercetin, luteolin, and genistein reduced significantly ($p<0.05$) the carcinogen-induced DNA damage in BEAS-2B cells. Therefore, consumption of fruits and vegetables rich in flavonoids such as quercetin, luteolin, and genistein may have a positive effect on reducing the risk of cancer, and further investigations are suggested.

Session 5. Regular author oral presentations: Genetics, Biotechnology and Breeding

21. Genetic stability analysis of stem solidness and grain yield in spring wheat

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The wheat stem sawfly, *Cephus cinctus* Norton (Hymenoptera: Cephidae), is a major pest of wheat (*Triticum aestivum* L.) in the northern Great Plains where it is a constant threat in Montana and is resurging in Alberta, Saskatchewan and North Dakota. Adoption of solid-stemmed cultivars is an important management tool for wheat growers; however, the inconsistent pith expression first noted with the release of 'Rescue' has been repeatedly observed in modern cultivars in Canada. Given the extensive hectares planted to solid-stemmed wheat cultivars during an outbreak, identification of cultivars that display stable stem solidness and grain yield across a wide range of environments where stem sawfly infestations occur is desirable. We assessed eight solid-stemmed and two hollow-stemmed spring wheat genotypes grown across diverse environments for their response in stem solidness and yield using multiple statistical models. Study sites included southern Alberta and Saskatchewan, Montana and North Dakota. Most models agreed that the genotypes, 'Choteau' 'BW925' and 'Mott' consistently displayed high and stable stem solidness concomitant with high grain yield. 'Choteau' and 'BW925' also consistently met or exceeded the desired threshold of a 3.75/5 pith rating for optimum resistance whereas, 'Mott' developed optimal pith at a specific (early) phenological stage when resistance to WSS infestation is critical. The identified stable and ideal genotypes would be useful to enhance germplasm development, production and adoption of spring wheat cultivars in the WSS prone regions.

22. Role of NOX genes in *Verticillium dahliae's* pathogenicity

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NADPH oxidase (Nox) genes are crucial for the production Reactive Oxygen Species (ROS) and are important for many fungi's pathogenicity. Genome investigation of *Verticillium dahliae* revealed the existence of three Nox-related genes namely *NoxA*, *NoxB*, and *NoxC*. Here we investigated the role of these genes in the pathogenicity of *V. dahliae*. *In vitro* expression of *NoxA*, *NoxB*, and *NoxC* showed significantly higher expression of *NoxB* in the highly than the weakly aggressive isolate of *V. dahliae* after treatment with different potato extracts. More transcripts of *NoxA* were detected in the weakly than the highly aggressive isolate in response to leaf and stem extracts. Significantly higher expression of *NoxC* was observed in the highly aggressive isolate treated with stem extracts. Single gene disruption mutants were generated for each of these genes to better understanding of the role of these genes in the pathogenicity of the highly aggressive isolates. Knocking out of both *noxa* and *noxb* genes, significantly decreased pathogenicity of the fungus, indicating the essential roles of these genes for *V. dahliae*'s against its hosts. The penetration ability of both *noxa* and *noxb* knock-out strains was drastically reduced, compared to the wild type. Gene complementation restored the pathogenicity as well as penetration capability of the fungus in both *noxa* and *noxb* mutants. Our data revealed that NoxA and NoxB genes play important roles in the pathogenicity of *V. dahliae*. These findings shed more light on the biology of *V. dahliae* and the mechanisms of its pathogenicity.

23. Functional characterization of minor genes of *Brassica napus* in response to blackleg disease

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Blackleg, mainly caused by fungal pathogen *Leptosphaeria maculans*, is one of the most devastating diseases in canola (*Brassica napus* L.) resulting in significant yield loss worldwide. An important element for bottom line profit and sustainability of the crop and environment is to mitigate pathogens through genetic resistance. In this study, we conducted genome wide identification and characterization of the *VQ* (Valine-Glutamine) gene family in *B. napus*. To understand the function of *B. napus VQ* genes in response to blackleg disease, we overexpressed *BnVQ7* (BnaA01g36880D, also known as *MKS1* gene) in a blackleg-susceptible canola variety Westar. Overexpression of *BnMKS1* in canola did not improve resistance to blackleg disease at seedling stage. However, transgenic canola plants overexpressing *BnMKS1* displayed enhanced resistance to *L. maculans* infection at the adult plant stage. In addition, we identified and characterised *BnNCED3* (9-cis-epoxycarotenoid dioxygenease) and *BnTX1* (Trithorax-like factor) from *B. napus*. Transgenic *B. napus* Westar plant overexpressing *BnNCED3* which shows enhanced adult plant resistance against blackleg infection. BnTX1 was confirmed to bind to the promoter region of *BnNCED3* gene using chromatin immunoprecipitation (ChIP)-qPCR. However, overexpression of *BnTX1* in transgenic plants displays decreased adult plant resistance in response to blackleg pathogen infection. These results indicated that minor genes play important roles in canola against blackleg disease.

24. Characterizing the common wheat accession KU168-2 for the stem rust resistance

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Wheat stem rust, caused by a biotrophic fungal pathogen *Puccinia graminis* f. sp. *tritici* (*Pgt*), is a historically devastating disease of wheat. With the ongoing evolution of virulent *Pgt* races, especially the Ug99 group (TTKSK and 13 variants), there is potential for more destruction in the future. Deployment of effective resistance (R) genes in cultivars is the preferred approach to combat this threat. In the current study, a genetic study was conducted on a common wheat double haploid (DH) population developed from a cross between RL6071 (susceptible) × KU168-2 (resistant). Phenotyping the DH population with *Pgt* races TTKSK and TPMKC showed resistance to these races was conferred by a single R gene. The R gene was genetically mapped to a region of chromosome arm 6AL known to be associated with *Sr13*. Till now, four resistance haplotypes R1-R4 have been reported for the *Sr13* region. A phenotypic analysis was conducted using six differentiating *Pgt* races TTKSK, QFCSC, QTHJF, RCRSF, TMRTF, and TPMKC on carriers of the four *Sr13* resistance haplotypes, KU168-2, RL6071, and selected R and S class DH lines which revealed that KU168-2 is functionally unique. A genetic characterization with the *Sr13* linked KASP and STARP markers indicated no amplification for the KU168-2 line, suggesting it carriers a new gene or a new allele of *Sr13*. To resolve this, we are planning to sequence the *Sr13* region in KU168-2. With more effectiveness as compared to *Sr13* known haplotypes and hexaploid origin, *SrKu168-2* will be a good candidate for use in breeding programs.

25. Temporal dynamics of the virome composition and transcriptional response of three grapevine cultivars

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Grapevine can be affected simultaneously by several pathogens, with a complex interaction that has largely been understudied. Among these pathogens, viruses represent a widespread class of pathogens that interact differentially with grapevine cultivars. In a recent study, we revealed a diverse virome (all the viruses and viroids) of a leafroll-infected interspecific hybrid grapevine cultivar and compared it to the virome of *V. vinifera* cultivar. However, co-occurrence analysis revealed that the presence of grapevine leafroll-associated virus species was randomly associated with the development of virus-like symptoms. To understand what drives the expression of symptoms, we used RNA sequencing analysis to profile the virome and transcriptome of grapevine leaves collected at two different times during the growing season (early August and late September). For cultivars such as Vidal, a total of 7047 genes were identified as differentially expressed genes (DEGs) from August to September, of which 2465 were upregulated and 4582 were downregulated. Further analysis revealed that many of these DEGs are involved in RNA-silencing pathway. For example, endoribonucleases dicer homolog 1 and 2 were significantly overexpressed. All asymptomatic grapevine plants showed viral-like symptoms in late September. The virome also showed a shift in terms of diversity and abundance, and the titer of the economically important viruses decreased from August to September, except in one case.

26. A deep dive into the game of hide and seek in the *Brassica napus-Leptosphaeria maculans* pathosystem: combined transcriptome and proteome analysis

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Blackleg, caused primarily by the hemibiotrophic fungus *Leptosphaeria maculans* (Desmaz.) Ces. & De Not., is one of the most economically important diseases in many canola/oilseed rape (*Brassica napus* L.) growing regions in the world that often causes significant yield losses. Genetic resistance has been proven effective in mitigating blackleg infection at different growth stages (seedling and adult plant). Seedling resistance generally follows the gene-for-gene theory, with the exception that the recognition of avirulence genes *AvrLm3* and *AvrLm9* by the respective resistance genes *Rlm3* and *Rlm9* is masked by the presence of *AvrLm4-7*, known as the 'game of hide and seek'. Recent evidence has shown that there is no direct interaction between *AvrLm4-7* and *AvrLm3* or *AvrLm9*, or between *Rlm9* and *AvrLm9* or *AvrLm4-7*, suggesting *AvrLm4-7* may conform to the guard or decoy models and interact with unknown targets in the host that represses the recognition of *AvrLm3-Rlm3* and *AvrLm9-Rlm9*. To reveal molecular networks underlying the masking effect, we combined RNA sequencing (NovaSeq 6000 System, Illumina) and proteomic (TMT-based technology) studies on *B. napus* 02-22-2-1 (*Rlm3* carrier) seedlings at 3-, 7- and 11-days post inoculation (dpi) and Goéland (*Rlm9* carrier) seedlings at 3 and 7 dpi with *L. maculans* isolates carrying *avrLm4-7-AvrLm3-AvrLm9* and *AvrLm4-7-AvrLm3-AvrLm9*, respectively. Hundreds to thousands of genes were identified concurrently or specifically in these typical and masked interactions, in addition to a number of differentially expressed proteins. The further downstream analysis in this multi-omics study will be instrumental to pinpoint key players in the 'game of hide and seek' for this pathosystem and possibly illuminating similar interactions in other pathosystems.

27. Using molecular biology and omics to manage clubroot of canola

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Clubroot, caused by *Plasmodiophora brassicae*, is one of the most important diseases of canola (*Brassica napus*) in Canada. Disease management relies heavily on planting clubroot resistant (CR) cultivars, but in recent years, new resistance-breaking pathotypes of *P. brassicae* have emerged. While efforts to develop new CR varieties using traditional breeding are underway, omics and molecular biology technologies can help to search for novel sources of resistance, improve understanding of host-pathogen interactions, and facilitate diagnosis. We performed two transcriptomic studies with two cultivar resistance-breaking pathotypes (3A and 5X) on *B. napus* hosts presenting contrasting resistance/susceptibility. The interaction with pathotype 5X showed a clear salicylic acid (SA)-mediated immunity response, especially in the resistant genotype. Inoculation with pathotype 3A showed that SA and ethylene were important as part of the defense mechanism of the resistant cultivar. As expected, susceptible hosts showed features of early cell growth modification. The *P. brassicae* reads from each interaction were used to predict putative effectors, indicating a predominance of effectors with interacting domains (e.g., ankyrin), supporting previous studies. Genes like benzoic acid/SA methyltransferase (*BSMT*), which methylates SA to render it inactive, showed higher levels of expression in the compatible interactions. We also sequenced 45 *P. brassicae* single spore and field isolates using Illumina short-reads, with reference-based mapping conducted to identify polymorphic sites that could be targeted for molecular pathotyping. Isolate clusters corresponding to pathotypes 5X and 3H could be distinguished by rhPCR and SNapShot. These molecular diagnostics methods show promise for distinguishing additional pathotypes for proactive clubroot management.

28. Clathrin mediated endocytosis is involved in the uptake of exogenous double-stranded RNA in the white mold phytopathogen *Sclerotinia sclerotiorum*

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RNA interference (RNAi) technologies have recently been developed to control a growing number of agronomically significant fungal phytopathogens, including the white mold pathogen, *Sclerotinia sclerotiorum*. Exposure of this fungus to exogenous double-stranded RNA (dsRNA) results in potent RNAi-mediated knockdown of target genes' transcripts, but it is unclear how the dsRNA can enter the fungal cells. In nematodes, specialized dsRNA transport proteins such as SID-1 facilitate dsRNA uptake, but for many other eukaryotes in which the dsRNA uptake mechanisms have been examined, endocytosis appears to mediate the uptake process. In this study, using live cell imaging, transgenic fungal cultures and endocytic inhibitors, we determined that the uptake mechanism in *S. sclerotiorum* occurs through clathrin-mediated endocytosis. RNAi-mediated knockdown of several clathrin-mediated endocytic genes' transcripts confirmed the involvement of this cellular uptake process in facilitating RNAi in this fungus. Understanding the mode of dsRNA entry into the fungus will prove useful in designing and optimizing future dsRNA-based control methods and in anticipating possible mechanisms by which phytopathogens may develop resistance to this novel category of fungicides.

Session 6. Invited keynote speaker

29. Genomics: changing how we improve crops

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Genomics is a rapidly changing field with the power to disrupt and enable scientific breakthroughs in many disciplines of biology. The immense size and complexity of many plant genomes hindered early genome sequencing progress of several crops, but recent technological advances in sequencing and assembly have made it possible to achieve chromosome scale assemblies for even the most complex genomes. Coupled with reduced costs and increased throughput, it is now possible to capture genome information of multiple individuals, or even large populations. By comparing the genome assemblies of multiple individuals, we are able to uncover the full complement of genomic diversity available to plant breeders and guide the identification of causal genes for in-demand traits. With genomics tools at our fingertips, it is truly an exciting time to be working towards plant improvement and to witness these technologies drive the development of the next generation of crops. It is with this next generation of crops that we will be meeting the needs of our increasing human population and challenges of intensified agriculture and climate change.

Session 7. Student oral competition: Genomic Applications for Crop Improvement

30. Bye-bye fungicides, hello RNAi: Understanding the uptake of RNAi-based controls and application of RNAi in controlling obligate biotrophic oomycetes

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Canada's crops are constantly threatened by fungal and oomycete pathogens that can cause serious yield losses. While fungicides are often used to control them, there are increasing concerns about off-target effects and the rise of pathogen resistance. RNA interference (RNAi) is emerging as a control method of phytopathogens and permits species-limited control using gene sequence-specific double-stranded RNAs (dsRNAs). Growth of *Sclerotinia sclerotiorum* can be inhibited using linear dsRNAs, hairpin RNAs (hpRNAs) and paperclip RNAs (pcRNAs), but the cellular uptake mechanisms of these different structured molecules differ. While linear dsRNAs are taken up by *Sclerotinia* via clathrin-mediated endocytosis, hpRNAs and pcRNAs enter by an unidentified pathway. By challenging *Sclerotinia* with chemical inhibitors and RNAi-mediated knockdown of different uptake proteins, we are elucidating the different dsRNA uptake mechanisms in this fungus. Our findings could prove valuable in future designs of dsRNAs to either overcome natural or acquired uptake resistance. In addition to our research on necrotrophic fungi, we have extended our applications of RNAi to obligate biotrophic oomycete pathogens. DsRNAs have been designed to target genes associated with a range of cellular functions in the downy mildew pathogen *Hyaloperonospora arabidopsidis*, which infects the model plant *Arabidopsis thaliana*. The efficacies of the different dsRNAs were evaluated by measuring transcript knockdown, leaf staining, and by a novel *Hyaloperonospora in vitro* spore germination assay. Our findings have led to improved ways in measuring RNAi-based treatments in obligate biotrophic pathogens and serve as the basis for future RNAi analysis within *Hyaloperonospora*.

31. Improving biosurveillance in the genomics era: using large-scale genome comparisons with machine learning to predict fungal phytopathogenic lifestyles

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Fungal phytopathogens employ a diverse array of trophic modes, or lifestyles, that influence host-pathogen interactions and give plant pathologists important information on how a fungus is causing disease, how it might spread through an ecosystem, and ultimately, how best to approach disease mitigation. While current biosurveillance strategies enable regulatory agencies to identify known pathogens, they fail to monitor unknown or taxonomically unclassified pathogens, and they cannot determine the specific biological traits and lifestyles that facilitate disease outbreaks. We are demonstrating a genomics-based approach to address these challenges. Our research tested the hypothesis that there are genomic signatures associated with fungal phytopathogenic lifestyles that can be harnessed to develop more effective biosurveillance approaches. We compiled a database containing lifestyle and biological trait information for 537 fungal species, spanning the Ascomycota and Basidiomycota phyla, from the fungal genome portal MycoCosm. Using the gene annotation data from a subset of 387 species with published genomes, we performed both principal component analyses (PCAs) and machine learning to determine whether there were patterns associated with specific lifestyles or biological traits. While there were few discernable patterns beyond phylogeny from the PCAs, our novel machine learning approach, DendroNet, was able to separate the signals from phylogeny and gene content and successfully predict the lifestyles of species from their genomes with AUROC (area under the receiver operating characteristic curve) scores ranging from 0.84 to 1.00. These results have important implications for the future of phytopathogen biosurveillance as well as the development of more effective disease mitigation strategies.

32. Comparison of qPCR, Illumina amplicon sequencing, and Oxford Nanopore MinION sequencing for the detection and quantification of airborne plant pathogens

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Currently in Alberta, Canada, several associations and research groups are independently monitoring the air for spores of important plant pathogens: *Sclerotinia sclerotiorum* (Lib.) de Bary in dry bean and canola, *Puccinia* species in wheat, and *Phytophthora infestans* (Mont.) de Bary in potato. Methods used for this monitoring rely on either real-time polymerase chain reaction (qPCR) or microscopy. The current research project is designed to assess whether next-generation sequencing techniques could simultaneously streamline existing sampling efforts and expand the number of pathogens detected. We collected daily air samples in (i) canola experimental plots at four sites across the province of Alberta, and (ii) dry bean, wheat, canola, and potato fields (n = 7) in southern Alberta. Following DNA extraction, samples were sent for Illumina amplicon sequencing of the fungal ITS1 and ITS2 regions. Additionally, the number of *S. sclerotiorum* ascospores in each sample was quantified using a qPCR assay. To assess the potential of in-field analysis of samples, a subset of DNA was also sequenced with the Oxford Nanopore MinION. Preliminary analysis of the canola data set revealed many common and plant pathogenic fungal ITS sequences and variation in community composition between sample sites. Comparing sequence counts of *S. sclerotiorum* from Illumina amplicon sequencing with the estimates of *S. sclerotiorum* DNA from qPCR revealed that qPCR could quantify lower levels of *S. sclerotiorum* DNA than amplicon sequencing. Results of this study will help to lay the foundation for a potential province-wide air monitoring network for plant pathogens.

33. Continuing the vital search for Fusarium head blight resistance

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Fusarium head blight (FHB) reduces yield, grade, and ultimately the economic return of harvested wheat. Integrated pest management strategies are used to mitigate FHB infection and genetic resistance is a key component. FHB resistance is elusive, and additional sources are continually needed to improve resistance. To continue the search for FHB resistance, 10,000 bread wheat (*Triticum aestivum* L.) accessions from Plant Gene Resources of Canada were evaluated for FHB resistance in field disease nurseries over six years. Four thousand accessions were re-evaluated over three years, followed by continued evaluation of the 400 accessions with the greatest resistance. The top 200 accessions were selected for type II resistance evaluation in the greenhouse by single spikelet inoculation with *Fusarium graminearum.* The in-field and greenhouse phenotypic data will be combined with genotypic data, obtained by 90K Infinium SNP array, to generate a Genome Wide Association Study to reveal quantitative trait loci associated with FHB resistance. Previous results have identified quantitative trait loci on chromosomes 1A, 4A, 6A, 2B, 5B, 7B, 1D, 2D, and 3D. The information obtained from this study will aid in FHB resistance breeding efforts and will benefit the wheat industry.

34. The regulation of intrinsic signaling in Brassica napus defending against *Leptosphaeria maculans*

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Plants are able to trigger multiple signaling pathways to cope with pathogenic invasion. Gene-for-gene interaction, one of the effective mechanisms, is triggered by the interaction between pathogenic Avr effectors from the pathogen and plant R proteins. Plant tissues induce distinct activities when they have, or have no HR, and those differences help to find out the factors in efficient defense against plant pathogens. An excellent pathosystem to investigate this is the *Brassica napus* – *Leptosphaeria maculans* pathosystem. Three cultivars of *B. napus* - Westar, Surpass400 and 01-23-2-1 that are susceptible, intermediate-resistant and resistant respectively, were inoculated by two *L. maculans* isolates (HCRT75 8-1 (Genotype: *avrLm1, AvrLm2,*

Abstracts

avrLm3, avrLm4, AvrLmJ1-5, AvrLm7, AvrLm6, avrLm9, AvrLm11, avrLepR1 and AvrLepR2) and HCRT77 7-2 (Genotype: *AvrLm1, avrLm2, avrLm3, AvrLm4, AvrLmJ1-5, AvrLm7, AvrLm6, avrLm9, AvrLm11, avrLepR1 and avrLepR2*)) to cause three distinct levels of severity: susceptible, intermediate and resistant. Expression studies using RT-qPCR, histochemical assays (such as trypan blue staining) were applied on the cotyledons of those cultivars to search the differences in defense response from those cultivars (with distinct severities). Histochemical assays suggested that the intermediate and resistant genotypes (i.e. Surpass400 and 01-23-2-1) displayed earlier H2O2 accumulation and cell death on the cotyledons. Transcriptional analysis (RT – qPCR) also observed that the genes related to salicylic acid (SA) and ROS were activated from the two genotypes as early as 3 and 5 dpi. The results indicated that the early activation of SA/ROS signaling is one of the crucial components for *B. napus* to defend against *L. maculans*.

35. Genetic responses of alfalfa (*Medicago sativa* L.) populations to long-term grazing

H. WANG AND B. BILIGETU. *Department of Plant Sciences, University of Saskatchewan, 51 Campus Dr., Saskatoon, SK S7N 5A8, Canada.*

Stand persistence under grazing is a key improvement goal for alfalfa breeding. This study collected alfalfa populations from 14 long-term rancher sites across four soil zones of Saskatchewan. From 2018-2020, the 14 alfalfa populations were evaluated in a field nursery for seven agro-morphological traits and three nutritive traits. DNA of random samples from each population were sequenced by genotyping-by-sequencing. There were significant differences in the forage yield among the 14 alfalfa populations at first and second cuts ($p < .05$). A two-way clustering analysis on the best linear unbiased prediction (BLUP) values of ten traits (seven agro-morphological traits and three nutritive traits) from the three years generated three clusters. Cluster I was characterized by the highest forage yield containing plants from MacDowall, Duck Lake, Dalmeny and Arcola populations. Based on 19,853 single nucleotide polymorphisms (SNPs), no apparent genetic separation was detected among the 14 populations, but there was a genetic shift by soil zone with the populations from Black and Brown Soil zones being most unique. A genotype-environment association analysis found 283 SNPs within the 14 alfalfa populations including 114 SNPs associated with soil nutrient, 67 SNPs with annual precipitation, 39 SNPs with soil pH, 33 SNPs with soil zone and 30 SNPs with annual air temperature. Alfalfa populations from long-term grazing sites is promising to discover highly adapted germplasm to long-term grazing in the Canadian prairies.

36. Transcriptomic profiling of the host-pathogen interaction in tan spot of wheat

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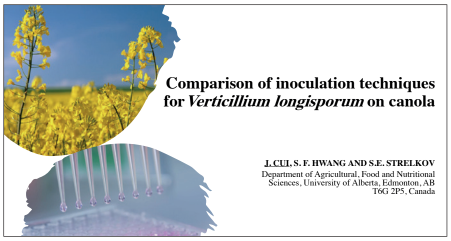
Tan spot, caused by the necrotrophic fungus *Pyrenophora tritici-repentis*, is a foliar disease that affects wheat (*Triticum aestivum* and *Triticum turgidum*) by decreasing the kernel weight and number of kernels per spike. In recent years, tan spot has become one of the most detrimental diseases of wheat in Canada. Research on this pathosystem has focused on understanding the genetic basis of host resistance, yet important aspects of the plant-pathogen interaction remain unanswered. Using high-throughput RNA-sequencing, we have identified differences between isolates of *P. tritici-repentis* during saprophytic vs. parasitic growth. Differences were also identified *in planta*, at 12, 36 and 72 h after inoculation, between isolates producing the necrotrophic effectors ToxA and ToxB. The number of reads recovered indicated an increase in the ToxA-producer, while minor changes in read numbers were found for the ToxB producer. Preliminary analysis showed that the expression patterns correctly clustered the biological replicates according to each treatment, validating the experiment. For the ToxA-producing isolate, the number of differentially expressed genes decreased over time, in contrast with the ToxB-producing isolate, which presented a constant pattern of expression. This study will provide genomic-based resources to improve understanding of virulence mechanisms in *P. tritici-repentis* and identify patterns of molecular interactions between the host and pathogen. The knowledge can be applied to the development of improved tan spot management programs, by identifying genes involved in virulence and potential targets in the host. Additionally, through comparative genomics with other necrotrophic fungal pathogens, these genes can provide insights into pathogenicity-related processes.

Session 8. Student oral competition: Plant and Soil Health

37. Comparison of inoculation techniques for *Verticillium longisporum* on canola

J. CUI, S. F. HWANG AND S. E. STRELKOV. *Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB T6G 2P5, Canada.*



Comparison of inoculation techniques for *Verticillium longisporum* on canola

J. CUI, S. F. HWANG AND S.E. STRELKOV
Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB T6G 2P5, Canada

Verticillium stripe, caused by *Verticillium longisporum* (VL), is an emerging soilborne disease of canola (*Brassica napus*) in Canada. Improved inoculation protocols will facilitate study of this disease and its management. Two inoculation techniques, a root-dip method at two inoculum concentrations and a grain inoculation method at four inoculum concentrations, were compared with the canola cultivars ‘45H31’, ‘CS2000’ and ‘Westar’ under greenhouse conditions. Symptoms of Verticillium stripe appeared at early growth stages following root dip inoculation, resulting in seedling mortalities of 13%, 34%, and 33%, respectively, for ‘CS2000’, ‘45H31’ and ‘Westar’ at 35 days post-inoculation. Plants inoculated by the root dip method incurred much greater mortality at the high vs. low inoculum concentration. In the surviving adult plants, ‘45H31’ became strongly resistant while ‘CS2000’ became more susceptible to VL. The grain inoculation method did not cause early stage mortality, although Verticillium stripe severity at the adult stage was significantly different between control and high inoculum concentrations for all cultivars. In addition, dry weight and plant height decreased as inoculum concentration increased. Inoculation of 1-week-old, 2-week-old, and 3-week-old seedlings of ‘CS2000’ and ‘Westar’ was also compared by the root-dip method. Symptoms were more severe when VL was inoculated at the later growth stages, perhaps because infected seedlings died following early inoculation. It seems that the timing and method of inoculation with VL will need to be carefully considered with respect to the objectives of a particular study.

38. Disease dynamics of root rot complex in field pea

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Pea root rot is a disease complex comprised of multiple biotic and abiotic stressors resulting in decay of the root system. Pathogens contributing to root rot in field peas include *Aphanomyces euteiches* and various *Fusarium* spp. However, little is understood of the nature of the interspecific interactions between pathogens and disease severity, as well as environmental influence on these interactions. The objective of our study was to simulate multiple infection scenarios in a greenhouse experiment to (i) characterize the nature and effect of pathogen interactions on disease severity and (ii) determine effect of multiple pathogens on pathogen biomass and host colonization patterns using quantitative PCR (qPCR). ‘CDC Meadow’ was grown in soil inoculated with varying concentrations of *Fusarium avenaceum*, *Fusarium redolens* and *Aphanomyces euteiches*. Four weeks post seeding, disease severity of roots was rated using a visual scale and fresh biomass measurements were taken. DNA was isolated from the tap and lateral roots for pending qPCR analysis. Results showed a positive correlation between pathogen load and disease severity in the case of all three pathogens. The presence of *F. redolens*, a weak pathogen, in the mixture resulted in a lower disease severity compared to single inoculations in some trials, but this was not consistent across all repeated trials. These results highlight that, even under controlled conditions, it is difficult to ascertain the nature of multiple pathogen interactions. This emphasizes the challenge of understanding pea root rot development under field conditions where more than three pathogens are often present.

39. Cucumber powdery mildew detection using non-georeferenced multispectral images.

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Powdery mildew, which is caused by the fungus *Podosphaera xanthii,* is a major disease in cucumber greenhouses and may lead to yield losses between 30 to 50% of the total production This study evaluated three geometric transformations in an image registration method applied to non-georeferenced multispectral images acquired at close range over greenhouse cucumber plants with a Micasense® RedEdge camera. The detection of matching points was performed using SURF features, and outliers matching points were removed using the MSAC algorithm. For each geometric transformation (affine, similarity, and projective), we mapped the matching points of the blue, green, red, and NIR band images into the red-edge band space and computed the root mean square error (RMSE in pixel) to estimate the accuracy of each transformation. Then, registered band images were used to create an aligned RGB image and different vegetation indices. Using a pixel-by-pixel approach, a fine Gaussian support vector machine was trained to classify healthy and infected pixels. Our results achieved an RMSE of less than 1 pixel with the similarity and affine transformations and of less than 2 pixels with the projective transformation, whatever the band image. We determined that the best transformation was the affine transformation because it produces RMSEs of less than 1 pixel and having a Gaussian distribution. The classification using the RGB images presented a precision and F1 Score of 82 and 88%, respectively. Nevertheless, Cucumber powdery mildew detection is feasible using the five registered bands, reaching a precision and F1 Score of 97 and 98%, respectively.

40. Understanding the effects of landscape structure on the abundance of cabbage seedpod weevil and lygus bugs, and associated crop damage

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Canola is a major oilseed crop grown in the Canadian Prairies. Cabbage seedpod weevils and lygus bugs are two major insect pests damaging canola and affecting yield. These insects feed mainly on reproductive structures of canola such as buds, flowers, and pods. Chemical insecticides are the only available option for canola growers to manage these pests. Given the expense and potential harmful impacts of pesticides on the environment and biodiversity, biological control is an attractive option worth researching. Biological control has been investigated as a feasible option to keep these two canola pests below economic thresholds. Recent research has focused on classical biological control using efficient parasitoids from Europe. Previous studies suggest that surrounding landscape structure and configuration could affect the success of biocontrol of pests by natural enemies. Our study aimed to measure the effects of landscape on the abundance of cabbage seedpod weevil and lygus bugs, and associated crop damage in canola. To assess these effects, independent canola field sites were selected, and landscape structure and configuration were documented. Digital maps were constructed using ArcGIS Pro. From the resulting data and maps, the proportion of various habitats and non-crop habitats were calculated. Cabbage seedpod weevil and Lygus bugs abundance were estimated by sweep net sampling. Weevil damage was estimated by counting the exit holes in canola pods. Preliminary analysis was conducted using regression models. The results will elucidate the effect of landscape structure on the abundance of cabbage seedpod weevil, lygus bugs, crop damage and provide knowledge to improve sustainable management of these pests.

41. Role of tomato ringspot virus in tree fruit decline in the Niagara region

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Stone fruits are economically important crops in the Niagara region, producing $66 million annually, and have recently come under threat from a devastating disease. Tree Fruit Decline (TFD) is an emerging disease that results in rapid decline and death, up to 25% mortality, of stone fruit trees to which there is no known cause. Numerous symptoms have been observed including leaf chlorosis and wilting, increased gummosis, cankers, and death. Viral infection of fruit trees can result in similar symptoms to TFD. In order to identify the potential cause of TFD, we employed RNAseq to identify all viruses present in diseased fruit trees. Total RNA was extracted from diseased tree samples and sequenced using Ilumina NovaSeq. Multiple plant viruses were identified including Prunus necrotic ringspot virus, Tobacco streak virus, Grapevine associated ilarvirus, Tomato ringspot virus (ToRSV), and Peach latent mosaic viroid. ToRSV was the most prominent virus in these samples and infection by ToRSV often results in similar symptoms to TFD. To investigate further, PCR screening of 507 trees in the Niagara region revealed that ToRSV was present in 13% of fruit trees. ToRSV was most prominent in peach trees with 27% prevalence rate. Whereas the least prominent were plum and cherry trees with 6% and 5%, respectively. We observed that multiple diseased trees failed to test positive for ToRSV and multiple healthy trees did test positive for ToRSV. Therefore suggesting that ToRSV is likely not the sole cause of TFD but may be a contributing factor in diseased trees.

42. Potential use of vegetative indices to detect and estimate disease severities of Monilinia and Botrytis blight on wild blueberry fields

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Monilinia blight (MB) and Botrytis blossom blight (BB) diseases are endemic to most wild blueberry fields and affect both foliage and flowers. The severity of these diseases depends on the conditions present on the field. Present disease monitoring depends on the use of intensive sampling, using line transect among population structure. Therefore, the objective of this study is to assess the potential of using vegetative indices (VI's) to detect and assess the severities of Monilinia blight and Botrytis blight disease on wild blueberry plants. Three patches each of Monilinia, Botrytis blight and healthy plant treatments were identified, and disease progression monitored. Disease sampling were grouped into 3 forms: low (1 – 30%), moderate (30 – 70%), and severe (70 – 100%) disease damage. Assessments of plant damage was conducted using VI's and data analyzed using analysis of variance. Results indicated that there were significant differences ($p<0.05$) between the VI's computed for the healthy, Monilinia and botrytis blight diseased patch. At each damage level, healthy plants showed the highest significance, with Botrytis blight being significantly different from Monilinia blight. A discriminant accuracy of 94.4% showed that, normalized difference vegetative index (NDVI) can be used to differentiate between healthy and diseased plants. Green leaf index (GLI) gave an accuracy of 83.3% with enhanced NDVI (ENDVI) giving 72.2% accuracy. NDVI performed better than the other VI's in the determination of disease severity. These results have illustrated the potential to use VI's to discriminate healthy and disease plants and to assess disease pressures on wild blueberry fields.

43. Metalaxyl sensitivity of *Phytophthora* spp. associated with red raspberry in British Columbia

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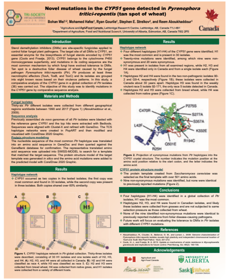
Root rot and wilting complex (RRWC), caused by *Phytophthora* spp., is the most devastating disease of red raspberry in British Columbia (BC). Metalaxyl is the most commonly used fungicide to manage the disease in the province. *P. rubi* and *P. gonapodyides* were isolated from red raspberry samples showing symptoms of RRWC. The metalaxyl sensitivity of strains of *Phytophthora* spp. (12 strains of *P. rubi* and 6 strains of *P. gonapodyides*) isolated from diverse raspberry farms of BC were evaluated *in vitro* using the radial growth method. Metalaxyl was amended to 20% clarified V8 agar to yield final concentrations of 0, 0.001, 0.01, 0.1, 1, 10 $\mu g\ ml^{-1}$. Each strain was tested in triplicate for treatments and experiments were repeated twice independently. Fifty percent effective concentration (EC_{50}) values and dose response curves were determined for each strain. Results showed that ~ 83% of *P. rubi* and 100% of *P. gonapodyides* strains were highly sensitive to metalaxyl with mean EC_{50} values of 0.0576 (range from 0.0375 to 0.0738) for *P. rubi* and 0.0542 (range from 0.0244 to 0.0758) for *P. gonapodyides*. A detailed sensitivity study of a large number of *Phytophthora* isolates is in progress.

Session 9. Student poster flash-talks: Genetics, Biotechnology and Breeding

44. Novel mutations in the *CYP51* gene in a global collection of *Pyrenophora tritici-repentis* (tan spot of wheat)

B. WEI, M. HAFEZ, R. GOURLIE, S. E. STRELKOV AND R. ABOUKHADDOUR. *(B.W., M.H., R.G., R.A.) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1 Ave S, Lethbridge, AB T1J 4B1, Canada; (B.W., S.E.S.) Department of Agricultural, Food & Nutritional Science, University of Alberta, 410 Agriculture/Forestry Centre, Edmonton, AB T6G 2P5, Canada.*



Sterol demethylation inhibitors (DMIs) are a group of site-specific fungicides applied to control fungal plant pathogens. The target site of all DMIs is CYP51, belongs to the cytochrome P450 monooxygenase superfamily, an essential enzyme for the biosynthesis of fungal sterols. Mutations in *CYP51* are the most common mechanism by which fungi evolve tolerance to DMIs. In this study, mutations in the *CYP51* gene were explored in a global collection of 36 isolates of *Pyrenophora tritici-repentis*, the pathogen causing tan spot of wheat. The mutations at the DNA and protein levels were determined. The results showed that *CYP51* occurred as two gene copies in the tested isolates, the first copy was most common and found in 33 isolates and the second copy was only found in three isolates with over 60% similarity. Four different haplotypes of *CYP51* were identified (H1- H4). Haplotype H1 was the most common and found in 30 of the isolates. In contrast, the two non-pathogenic isolates and a weakly virulent race 5 isolate from Canada all carried different haplotypes. Eight non-synonymous mutations were identified, but none were identical to previously reported mutations. The non-pathogenic isolates were collected from grasses and likely were not subjected fungicide application. Further work to estimate the tolerance to DMIs in relation to these *CYP51* mutations is *P. tritici-repentis* is needed.

45. Modern breeding strategies assist development of disease-resistant, two-row malting barley adapted for production in western Canada

J. R. TUCKER, C. W. HIEBERT, W. XU, A. BADEA AND W. G. D. FERNANDO.

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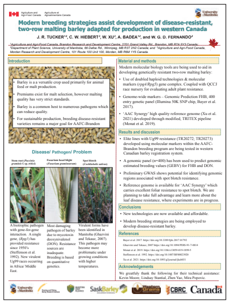
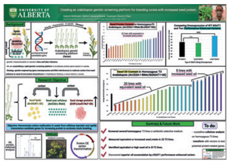


Barley (*Hordeum vulgare* L.) is a versatile crop used primarily for animal feed or malt production, and is of major economic importance to western Canadian farmers. However, barley is a common host to numerous plant pathogens, which impose constraints on production that can affect both yield and grain quality. Plant breeding is a successful approach for disease management in barley, which minimizes reliance on pesticides, helps Canada's approach for IPM and sustainability. Molecular marker assisted selection for *rpg4/Rpg5* gene complex has supported development of elite germplasm with resistance to virulent races (Ug99) of stem rust (*Puccinia graminis* f. sp. *tritici*). Advances in Genomic sciences have supported new approaches that exploit genome-wide markers for genomic prediction and enhancement of resistance to fusarium head blight (*Fusarium graminearum*) and low deoxynivalenol accumulation. With the recent release of the first reference genome of a Canadian malting cultivar 'AAC Synergy', it will be possible to investigate unique foliar disease resistance mechanisms for further use in developing improved germplasm. Accelerated development of disease-resistant cultivars will help maintain competitiveness of barley in face of evolving pathogens.

46. Creating an *Arabidopsis* genetic screening platform for breeding canola with increased seed protein.

K. MCDONALD, K. JAYAWARDHANE AND G. CHEN. *Department of Agricultural, Food, and Nutritional Science, 410 Agriculture/Forestry Center, University of Alberta, Edmonton, AB T6G 2P5, Canada.*

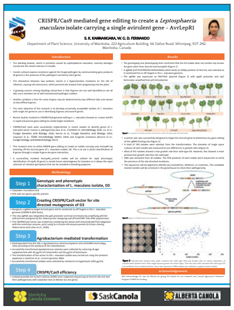


Canola (*Brassica napus* L.) is the major oilseed crop cultivated in the Canadian Prairies. After oil extraction, the protein and carbohydrate meal by-product is mainly used as animal feed. The carbohydrate component of the meal can inhibit animal digestion and has low value, while the seed protein has potential for higher-value use in the plant-based protein industry. It is of great interest to increase the value of canola meal by manipulating carbon flow from seed coat cellulose to seed storage proteins. Since characterization of candidate genes for increasing canola seed protein is time and labor intensive, we propose creating a rapid genetic screening platform using *Arabidopsis thaliana* L., a relative of canola. We have metabolically engineered *A. thaliana* with reduced seed cellulose through seed-specific At*CESA1*-RNAi downregulation and increased seed oil through Bn*DGAT1* overexpression. This platform would be used by breeders to rapidly characterize candidate genes for increasing protein content in canola without penalizing seed oil. So far, we have created a population of T2 *A. thaliana* with At*CESA1*-RNAi-downregulation and Bn*DGAT1*-overexpression and have confirmed increases in seed oil content by 4-8% in eight transgenic lines. These lines have been advanced to the T3 generation, from which many homozygous lines have been identified for seed oil and carbohydrate analysis. Once we have acquired a population of homozygous T3 lines with high seed oil and low seed cellulose, they could be used as a platform in characterizing candidate genes for increasing seed protein, thereby accelerating the genetic research needed to support canola breeding.

47. CRISPR/Cas9 mediated gene editing to create a *Leptosphaeria maculans* isolate carrying a single avirulent gene - *AvrLepR1*

S. K. KANNANGARA AND W. G. D. FERNANDO

Department of Plant Science, University of Manitoba, 222 Agriculture Building, 66 Dafoe Road, Winnipeg, R3T 2N2, Manitoba, Canada.



Blackleg disease in canola, caused by *Leptosphaeria maculans,* is a major constraint to yield and trade. Although there is much research done on the interaction and identification of resistance, there is a significant limitation in characterizing the genes. A growing concern among blackleg researchers is that resistance (*R*) genes are not correctly identified as not all research labs use a standard set of well-characterized isolates. Further, the same *R*-gene may be determined by two different labs and named as two different genes. Therefore, the objective of the research is to develop universally acceptable isolates of *L. maculans* with single avirulent (*Avr*) genes that can be used for the identification of *R* genes and novel *R* genes. The clustered regularly interspaced short palindromic repeat (CRISPR)/Cas9 mediated gene editing is a promising tool in mutating *Avr* genes. We aim to create an isolate carrying only *AvrLepR1* by knocking off the *AvrLm5* gene of *L. maculans* isolate, D3. The CRISPR/Cas9 system was delivered to the *L. maculans* genome through the vector sgAvrlm5_pKHT332 via Agrobacterium-mediated transformation. The vector, sgAvrlm5_pKHT332, was created by combining a sgRNA, which was designed to bind *AvrLm5* gene at 192 nucleotide position, and a section of *pFC334* plasmid containing *Aspergillus nidulans tef1* promoter, Cas9 gene and *A. nidulans tef1* terminator via In-Fusion cloning. Antibiotic-resistant isolates were selected, and the mutant will be identified by sequencing the respective portion of the target gene. A successfully mutated *AvrLepR1_avrlm5* isolate will be utilized for rapid phenotypic identification of the *LepR1* gene in canola.

48. Genomic methylation levels appear adverse effect on total phenolic content between in vitro and greenhouse grown lingonberry (*Vaccinium vitis-idaea*)

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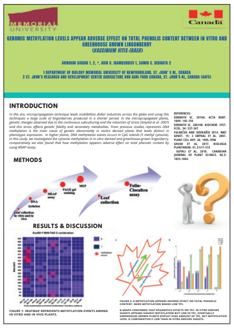
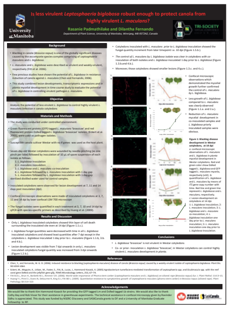


Methylation events play a role in developmental gene regulation, response to the environment, and natural variation of gene expression levels in crop plants. The purpose of the study is to investigate cytosine methylation and total phenolic content of lingonberry (*Vaccinium vitis-idaea*) among in in vitro derived and greenhouse-grown plants. Methylation event was analyzed by using Methylation Sensitive Amplified Polymorphism (MSAP) assay where the primers were cleaved in cytosine residues at 5'-CCGG-3' sites in CpG-islands. We observed that in vitro derived shoots showed higher methylation bands than tissue-culture derived greenhouse-grown (TC) plants. Cutting propagated greenhouse-grown (CP) plants was used as control where methylation was not displayed. On the other hand, total phenolic content were higher in TC and CP plants compared to in vitro-grown shoots. Thus, in this study we found that total phenolic content has an adverse effect on cytosine methylation, where methylation was high in in vitro derived shoots but low amount of phenolic content was observed.

49. Is less virulent *Leptosphaeria biglobosa* robust enough to protect canola from highly virulent *L. maculans*?

K. R. E. PADMATHILAKE AND W. G. D. FERNANDO. *Department of Plant Science, University of Manitoba, Winnipeg, MB R3T2N2, Canada.*



Leptosphaeria biglobosa is a less virulent pathogen that causes blackleg disease in canola (*Brassica napus*). Previous literature has shown the inoculation of less virulent *L. biglobosa* can boost the host resistance of canola against the highly virulent *L. maculans*. This study focused to study the effectiveness of *L. biglobosa* as a biocontrol agent against *L. maculans* in depth at morphological and transcriptomic levels. The *in-situ* development of two *Leptosphaeria* species inoculated at different timepoints was assessed using fluorescent-protein-tagged isolates: GFP-tagged *L. maculans* and DsRed-tagged *L. biglobosa*. The control of *L. maculans* mycelia with pre inoculated and co-inoculated *L biglobosa* was clear in fluorescence protein tagged mycelial observations under confocal microscope. The quantification of each pathogen done by qPCR and host defense related real time gene expressions confirmed the potential of *L. biglobosa* in the management of blackleg disease. The study shows how the less virulent species *L. biglobosa* protect the canola crop from the invasion of the highly virulent *L. maculans* in canola. Morphological and Transcriptomic data are being evaluated, and will be presented at the conference.

50. Evaluation of plant-pollinator ecosystem health and rapid detection of plant and bee pathogens by high-throughput sequencing of European honey bee (*Apis mellifera)*

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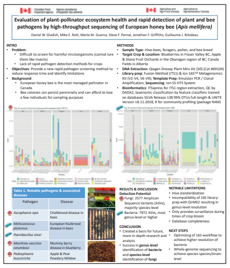

The European honey bee, *Apis mellifera*, is Canada's most prevalent managed pollinator. Honey bee pollination services are valued up to 5.5 billion dollars annually in Canada. Being associated with microorganisms in their environment, they have the potential to interact with and acquire pathogens. As a result, they can serve as vectors, transporting bee pathogens back to their hive or transferring pathogens between individual plants. In our proof-of-concept experiment, we exploited this bee-pathogen relationship to develop a new way to rapidly detect pathogens in the environment and assess the health of plant-pollinator systems. High-throughput sequencing (HTS) of the conserved ITS1 and 16S regions in samples from pollen collected in hive-mounted pollen traps, hive-stored pollen, and bee foragers was used to categorize fungi and bacteria, respectively. Over 19 million reads per run were generated from 44 samples. The QIIME2 pipeline was used to do quality control, produce amplicon sequence variants, and conduct taxonomic classification. Using this method, we created community pathogen profiles for apples and blueberries from British Columbia and Ontario. Identified plant pathogens include fungi *Monilinia* spp. and *Podosphaera leucotricha*. Bee pathogens include the fungus responsible for chalkbrood disease, *Ascosphaera apis*, as well as the bacteria *Melissococcus plutonius,* the causative agent of European foulbrood disease, and its secondary invader *Paenibacillus alvei*. With this pilot project, we seek to determine the capacity of this approach to evaluate plant-pollinator ecosystem health, identify limitations, and set up a foundation from which future screening programs may be built.

51. Determining resistance of asparagus (*Asparagus officinalis L.*) cultivars to *Stemphylium vesicarium*

G. AUSTIN, D. WOLYN, M.R. MCDONALD and Y. GAN. *Department of Plant Agriculture, University of Guelph, 50 Stone Rd E, Guelph, ON N1G 2W1, Canada.*

Purple spot of asparagus, caused by *Stemphylium vesicarium* (Wallr.) E. Simmons, decreases the marketability of spears and causes premature defoliation, leading to reduced yields in subsequent years. Field surveys of the resistance of asparagus cultivars to *S. vesicarium* have provided inconsistent results, leading to controlled environment studies with inoculated detached spears. Four cultivars, 'Guelph Millennium', 'Guelph Eclipse', 'Jersey Giant', and 'Gijnlim', were examined in field and controlled environment studies to evaluate methods to assess field resistance through inoculating detached spears. A bioassay was developed that produced consistent results. Nearly a dozen factors were assessed to further understand the mechanisms of resistance. Inoculation location on the spear, near the tip or base, was a significant factor and interacted with cultivar. Creating wounds by rubbing the surface, or keeping spears under continuous darkness, both increased lesion numbers; all cultivars were similarly affected. Treating spears with acibenzolar-S-methyl to trigger systemic acquired resistance countered the effect of continuous darkness. The difficulty in determining resistance in the field may be due to an interaction between cultivar resistance and acute weather during a critical infection period. The detached spear bioassay was largely consistent with field assessments conducted after wet or windy weather, but diverged when weather was drier and calm. The bioassay, with consistent water, high humidity, moderate temperature, fresh spears and location of inoculation on the spear, is useful for identifying some mechanisms of resistance among cultivars. However, inoculating attached spears in the field while accounting for weather will provide the most realistic results.

52. Polyphenols-rich apples exhibit anti-diabetic properties *in vitro.*

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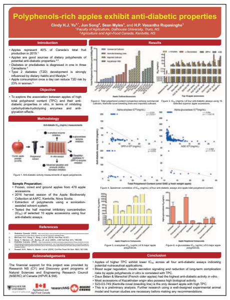
Polyphenols-rich apples exhibit anti-diabetic properties

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Introduction

- Apples represent 40% of Canada's total fruit production in 2019.[1]
- Apples are good sources of dietary polyphenols of potential anti-diabetic properties.[2,3]
- Diabetes or prediabetes is diagnosed in one in three Canadians.[4]
- Type 2 diabetes (T2D) development is strongly influenced by dietary habits and lifestyle.[5]
- Apple consumption once a day can reduce T2D risk by 23% in women.[3]

Objective

- To explore the association between apples of high total polyphenol content (TPC) and their anti-diabetic properties *in vitro*, in terms of inhibiting carbohydrate-hydrolyzing enzymes and anti-glycation effects.

Methodology

Figure 1. Anti-diabetic activity measurements of apple polyphenols.

Sample Preparation:

- Frozen, cored and ground apples from 478 apple accessions.
- 2016 harvest season of the Apple Biodiversity Collection at AAFC, Kentville, Nova Scotia.
- Extraction of polyphenols using a sonication-assisted solvent system.
- Tested the half maximal inhibitory concentration (IC_{50}) of selected 10 apple accessions using four anti-diabetic assays.

References

Results

Figure 2. Total polyphenol content comparison among commercial cultivars, Kentville novel breeding lines and imported cultivars.

Figure 3. IC_{50} (mg/mL) of four anti-diabetic assays using 10 selected superior apple accessions.

Figure 4. Spearman correlation of IC_{50} (mg/mL) of four anti-diabetic assays and apple total polyphenol content.

Figure 5. α-amylase IC_{50} (ug/mL) of 6 major apple polyphenols.

Figure 6. α-glucosidase IC_{50} (ug/mL) of 6 major apple polyphenols.

Acknowledgements

The financial support for this project was provided by Research NS (CY) and Discovery grant programs of Natural Sciences and Engineering Research Council (NSERC) of Canada (HPVR & SM).

Conclusion

- Apples of higher TPC exhibit lower IC_{50} across all four anti-diabetic assays indicating potential nutraceutical applications.
- Blood sugar regulation, insulin secretion signaling and reduction of long-term complication risks by apple polyphenols *in vitro* is correlated with TPC.
- Daux Belan & Marechal (French cider apples) had the highest anti-diabetic activity *in vitro*.
- Most accessions of Kazakhstan origin also possess high biological activity.
- S23-03-749 (Kentville novel breeding line) is the only dessert apple with high TPC.
- This is a preliminary analysis. Further research using a well-designed experimental animal model and human studies are necessary before making any recommendations.

Type 2 diabetes is a rising global health problem. The beneficial effect of dietary polyphenols on post-prandial glycemic control is recognized. Polyphenols are ubiquitous in plant-based diets and do not cause undesirable side effects. Apples are rich in dietary polyphenols and represent 40% of Canada's total fruit production. In this study, we have screened over 300 apple accessions from Canada's Apple Biodiversity Collection for inhibition of carbohydrate-hydrolyzing enzymes and dipeptidyl-peptidase IV (DPP-4) enzyme. The parameters were compared with respective commercial anti-diabetic drugs, Acarbose (α-amylase IC_{50} = 3.15 ug/mL; α-glucosidase IC_{50} = 236 ug/mL), and Sitagliptin (DPP-4 IC_{50} = 0.0014 ug/mL). The six most abundant polyphenols of apples (chlorogenic acid, epicatechin, phlorizin, procyanidin B_2, cyanidin-3-galactoside, and quercetin-3-galactoside) were also assessed to understand their contribution toward anti-diabetic properties of apples. A negative correlation was observed between total polyphenol content and IC_{50} values of α-amylase (r_s = -0.715; P = 2.87E-14), α-glucosidase (r_s = -0.554; P = 1E-16), and DPP-4 (r_s = -0.534; P = 0.0104) enzyme inhibition. Cider apples such as 'Marechal' (α-amylase IC_{50} = 5.3 mg/mL; α-glucosidase IC_{50} = 7.1 mg/mL), 'Daux Belan' (α-amylase IC_{50} = 14.4 mg/mL; α-glucosidase IC_{50} = 10.9 mg/mL), and 'Gros Frequin' (α-amylase IC_{50} = 7.7 mg/mL; α-glucosidase IC_{50} = 12.1 mg/mL), and wild apples from Kazakhstan such as 'Kaz 95 18-10' (α-amylase IC_{50} = 8.2 mg/mL; α-glucosidase IC_{50} =11.3 mg/mL), had the greatest anti-diabetic activities. This study will be continued to select specific apple varieties to produce nutraceuticals for the management and prevention of T2D.

Session 10. Regular author oral presentations: Pathogen Challenges and Genomic Applications

53. Use of high throughput sequencing for the identification of plant pathogens

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Field and vegetable crops are susceptible to many diseases which are caused by pathogenic organisms. These organisms co-exist on affected tissues, which complicates the diag-

Abstracts

nostic process. The decision-making process of disease diagnosis may involve the use of multiple microbiological, immunological and molecular assays, which can be time consuming, labor intensive and costly. The advent of high throughput sequencing (HTS) techniques makes it possible to accurately identify most pathogenic organisms in a single analysis. By coupling available taxonomic information and using the latest sequencing data filtration strategies, it is now possible to assess unique genetic variants that can precisely identify pathogenic organisms. We evaluated the identification accuracy potential by HTS on nearly 500 diagnosed cases received at the Laboratoire d'expertise et de diagnostic en phytoprotection (MAPAQ) and at the Centre de recherche sur les grains (CEROM). These cases represented diverse crops (crucifers, cucurbits, potatoes, field crops and tomato) and pathogens. Amplicon-based HTS was used to assess pathogenic groups by targeting respective DNA regions, including the fungal Internal transcribed spacer ITS, bacterial and archaeal 16S rDNA gene, eukaryota18S rDNA and Fusarium Elongation factor 1-alpha (EF1α) regions. The HTS approach is based on an adapted sequence processing strategy, involving the use of public and custom-curated reference sequence databases. The HTS-based diagnostics results showed a good agreement with the diagnostic approaches used by LEDP for several pathogenic genera including *Fusarium*. The HTS data will be stored in a relational database and analysed to define interpretation thresholds. A web application is to be developed to facilitate visualization of diagnosis based on HTS data.

54. Molecular diagnostics for bronze leaf disease affecting Canadian poplar and aspen trees

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Bronze leaf is a destructive disease that affects 'Tower' poplar *(Populus × canescens* Smith), Swedish columnar aspen *(P. tremula* L.), and Trembling Aspen (*P. tremuloides* Michx) and can cause economic losses to the nursery crop, processed wood industries and property owners where poplar and aspen trees are often used in amenity and shelterbelt plantings. *Apioplagiostoma populi* Barr (anamorph: *Discula* sp.) is the casual agent of bronze leaf disease; however, confirmation of the causal pathogen is challenging as it relies on observation of disease symptoms and morphological characteristics of *A. populi* when fruiting bodies form on infected leaves. Affected tissues develop a conspicuous, bronze-colored pigment that becomes pronounced in late summer. The symptoms reduce the aesthetic and commercial value of infected trees and dieback can lead to premature death. In this study, we characterized the bronze leaf disease morphology in Canada and identified pathogen-specific sequences for sensitive diagnostics that indicate systemic infection of vascular tissues. Leaf samples from symptomatic trees were collected from British Columbia, Alberta and Manitoba and examined for perithecia to microscopically characterize *A. populi* asci and ascospores. Disease-associated β-tubulin 2, translation elongation factor-1- ɣ chain, and the internal transcribed spacer (ITS) 5.8S region of the nuclear ribosomal DNA sequences were isolated from perithecia and symptomatic tree samples. Morphological and molecular biological data were used to characterize the relationship and epidemiology of *A. populi* to develop a rapid diagnostic test to facilitate reliable, early detection and thereby help prevent and/or reduce aesthetic and economic losses from this devastating disease.

55. The 168-year taxonomy of Claviceps in the light of variations: From three morphological species to four sections based on multigene phylogenies

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Abstract Withdrawn

56. Characterization of genomic and pathogenic diversity in *Sclerotinia sclerotiorum* population needed for development of resistant canola

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Sclerotinia sclerotiorum causes yield loss in dicotyledonous crops worldwide. In order to select suitable isolates for resistance screening in canola breeding programs, we genotyped 127 isolates collected in western Canada using simple sequence repeat (SSR) markers representing all chromosomes. The result revealed each isolate was an unique haplotype. Isolates from Manitoba were highly interconnected, since 61% of the isolates were mycelium compatible forming three clones of three to five isolates, with 86-95% similar SSR haplotype, as well as long stings of pairwise compatible isolates. In contrast, only 35% and 39% of isolates were mycelium compatible in Alberta and Saskatchewan, with a single clone of six isolates, but no strings. The difference can be explained by wetter growing seasons and more susceptible crops species in Manitoba favouring frequent mycelium interaction and more life cycles over time. Analysis of linkage disequilibrium rejected random recombination consistent with a self-fertile fungus. Genomic recombination between non-sister chromatids during meiosis in the ascospore stage is rare, since mycelium incompatibility inhibits isolates with different nuclei coming together. More probable sources of genomic diversity is slippage during DNA replication and point mutation of single nucleotides. A phylogenetic tree based on SSR haplotype grouped isolates into 17 sub-populations. Aggressiveness was tested by inoculating one isolate from each sub-population onto six *B. napus* lines with quantitative resistance. Subsequent analysis of variance was significant for isolate, line and isolate by line interaction. These 17 isolates represent the genomic and pathogenic diversity in western Canada and are suitable for resistance screening of new canola varieties.

57. Physiological and RNASeq analysis of the wheat cultivar "AAC Tenacious" under *F. graminearum* infection

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Abstract Withdrawn

58. Levels of mycotoxins in barley grains as infected by *Fusarium* head blight species in Manitoba, Canada from 2017 to 2020

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FHB can cause dramatic yield loss, lower grade, and contaminate small cereal grains (e.g., barley, oat, wheat) with fungal toxins (mycotoxin). This disease can savage crop and be responsible for up to $1.5 billion in income loss every year in Canada. Mycotoxins in barley have resulted in a growing concern of human and animal health hazards as recent increase of FHB in barley. We surveyed 180 barley fields over the four consecutive (2017-2020) seasons in Manitoba. *Fusarium poae* (*FP*), *F. graminearum* (*FG*), *F. sporotrichioides* (*FS*), *F. equiseti* (*FE*), and *F. avenaceum* (*FA*) were isolated, and multiplex PCR confirmed the presence of these pathogens in barley grains. *FP* and *FG* were predominant in barley grains in all four years. *FP* was detected in 84%, 65.9%, 61.7%, and 55.2%, compared to 34%, 56.8%, 40.4%, and 43.4% of barley fields infected with *FG* from 2017-2020, respectively. DNA concentration of *FP* (7.5, 2.87, 1.1 pg/ng) and *FG* (3.1, 1.1, 1.4 pg/ng) were also quantified using RT-qPCR from 2017-2019. Both PCR analyses indicate that last 4-year, the *FP* was detected as the most dominating species over *FG*. NIV appears to be the most common mycotoxin, was detected in 94% (mean 216 ppb, maximum 3252 ppb) and 66% (mean 412 ppb, maximum 2377 ppb) of barley fields from 2018-2019, respectively. DON was detected in 26% (mean 56 ppb, maximum 1488 ppb) and 24% (mean 65 ppb, maximum 2051 ppb) of barley fields. Results will help researchers to investigate potential management strategies to suppress barley-FHB in Manitoba.

59. A double agent: The mycotoxin patulin serves multiple roles during host-fungal-nonhost interactions

H. P. BARTHOLOMEW, M. J. BRADSHAW, O. MACARISIN, V. L. GASKINS, J. M. FONSECA AND W. M. JURICK II. *USDA-ARS, Food Quality Laboratory, 10300 Baltimore Ave, Beltsville, Maryland, USA.*

Mycotoxin contamination is a leading cause of food spoilage globally. One of the top mycotoxins of concern is patulin, which is found in processed pome (apple, pear, quince) fruit products. Produced mainly by *Penicillium* and *Aspergillus* species, patulin is a lactone polyketide that has cytotoxic effects in humans, survives pasteurization, and is stable during fermentation. While much is known regarding the impact of patulin on human health, there are significant knowledge gaps for how it affects plants and fungi. Here, we utilized purified patulin at physiologically relevant concentrations to determine if the toxin alone could mimic *Penicillium expansum* symptoms in apple fruit. Direct inoculation of six apple cultivars with patulin revealed a cultivar-independent susceptibility, as well as a dose response with toxin concentration. The symptoms were also observed in pear, another host of *P. expansum*, and the non-host citrus fruit mandarin. Patulin biosynthesis was recently shown to be completed outside of the fungal cell. Therefore, impacts on the fungus were investigated using five *P. expansum* strains and one *Penicillium crustosum* strain. Levels of tolerance to exogenously applied toxin varied as germination rates differed greatly when challenged, but all strains were able to produce viable colonies. However, other postharvest phytopathogenic fungi, *Colletotrichum fiorinae* and *Alternaria alternata*, were completely inhibited and did not germinate. We predict that these findings will provide a foundation for intervention technologies to block decay, preserve fruit quality, and abate toxin production in the fungus.

60. Modernization of Canadian Potato Post Entry Quarantine program by introducing molecular and genomic diagnostic methods for detecting virus and viroid pathogens in imported potato germplasm

H. XU AND D. L. HAMMILL. *Canadian Food Inspection Agency, Charlottetown Laboratory, 93 Mount Edward Road, Charlottetown, PEI, C1A 5T1, Canada.*

Abstact Withdrawn

Session 11. Invited keynote speaker

61. Soil bacteria and plant growth

B. R. GLICK. *Department of Biology, University of Waterloo, ON, Canada.*

How can we continue to feed all of the people in the world as the world's population continues to increase? We can increase crop productivity through the use of (i) transgenic plants, (ii) plant genome modification or (iii) the application of plant growth-promoting bacteria (PGPB). PGPB are soil bacteria that facilitate plant growth through their association with roots, shoots, leaves, fruits or other plant tissues. PGPB may promote plant growth directly by synthesizing auxin, cytokinin, or gibberellin, fixing nitrogen, lowering ethylene levels, sequestering iron, or solubilizing P or K. PGPB may also facilitate plant growth indirectly by preventing or decreasing the inhibitory effects of phytopathogens, through a variety of mechanisms. Some PGPB encode the enzyme ACC deaminase which cleaves ACC, the immediate precursor or ethylene in all higher plants, and thereby lowers ethylene levels which would otherwise be increased to growth inhibitory levels following various abiotic or biotic stresses. These stresses include fungal and bacterial phytopathogens, high levels of salt, flooding, drought, the presence of heavy metals or organic contaminants, extremes of temperature and the presence of nematodes. Plants treated with PGPB (with ACC deaminase) typically have greater root and shoot growth and are significantly healthier than untreated plants. Some of the other mechanisms possessed by PGPB (such as IAA synthesis, N fixation and trehalose biosynthesis) can act synergistically with ACC deaminase in promoting plant growth. Also, the functioning of Rhizobia, that form specific relationships (nodules) with legume roots and fix nitrogen for the host plant, is significantly promoted by the presence of ACC deaminase. In the past 10-20 years scientists worldwide have developed a much better understanding of the mechanisms used by PGPB so that many strains of these bacteria have begun to be commercialized throughout the world including Canada.

Session 12. Invited keynote speaker

62. The second century of phytobiome research

C. T. BULL. *Department of Plant Pathology and Environmental Microbiology and The Penn State Microbiome Center, The Pennsylvania State University, 111 Buckhout Laboratory, University Park, PA, 16802 USA.*

Researchers in plant sciences, environmental microbiology, and plant pathology have been studying phytobiomes for over a century using principles based on Koch's 1890 publication to attribute plant health, resiliency, and productivity phenotypes to interactions with microorganisms. In the past 50 years, the methods used to catalogue the presence and absence or diversity of microorganisms associated with these phenotypes have changed, but the principle of consistent association remains the same. The move from culture-dependent to culture-independent characterization of microbiomes associated with plants relies on high-throughput sequencing and analysis using either an amplicon or metagenomic approach. Diagnostic metagenomic approaches are emerging by coupling metagenomics to available whole genome sequences type strains and other reference strains. These methods changed the type of labor required, the volume of resulting data collected, and the training needed by researchers to plan, execute, and analyze these experiments. Furthermore, culture-independent methods (-omics) are moving us beyond cataloging organisms associated with plants, to understanding the functional relationships among members of the phytobiome *in situ*. Spatial and temporal multi-omic studies are required to tease apart complex phytobiome interactions. Innovative approaches to capture, store, and use microbiome assemblages are allowing us to assess the impact of these assemblages and circle back to principles attributed to Koch. In addition to examples of current work and new frontiers, with this presentation I hope to provide a few first steps for those who have not yet used microbiome sciences tools to help test their hypotheses.

Session 13. Student oral competition: Plant and Soil Health and the Microbiome

63. Does application of *Trichoderma gamsii* T6085 for control of Fusarium head blight alter the microbiome of wheat?

A. S. ALUKUMBURA, W. G. D. FERNANDO, S. SARROCCO, A. BIGI, G. VANNACCI AND M. G. BAKKER. *Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB R3T 2N2, Canada; (M.B.) Department of Microbiology, 45 Chancellor's Circle, Winnipeg, MB R3T 2N2, Canada; and (S.S., A.B., G.V.) Department of Agriculture, Food and Environment, University of Pisa, Lungarno Pacinotti 43, 6126 Pisa, Italy.*

Fusarium head blight (FHB), caused mainly by *Fusarium graminearum*, is a major constraint to wheat production worldwide. *Trichoderma gamsii* has shown promise as a potential biocontrol agent to manage FHB in wheat. However, the impact of *T. gamsii* application on the wheat microbiome is not known. The objective of this study is to evaluate the impact of *T. gamsii* application on bacterial and fungal communities associated with different wheat tissues. *T. gamsii* was applied on soil, crop residues at the beginning of stem elongation of wheat plants, and wheat spikes at anthesis. Wheat spikes, kernels and residue from the previous year's wheat crop were collected at different time points for microbiome profiling and quantification of *F. graminearum* and *T. gamsii* densities. Densities of *T. gamsii* and *F. graminearum* were considerably high in residue while their detection rates in spikes and kernels were lower. The application of *T. gamsii* did not change the *F. graminearum* density. Despite the limited impacts of *T. gamsii* application, there were clear differences in microbial community structure over time. In crop residue, the *F. graminearum* density had decreased over time while in wheat spikes, it had increased over time. The crop residue had the highest microbial diversity and comparatively different microbial community structure. In wheat spikes and kernels, the predominant bacterial genera were *Pseudomonas*, *Pantoea*, and *Enterobacter* and the predominant fungal genera were *Alternaria* and *Fusarium*. These results indicate a minor impact of *T. gamsii* application on the microbiome associated with wheat tissues.

64. Creeping bentgrass microbiome: traditional culturing and sequencing results compared to metagenomic techniques.

E. MCNAB, D. BENEDETTO AND T. HSIANG. *School of Environmental Sciences, University of Guelph, 50 Stone Road East, Guelph, ON N1G 2W1, Canada*.

Recent metagenomic studies have been probing the fungal microbiome of intensively managed turfgrasses to better understand organisms present which might be potentially beneficial or harmful, but the taxonomic resolution obtained in these studies is often limited to the family or genus level. This may be related to the common practice of targeting short sequences of rDNA (18S, ITS1, or ITS2 regions) for the estimation of fungal abundance and phylogenetic relationships. In this study, we collected samples from Guelph, Ontario, of intensively managed creeping bentgrass (*Agrostis stolonifera* L.) across two growing seasons and obtained 2204 foliar epiphytic fungal isolates. Subsequent sequencing of the entire ITS region of 248 representative isolates resolved these to 54 species in 31 genera. A comparison of the taxa identified in the present study as compared to those reported in five metagenomic studies revealed similarities. However, of the 31 genera we identified by sequencing, 18 genera (52%) were not reported in the metagenomic studies. The five metagenomic studies identified an average of 44 genera with 46% being unique to a particular study, and this ranged from 4% to 72% in the different studies. In addition to revealing genera which were not reported in other studies, an advantage of full length ITS sequencing was that it could resolve to species. Until sequencing technologies can yield full length ITS sequencing, laborious traditional culturing followed by sequencing of the entire ITS region can give insights into microbiomes not revealed by current metagenomic methods.

65. Cover crops differentially affect root disease susceptibility by changing the soil microbiome

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Barley and soybean, two of the most important crops in PEI, are both susceptible to root disease caused by *Fusarium* spp. The influence of cover crops on the soil microbiome and subsequent root disease of cash crops caused by *Fusarium* spp. is not clear. Cover crop effects on the soil microbiome and influence on subsequent crops' susceptibility to root disease was studied at the AAFC Harrington Research Farm, PE from 2018 to 2020. Year 1, field trials were planted in a split-plot design with, 8 individual cover crops, as well as 3 cover crop mixtures, and year 2 planted to barley or soybean, seeded no-till. Destructively sampled barley and soybean were rated for *Fusarium* root and crown rot (FRCR). The effects of cover crop soil on FRCR of soybean and barley were further analyzed in a greenhouse (GH) trial. In the field, high level of FRCR was observed in both cash crops, and cover crops were found to significantly influence disease. Barley planted after oilseed radish had high disease, whereas, barley planted after sorghum-sudangrass or the phacelia/brown mustard mix had low disease incidence. Similarly, soybean planted after alfalfa or oilseed radish consistently had high disease, whereas, soybean planted after phacelia had low disease incidence. FRCR observed in the GH trial was also significantly affected by preceding cover crop. Results indicate that certain cover crops affect root disease in subsequent crops by influencing the microbial composition in the soil, and that sorghum-sudangrass may have disease suppressive effects on FRCR in barley.

66. Impacts of ditch-buried garlic straw fortified with chemical fertilizer on soil microbial biomass, bacterial community and yield of a tunnel-grown chili

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A study was conducted to investigate the impacts of burying garlic residue in ditches, fortifying same with different rates of chemical fertilizer, on the soil microbial biomass and rhizospheric bacterial community diversity and structure, and yield of a plastic-tunnel grown chili. The experimental treatments comprised – residue with 25% recommended chemical fertilizer (R25), residue with 50% chemical fertilizer (R50), sole residue (SR), 100% chemical fertilizer (CF) and unfertilized control with no residue (C). Chili yield in CF was 20 - 45% significantly higher than those elicited by the other treatments. The soil microbial biomass carbon and nitrogen in fortified-residue and CF plots were higher than in SR and the control, even though they were statistically similar. Total carbon content in R25 and R50 were higher than those from the CF, SR and the control. NH_4^+-N was significantly increased by R50 treatment while CF plot had the highest NO_3^- -N, followed by R50. Soil microbial quotient and N-mineralization quotient were not influenced by the treatments. Results obtained from 16S rRNA high throughput sequencing revealed that CF influenced the diversity in the rhizospheric microbiome with a higher Chao 1 index and phylogenetic diversity, although the bacterial community composition at both phylum and genus levels were not enriched by the treatments. Proteobacteria, Acidobacteria, Chloroflexi and Actinobacteria were found to be the most abundant in the crop's rhizosphere. Fortifying garlic residue with chemical fertilizer helps to sequester carbon, but does not improve soil bacterial community and vegetable yield.

67. How oomycete community structure responds to crop rotation and tillage

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Soil-borne oomycete pathogens cause devastating crop losses; thus, it is critical to find means of controlling them with standard agronomic practices. Past research has revealed little about how oomycete community structure changes in response to management strategies such as tillage and crop-rotation. Furthermore, despite their economic importance as serious pathogens, such as species from genera *Pythium* and *Phytophthora,* oomycete communities are still underrepresented in large soil microbiome studies. To address these knowledge gaps, 224 composite soil samples were collected from a split-plot tillage and rotation experiment over a three-year period. An amplicon sequencing strategy was employed to assess oomycete community changes. To improve detection specificity, novel oomycete-specific primers targeting two DNA markers, the internal transcribed spacer 1 (ITS1) of ribosomal DNA and the ribosomal protein S10 gene (*rps10*), were used. This led us to develop a high-quality reference database (refDB) for the ITS1 region and to obtain a *rps10* refDB from http://oomycetedb.cgrb.oregonstate.edu/. While both markers had a good coverage of *Pythium* which was most prevalent in soils, the *rps10* marker recovered higher *Phytophthora* diversity as well as *Aphanomyces* which was not detected by the ITS1 marker. Preliminary analyses suggested that no-till increased oomycete diversity, while rotation effects were more complex. This study will shine a light on how common agricultural practices could help in managing and mitigating these important soil phytopathogens.

Abstracts

68. Identification of exotic forest pests by metabarcoding from a unique trap

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With the growing volume of international trade, we observe an increase in the number and diversity of exotic pests introduced in North America. When these pests become established, it is generally difficult to eradicate them. For this reason, the early detection of a new incoming pest is a priority. To do so, high-throughput sequencing techniques were developed to simultaneously process and screen a large number of samples. These methods are cost- and time saving while very effective for large numbers of samples. We applied these methods to the detection of emerging pests collected in insect traps and aerial spore traps. We designed a single trap and protocol for the simultaneous identification of pathogenic fungi and invasive insects from insect trap preservative fluids. We did the proof of concept that insect cells present in preservative liquids from insect traps can be used to identify insects. We screened numerous present and potentially introduced pests in North America using Illumina sequencing technology with specific primers for the fungal ITS region and the COI gene of insects. Hundreds of samples collected in British Columbia, Ontario, Quebec and New Brunswick were sequenced. We detected the presence of the fungus *Heterobasidion occidentale* Otrosina & Garbelotto in Sault.Ste. Marie (ON) and the presence of the bark beetle *Anysandrus maiche* Stark in Hamilton's (ON) 2019 sampling.

69. Characterization of wireworm populations in the floodplains of Lac Saint-Pierre

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Wireworms (Coleoptera: Elateridae) are serious agricultural pests across the world and their spread increases consistently. Damages are usually below ground, for example, to root crops and seedlings of field crops. It is commonly controlled by synthetic insecticides applied as soil or seed treatments before planting. This study focused on the wireworm population in the flood plains of Lac Saint-Pierre, QC (LSP) as some conventional agricultural practices (i.e., tillage, pesticides and fertilizers use) in the region have negatively affected the lake biodiversity and water quality. Objective of this project is to evaluate the wireworm economic threshold in different crops and propose recommendations regarding the insecticide use in the floodplain. Firstly, the wireworm population was evaluated across corn, soybean and forage commercial fields in the LSP region. Secondly, the negative effects on wireworm populations of growing buckwheat (*Fagopyrum esculentum* Moench.) was also tested. Six species of wireworms were found (*Agriotes* sp., *Aeolus* sp., *Dalopius* sp., *Hypnoidus abbreviatus*, *Limonius* sp., *Melanotus* sp.,) and their population varied across different regions (St. Barthélemy, Pierreville, La Visitation de l'île-Dupas and Baie-du-Febvre) in LSP. Based on the cultivated crops in those regions, the wireworm population level was considerably higher in forage crops and corn fields than in soybean fields. In the buckwheat plots, the initial wireworm populations were not sufficiently high to clearly determine its potential repressive effects. Since the wireworm population were below the economic thresholds for all scouted fields, the usage of insecticide seed coating could be reduced in the floodplain.

Session 14. Student oral competition: Plant and Soil Health

70. Effect of clubroot (*Plasmodiophora brassicae*) on yield of canola (*Brassica napus*)

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Clubroot, caused by *Plasmodiophora brassicae,* is a major disease of canola (*Brassica napus*). The aim of this study was to evaluate the effect of clubroot development on the yield of canola under field and greenhouse conditions. Three canola hybrids, '45H31' (susceptible), '45H29' (1st generation resistance) and 'CS2000' (2nd generation resistance), were inoculated with different quantities of *P. brassicae* inoculum and monitored for yield, pods per plant and 1000-grain weight. The field experiment was conducted over 2 years in biosecure clubroot nurseries inoculated with pathotype 5X or a mix of pathotypes 5X and 3H at 5×10^8, 5×10^6 and 5×10^4 resting spores per plant. In the greenhouse experiment, plants were inoculated with pathotypes 5X, 3H or a mixture of both at 1×10^3, 1×10^4 and 1×10^6 resting spores per plant. In both the field and greenhouse, clubroot incidence and disease severity index (DSI) increased along with inoculum density; the highest levels of disease were observed in the susceptible hybrid, while the lowest were found in '45H29.' Yield, pods per plant and 1000-grain weight decreased as the DSI increased in all hybrids. Yield was affected by DSI and canola hybrid, but not by pathotype. Regression analysis indicated that under greenhouse conditions, an increment of 1% in the DSI resulted in a decrease of 0.49% in yield; under field conditions, this percentage was reduced to 0.26%. While the rate of yield reduction was similar among hybrids, overall yield losses were lower in the clubroot resistant hosts, since clubroot was less severe.

71. Fungal pathogen emergence: an *Ustilago maydis* x *Sporisorium reilianum* model

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The emergence of fungal hybrid pathogens threatens sustainable crop production worldwide. To investigate hybridization, the related smut fungi, *Ustilago maydis* and *Sporisorium reilianum,* were selected, because they infect a common host (*Zea mays*), can hybridize, and there are tools available for their analysis. Hybrid dikaryons demonstrated filamentous growth on plates, similar to *U. maydis* dikaryons, but showed reduced virulence and colonization of *Z. mays* compared to both parental dikaryons. To understand the hybrid's limited pathogenic development, select virulence gene transcript levels were assessed during pathogenic time courses, using RT-PCR and/or RT-qPCR with species-specific primers. These genes included transcription factors, cell signalling proteins, and effectors characterized in *U. maydis,* as well as their orthologs in *S. reilianum*. During the hybrid infection, these virulence genes had altered transcript levels relative to the parental dikaryon infections. Genes involved in late development were either downregulated or not detected in the hybrid, suggesting that the hybrid's pathogenic development had stalled. To determine if hybrid pathogenesis could be altered, characterized *U. maydis* virulence genes were constitutively expressed in the *U. maydis* nucleus of the hybrid. Little impact was observed in hybrids with increased expression of *tin2, pit2,* and *cce1* effectors, which are known to modify host response. However, increased expression of *rbf1* and *hdp2,* transcription factors that are known to regulate early-stage specific pathogenic development, increased the hybrid's ability to infect and induce symptoms, including the rare induction of small leaf tumors. These results establish a base for investigating molecular aspects of fungal hybrid pathogen emergence.

72. The chemotypes 3ADON, 15ADON, NIV, and NX-2 of *Fusarium graminearum* vary in aggressiveness on wheat

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The aggressiveness of *Fusarium graminearum* chemotypes was assessed in a greenhouse experiment on spring wheat genotypes that varied in resistance to Fusarium head blight (FHB). Fifteen isolates (five 3ADON, five 15ADON, three NIV, and two NX-2) of *F. graminearum* isolated from Saskatchewan wheat fields were evaluated using point inoculation (Type II resistance assay). Evaluation was on three wheat genotypes assessed as resistant, moderately resistant, and susceptible to FHB and near-isogenic lines (NILs) in the CDC Go (moderately susceptible) background, carrying *Fhb* quantitative trait loci (QTL) in four combinations: *Fhb1*, *Fhb2*, *Fhb5,* and *Fhb1*+*Fhb2*+*Fhb5*. All four *F. graminearum* chemotypes were pathogenic on wheat and varied in aggressiveness. Disease severity caused by 3ADON, 15ADON, NIV, and NX-2 isolates differed, with 3ADON (29.7 ± 3.6) and 15ADON (22.4 ± 2.9) isolates more aggressive than NIV (16.7 ± 2.8), and NX-2 (16.2 ± 3.1) isolates. Significant differences were observed for mycotoxin accumulation among chemotypes, which was highest for 3ADON (14.1 ± 2.26 µg kg^{-1}). There was no interaction between chemotype and wheat line for disease severity or mycotoxin.

73. Impact of long-term nitrogen fertilization on soil organic carbon, total soil nitrogen and future production in continuous corn (*Zea mays* L.) in Ontario

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Synthetic nitrogen (N) fertilization can change soil properties such as soil organic carbon (SOC) over time, leading to longer-term changes in crop productivity in corn-based cropping systems. However, existing studies have found positive, negative, and neutral responses of SOC to long-term N fertilization. To investigate the impact of long-term N fertilization on soil properties in a continuous corn rotation, a ten-year N rate (2009 –2018) experiment was established in Elora, Ontario. Plots received one of six N rates (30-260 kg-N ha^{-1}) each year. SOC, total soil N, and other soil properties were measured in each plot at the start and end of the trial. To investigate the legacy effect of historic N rate on crop productivity, in 2019 after trial conclusion all plots were planted to corn and fertilized with a N-limiting rate to 58 kg-N ha^{-1}. SOC increased in all treatments over ten years, with no significant effect of N rate on SOC accumulation despite large differences in residue C additions. No differences in total soil N were observed after 10 years across N rates despite large differences in N balances across treatments. At higher N rates with positive N balances, fertilizer N not taken up by the crop does not accumulate in soil and appears to be lost to the environment. Corn yield in 2019 was unaffected by historic N rate. These results suggest that variations in N rate within the typical range common in Ontario corn production has minimal impact of agronomic relevance on soil properties.

74. *Fusarium graminearum* infection of differentially resistant barley cultivars reflect growth and deoxynivalenol production during malting

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Fusarium head blight (FHB) of barley causes significant losses for the malting and brewing industry; however, there has been insufficient attention towards understanding fungal growth and deoxynivalenol mycotoxin production during the malting process. Barley varieties: Newdale (moderately resistant to moderately susceptible to FHB) and AAC Goldman (moderately resistant to FHB) were inoculated with single strain conidial suspensions of each of seven different *Fusarium graminearum* strains (plus a non-inoculated control). In 2019, FHB severity was higher in Newdale (9%, by visual assessment) than in AAC Goldman (3%), and similar differences were observed for the fungal load (940.6 vs. 423.7 *Fusarium*: barley gene abundance ratio) and deoxynivalenol content (3.2 vs. 2.8 ppm via ELISA). We micro-malted this barley and found that cultivar differences in *Fusarium*-related variables persisted after malting; fungal load in the final malt was 17.03 in Newdale vs. 12.14 in AAC Goldman, and deoxynivalenol content was 3.8 vs. 1.4 ppm. Deoxynivalenol content increased in Newdale through the malting process but was reduced in AAC Goldman. Differences among cultivars were again evident in 2020: FHB severity was 38% in Newdale vs. 21% in AAC Goldman, the fungal load was 9.7 vs. 4.4, and deoxynivalenol content was 1.2 vs. 0.7 ppm. Toxin production varied among the seven pathogen strains as it was higher for 3-acetyl-deoxynivalenol compared to 15-acetyl-deoxynivalenol isolates. The outcome of this work will help to develop novel management strategies that could improve malt quality.

75. Pathogenicity of *Fusarium graminearum* and *F. poae* Causing Fusarium Head Blight on Barley Under Controlled Conditions

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Fusarium head blight (FHB) is one of the most damaging diseases of barley. FHB is caused by a species complex that includes different *Fusarium* spp. and *Fusarium graminearum* is the species of greatest concern for FHB of barley in Canada. Field surveys show that two or more FHB species often co-exist within the same field or grain sample and currently *F. poae* has been reported as another dominant FHB species in barley growing regions. The aim of this study is to understand the pathogenicity of F. graminearum, F. poae and mixture of both species in co-inoculation causing FHB in barley under control condition. Spray inoculation was performed on two susceptible barley genotypes at 10 to 14 days after heading. Heads were assigned a visual FHB rating on a scale of 0-9 at 4, 7, 14, 21, and 28 days after inoculation. There was a significant difference in FHB symptoms between *F. graminearum* and *F. poae*, with *F. graminearum* being the most pathogenic species. *F. poae* was least pathogenic and not statistically different than the control treatment (inoculated with deionized water only). When heads were co-inoculated with the mixture of both FHB species, FHB symptoms were lower than the *F. graminearum* treatment, indicating that the presence of *F. poae* may reduce the pathogenicity of *F. graminearum.*

76. Fusarium Head Blight species diversity and deoxynivalenol (DON) levels in Western Canadian producer wheat fields

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Fusarium Head Blight (FHB) is a devastating disease in Western Canada that affects both the quantity and qualitity of wheat grain, mainly due to mycotoxin contamination (deoxynivalenol-DON and nivalenol-NIV). *Fusarium graminearum* is the principal causative agent associated with FHB of wheat in Western Canada. Wheat spikes were collected in 2020 from an area not treated with fungicide in 65 participating farmers' fields in Western Canada to evaluate the presence of *Fusarium* species and their chemotypes. Inoculum availability was measured by setting up spore traps in each field from flowering until the soft dough stage. Both grain and chaff from spring wheat were subjected to mycotoxin testing by high sensitive 5/5 Vomitoxin kits from Neogen and fungal species and chemotype testing by DNA-based methods (PCR). The initial DON testing showed that the 2020 growing season experienced mild levels of FHB toxin contamination. In spring wheat, the highest mean DON content was recorded from Manitoba samples (0.3 ppm in grain and 2.12 ppm in chaff), while both Saskatchewan and Alberta samples contained average DON levels <0.2 ppm in grain and <1.00 ppm in the chaff. The chaff contained a significantly higher DON level than the grain, suggesting that chaff removal during harvest can reduce the impact of DON on the grain. The total genomic DNA was extracted from 24 *Fusarium* damaged kernels and ~0.5 g of chaff from each spring wheat sample. Different *Fusarium* species, including *F. graminearum* and their chemotype-producing genes, will be identified by 24 species-specific PCR assays and presented.

77. The virulence of *Plasmodiophora brassicae* on canola with '2nd generation' clubroot resistance

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Clubroot, caused by *Plasmodiophora brassicae*, is a damaging soilborne disease of canola (*Brassica napus*) first identified on the Canadian Prairies in 2003. Clubroot resistant (CR) canola cultivars, carrying what is now known as '1st generation' resistance, were introduced in 2009-10 and soon became the most effective and widely used clubroot management tool. Unfortunately, new pathotypes of *P. brassicae* have emerged that can overcome 1st generation resistance, and are found in an increasing number of fields. In response, canola breeders have developed a new set of cultivars with so-called '2nd generation' resistance. While the nature of this resistance is not in the public domain, and may differ among cultivars from different companies, it is believed to be distinct from 1st generation resistance and is either conferred by a different resistance gene(s) or represents stacked resistance genes. Studies are underway to characterize the virulence of *P. brassicae* populations on different hosts with 2nd generation resistance. Isolations of the pathogen were made from symptomatic 2nd generation CR canola crops identified in the field, and tested for their virulence on a suite of eight commercial canola cultivars carrying 2nd generation resistance. These cultivars were also tested with selected *P. brassicae* pathotypes that break 1st generation resistance. Preliminary results indicate that about half of these cultivars developed moderate to severe levels of clubroot when challenged with pathotypes that can overcome 1st generation resistance. This suggests that resistance-breaking strains of *P. brassicae* may be difficult to control with resistance alone.

Session 15. Regular author oral presentations: Plant and Soil health

78. Trends in symbiotic nitrogen fixation over 100 years of soybean breeding

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Soybean [*Glycine max* (L.) Merr.] is the world's most important legume crop and the largest oilseed crop. It forms a symbiotic relationship with rhizobia bacteria resident in root nodules that provide fixed nitrogen to host plants through symbiotic nitrogen fixation (SNF). Similar to many programs globally, decades of conventional soybean breeding in Ontario have mostly focused on yield and grain quality parameters, instead of SNF *per se*. However, given the focus on improving yield in the absence of adding inorganic N fertilizer, we hypothesized that there has been indirect selection pressure to improve nitrogen fixation. To test this hypothesis, in this study, SNF-related traits were evaluated in pedigree-related historical germplasm (19 cultivars) and 25 modern cultivars derived from the University of Guelph's, Canada, breeding program. Field trials were conducted at Woodstock, ON, Canada in 2016 and 2017, and various agronomic traits were measured, including nitrogen fixation capacity. Considerable variation was observed among Canadian soybean cultivars released over the past 100 years for nitrogen fixation. The modern soybean cultivars had similar or moderately higher SNF compared to the historical lines in terms of the percentage of nitrogen derived from the atmosphere (%Ndfa) and total shoot nitrogen fixed. These findings suggest that, despite a lack of direct selection for SNF traits, SNF has been maintained and possibly improved in modern soybean breeding. There are opportunities for deliberate selection for improved SNF, where historical and modern soybean cultivars were identified as potential parents for targeted breeding for improved SNF.

79. Altering nitrogen management to improve winter wheat yields and nitrogen efficiency in the Northern Great Plains

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Optimizing nitrogen management for winter wheat crops can maximize agronomic performance and reduce greenhouse gas emissions, but these factors are rarely considered together. We conducted two experiments at seven sites throughout the Canadian Prairies over three to four crop cycles. We measured grain yield and protein at all sites, and greenhouse gas emissions from one site (Lethbridge, Alberta). Experiment I applied: urea, urea+eNtrench® (nitrification inhibitor), SuperU® (urease and nitrification inhibitor), and Environmentally Smart Nitrogen® (ESN®), a polymer-coated urea. All N was applied: 100% side-banded at planting, 30% side-banded at planting and 70% broadcast in-crop in late fall, and 30% side-banded at planting and 70% broadcast in-crop in early spring. Experiment II applied: urea ammonium nitrate (UAN), UAN+eNtrench®, UAN+Agrotain Ultra® (urease inhibitor), UAN+Agrotain Plus® (urease and nitrification inhibitors), and a 50-50 mix of urea and ESN®, with all N applied 50% side-banded at planting and 50% broadcast in-crop in early spring. All N banded at planting and split applying in spring produced similar yields and protein, but grain yields and protein were 4.2% and 1.8% when N was split applied in late fall compared to all N banded at planting ($p \leq 0.05$). Including urease or urease and nitrification inhibitors also incrementally improved yields and N uptake. Greenhouse gas emissions scaled per unit grain yield, grain-N, and total N uptake did not vary significantly between treatments showing improvements in winter wheat agronomic performance did not equate to substantial reductions in greenhouse gases linked to climate change.

80. Effect of wood ash, sludge, and biochar on heavy metals mobility in plant-soil system of annual ryegrass and kale

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Paper industry produces tremendous amount of waste material, such as wood ash (WA) and paper sludge (SL). WA and SL contains mineral nutrients and high pH, hence could be used as potential liming and nutrient source. However, WA and SL may contain heavy metals that could adversely affect crop growth, produce quality and eventually human health. Biochar (BC) is known to mitigate heavy metals uptake by plants. Herein, we conducted a greenhouse study to evaluate the effect of WA, SL alone and in combination with BC on heavy metals mobility in soil-plant system of annual ryegrass, (*Lolium perenne L.*) and kale, (*Brassica oleracea*). Experimental treatments were: 1) limestone as control (L), 2) WA, 3) SL, 4) WASL, 5) LBC, 6) WABC, 7) SLBC, 8) WASLBC. Limestone, WA, SL, WA+ SL and BC application rates were 7.1 Mg ha^{-1}, 17.25 Mg ha^{-1}, 55 Mg ha^{-1},13.8 + 11 Mg ha^{-1} and 20 Mg ha^{-1}, respectively. Results indicated that SL application increased Pb concentration in annual ryegrass soil, whereas WASL enhanced Ni concentration in kale soil compared to control, though within CCME limits. Furthermore, BC addition significantly reduced Pb uptake by 17 % in annual ryegrass shoots, and Ni uptake by 32% in kale shoots, respectively, compared to non amended BC treatments. Based on results, it can be concluded that WA could be used as soil amendment without heavy metal contamination risk in soil. Nonetheless, BC addition mitigated the risk of heavy metal uptake in both annual ryegrass and kale.

81. Effect of biofumigation and fumigation on population density of root-lesion nematodes, *Verticillium dahliae* and potato yield in New Brunswick

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Potato early dying disease complex (PED) is an endemic and a major yield-limiting factor for potato production in New Brunswick (NB). PED is primarily caused by *Verticillium dahliae, and* is exacerbated by the root-lesion nematode, *Pratylenchus penetrans*. In NB, PED management is mainly done through a two-year potato-cereal crop rotation, but is ineffective despite cereals being a less favorable host. Soil fumigation with either metam sodium or chloropicrin can be used to control PED, but is not commonly practiced in Canada. Chloropicrin was demonstrated to reduce visual PED severity in some observational trials in NB, but its effect on pathogen population density and potato yield was not well studied. Biofumigation using mustard crops, as an alternative to chemical fumigation, showed potential in managing PED and other soil-borne pests, but its effectiveness needs to be evaluated under potato production systems of NB. Two trials were conducted to compare the effect of biofumigation and chloropicrin fumigation on PED management in a two-year-rotation production system in commercial fields in NB from 2017 to 2020. The treatments included 1) spring barley representing conventional management, 2) spring barley plus fall chloropicrin fumigation, and 3) two crops of brown mustard as biofumigation. Biofumigation and fumigation significantly increased tuber yield by 10% and 15% of marketable yield, respectively, in trial one, and 3% and 19% of marketable yield, respectively, in trial two. Results indicate that both biofumigation and fumigation have a potential to suppress PED pathogens and increase potato yield in fields with high PED pathogen pressure.

82. Potential role of root neutral lipids in mediating forage soybean acclimation to cultivation on acidic soil in boreal climate

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Crop plants are known to adapt to their environment to produce desirable harvest by modulating their membrane lipids. Conversely, less is known concerning storage lipid's role in successful plant adaptation and acclimation to abiotic stressor in the growth environment. Triacylglycerol (TAG) and diacylglycerol (DAG) are the main storage lipids and limited information suggest that their metabolism appears to be important in plant response to different abiotic stresses such as phosphorus or nitrogen starvation. To improve our understanding of neutral lipids contributions to successful plant acclimation to environmental stress we assessed TAG and DAG metabolism in soybean roots exposed to varying soil pH (6.8, 6.0 and 5.1) and their possible relationship with plant agronomic performance and adaptation during cultivation in boreal climate. A field study was conducted in Newfoundland where root membrane lipids were determined at pod formation stage using ultra high-performance liquid chromatography linked to hydrophilic interaction chromatography coupled to heated electrospray ionization accurate mass tandem mass spectrometry. We observed a significant decrease in total neutral lipids across the soil pH continuum {from neutral soil pH (79.93±0.60 nmol%) to acidic soil pH – 5.1 (70.60±0.39 nmol%)} whereas a concomitant increase was noticed in forage biomass production. Soybean plants produced significantly higher biomass of 3.59±0.13 Mg ha^{-1} at pH 5.1, (3.55±0.07 Mg ha^{-1}at pH 6 compared to lower biomass (2.18±0.23 Mg ha^{-1}) at pH 6.8 which suggests that neutral lipids remodulation appears to assist forage soybeans plants to adapt and attain higher forage biomass at low soil pH in boreal climate.

83. Adapting precision planters for pulse crop production in southern Alberta

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Precision planting technology provides uniform seed placement at precise distances along the rows and superior depth control compared to conventional air seeding systems. Thus, precision planters have the potential to improve the proportion and uniformity of crop emergence, reduce interplant competition, and increase yield. This study compares the performance of precision planters and conventional air drill seeders for seeding pulse crops, including chickpeas (*Cicer arietinum*), lentils (*Lens culinaris*), faba beans (*Vicia faba*), soybeans (*Glycine max*), and field peas (*Pisum sativum*) across three locations in southern Alberta from 2019 to 2021. The crops were seeded at normal (100 seeds m^{-2} for lentils and pea; 50 seeds m^{-2} for faba beans, soybeans, and chickpeas) and low (50 seeds m^{-2} for lentils and pea; 25 seeds m^{-2} for faba beans, soybeans, and chickpeas) seeding rates and at 30.5 cm row spacing for both seeders. Initial results from the data collected from six site-years (2019 and 2020) indicate a statistically significant increase in plant emergence for chickpeas, faba beans, and field peas and seed yield for field peas and chickpeas for the precision planter. Seed yield of precision planted lentils was higher than the air drill, but the difference was not statistically significant ($p = 0.08$). Crop yields were higher at normal compared to lower seeding rates, but the interaction between seeder type and seeding rate was not statistically significant ($p < 0.05$) for any crop, thus indicating that precision planting of the crops did not reduce the optimum seeding rates for maximum yields.

84. Cell-wall reinforcement contributes to clubroot resistance

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Clubroot (caused by *Plasmodiophora brassicae* Woronin) is a serious disease of canola (*Brassica napus* L.), and genetic resistance remains the most cost-effective strategy for management of this disease. While monogenic resistance has been widely used, the breakdown of clubroot resistance (CR) has been increasingly reported. Pyramiding CR genes may lead to broader-spectrum and more durable resistance. We investigated the mechanisms of resistance conferred by CR genes residing on chromosomes A03 and A08, singly and in stack, using fluorescent and electronic microscopy assisted with microspectroscopy. Inoculated with pathotype 3H, canola lines carrying either single or stacked CR genes showed strong resistance, with the arrest of infection process within root-hairs and/or exodermis. Lines with a single CR gene showed a high level of infection in root hairs as in the susceptible cultivar Westar, but effectively restricted secondary plasmodia to exodermal cells and blocked the further invasion into root cortex. In contrast, the line with stacked CR genes prevented the infection in root hairs, causing fewer secondary infection which was also restricted to the exodermis. There was strengthening of cell wall with the resistance, relative to the susceptibility, and the main components for this cell-wall modification appeared to be increased carbohydrate and phenolic compounds. Genes involved in the corresponding pathways of these metabolites were also upregulated. These results show the role of cell-wall reinforcement in clubroot resistance, as well as the stages where *P. brassicae* may be arrested by resistance mechanisms during the infection process.

85. Elimination of zebra chip in Canada

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Zebra chip is a potentially devastating disease of solanaceous crops caused by '*Candidatus* Liberibacter solanacearum' (Lso), a phloem-limited gram-negative bacterium that is transmitted by the potato-tomato psyllid (TPP) *Bactericera cockerelli* (Šulc). Originating in Mexico, the disease has become more prevalent and migrated northward through the US over several decades. To determine occurrence and epidemiology in Canada, TPP were collected from thousands of yellow sticky cards, and hundreds of samples from plants that exhibited putative disease symptoms, were collected during 2013 to 2020 from commercial farms. The TPP vector was observed primarily in AB, with fewer found in SK and MB. Under 100 TPP were observed annually except in 2017. Total nucleic acid was isolated from psyllids or plant samples and the cytochrome oxidase I or 16S ribosomal DNA was amplified with TPP and Lso specific PCR primers, respectively. All samples were negative for Lso except four TPP and a single post-harvest potato tuber recovered from southeastern Alberta in 2017. The Lso-positive potato tuber produced symptomatic plants with the proliferation of axillary shoots and abnormal tubers. BLAST analysis of the TPP and plant Lso showed central and western TPP haplotype and an identical match to Lso haplotype A isolates from the United States. Detection of Lso in Canada indicates the pathogen may be spreading to new areas, possibly due to favorable environmental conditions, and industry should continue to monitor movement of the vector and disease to minimize losses.

Session 16. Society award winners

86. A. Levesque: CPS Lifetime career award

Riding the wave of digitization – towards a better understanding of the role and impact of fungi and oomycetes.

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In plant pathology, identifying the causal agent of a disease, from the species to the most critical expressed genes, and predicting its impact and managing it can provide significant economic and environmental benefits. As a graduate student I recognized that identification of soil-borne isolates of *Pythium* Prings. and *Fusarium* Link was a major bottleneck affecting my research into the mode of action of the herbicide glyphosate. There were very few taxonomy specialists for these genera who could help me identify and separate those species which were pathogenic, saprophytic or even used as biological control agents among the many strains that I had isolated. After I obtained my Ph.D., PCR technology became available and DNA-based technologies improved significantly as a result of that. I became a specialist on zoosporic fungi and in collaborations with other taxonomists I was involved in generating many reference DNA sequence databases. With the advent of high throughput sequencing technologies, the ability to digitally identify or detect zoosporic fungi has been streamlined to near real-time. Species identification is now supported by the large body of fully annotated genomes available and can be carried out with practically any expressed genes. There is a growing public understanding of epidemiology of emerging diseases and DNA-based technologies because of SARS-CoV-2. This offers a new opportunity for plant pathologists to explain the importance of their work to the general public and continue to build on the momentum digitization has provided towards a better understanding of the role and impact of fungi and oomycetes.

87. Widespread Herbicide Resistance in Pigweed Species in Ontario Carrot Production is Due to Multiple Photosystem II Mutations.

DAVIS G, LETARTE J, GRAINGER CM, RAJCAN I, TARDIF FJ. 2020. Can. J. Plant Sci. 100: 56–67. doi: 10.1139/cjps-2019-0114. François Tardif: CSA Best CJPS paper award.

Widespread Herbicide Resistance in Pigweed Species in Ontario Carrot Production is Due to Multiple Photosystem II Mutations

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The apparent efficacy of linuron to control pigweeds (*Amaranthus* spp.) has declined in Ontario, Canada, in past decades, possibly due to resistance. Samples were collected in multiple fields across Ontario with reported linuron failure. These were characterized at the whole plant and molecular levels. Screening with linuron revealed resistance in six out of nine green pigweed (*A. powellii* S. Watson) populations and 36 of 38 populations of redroot pigweed (*A. retroflexus* L.). Sequencing of the *psbA* gene showed resistant plants had mutations conferring resistance to PSII inhibitors. The most commonly seen mutation was coding for a Val219Ile substitution while other populations had Ala251Val or Phe274Val. Two populations were documented with a double mutation at Val219Ile and Phe274Val. All substitutions endowed plants with low to moderate resistance to linuron, with various levels of cross resistance to other PSII inhibitors. The double mutants were characterized by higher levels of resistance to linuron and diuron compared to each single substitution. The widespread failure of linuron to control pigweed species in many carrot fields in Ontario is due to selection of PSII mutants. This is the first report of double mutation in *psbA* in any weed species and the first report of the Ala251Val and Phe273Val in pigweed species. The presence of a double mutation is probably the result of continuous selection of plants already resistant due to a single mutation. Our results illustrate the need for diversified weed management strategies in crops where herbicide options are limited.

88. Response of growth, yield and quality of edible-podded snow peas to supplemental light-emitting diode lighting during winter greenhouse production

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Low natural light level during winter months is a major limiting factor for greenhouse crop production in northern regions. To determine the effects of supplemental lighting (SL) on winter greenhouse production of edible-podded snow peas (*Pisum sativum* L.), plant growth, pod yield and quality were investigated under SL at a photosynthetic photon flux density (PPFD) of 50, 80, 110, and 140 µmol · m^{-2} · s^{-1}, plus a no-SL control treatment, inside a Canadian greenhouse from January to March. Light-emitting diodes with a red:blue PPFD ratio of 4:1, and a 16-h photoperiod were used for the lighting treatments. During the trial period, the average natural daily light integral (DLI) inside the greenhouse was 6.6 mol · m^{-2} · d^{-1}, and the average daily temperature was around 13°C. Comparing with the control, all SL treatments increased pod yield (g · plant^{-1}) and promoted plant growth as demonstrated by faster main stem extension and greater aerial biomass. Also, total pod yield (g · plant^{-1} or no. · plant^{-1}) and some growth traits (e.g., stem diameter, branch number, leaf thickness, and leaf chlorophyll content) were proportional to supplemental PPFD within the range of 0–140 µmol · m^{-2} · s^{-1}. However, SL levels 50–80 µmol · m^{-2} · s^{-1}, corresponding to a total (natural + supplemental) DLI of 9.4–11.1 mol · m^{-2} · d^{-1}, resulted in the best pod quality based on evaluations of individual fresh mass, length, soluble solids content, succulence, and firmness. Therefore, a total DLI ranging between 9.4 and 11.1 mol · m^{-2} · d^{-1} can be recommended as a target light level for winter greenhouse production of pea pods using SL under environmental conditions like this trial.

89. Innovations in sustainable agricultural intensification to address climate change, food security, nutrition and resilience

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Grand challenge of increasing productivity of nutritious and safe food under climate crisis requires a systems and transdisciplinary approach towards agri-food systems. Innovation is to key to improve global food and nutritional security, and resilience of agriculture and people. Climate extremes negatively impacts productivity and quality of grain and horticultural crops. Climate change influences occurrence, intensity and spread of pests and disease. There is an urgent need to develop and scale climate smart agricultural practices to improve resilience of cropping systems through adaptation and mitigation strategies, and resilience people through building social capital and support system. Innovations should emphasize broader one-health (soil, plant, animal and human) with end-to-end programing (production to consumption) and circularity (recycling waste) in agri-food systems. Our approach must positively impact productivity, nutrition, health and environmental outcomes. Sustainable agricultural intensification (SAI) provides a platform that focuses on increasing agricultural productivity and efficiency from existing farmland without any adverse environmental impacts. It provides a framework to measure impacts across key domains (productivity, environment, economic, social and human condition) to better understand the complexities in the system. Innovations in genetic, agro-ecological and social components of SAI along with creating enabling environments and building social capital is a prerequisite for success. This requires collaboration between multiple disciplines, organizations, stakeholders, private-sector and donors. Current investments in innovation in SAI in the Global South is extremely low and requires transformation to meet sustainable development goals and support climate action. Present status, innovation gaps and future opportunities will be presented and discussed.

Session 17. Student oral competition: Plant Health and Resilience

90. Building a better cell wall- How structural modifications in pectin impact the role of the cell wall as a barrier to both abiotic and biotic stress

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Climate change continues to threaten plant populations, as the frequency and severity of stresses mount. Structural modifications in the cell wall through pectin cross linkages between calcium ions and boric acid, may be key to mitigating damage caused by stress. The objective of this research was to examine how changes in calcium and boron within various plant spp. may translate to increased resistance to multiple stresses. Calcium was found to significantly ($p<0.05$) reduce water loss in high methylated citrus pectin, used as a model for pectin in *Allium*. However, the efficacy of calcium in mitigating drought stress in *Allium* was inconsistent between species and lengths of dehydration. Nonetheless, *A. fistulosum* (freezing tolerant), was significantly ($p<0.05$) more resistant to water loss compared to *A. cepa* (freezing susceptible). Moreover, we found BOR1, a boron transporter in *Arabidopsis*, impacts tolerance to stress caused by dehydration and *Colletotrichum higginsianum*, a hemibiotrophic pathogen that uses physical pressure to circumvent the cell wall. *bor1* had a higher rate of water loss and percent electrolyte leakage following dehydration stress. Furthermore, the addition of boron to pure pectin significantly ($p<0.05$) reduced water loss. In addition, *bor1* had the most rapid rate of *Colletotrichum higginsianum* infection. Lesions were generally larger and appeared ~48hr earlier. In conclusion, response to stress is complex and pectin modifications are likely not a silver bullet. Nonetheless, our research demonstrates connections between dehydration stress, freezing stress and *Colletotrichum higginsianum* and is indicative that the cell wall and pectin likely play a critical role in defence.

91. The role of drought stress on the acquisition of freezing tolerance in asparagus (*Asparagus officinalis* L.) under controlled conditions

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Cold acclimation induces freezing tolerance in asparagus (*Asparagus officinalis* L.) which is important for survival and longevity in temperate climates. Previous studies indicated that cultivar "Guelph Millennium"(GM), adapted to Southern Ontario, acquired freezing tolerance earlier in the fall and maintained it later in the spring than "UC157"(UC), a cultivar commonly grown in desert climates. Since the cold acclimation and drought response pathways in plants overlap with common cellular responses, the objective of this research was to determine if drought alone induced freezing tolerance or interacted synergistically with cold temperatures. Seedlings of GM and UC were subjected to control, drought, or cold acclimating conditions for six weeks. Additional treatments included six weeks of drought or cold conditions followed by six weeks of cold acclimation, and plants grown for 12 weeks under control conditions. LT_{50}, the temperature at which 50% of plants die, and metabolites/parameters associated with freezing tolerance were measured. GM had decreased LT_{50} levels (increased freezing tolerance) compared to UC under both drought and cold acclimating conditions, with no cultivar difference observed under control conditions. Drought stress prior to cold acclimation increased LT_{50} (reduced freezing tolerance) in UC and no synergism was observed for GM. High root:shoot ratio and low crown percent water was associated with increased freezing tolerance in GM, while a high crown sucrose concentration in UC was related to decreased freezing tolerance for the drought treatment. Overall, drought stress induced cultivar specific adaptations causing differences in freezing tolerance, thus confirming the interrelationship between these two physiological pathways.

92. Effects of two bacterial inoculants on the physiology and transcription of osmoprotectant related genes in four generations of alfalfa breeding lines

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Soil salinity is a malady inhibiting crop growth on 397 million ha of land worldwide, and 3.75 million ha in Western Canada. Planting deep rooted perennial forages such as alfalfa in salt affected land can act both as a means of land remediation by lowering the salt-laden groundwater table, and as a supplemental revenue stream for producers. Increased production of osmoprotectants is one means of raising the salinity tolerance of a plant. Mutualistic soil bacteria as well as selection for salt tolerant plant genotypes have both been demonstrated to be mechanisms capable of increasing the production of anti-stress related compounds in plant tissues. This experiment aims to explore whether 2 strains of soil bacteria (*Ensifer meliloti, Halomonas maura*) can increase concentrations of osmoprotectants in alfalfa, whether salt-adapted genotypes from a multi-generation breeding program targeting salinity tolerance produce greater concentrations of osmoprotectants, and whether soil bacteria can interact with salt-adapted genotypes to produce more osmoprotectants compared to earlier generations in 0, 8, and 16 ds/m soils. If increased levels of osmoprotectants are found among treatments, an rt-qPCR study will be conducted to deduce the cause(s) of increased osmoprotectant production among treatments. This study will aid in adapting alfalfa cultivars to growth on saline soil thereby producing a revenue stream for producers from marginal agricultural land.

93. Understanding the genetic basis for nitrogen fixation in early maturity soybean under the drought stress

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Soybean [*Glycine max* (L.) Merr.] is the leading legume crop in the world. It fixes atmospheric nitrogen through the symbiotic rhizobia bacteria that inhabit root nodules. Drought stress limits plant growth, yield, and symbiotic nitrogen fixation (SNF) in soybean. The main objective of this study is to identify allelic variation associated with SNF in a short-season soybean diversity panel under drought stress. A diversity panel of 100 early-maturity Canadian soybean varieties for which genome-wide genotypic data are available was used in this study. A greenhouse pot experiment was conducted to determine plant phenotypic traits and SNF under drought stress. Seedlings were inoculated with *Bradyrhizobium japonicum* USDA 110, and the initial soil moisture content was maintained at 80% field capacity. The drought treatment was imposed after 3-weeks of plant growth, where half of the plants were maintained at 30% field capacity and the rest at 80% field capacity until maturity. Results showed a reduction in stomatal conductance, number of pods per plant, number of seeds per plant, and seed yield, whereas an increase in leaf chlorophyll content under drought stress. Genotypic variability was found for leaf chlorophyll content, stomatal conductance, photosynthesis (at flowering), number of pods per plant, number of seeds per plant, and seed yield (at maturity). The % nitrogen derived from the atmosphere (%NDFA) will be measured using the ^{15}N-dilution method. A genome-wide association study will be performed to identify allelic variation associated with SNF under drought stress and provide molecular markers useful in future soybean breeding programs.

94. Breeding for improved nitrogen fixation in pea

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The process of biological nitrogen fixation (BNF) through nodules of legumes benefits soil fertility, increases crop productivity and reduces the requirement for chemical fertilizers. Pea is an important pulse crop in western Canadian prairies with considerably high N fixation potential and nutritional value. The N fixation capacity of pea in Canadian environments ranges from 50 to 55% of crop N requirement. Nodulation mutants such as *nod3*, *Sym28*, *Sym29* and *nod4* have been developed by researchers in Europe for improved N fixation but not evaluated in a breeding program. We evaluated the potential of 20 pea lines derived from crosses between two of these nodulation mutants (*nod3* and *Sym29*) and Saskatchewan adapted pea cultivars CDC Meadow and CDC Dakota, for N fixation and agronomic traits. N fixation capacity of tested pea lines ranged from 50-80%. Best linear unbiased predictions (BLUPs) and orthogonal contrasts showed that pea lines under study performed better than checks. Pea lines, especially those arising from crosses with CDC Dakota, had on average 10% more grain yield, 2-3% more seed protein, and 5% more total N fixed than checks. The amount of fixed N showed moderately high and significantly positive correlation with days to maturity ($r=0.6$, $p<0.01$) and seed protein concentration ($r=0.5$, $p<0.01$). Root architecture and association mapping studies involving these pea lines will further explore different N-fixation mechanisms at interplay in these lines. In the future, it may be possible to pyramid these mechanisms to produce lines with even greater N fixation capacity.

95. Fungicide sensitivity of *Stemphylium vesicarium* in Ontario

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Stemphylium leaf blight (SLB), caused by *Stemphylium vesicarium* (Wallr.) E. G. Simmons, has become an important disease of onion in Ontario, Canada and north-eastern USA in recent years. Commercial cultivars are highly susceptible, so growers apply foliar fungicides at 10–14-day intervals to manage the disease. However, the efficacy of several fungicides has declined over time. Isolates of *S. vesicarium* collected in southern Ontario from onion, asparagus, and leek in 2012–2020 were assessed for sensitivity to the technical grade active ingredients of commonly used fungicides. Two isolates collected from oat in Saskatchewan in 1995 provided an historical baseline. The oat isolates were sensitive to azoxystrobin (FRAC 11), fluopyram (FRAC 7) and difenoconazole (FRAC 3), but insensitive to pyrimethanil (FRAC 9). Sensitivity to azoxystrobin was present in isolates collected from asparagus in 2012, but the population trended towards insensitivity by 2016, with 97% insensitive in 2020. Isolates from 2012 were sensitive to fluopyram, but 37% of the 95 isolates collected in 2018 and 2019 and 100% of 30 isolates in 2020 were insensitive. Most isolates (99%) were sensitive to difenoconazole based on a mycelial growth assessment, but conidial germination was not inhibited even a high rate (100 ppm). For pyrimethanil, 94% of isolates from 2018 and 2019 were insensitive. These active ingredients, which have been and are being used on onion in Ontario, no longer provide effective SLB suppression. Identification of alternative management strategies is required.

96. Photoperiodic response of in vitro *Cannabis sativa* plants

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With the increased legality of cannabis (*Cannabis sativa*) worldwide, there is high demand to improve production. A majority of commercial cultivators opt for a 12.0-hour uninterrupted dark period to induce flowering of cannabis plants; however, if certain genotypes can flower under a shorter dark period, then longer photoperiods could be used to improve cannabis yield. To determine if the floral initiation of female cannabis explants respond to varied photoperiod, female '802' explants were grown in vitro for four weeks under one of six photoperiod treatments: 12.0, 13.2, 13.8, 14.4, 15.0, and 16.0 hours per day. The percentage of flowered explants were highest in the 12.0- and 13.2-hour treatments, with 76% and 72%, respectively. There were no photoperiod effects on final height, growth index, or fresh weight. These findings suggest that an uninterrupted dark period of at least 10.8 hours (i.e., 13.2-hour photoperiod) is suitable to induce flowering of the '802' genotype. Further research is required to investigate the photoperiodic response on a whole-plant level to determine if in vitro studies can be used to determine genotype-specific photoperiods to optimize production.

Session 18. Student oral competition: Plant Health and Innovations in Agronomy

97. Weather-based models for forecasting and managing Fusarium head blight risk in western Canadian cereal production

T. T. MATENGU, P. BULLOCK, M. S. MKHABELA, F. ZVOMUYA, M. A. HENRIQUEZ, T. OJO, R. PICARD, R. AVILA AND M. HARDING. *Department of Soil Science, University of Manitoba, Winnipeg, MB, Canada; (M.A.H.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, Morden, MB, Canada; (T.O.) Soil and Ag Weather Surveillance, Manitoba Agriculture and Resource Development, Winnipeg, MB, Canada; (R.P.) Crop Production Extension, Manitoba Agriculture and Resource Development, Somerset, MB, Canada; (R.A.) Ministry of Agriculture, Government of Saskatchewan, Regina, SK, Canada; (M.H.) Plant and Bee Health Surveillance, Alberta Agriculture and Forestry, Brooks, AB, Canada.*

Predicting the risk of Fusarium Head Blight (FHB) disease occurrence in cereal crops is critical for determining the need for and timing of fungicide sprays. Existing models for predicting FHB risk developed many years ago may no longer be suitable for the current Fusarium species complex that has evolved in Canada. Therefore, this study aims to develop and validate weather-based risk models around flowering for predicting FHB index (FHBi), Fusarium damaged kernels (FDK), and deoxynivalenol (DON) in spring wheat, winter wheat, barley, and durum across three Canadian Prairie provinces. Data collected from 15 sites in western Canada in 2019 and 2020 were used to classify an epidemic at a 5% FHBi (all crops), or 1 mg kg^{-1} DON (all crops) or 0.2, 0.3, 0.8, and 2% FDK thresholds for barley, spring wheat, winter wheat, and durum, respectively, to develop weather-based models for *Fusarium* epidemics. Kendall correlation and stepwise logistic regression analysis identified suitable combinations of temperature (temp), relative humidity (RH), precipitation (prec), and solar radiation (SR) at 4, 7, 10, 14 days pre-anthesis, and 3 days pre to 3 days post-anthesis for predicting FHB risk. The weather variables chosen across crop types for the FHBi models were RH, temp, and prec, and for the FDK and DON models RH was selected. Prediction accuracy of the models ranged from 74.6 to 80.6, 76.5 to 78.1 and 78.3 to 79.3% for FHBi, FDK, and DON, respectively. Fusarium head blight pressure was low in 2019 and 2020, most likely due to drier than normal weather conditions, which were unfavorable for the disease. The models will be used to power an interactive, online digital viewer and provide early warning of potential FHBi, FDK, and DON epidemics in prairie cereal crops.

98. Greenhouse and field evaluation of Amisulbrom for clubroot management

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Clubroot, caused by *Plasmodiophora brassicae*, is an important constraint to Canadian canola (*Brassica napus*) production. The fungicide amisulbrom, a quinone inside inhibitor (QiI), was evaluated for effectiveness as a clubroot management tool. Liquid (GWN10440, 1000 g active ingredient (ai) ha^{-1}) and fertilizer formulations (GWN10750, 700 g ai ha^{-1}; GWN10751, 1000 g ai ha^{-1}; GWN10752, 1500 g ai ha^{-1}) of amisulbrom were compared on clubroot susceptible and moderately resistant canola hybrids under greenhouse conditions, and in field trials conducted in Edmonton in 2019 and 2020. No significant differences were observed among the amisulbrom treatments in the field in 2019, possibly due to excessive raining. In 2020, treatment with amisulbrom resulted in significant reductions in the clubroot disease severity index (DSI) in the field; the best control (nearly 60% reduction in DSI) was obtained with GWN10752 and GWN10440. Under greenhouse conditions, the treatments were tested at low (1×10^5 resting spores g^{-1} soil) and high (1×10^7 resting spores g^{-1} soil) inoculum pressure. Clubroot severity decreased with increasing amisulbrom rate for all fertilizer formulations, with a DSI < 20% observed in both cultivars following treatment with GWN10752 at the low inoculum level. The greatest reductions in DSI were achieved with the liquid formulation GWN10440 at both the low and high spore concentrations. While both liquid and fertilizer formulations of amisulbrom show promise as part of an integrated clubroot management strategy, the fertilizer form may be more suitable for Canadian canola growers given the costs of equipment, time and labour.

99. Development of a consistent greenhouse inoculation method for *Fusarium avenaceum* for screening germplasm of *Pisum sativum*

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Fusarium avenaceum is the most dominant pathogen in the pea (*Pisum sativum*) root rot complex in the prairies. Management of fusarium root rot (FRR) is challenging as fully resistant cultivars are absent and control options are limited to crop rotation. To develop a screening system for breeding purposes, three experiments were conducted. In the first experiment, disease severity (DS) of two cultivars ('CDC Meadow' and 'Carmen') in response to seed soak inoculation by three *F. avenaceum* isolates at four concentrations (1000, 5000, 10000, 50000 macroconidia/ml water) was measured. Results indicated that 10,000 macroconidia/ml was the best inoculum dose to achieve moderate disease severity. 'CDC Meadow' had significantly higher DS at all inoculum concentrations compared to 'Carmen'. In the second experiment, 13 pea germplasm lines were screened in a *Fusarium* disease nursery, and in a greenhouse using the seed soak method. Germplasm lines 'K-2', '5005', and '5004' had significantly lower DS in the 2019 field nursery while none of the lines performed differently from the susceptible control in 2020 field or greenhouse trials. Due to inconsistent results between greenhouse and field screening, four different inoculation methods were then compared in two cultivars ('CDC Meadow' and 'CDC Dakota'). The inoculation methods were: 1) seed soaking; 2) pipetting inoculum to seed at planting; 3) pipetting inoculum to lower stem and roots two weeks after planting; or 4) soaking roottrainers in inoculum two weeks after planting. Root soaking resulted in consistent FRR development in both cultivars, and will be tested further on more germplasm lines.

100. Growing wheat and liming to manage clubroot

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Clubroot, caused by *Plasmodiophora brassicae* Woronin, can dramatically reduce quality and yield of brassica crops. The resting spores can persist in soil for many years. Crop rotation is an important management strategy because a 2-year break from a host can reduce concentrations of resting spores in soil. Bait crops can reduce inoculum levels by stimulating the germination of resting spores, and the resulting zoospores ultimately die if a susceptible host is not available to complete the life cycle. Also, application of lime to raise soil pH levels above 7.2 reduces clubroot severity, in part by inhibiting resting spore germination. The interaction of bait crops and liming on spores of *P. brassicae* was not known. The effect of selected field/cover crops (wheat, barley, soybean, field pea, perennial ryegrass) on concentrations of spores in soil and the combined effect of growing wheat, a potential bait crop, and three liming rates on concentrations of spores were assessed in short-duration (8 weeks) studies under controlled conditions. Wheat reduced the concentrations of spores compared to a no-plant control. However, the hypothesis that root weight of a crop would be correlated with spore reduction was not supported. This indicated that crops with more extensive root systems did not induce more spore germination or reductions in spores. Increasing the rate of lime reduced spore numbers and there was no interaction between growing wheat and applying lime. Therefore, the two approaches do not counteract each other, and can both be used by growers.

101. Estimating fresh weight of pea shoot using measurable morphological traits

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Non-destructive estimation of shoot fresh weight (FW) using measurable morphological traits can potentially benefit robotic harvesting and other decision-making processes in pea shoot production. To predict shoot FW, nine regression models were developed, including two power models using stem diameter (SMD) or stem length (SML) as a variable, and seven linear models using part or all the following variables: SMD, SML, leaflet length (LL), leaflet width (LW), stipule length (SEL), and stipule width (SEW). Among the nine models, the 6-variable linear model was the most effective at explaining the variation in FW, and the linear models with only one variable, SMD or SML, were equally as least effective as the nonlinear models (i.e., power models), suggesting a linear rather than non-linear relationship between FW and the morphological variables. Stepwise regression and path analysis indicated that SMD, SML, SEL, and LL were the most important four predictor variables for multi-variable linear regression models for estimating FW. The 4- and 3-variable linear models (i.e., FW = -1.437 + 0.276 SMD + 0.010 SML + 0.022 LL + 0.013 SEL and FW = -1.383 + 0.308 SMD + 0.011 SML + 0.030 LL, respectively) were selected for their more accurate predictions than the 2- and 1-variable linear models, and relatively simpler forms than the 6-variable linear model. Although the prediction accuracy can potentially be affected by air temperature, light conditions and harvesting time, the multi-linear regression model is an effective approach for estimating FW of individual pea shoots using measurable morphological traits.

102. Genetic study of germination and seed shattering in *Euphorbia lagascae* Spreng in response to different seed treatments

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Euphorbia lagascae Spreng is grown because of its valuable seed oil, which is around 50% of the seed weight in which two-thirds is vernolic acid that has multiple industrial uses such as stabilizer-plasticizer and natural dye. Seed shattering resistance and germination have been reported as targets for improvement in E. *lagascae* before it can be used as a successful new industrial crop for Ontario that would grow well and be harvested easily. The objective of this study was to determine the genetic control of seed germination and seed shattering traits. Five different wild-type genotypes of E. *lagascae* that demonstrated high germination potential were crossed with an EMS mutant genotype that produces non-shattering capsules. The F2 populations for two successful crosses were separated into three different treated groups for seed germination evaluation and to study the segregation of 200 individuals per F2 population. The three treatments were: light treatment, gibberellic acid (GA3) treatment, and control. Consequently, plants treated with around approximately 250 µmol of light showed significant improvement in germination up to 75% in cross A and 82.4 % in cross B compared with the control plants and the group treated with 0.05% GA3 in the last week of collected data. The chi-square test indicated that the expression of seed germination, when treated with light, is simply inherited as it exhibited a 3:1 segregation ratio for germinated vs. not germinated seeds, indicative for one gene and dominance gene action in F2. The same conclusion was reached when phenotyping for the shattering trait for the subpopulations treated with light, which was also simply inherited as a 3:1 ratio for shattering vs. non-shattering capsules. Our results emphasize the importance and significance of light treatment in producing uniform populations through good germination and shattering resistance of the mutant genotypes of E. *lagascae*. This is the first report of light treatment significantly improving seed germination of E. *lagascae*, which may enhance efforts in the development of this new industrial crop.

103. Validation of prediction models for sclerotinia stem rot (*Sclerotinia sclerotiorum*) in soybean (*Glycine max*) in Quebec

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Sclerotinia stem rot (SSR) in soybean [*Glycine max* (L.) Merr] is a disease caused by the fungal pathogen *Sclerotinia sclerotiorum* (Lib.) de Bary which leads to yield losses for farmers in many regions, including Quebec. The disease is commonly kept at bay by chemical fungicides sprayed during the crop's vulnerable growth stages or using tolerant cultivars. However, whether pesticides are needed depends on the risk of disease outbreak, which is largely influenced by environmental conditions prevailing prior to and during the soybean flowering period. Unnecessary or improperly timed fungicide applications are costly not only economically, but also environmentally. To evaluate the risk of SSR disease development, researchers have created multiple SSR prediction models. In 2019 and in 2020, pre-conditioned *S. sclerotiorum* sclerotia were placed in commercial and research soybean plots throughout Quebec. Plots were scouted for the presence of apothecia and SSR disease development. Observations were used to evaluate the ability of previously published bioclimatic models to predict the formation of *S. sclerotiorum* apothecia under Quebec's agro-environmental conditions through receiver operating characteristic (ROC) curve analysis. Upon validation, models were customized using the data collected in Quebec to improve their predictive ability in the local context. The most accurate published models used maximum temperature alone or maximum temperature, wind speed and relative humidity, with an accuracy of 80.0% and 75.9% respectively at a probability threshold of 40%. These results suggest that published models provide a reliable basis for the development of an adapted SSR forecasting system for Quebec soybean growers.

Session 19. Student poster flash-talks: Biotic and Abiotic Challenges

104. Characterization and developing effective screening methods of bacterial blight of highbush blueberry in the Lower Mainland of British Columbia

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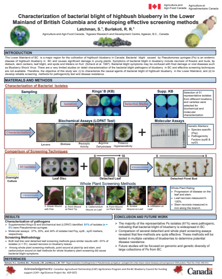

Characterization of bacterial blight of highbush blueberry in the Lower Mainland of British Columbia and developing effective screening methods

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Agriculture and Agri-Food Canada, [1]Agassiz Research and Development Centre, Agassiz, B.C., Canada

INTRODUCTION

The Lower Mainland of BC is a major region for the cultivation of highbush blueberry in Canada. Bacterial blight caused by *Pseudomonas syringae* (Ps) is an endemic disease of highbush blueberry in BC and causes significant damage in young plants. Symptoms of bacterial blight in blueberry include necrosis of flowers and buds, tip dieback, stem cankers, leaf blight, and spots and blisters on fruit (Scheck et al. 1997). Bacterial blight symptoms may be confused with frost damage or viral diseases such as Blueberry Shock Virus. There are a very limited studies on detail characterization of the bacterial blight pathogens of blueberry in BC and effective screening techniques are not available. Therefore, the objective of this study are: (i) to characterize the causal agents of bacterial blight of highbush blueberry in the Lower Mainland, and (ii) to develop reliable screening methods for pathogenicity test and disease resistance.

MATERIALS AND METHODS

Characterization of Bacterial Isolates

Selection of 51 representative isolates from different locations, and varieties were selected for biochemical and molecular characterization

Biochemical Assays (LOPAT Test)

Molecular Assays

Genetic Markers:
- Species specific (Psy)
- Pathogenicity Factors (syrB & syrD)

Comparison of Screening Techniques

Whole Plant Screening Methods

Whole Plant Rating:
- Progression of disease on the leaf and stem.
- Leaf necrosis measured 0-100%.
- Stem necrosis measured in mm along the branch.

RESULTS

Characterization of pathogens
- Supplemented King's B and biochemical test (LOPAT) identified 61% of isolates (n = 51) were *Pseudomonas syringae*.
- Molecular assays: 37%, 35%, and 24% of isolates had Psy, syrB , syrD markers, respectively.

Screening Methodology
- Both leaf disc and detached leaf screening methods gave similar results with ~61% of isolates (n = 51) caused necrosis on blueberry leaves.
- Among whole plant screening methods, point wound at plant tip and stem, and carborundum wound on leaf methods for whole blueberry plant screening did cause bacterial blight symptoms.

CONCLUSION AND FUTURE WORK
- The majority of the representative Ps isolates (61%) were pathogenic, indicating that bacterial blight of blueberry is widespread in BC.
- Comparison of several detached and whole plant screening assays revealed that few methods are quite effective. These methods will be tested in multiple varieties of blueberries to determine potential disease resistance.
- Future studies will be focused on genomic and genetic diversity of large collections of Ps from BC.

REFERENCES

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The Lower Mainland of BC is a major region for the cultivation of highbush blueberry in Canada. Bacterial blight caused by *Pseudomonas syringae* (Ps) is an endemic disease of highbush blueberry in BC and causes significant damage in young plants. The objectives of this study were: (i) to characterize isolates of Ps and assess their virulence; and (ii) to develop reliable screening methods for pathogenicity test and disease resistance. About 200 isolates of Ps were collected in 2019 from suspected bacterial blight-infected plant samples. Of these, 51 representative isolates were used for characterization and virulence diversity. Isolates were confirmed as Ps by growing them on the Ps-selective media KBC (King's B media with boric acid, cephalexin, and cycloheximide), and further characterized using the LOPAT test (levan, oxidase, pectolytic activity, arginine dihydrolase, and tobacco hypersensitivity reaction). Pathogenicity and virulence of these isolates were performed using blueberry leaf disc and detached leaf assays. About 61% of the tested isolates (n = 6) were confirmed as Ps and were pathogenic. Six pathogenic isolates were further evaluated by inoculating flower buds of two varieties 'Chandler' and 'Duke'. All six isolates caused bacterial blight on flower buds of both varieties. In addition, six screening methods were compared by inoculating Ps in intact blueberry plants and three methods (wounding stem apex, removing leaf and wounding stem, and wounding leaf with carborundum) performed better than the remaining of screening methods.

105. Comparing extraction methods to quantify *Aphanomyces euteiches* inoculum levels in field soils

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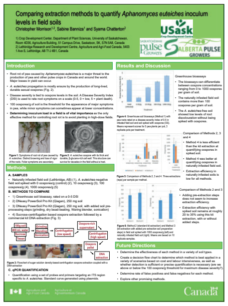

Root rot of pea and lentil caused by the oomycete pathogen *Aphanomyces euteiches* is a serious threat to pea and lentil production in Canada and elsewhere around the world. Accurate detection and quantification of the inoculum of this pathogen, in the form of long-lived oospores, is a necessary tool for growers as control of this disease is limited to avoiding peas or other hosts in a field until inoculum load is reduced sufficiently. Standard commercial kit DNA extractions coupled with quantitative polymerase chain reaction amplification (qPCR) can be used to quantify this pathogen in soil samples but can provide inconsistent results for some soil types. To improve upon existing methods, multiple extraction methods were performed followed by standard qPCR to assess detection limits, precision, and accuracy. Methods include a sugar-based centrifugation oospore extraction with subsequent DNA extraction, standard commercial kit DNA extraction coupled with pre-extraction steps including grinding, bead-beating and sonication of soil samples, and greenhouse bioassays. Both naturally infested field soil and spiked soil were used. Pre-extraction steps involving grinding and bead-beating slightly increased extraction efficiency, likely by helping to separate the oospores from the soil matrix. Extraction efficiency from naturally infested field soils remained low, but the alternative extraction methods using substantially larger volumes of soils (two orders of magnitude) than the 250 mg required for the commercial kit may be needed in soils where oospore counts are low. Comparing these methods in different soil types will be important to determine whether methods are reproducible across soil types.

106. Effects of low temperature stress on physiological and biochemical processes of silage-corn genotypes

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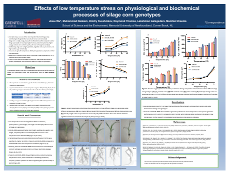

Low temperature stress hampers seedling establishment, growth and productivity of crops. However, low temperature stress tolerance varies within crop species and genotypes. In this study, we conducted a growth chamber experiment to determine the effects of low temperature regime on the seedling establishment, physiological and biochemical parameters of three silage corn genotypes. Experimental treatments were five temperature regimes including 25°C (control), 20°C, 15°C, 10°C and 5°C and three genotypes (Yukon-R, DKC26-28RIB, A4177G3-RIB) with different genetic traits. The experiment was set up in a completely randomized design in split-plot arrangement with three replications. Low temperature stress was imposed at the third leaf stage for five days, and then physiological and biochemical parameters were recorded. Results depicted that silage-corn vegetative growth, photosynthetic system and redox homeostasis were affected when seedlings were exposed to 15°C or lower temperatures. Silage-corn genotypes Yukon-R and DKC26-28RIB expressed significantly ($p < 0.05$) higher agronomic performance than A4177G3-RIB, particularly root development. Similarly, Yukon-R and DKC26-28RIB showed minimum stress-induced malonaldehyde and hydrogen peroxide content. However, photosynthesis rate and photochemical efficiency (*Fv/Fm*) were higher in Yukon-R and DKC26-28RIB compared to A4177G3-RIB under low temperature conditions. Taken together, our data suggested that Yukon-R and DKC26-28RIB have better adaptation and low temperature stress tolerance, which could be considered as the candidate genotypes to be grown in boreal climate. The outcome of this research will further enhance our insights in understanding low temperature stress tolerance mechanisms of silage-corn and designing future field experiments to enhance forage production in boreal climates.

107. Yield Losses in Canola Caused by *Verticillium longisporum*

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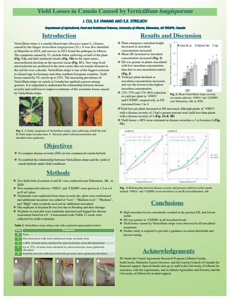

Verticillium stripe, a novel disease of canola (*Brassica napus*) caused by *Verticillium longisporium*, was first reported on the Canadian Prairies in 2014. The increasing prevalence of this soilborne disease has

Abstracts

sparked concern among growers, since the potential for yield losses could be high. The relationship between Verticillium stripe severity and yield was evaluated at two infested field sites near Edmonton, Alberta, in 2020, using the canola hybrids ‘45H31’ and ‘CS2000’. The disease severity was assessed on a 0 – 4 scale developed for this study, based on symptoms on the main stem and the amount of premature pod senescence, where 0 = no disease, 1 = discolouration with dark unilateral stripe on main stem, 2 = less than 25% of microsclerotia colonized on stem cortex, 3 = up to 75% of main stem colonized by microsclerotia, and 4 = entirely necrotic. Both canola hybrids developed symptoms of Verticillium stripe. Regression analysis indicated that seed yield declined with increasing disease severity. Seed yield per plant decreased by 12% to 75% and 17% to 86% in ‘45H31’ and ‘CS2000’, respectively, as disease severity increased from 1 to 4. A greater percentage yield loss was observed on ‘CS2000’ vs. ‘45H31’. At a disease severity of 3, yield losses in both cultivars exceeded 60% at one location. These preliminary results suggest that Verticillium stripe can cause very significant yield losses at high disease severity levels. The field trials are being repeated in 2021.

108. Impact of blackleg (*Leptosphaeria maculans*) on canola yield

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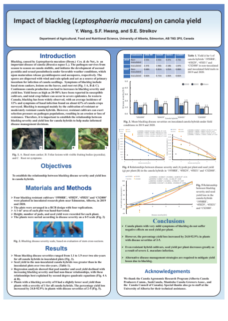

Impact of blackleg (*Leptosphaeria maculans*) on canola yield

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Introduction

Blackleg, caused by *Leptosphaeria maculans* (Desm.) Ces. & de Not., is an important disease of canola (*Brassica napus* L.). The pathogen survives from season to season on canola stubble, and initiates the development of asexual pycnidia and sexual pseudothecia under favorable weather conditions, which upon maturation release pycnidiospores and ascospores, respectively. The spores are dispersed with wind and rain splash and act as a source of primary inoculum for infection of canola seedlings. Symptoms of blackleg include basal stem cankers, lesions on the leaves, and root rot (Fig. 1 A, B & C). Continuous canola production can lead to increases in blackleg severity and yield loss. Yield losses as high as 30-50% have been reported in susceptible cultivars, and total crop failure can occur in severe epidemics. In western Canada, blackleg has been widely observed, with an average incidence of 12% and symptoms of basal infection found on about 63% of canola crops surveyed. Blackleg is managed mainly by the cultivation of resistant or moderately resistant canola hybrids. However, resistant cultivars can exert selection pressure on pathogen populations, resulting in an erosion or loss of resistance. Therefore, it is important to establish the relationship between blackleg severity and yield loss for canola hybrids to help make informed disease management decisions.

Fig. 1. A. Basal stem canker; B. Foliar lesions with visible fruiting bodies (pycnidia); and C. Root rot symptoms.

Objectives

To establish the relationship between blackleg disease severity and yield loss in canola hybrids.

Materials and Methods

- Four blackleg resistant cultivars ‘1950RR’, ‘45H29’, ‘45H31’ and ‘CS2000’ were planted in inoculated research plots near Edmonton, Alberta, in 2019 and 2020.
- The plots were arranged in a RCB design with four replications.
- A 1-m² area of each plot was hand-harvested.
- Height, number of pods, and seed yield were recorded for each plant.
- The plants were sorted according to disease severity on a 0-5 scale (Fig. 2)

Fig. 2. Blackleg disease severity scale, based on evaluation of stem cross-sections.

Results

- Mean blackleg disease severities ranged from 1.1 to 1.9 over two site-years for all canola hybrids in inoculated plots (Fig. 3).
- Seed yield in the non-inoculated canola hybrids was greater than in the inoculated plots over two site-years. (Table 1).
- Regression analysis showed that pod number and seed yield declined with increasing blackleg severity and had non-linear relationships, with these relationships best explained by second degree quadratic equations (Fig. 4 A & B).
- Plants with a blackleg severity of 0 had a slightly lower seed yield than plants with a severity of 1 for all canola hybrids. The percentage yield loss increased by 24.8-92.9% in plants with disease severities of 2-5 (Fig. 5).

Table 1. Yield (t ha⁻¹) of canola hybrids ‘1950RR’, ‘45H29’, ‘45H31’ and ‘CS2000’ in non-inoculated and inoculated field trails in 2019 and 2020.

Fig. 3. Mean blackleg disease severities on inoculated canola hybrids under field conditions in 2019 and 2020.

Fig. 4 Relationships between disease severity and (A) pods per plant and seed yield (g) per plant (B) in the canola hybrids in ‘1950RR’, ‘45H29’, ‘45H31’ and ‘CS2000’.

Fig. 5 Relationship between blackleg severity and seed yield loss in the canola hybrids ‘1950RR’, ‘45H29’, ‘45H31’ and ‘CS2000’.

Conclusions

- Canola plants with very mild symptoms of blackleg do not suffer negative effects on seed yield per plant.
- However, the percentage yield loss increased by 24.8-92.9% in plants with disease severities of 2-5.
- Even resistant hybrid cultivars, seed yield per plant decreases greatly as a result of severe *L. maculans* infection.
- Alternative disease management strategies are required to mitigate yield losses due to blackleg.

Acknowledgements

We thank the Canola Agronomic Research Program (Alberta Canola Producers Comm., SaskCanola, Manitoba Canola Growers Assoc., and the Canola Council of Canada). Special thanks also go to staff at the University of Alberta for their technical assistance.

Blackleg, caused by *Leptosphaeria maculans*, is an economically important disease of canola (*Brassica napus*) worldwide. Severe epidemics can result in yield losses of 30-50% and total crop failure can occur when susceptible canola cultivars are grown. In western Canada, blackleg have been widely observed, while growers plant blackleg resistant cultivars to manage the disease. In order to establish the relationship between blackleg severity and the yield of blackleg-resistant canola hybrids, field experiments were conducted over 2 years in four canola hybrids, ‘1950RR’, ‘45H29’, ‘45H31’ and ‘CS2000’. Adult plants were assessed for blackleg disease on a 0 to 5 scale, where 0 indicates a completely healthy plant and 5 indicates plant death. The average disease severity on the inoculated canola ‘1950RR’, ‘45H29’, ‘45H31’ and ‘CS2000’ over 2 years was 1.4, 1.6, 1.9 and 1.1, respectively. Seed yield in non-inoculated plots were higher than inoculated plots for all four canola hybrids. Regression analysis indicated that there were polynomial relationships between blackleg severity and pod number and seed yield. Plants with a blackleg severity of 0 had a slightly lower seed yield loss than plants with a severity of 1 for ‘1950RR’, ‘45H29’ and ‘CS2000’, while as disease severity increased to 2–5, yields began to decline. Seed yield decreased as disease severity increased from 0-5 for ‘45H31’. The results suggest the potential for significant losses in blackleg-resistant canola hybrids, and integrated disease management strategies should be employed to mitigate the impact of *L. maculans* on canola.

109. Evaluation of the pH sensitivity of *Plasmodiophora brassicae* strains

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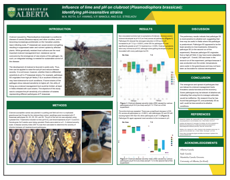

UNIVERSITY OF ALBERTA

Influence of lime and pH on clubroot (Plasmodiophora brassicae): Identifying pH-insensitive strains

M.N. ROTH, S.F. HWANG, V.P. MANOLII, AND S.E. STRELKOV

INTRODUCTION

METHODS

RESULTS

DISCUSSION

CONCLUSION

REFERENCES

ACKNOWLEDGEMENTS

Alberta Canola

Sask Canola

Manitoba Canola Growers

University of Alberta (In Kind)

Clubroot, caused by *Plasmodiophora brassicae*, has emerged as a serious disease of canola (*Brassica napus*) in western Canada. Since development of this disease is favored in acidic soils, lime can be applied to increase soil pH and suppress clubroot outbreaks. It is not known, however, whether there is differential sensitivity to pH in *P. brassicae* strains, or whether lime can exert selection pressure on the pathogen, favoring pH insensitive strains. Clubroot-susceptible canola was grown in a potting medium/field soil mix inoculated with pathotypes 3A, 3H, 3D, 5G or 5X of *P. brassicae*, at pH 6.1 (no lime) or pH 7.2 and pH 8.0 (limed treatments) in replicated greenhouse trials. Clubroot severity was assessed after 6 weeks. Non-inoculated controls were grown in soil mix free of the pathogen. No symptoms of clubroot were observed in the non-inoculated controls, while severe clubroot developed at pH 6.1 regardless of pathotype. At pH 7.2, there was a large and significant decrease in clubroot severity for pathotype 5X. In contrast, pathotypes 3D and 5G caused moderate disease at this pH, while levels of disease for pathotypes 3A and 3H were in between those for 5X and 3D/5G. At pH 8.0, symptom development was very limited for most pathotypes. Experiments are underway to further characterize the pH response of pathotypes 3D and 5G. The results indicate some variation in the sensitivity of *P. brassicae* to soil pH, which could have implications for the utility of lime application as a clubroot management strategy in certain fields.

Session 20. Theme: Climate change and biodiversity

110. Impact of changing climate on the Canadian prairies on pest threats, canola yields and quality

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The Canadian prairies are one of the world’s most highly productive agricultural regions, especially given constraints on growing season duration and moisture. The climate change projections described in the Intergovernmental Panel on Climate Change are based on scenarios called Representative Concentration Pathways (RCPs) that cover from 2006 onward and are identified by a number indicating the change in radiative forcing by the end of the 21st century. The RCP2.6 represents a low emission pathway with a change in radiative forcing of roughly 2.6 W/m2, RCP4.5 and RCP6 represent intermediate emission pathways, and RCP8.5 represents a pathway with continued growth in GHG emissions (high emissions), leading to a radiative forcing of roughly 8.5 W/m2 at the end of the century. The RCP2.6 scenario is consistent with limiting global temperature increase to roughly 2°C above the pre-industrial value and aligns goals agreed to in the Paris Agreement. Increased atmospheric CO_2 concentrations may stimulate growth and yield of canola as CO_2 is the substrate for photosynthesis and therefore a macronutrient ("CO^2 fertilization effect") and this can offset some of the negative effects of extreme climate. This paper examines the potential impact of these projected climate change scenarios and resultant changes in CO_2 concentrations, temperature, moisture, growing degree days, and increase in frequency and severity of extreme events on canola yields and quality. Current and emerging pest distributions and severity, along with biodiversity on the Canadian prairies were also assessed under climate change scenarios. Adaptive strategies for continued profitable canola production are also discussed.

111. Machine learning-based canola yield prediction and site-specific nitrogen recommendation

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An effective crop yield prediction is critical for precise nitrogen (N) fertilization. However, crop yield forecasting is highly complex due to many influenced factors, such as genotype and environment. The objective of this study is to develop a machine-learning algorithm, i.e., random forest regression (RFR) to make decisions in site-specific N recommendation at an early growth stage through canola yield prediction. A 4-yr (2013-16) field experiment with series of N rates (0200 kg N ha^{-1}) and timing (at planting or split application at GS16) was conducted at 5 locations in eastern Canada. Hybrids InVigor 5440 and L150 were used in 2013 and 2014 while L150 was replaced with L140P since 2015. The pre-planting soil properties (texture, pH, P, K, and organic matter), weather (precipitation and temperature), N rate, plant phenotypes (height and density), and vegetative indices (NDVI and SPAD) collected before the 6-leaf stage were used to train the validate the models. Results showed that weather condition is the most important factor to determine seed yield, with a GINI score of 22%. Single vegetative index (NDVI or SPAD) could illustrate over 55% of seed yield in terms of relative error (RE). However, a high root-mean-square error (RMSE), approaching 30% of average yield, was observed. Incorporating other features (soil properties, weather, etc.) with vegetative indices could greatly improve the predicting reliability of RFR up to 85%, with 53-57% lower RMSE compared to NDVI- or SPAD-based models. As such, all features RFR was used to make precise N recommendations. A rate of 150 kg N ha^{-1} was suggested for most scenarios in eastern Canada with a slightly higher (160 kg N ha^{-1}) for those sites of even precipitation distribution.

112. The role of canola in carbon sequestration in Western Canada soils

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Soil Organic Carbon (SOC) in agricultural lands is vital for global food production and greenhouse gas (GHG) mitigation. Over the past several decades canola acres have rapidly increased, while at the same time summerfallow acres have declined, leading to an increase SOC. Low-till and no-till farming practices allow Canadian farmers to sequester 11 million tonnes of greenhouse gases (GHG) in their fields each year. Less tilling means farmers are making fewer passes over the field with tractors and tillage implements, reducing fuel and GHG emissions. As a result of increased conservation tillage practices, Canadian farms now use between 126 and 194 fewer litres of diesel each year, reducing GHG emissions by about 450,000 to 750,000 tonnes per year. The majority of increased recent carbon input in Western Canada has been largely driven by the increasing area and yield of canola. In additions to increasing yields, crops with larger root systems and higher root to shoot ratio like canola, provide higher belowground carbon input and impact radiative forcing. Based on carbon calculations which attribute carbon change to individual crops, increasing canola yields to an average of 52 bushels per acre by 2025 will sequester an additional five million tonnes of greenhouse gases in Canadian soils each year, relative to 2005. The impact of canola production practices and yields will be presented in context of canola industries commitment to Canada and UN sustainability goals. Canola has a strong history of helping Canada reduce its overall GHG emissions and will play a critical role in further reductions.

113. Wild berries for northern agriculture - selection, propagation, conservation and production

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Wild blueberry (*Vaccinium* spp. L.), cranberry (*V. macrocarpon* Ait.), lingonberry (*V. vitis-idaea* L.) and cloudberry (*Rubus chamaemorus* L.) are native to northern Canada. While blueberry (lowbush and highbush) is the most important fruit crop in Canada with highest farm gate value followed by apple, grape and cranberry, lingonberry and cloudberry are two important indigenous food crops rich in antioxidant metabolites. Wild berries and hybrids between wild and cultivated berries are of significant importance for conserving genetic resources and community food production due to their higher production and winter hardiness compared to existing cultivars. New techniques for conservation, propagation and selection of pest resistant and high antioxidant containing wild germplasm will play significant role for preserving valuable biodiversity and for a sustainable production system in the North. The current review deals with the in-depth progress on different aspects of wild berry germplasm characterization at molecular and biochemical levels, their propagation in vitro and use of molecular markers for the clonal fidelity of micropropagated wild berries. The paper also covers the utilization of epigenetics in tissue culture berry crop improvement.

114. Assessing the yield and stability of cropping systems in the major ecozones on the Canadian Prairies

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Agriculture faces grand challenges of meeting growing food demands while reducing environmental impacts. An integrated approach is required to design cropping systems and achieve the goal of agricultural sustainability under climate change. A 4-year crop rotation study was established in 2018 at seven sites across the Canadian Prairies, including Beaverlodge, Lacombe, and Lethbridge, AB; Melfort, Scott, and Swift Current, SK; and Carman MB. The overall objective of this project is to develop resilient cropping systems in different ecozones on the Canadian Prairies. This study tested six cropping systems consisting of 1) conventional cropping system (Control), 2) pulse- or oilseed-intensified cropping system (POS), 3) diversified cropping system (DS), 4) market-driven cropping system (MS), 5) high risk and high reward cropping system (HRHRS), and 6) green-manure incorporated soil-health focused cropping system (GMS). Averaged across all site-years, the system yield (e.g. canola equivalent yield) for MS (2167 kg ha^{-1}) and POS (1758 kg ha^{-1}) were 33 and 8% higher than Control (1632 kg ha^{-1}), respectively; while the CEY for DS (1537 kg ha^{-1}), HRHRS (1451 kg ha^{-1}) and GMS (1319 kg ha^{-1}) were 6, 11, and 19% lower than Control, respectively. Yield stability as indicated by the coefficient of variation follows the order of GMS > POS > Control > DS > MS > HRHRS. The preliminary results suggest that a balance between yield and stability need to be achieved when designing a cropping system.

115. Is plant growth regulator application reliable option for forage seed crop management in the Peace River Region of Canada?

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Lodging related impairment of fertilization and seed development is one of the major constraints to seed yield in forage and turfgrass seed crops. Plant growth regulators (PGRs) that reduce cell elongation through the control of gibberellic hormonal activities are increasingly used for temperate forage seed crops around the world. Various study results show that the anti-gibberellic PGRs reduce plant height, diminish lodging and increase seed yield. A number of field experiments with PGRs were conducted on creeping red fescue (*Festuca rubra* L. ssp. *rubra* Gaudin), meadow bromegrass (*Bromus riparius* Rehm) and timothy (*Phleum pratense* L.) seed crops at Beaverlodge Research Farm and its outreach areas in the Peace River region. Two PGRs, trinexapac-ethyl and chlormequat chloride, were applied at two-node (BBCH 31-32) and/or early heading (BBCH 51-52) growth stages. The seed crop species exhibited differential responses to PGR application, in that creeping red fescue was least responsive, while meadow bromegrass and timothy showed moderate to high response in terms of reduction in plant height and lodging, and increasing seed yield. Those responses were highly dependent on the growing season weather condition. Generally, PGR application was more effective on seed crops with vigorous growth that received well distributed rainfall providing adequate moisture in the soil. Further studies are needed to understand physiological mechanisms for differential responses of forage seed crops to PGR application.

116. Effect of time of seeding and stage of harvesting on MasterGarze corn in Northwestern Ontario

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Abstract Withdrawn

Session 21. Invited keynote speaker

117. Managing soil organic matter for global food and climate security

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Global prevalence of undernutrition for 690 million may have been increased by another 80 to 132 million (12 to 20%) by the end of 2020 through disruptions in food production and supply chains. In addition to undernutrition, 2 billion people are prone to malnutrition. The latter; caused by lack of one or more of several micro nutrients, protein and amino acids; is aggravated by degradation and decline in soil's capacity to produce ecosystem services essential to human wellbeing and nature conservancy. The Green Revolution of the 1960s was a global success story, and drastic increase in agronomic production (e.g., cereals such as wheat and rice) saved hundreds of millions from starvation. Between 1961 and 2020, global population increased by a factor of 2.5 (3.2 to 7.8 B). However, global cereal production increased by 3.3 times (0.99 to 3 Gt). Therefore, the per capita cereal production increased 32% (284 to 376 kg). In addition to adoption of input-responsive dwarf varieties, significantly high agronomic yields were obtained by drastic increase in input of fertilizers such as N (9.2 times), P (5 times) and K (4.8 times). Furthermore, the irrigated land are increased 2.4 times (144 to 350 M ha). Such an Increase in use of chemicals (e.g., fertilizers and pesticides) caused eutrophication of natural waters, pollution of air, and emission of greenhouse gases (GHGs). Global temperatures have already increased by 1.1 ℃, and ~30% of all anthropogenic emissions are attributed to agriculture. There also exists a serious problem of soil degradation by a range of processes (i.e., decline in soil structure, compaction, accelerated erosion, salinization, acidification, depletion of soil organic matter or SOM content, nutrient/elemental imbalance). Some soils are already extinct, some others are endangered, and the issue of "peak soil" is a global concern. Adverse effects of a severe depletion of SOM content (often below 0.5% in the surface layer in agricultural soils of South Asia, Sub-Saharan

Africa, Central American and the Caribbean etc.) necessitates the use of chemical fertilizers to alleviate nutrient-related constraints to crop production. However, fertilizers can be prohibitively expensive for resource-poor small land holders, and their effectiveness and use efficiency are low because of the widespread problem of soil degradation. Agro-ecosystems may have lost as much as 135 Gt of soil organic carbon (SOC), which must be restored to above the critical level (1.5 – 2.0 % in the 0-20 cm layer) to enhance and sustain productivity. While enhancing agronomic productivity by improving the use efficiency of inputs and increasing the drought resilience, restoration of SOC stock also increases adaptation to and mitigation of the global warming. Potential of SOC sequestration in managed soils of the world is 2.5 Gt C/yr. (1.5 – 3.4 Gt C/yr.) through adoption of site-specific best management practices (e.g. conservation agriculture, integrated soil fertility management, complex rotations and integration of crops with trees and livestock). The cumulative potential of SOC sequestration between 2020 and 2100 at 178 Gt, combined with that of C sequestration in forest/woodland biomass at 155 Gt, can create a drawdown of 157 ppm CO2 from the atmosphere. With adoption of non-carbon energy sources (i.e., wind, solar, geothermal), re-carbonization of the terrestrial biosphere (soil, vegetation) can still limit the global warming to below 2 ℃. Thus, managing SOC content is a win-win-win option. It is essential to advancing food and nutritional security, adaptation and mitigation of global warming, and strengthening of the biodiversity. Re-carbonization of the soil and biosphere can also put on track the Sustainable Development Goals of the Agenda 2030 of the United Nations. However, farmers/foresters/land managers must be motivated and incentivized through payments for ecosystem services at the societal cost of SOC (e.g., $120/t of SOC). Translating science into action, needs prudent governance and implementation of policies (at local, national and global level) which are pro-nature, pro-agriculture and pro farmer.

Session 22. Invited keynote speaker

118. Organic as a platform for ecological innovation in agriculture

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Agricultural policy is increasingly emphasizing the need for development and adoption of practices that reduce environmental impact. Environmental considerations have become a part of research programs as well, either as explicit program objectives or requests to consider environmental outcomes as a secondary impact of the science. Organic agriculture is an internationally recognized system of production guided by principles of environmental sustainability and regulated national standards. The organic system limits the use of non-ecological practices, and encourages adoption of practices that promote long-term stability and resilience in soil fertility and pest management. As such, organic farmers are particularly dependent on understanding agroecosystem processes that lead to financially, socially, and environmentally sustainable practices. Consumer demand continues to drive rapid growth in the global organic market even with premium prices. This demand provides an excellent platform for development and early adoption of ecologically-based practices that could evolve to benefit all of agriculture when up-scaled. The national Organic Science Cluster program in Canada provides examples of how organic agriculture can be used as a launch pad for agroecological innovation including: biological controls for *Fusarium* head blight, development of growing mediums for organic greenhouse production, optimization of green manures to displace nitrogen fertilizer application, development of integrated approaches to manage pests such as wireworm, and farmer participatory plant breeding.

Session 23. Student oral competition: Innovations in Agronomy and Crop Management

119. Effect of cereal and non-cereal crop sequences on Fusarium head blight severity across the Canadian prairies

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Fusarium head blight (FHB) is a disease of concern for cereal producers across western Canada. Approximately 60% of the area seeded to annual crops in the Canadian prairies consists of wheat and canola; this low crop diversity within rotations increases disease risk of cereals. This study focussed on the effect of a three-year crop sequences on FHB of wheat or barley in the third year of the experiments. From 2018 to 2020, five sites across the prairies were seeded with a core set of five crops including wheat, barley, canola, pea, and maize; at all sites, another one to four crops were included that were common to the area. The experiments consisted of a crop matrix arranged in a split block design. Disease severity (FHB index, Fusarium damaged kernels (FDKs) and deoxynivalenol content), yield and crop quality measurements were recorded. *Fusarium* spp. were isolated and identified from wheat and barley kernels. The crop stubble from the year immediately prior to cereal production had detectable effects on FHB severity, the predominant *Fusarium* spp. isolated, and the amount of FDK. *Fusarium graminearum* and *F. poae* were the predominate species isolated; the frequency of *F. poae* was similar in sequences with cereals and pulses. These findings reveal that including pulses and other non-cereal crops in a three-year crop sequence benefit yield and quality. The predominant *Fusarium* spp. isolated from infected kernels differed depended on the previous crop and the site.

120. Assessing the phenotypic response to phosphorus in a winter wheat (*Triticum aestivum* L.) diversity panel field screened in Ontario, Canada

K. SJONNESEN, I. RAJCAN AND E. LEE. *Plant*

Abstracts

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Phosphorus (P) is an essential macronutrient in crop production, and in past decades, there has been heavy P fertilizer application to Ontario soils. The subsequent P build-up in soils creates a scenario where many agroecosystems partake in or are at risk of contributing to P pollution of water systems. Breeding important crops like winter wheat (*Triticum aestivum* L.) for better P use efficiency (PUE) is a necessary strategy to addressing this issue in Ontario. However, there has been little success to date. The purpose of this study was to screen winter wheat genotypes for their response to P through field traits, and to evaluate the consistency of the P response across traits and environments. To achieve this, a 200-line winter wheat diversity panel was grown under applied P (100 kg/ha MAP) and no P applied (0 kg/ha MAP) conditions, and phenotyped for winter survival and recovery traits, phenological traits, and grain yield. Traits that revealed a clear P response were used to categorize genotypes for PUE. The yield P response could not be predicted with the P response from other traits, which is indicative of the numerous strategies acting at variable developmental stages that contribute to a plant's PUE. Furthermore, the P response was not consistent across environments, pointing to the importance of multi-environment trials to identify stable genotypes for PUE. With these findings, we also present a method for screening genotypes for PUE that is practical for field testing in regions with historically high P inputs.

121. Canopy management: the balance between lodging risk and nitrogen use in western Canadian spring wheat production

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Lodging risk has increased with the introduction of new high yielding wheat cultivars with increased nitrogen (N) fertility requirements. Agronomic management of the crop canopy has been used to reduce lodging risk. However, the short growing season and unpredictable moisture supply in western Canada may influence the adaptability of canopy management strategies. The objective of this study was to quantify the ability of agronomic practices to modify the canopy and lodging risk, and to determine how these practices influence N use and final grain N. Field trials in southern Manitoba evaluated three plant densities, split N fertilizer application, and a chlormequat chloride (CCC) application on canopy size (dry matter and height at anthesis), N uptake and remobilization (Rm), lodging risk, grain yield, protein, and N content on the cultivar AAC Brandon. Low plant density, split N, and CCC applications all showed potential to reduce lodging risk without reducing grain yield or protein. Additionally, PGR and split N applications increased final grain N content by 3 and 14 kg N ha^{-1}, respectively. Correlations between dry matter at anthesis and N uptake at anthesis (r=0.80), and N uptake at anthesis and N Rm (r=0.92) during grain fill were high. Grain N content wasn't limited by canopy management practices in this experiment, likely due to sufficient post-anthesis N uptake, compensating for reduced N Rm. Therefore, canopy management practices have potential in western Canada to reduce lodging risk without compromising grain N levels. Additional testing will be required for additional cultivars and growing regions.

122. Grass cover crops during vineyard establishment in southern Quebec: Their effects on weed control and soil aggregate stability to water

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Although cover crops can be competitive against weeds and improve soil health, their implementation at the northern limit of grapevine production is relatively uncommon and poorly documented. In such areas, vines have to be covered by soil (hilling) or geotextiles to be protected from frost during winter. A three-year (2018-2020) randomized complete block design experiment was conducted at Agriculture and Agri-Food Canada's (AAFC) research farm in Frelighsburg, QC. Weed control, aggregate stability and vine productivity were assessed following four interrow (3 m) management strategies: 1) cultivation; 2) cover cropping using an annual grass mixture (*Lolium multiflorum* Lamarck, *Avena sativa*, L.); 3) cover cropping using a perennial grass mixture (*Poa pratensis* L., *Lolium perenne* L., *Lolium multiflorum* Lamarck, *Festuca rubra* L.); and 4) a weedy control. A 1 m wide strip under the vine row was clean cultivated in all treatments and all vegetated treatments (i.e., 2, 3, 4) were regularly mowed. Measurements included weeds and intercrop density, cover and biomass (including roots), soil aggregate stability and gravimetric water content, vine pruning weight, biomass, leaf area, and yield. Cultivation was the most efficient strategy to control weeds and weed populations increased in both cover crop mixtures after the first year in comparison. Cover crop management also impacted weed population composition. Cover crops contributed to preserve the integrity of soil structure because mean weight diameter (average size of water stable aggregates) was greater in vegetated treatments compared to cultivation. Finally, cover crops did not reduce yield at harvest.

123. Wood ash and paper sludge: Potential liming and nutrient sources for podzolic soils

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Canadian paper industry produces a significant amount of wood ash (WA) and paper sludge (SL) as waste products each year. Contemporarily, these wastes are disposed off at landfill cites, causes financial and environmental implications. An alternative to landfilling could be recycling and reusing mill waste as soil amendments that might increase soil pH and provide essential nutrients. The objective of this study was to evaluate WA, SL alone and in combination with biochar (BC) as liming and nutrient source to increase soil pH, crop growth and yield in podzolic soil. We have conducted a greenhouse experiments at Wooddale Provincial Tree Nursery, Grand Falls-Windsor, Newfoundland. Experimental treatments were: 1) limestone as control (L), 2) WA, 3) SL, 4) WASL, 5) LBC, 6) WABC, 7) SLBC, 8) WASLBC. Annual ryegrass, (*Lolium perenne L.*) and kale, (*Brassica oleracea*) were used as test crops. Limestone, WA, SL and WA+ SL application rates were 7.1 Mg ha^{-1}, 17.25 Mg ha^{-1}, 55 Mg ha^{-1}, and 13.8 + 11 Mg ha^{-1} respectively, and were calculated based on (calcium carbonate equivalent (CCE) and BC was applied at 20 Mg ha^{-1}. Results indicated that application of WA significantly increased soil pH and achieved target pH in both crops. WA application produced 70% greater biomass in annual ryegrass and 28% higher kale yield compared to control. These study results suggest that WA has liming, and agronomic benefits thus could be used as an alternative source for liming and nutrients in the podzolic soil in boreal climate.

124. Agronomic analysis of sainfoin (*Onobrychis viciifolia* Scop.) and grass mixtures for forage production in western Canada

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Sainfoin is a palatable perennial legume that is gaining interest in the western Canadian beef industry since it does not cause frothy bloat in grazing ruminants. The objective of this study was to assess reduced sainfoin seeding rate and determine agronomic performance of sainfoin-grass mixtures. Two sainfoin cultivars (cv.), 'Melrose' and 'AAC Mountainview', were evaluated as monocultures and in mixtures with three grass species, crested wheatgrass (*Agropyron cristatum* L.) cv. 'AC Goliath', meadow bromegrass (*Bromus riparius* Rehm.) cv. 'Armada', and hybrid bromegrass (*Bromus riparius* x *Bromus inermis*) cv. 'AC Knowles', under one- and two-cut harvests at Swift Current, SK, Saskatoon, SK, and Brandon, MB. The sainfoin-grass mixtures compared favorably to a common industry mixture of 'Beaver' alfalfa (*Medicago sativa* L.) and 'Armada' meadow bromegrass, with acceptable winter survival (93-100% sainfoin survival compared to 100% alfalfa survival), forage yields (787 – 10 757 kg ha^{-2} in the sainfoin-grass mixtures compared to 2161 – 9427 kg ha^{-2} in the alfalfa-meadow bromegrass mixtures), and species compatibility for use in the western Canadian beef industry. 'Melrose' with crested wheatgrass at a 30:70 seeding ratio performed well in the Dark Brown soil zone. 'Melrose' and 'AAC Mountainview' with crested wheatgrass at a 30:70 seeding ratio performed well in the Black soil zone. 'Melrose' and 'AAC Mountainview' with crested wheatgrass at a 50:50 seeding ratio performed well in the Brown soil zone. Seeding rate of sainfoin monocultures could be reduced by at least 50% while maintaining forage yields to reduce seed cost for producers.

125. The effects of nitrogen fertilizer stabilizers on the growth, yield, and feed quality of silage corn in a boreal climate

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The application of nitrogen (N) fertilizer in agricultural production systems is lost approximately more than 50% to environment; thus, leading to an increase in cost of crops production, greenhouse gas emission and environmental pollution. Intensive agriculture production demands substantial N fertilizer application to boost yield but pose higher risks of N losses. Urease and nitrification inhibitors (UI and NI, respectively) are known to reduce N losses, synchronize N release, plant N uptake, and consequently enhance growth, biomass, and crop yield. A two-year field experiment was conducted to evaluate the effects of urea stabilized with UI [N-(n-butyl) thiophosphoric triamide (NBPT)] and NIs [nitrapyrin and dicyandiamide (DCD)] on the growth, yield, and quality of silage corn. Experimental treatments were: 1) urea (UR); 2) SuperU™ (SU, urea with DCD and NBPT); 3) Agrotain™ (AG, urea with NBPT); 4) eNtrench™ (EN, urea with nitrapyrin); and 5) No-N as control (CTRL). Results indicated that N fertilized treatments increased chlorophyll content and crop yield by 42 – 46% and 102 – 159% respectively compared to CTRL. SU produced 21% greater yield than UR, although it was not statistically significant. Crude protein, acid detergent fibre, starch, and minerals did not show significant responses to fertilizer stabilizers. However in the second year, SU increased the net energy of lactation (NEL) by 7% compared to CTRL. Based on current findings, SU could be used as potential N stabilizer to enhance yield and NEL in boreal climate. Further studies to confirm long-term responses from a wider range of forage crops are recommended.

126. Estimating the plant characteristics of cicer milkvetch (*Astragalus cicer* L.) using a remote sensing approach

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Stockpile grazing perennial forage can provide cattle with nutritious forage at a low cost during the fall and early winter. Cicer milkvetch (*Astragalus cicer* L.) is a perennial forage legume well suited to stockpile grazing in the moist areas of the Canadian Prairies because of its consistent yield and high nutritional value. Developing remote sensing tools to identify superior breeding populations could accelerate the development of new varieties of cicer milkvetch. The objective of this study was to compare the capacity of remote sensing green area estimates based on either a thresholded normalized difference vegetation index (NDVI) or a Blue-NDVI to estimate the stem length, forage yield, and rhizome spread of cicer milkvetch. Data was recorded at the stockpile harvest date in mid-October of 2020 on a cicer milkvetch nursery containing 27 populations arranged in a completely randomized design with two to three replications per population. Blue-NDVI was more highly correlated than NDVI with the stem length, forage yield, and rhizome spread of cicer milkvetch. Forage yield had the highest correlation with Blue-NDVI (Pearson's Correlation Coefficient [PCC]= 0.76, $p<0.001$), rhizome spread had the lowest correlation (PCC = 0.41, $p<0.001$), and stem length was an intermediate value (PCC=0.54, $p<0.001$). A remote sensing based green area estimate from a thresholded Blue-NDVI is effective at predicting the stem length, forage yield, and rhizome spread of cicer milkvetch and with further research could be an effective breeding tool.

Abstracts

Session 24. Student poster flash-talks: Progress in Plant Health

127. Effects of fertility management on the phenological development of dual-purpose intermediate wheatgrass and impact on grain yield and forage quality characteristics Ⓟ

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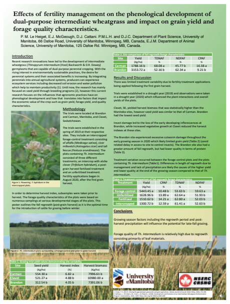

Intermediate wheatgrass (IWG; *Thinopyrum intermedium* (Host) Barkworth & D.R. Dewey) is a well-established perennial forage that has been developed more recently for grain yield. However maximum yield potential under western Canadian growing conditions has not yet been achieved. An in-depth understanding of phenological development of the crop may be used to establish optimal management practices, leading to greater overall yield potentials, increasing the potential return for producers. In two grain production experiments, this study evaluated phenological development of IWG across the Prairie region In Exp 1. small plot sites were established in MB (Carman, Brandon) and SK (Clavet) in 2019 and harvested in 2020. Treatments were: 1) non fertilized control (IWG only), 2) IWG with post-harvest fertility, 3) IWG intercropped with alsike clover, and 4) a forage control. Experiment 2, established in 2017 at Carman, had a fall, spring, split fall/spring and no fertility applications since 2018. After reproductive induction, tillers were sampled and measured to evaluate crop development in all Manitoba experiments. Grain yield was taken in 2020 and forage yield in fall of 2019. Drought conditions in 2020 impacted yield potential, however grain yield was higher for fall fertilized treatments compared to spring fertilized and unfertilized treatments. Forage control yielded higher biomass with generally higher fibre concentrations and lower Relative Feed Values than plots including IWG. Trials in Exp. 1 were in the first reproductive year and fertility treatments were not applied until after grain harvest, therefore variation amongst some treatments was the result of environmental variability.

128. Nutritive value of sainfoin (*Onobrychis viciifolia* Scop.) and grass mixtures for forage production in western Canada Ⓟ

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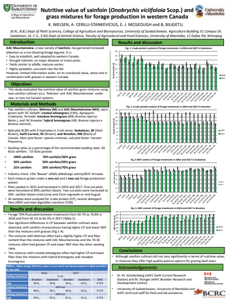

The objective of this study was to evaluate the nutritive value of sainfoin-grass mixtures using two sainfoin cultivars (cv.), 'Melrose' and 'AAC Mountainview'. They were evaluated as monocultures and in mixtures with three grass species, crested wheatgrass (*Agropyron cristatum* L.) cv. 'AC Goliath', meadow bromegrass (*Bromus riparius* Rehm.) cv. 'Armada', and hybrid bromegrass (*Bromus riparius* x *Bromus inermis*) cv. 'AC Knowles', under one (80% bloom)- and two (50% bloom and 25cm regrowth)-cut harvests at Swift Current, SK, Saskatoon, SK, and Brandon, MB. Plots were established in 2015 with sampling in 2016 and 2017. Samples were analyzed for crude protein (CP), neutral detergent fibre (NDF) and total digestible nutrients (TDN). Few significant differences in CP between sainfoin cultivars were observed, with sainfoin monocultures having higher CP and lower NDF than the mixtures with grasses. The mixtures with Melrose often had a slightly higher CP and fiber content than the mixtures with AAC Mountainview, and the 70:30 mixtures often had greater CP and lower NDF than the other seeding rates. The mixtures with crested wheatgrass often had higher CP and lower fiber than the mixtures with hybrid bromegrass and meadow bromegrass. Forage TDN fluctuated between treatments from 39.7% to 70.8% in 2016 and from 50.1% to 65.5% in 2017. Regardless of the mixture, pure sainfoin tended to be among the highest ranked for TDN overall. In conclusion, although sainfoin cultivars did not vary significantly in regard to their nutritive value, in mixtures they offer high quality pasture options for grazing beef cows.

129. Potential of dairy digestate as a biofertilizer: Effects on growth, yield and phytochemical profile of lettuce in hydroponics

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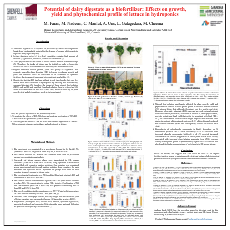

Lettuce (*Lactuca sativa* L) is a leafy vegetable containing an immense variety of minerals, vitamins and health-promoting secondary metabolites which are required for normal functioning of human health. Anaerobic dairy digestate (DD) contains mineral nutrient and proportionately higher ammonium-N (NH_4^+-N) compared to undigested materials, and therefore has the potential to be used as a mineral nutrient source in soil based and soilless culture. A pilot study was conducted to investigate the effects of anaerobic DD, inorganic nutrient solution (NS) and combine application of DD and NS on the growth, yield, and phytochemical profile of lettuce in hydroponics under controlled environment conditions. Experimental treatments were: 1) DD alone, 2) modified Hoagland solution (NS), 3) DD 50% + NS 50% (based on total N in DD) and replicated three times. DD used in this study was diluted ten times to reduce NH_4^+-N toxicity. Results showed that DD solution produced lower LA, chlorophyll contents, root dry weight, lettuce fresh biomass/yield and minerals and vitamins compared to NS. However, DD produced significantly higher concentration of phenolics (chicoric acid, chlorogenic acid, luteoline, quercitin-3-β-d-gluconide, quercitin-3-glucoside and quercitin-β-malonyl) and antioxidants. Romaine lettuce showed superior agronomic performance and produced higher LA, chlorophyll contents, root dry weight, yield, minerals, vitamins, total phenolics, total antioxidants and polyphenols than Newham. Based on results, we suggest that DD could be used as an organic fertilizer/nutrient source to sustain growth, yield, and enhanced phytochemical profile of lettuce in hydroponics under controlled environmental conditions.

130. Alternative products for management of Cercospora leaf spot (*Cercospora beticola* Sacc.) of sugarbeet (*Beta vulgaris* L. spp. *vulgaris*)

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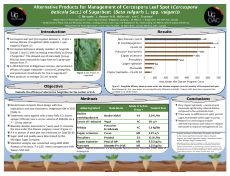

Cercospora beticola Sacc., causal agent of Cercospora leaf spot (CLS), is one of the most serious foliar pathogens of sugarbeets (*Beta vulgaris* spp. *vulgaris*). Resistance to FRAC Group 1 and 11 fungicides and increasing insensitivity to Group 3 fungicides challenge CLS management in Ontario. The active ingredient mancozeb, has been an important fungicide in standard spray programs, but has been re-evaluated with fewer applications permitted due to safety concerns. Evaluation of alternative fungicides is needed to identify mancozeb replacements. Potassium bicarbonate and phosphites showed potential in managing CLS of sugarbeets in a 2019 field trial. These alternative fungicides and the registered fungicides mancozeb, copper octanoate, *Bacillus amyloliquefaciens*, and copper hydroxide, with and without canola oil spray adjuvant, were evaluated in a field experiment at Ridgetown, Ontario in 2020. Applications occurred on a 7 to 10-day calendar schedule. CLS intensity was moderate; disease severity in the non-treated control was 27% on the final assessment date. The area under the disease progress curve (AUDPC) was lower in the mancozeb, copper hydroxide, and copper hydroxide + canola oil treatments than the non-treated control. Phytotoxicity was observed in plots treated with copper hydroxide and copper hydroxide + canola oil. No differences were found among treatments for the percent sugar recovered, beet yield, or sugar purity, possibly because of the relatively low disease pressure. This trial will be repeated in 2021 to confirm the results. Concurrent research on fungicide programs integrating these new tools is expected to provide growers with more options to combat CLS.

131. Assessing fungicide efficacy for improved management of the wild blueberry foliar disease complex in eastern Canada

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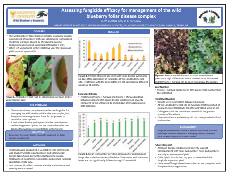

The wild blueberry foliar disease complex, comprised of blueberry leaf rust (*Thekospora minima*), Sphaerulina leaf spot (*Sphaerulina* vaccinii) and Valdensinia leaf spot (*Valdensinia heterodoxa*), significantly reduce yields when left unmanaged in the vegetative year of production. The once widely used chlorothalonil is no longer being used by many growers due to its deregistration in the European Union. Therefore, the objective of this study was to evaluate registered and future fungicide options for their impact on foliar diseases, leaf number and floral bud number. Field trials conducted in Collingwood Corner and Londonderry (Nova Scotia) consisted of ten treatments: untreated, mefentrifluconazole, mefentrifluconazole + fluxapyroxad, mefentrifluconazole + pydiflumetofen, pydiflumetofen, pydiflumetofen + difenoconazole, prothioconazole, fluopyram + prothioconazole, prothioconazole + benzovindiflupyr, and prothioconazole + pydiflumetofen. Mefentrifluconazole and pydiflumetofen are currently not registered for use on wild blueberries in Canada but, can are expected to be available within the next few years. Disease pressure was significantly higher at the Londonderry location. At both locations prothioconazole + benzovindiflupyr treatments recorded the highest leaf number, with prothioconazole + benzovindiflupyr and prothioconazole + pydiflumetofen treatments resulting in lowest disease incidence. At the Londonderry location, the untreated treatment had the lowest floral bud number. This study demonstrates that the current industry standard tank mix of prothioconazole + benzovindiflupyr offers the greatest control of foliar diseases. Furthermore, this study has also shown that pydiflumetofen combined with prothioconazole can be considered part of the foliar disease management strategy once pydiflumetofen is registered for use on wild blueberries in Canada.

Session 25. Student poster flash-talks: Plant Health and Resilience

132. *In vitro* screening of different forest tree species residues for their antifungal/antibacterial activity against strawberry pathogens

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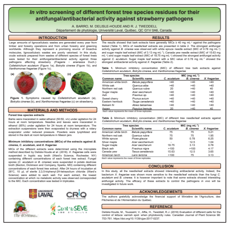

Large amounts of lignocellulosic wastes are generated every year from timber and forestry operations and from urban forestry and greening worldwide. Although they represent a promising source of bioactive molecules, lignocellulosic wastes are poorly valorised. In this study, crude extracts prepared from wastes (barks, needles, or leaves) of different species of forest trees were tested for their antifungal/antibacterial activity against three pathogens affecting strawberry (*Fragaria* × *ananassa* Duch.): *Botrytis cinerea* Pers., *Colletotrichum acutatum* J.H. Simmonds, and *Xanthomonas fragariae* Kennedy & King. Minimal inhibitory concentrations (MICs) of the crude extracts were determined using standard procedure. The strongest antifungal activity against *B. cinerea* was observed with white spruce [*Picea glauca* (Moench) Voss] needle extract while Canada yew (*Taxus canadensis* Marsh.) needle extract and sugar maple (*Acer saccharum* Marsh.) leaf extract showed the strongest antifungal activity against *C. acutatum*. Sugar maple leaf extract with a MIC value of 0.78 mg/mL showed the strongest antibacterial activity against *X. fragariae*. The efficacy of these extracts to control the pathogens *in vivo* will be investigated in future work.

133. Effect of *Brassica napus* seedling age at time of inoculation on fusarium wilt severity

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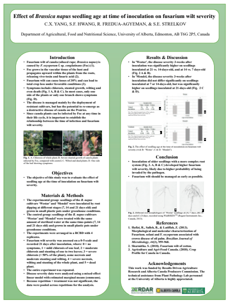

Fusarium wilt is a widespread vascular fungal disease caused by the soilborne pathogen *Fusarium oxysporum*. In Canada, fusarium wilt was first reported on canola (oilseed rape; *Brassica napus*) in 1999 in northeast Alberta, becoming more severe after 2002. At present, fusarium wilt is managed mainly by the deployment of resistant cultivars, but has the potential to re-emerge as a destructive disease of canola on the Prairies. The objective of this study was to evaluate the effect of seedling age at the time of inoculation on fusarium wilt severity. Seedlings of the *B. napus* cultivars 'Westar' and 'Mendel' were inoculated at different stages (7, 14 and 21 days old) under greenhouse conditions. Fusarium wilt severity was assessed on a 0-5 scale, where: 0 = no symptoms, 1 = mild chlorosis of one leaf, 2 = moderate chlorosis and stunting of one to two leaves; 3 = severe chlorosis (> 50% of the plant), some necrosis and moderate stunting and wilting, 4 = severe necrosis, wilting and stunting of the whole plant, and 5 = dead plant. The disease severity data were analyzed using a mixed-effect linear model with estimated marginal means, which showed that seedlings inoculated at 21 days old developed the highest disease severity, while those inoculated at 7 days had the lowest disease severity for both cultivars. These results suggest that fusarium wilt is more severe when older seedlings are inoculated with *F. oxyporum*.

134. The effect of plant age on the susceptibility of American ginseng (*Panax quinquefolius* L.) to replant disease

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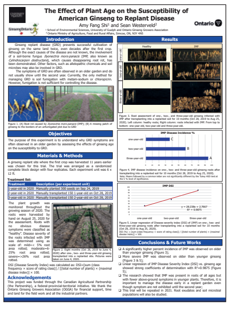

Ginseng replant disease (GRD) prevents successive ginseng cultivation on the same land without considerable crop losses. Although the cause of GRD is not fully understood, a fungal pathogen *Ilyonectria mors-panacis* (IMP) is known to be involved. The symptoms of GRD are often not observed until plants in replanted gardens are older. To understand whether this is due to progressive development of the disease over time or if older plants are more susceptible, three ages of ginseng were manually transplanted in fall 2019 from newly planted gardens to a replanted site where ginseng was harvested 10 years earlier. The trial was arranged in a randomized, complete block design with four replications. Foliar symptoms caused by IMP started to show on older plants in late July, nine months after transplanting. A root assessment was conducted to analyze disease incidence and severity in late August 2020. The Disease Severity Index (DSI) increased linearly with increasing age (R^2=0.9875). The results suggest that older plants are more susceptible to GRD. *Ilyonectria mors-panacis* was present in roots of all ages but younger plants displayed fewer symptoms. Therefore, it is important to manage GRD early in a replant garden even though obvious disease symptoms may not be present until the second year.

135. Seed germination responses to low-intensity monochromatic light spectra for 14 ornamental plant genotypes

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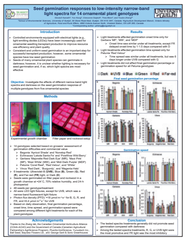

Electric lights are increasingly being used for transplant production in controlled environments. However, for seed germination, it is unclear whether lighting is necessary and what monochromatic light spectra are effective. Multiple ornamental genotypes from begonia, echinacea, gerbera, petunia, and vinca were germinated under red (R), blue (B), green (G), far-red (FR), ultraviolet-B (UVB) light, or darkness. Light-emitting diode fixtures provided the aforementioned monochromatic lights, except for UVB, which was sourced from narrow-band fluorescent light. The average photon flux density at seed level was ≈18 µmol m^{-2} s^{-1} for R, B, G and FR, and 0.4 µmol m^{-2} s^{-1} for UVB. Based on daily records, final germination percentage, onset time, time spread, and germination speed were compared among different light treatments for each of the plant genotypes. There were no promotive effects on final germination percentage, onset time, and time spread, under monochromatic lights compared to darkness. FR inhibited seed germination relative to darkness by reducing final germination percentage, delaying onset time, or decreasing germination speed in some genotypes. Under R, G, and UVB, compared to darkness, germination speed was increased for begonia 'Apricot Shade', a light-requiring genotype, and inhibited for vinca 'Burgundy', a light-inhibited genotype. Therefore, lighting is unnecessary for seed germination of the tested species except light-requiring genotypes, where R, G, and UVB are the most promotive among the monochromatic lights.

136. Efficacy of *Bacillus pumilus* and *Bacillus subtilis* to control gray mold on tomato and cucumber plants grown in greenhouse

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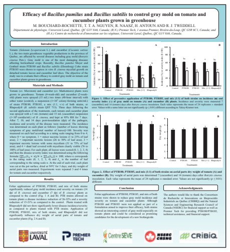

Gray mold (*Botrytis cinerea* Pers.) is one of the most damaging diseases affecting horticultural crops. Recent work reported the efficacy of *Bacillus pumilus* Meyer and Gottheil strain PTB180 and *Bacillus subtilis* (Ehrenberg) Cohn strain PTB185 to repress *in vitro B. cinerea* mycelial growth on detached tomato (*Solanum lycopersicum* L.) leaves and cucumber (*Cucumis sativus* L.) leaf discs. The objective of the study was to evaluate their efficacy to control gray mold on tomato and cucumber plants grown in greenhouse. Tomato and cucumber plants were sprayed two times (48 hours interval) with either water (control), a suspension (1×10^7 colony-forming units/mL) of strain PTB180, PTB185, a mix (1:1, v:v) of both strains, or Rhapsody® (*B. subtilis* strain QST 713). Three days following the second application of the treatments, each plant was sprayed with a suspension (1×10^6 conidia/mL) of *B. cinerea*. On days 7, 10, and 14 post-inoculation of the pathogen, incidence and severity of the disease were measured. Foliar applications of PTB180, PTB185, and mix (1:1) of both strains were shown to significantly reduce gray mold incidence and severity on tomato and cucumber plants as compared to the control. The efficacy of the strains PTB180 and PTB185 was compared with that of the Rhapsody®.

137. Screening for potential biological control agents against *Allorhizobium vitis*, the causal agent of crown gall disease of grapevine

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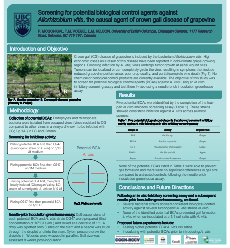

Crown gall disease of grapevine is an economically important disease in cold-climate grape growing regions around the world. The disease is characterized by its severe detrimental effect on grapevine performance and crop quality. Partial or complete vine death is common, especially in young vines. The causal agent of grapevine crown gall is the soil-dwelling bacterium *Allorhizobium vitis,* which can be introduced into vineyard soil via infected planting material. Current cultural management practices are often not effective and there are currently no commercial biocontrol products available. In this study, endophytic and rhizosphere bacteria collected from escaped vines (vines resistant to disease symptoms) in crown gall-diseased vineyards in British Columbia and Ontario were screened for inhibitory activity against several strains of *A. vitis.* The inhibitory screening assay employed consisted of four separate screens, each included to reduce the number of potential bacterial isolates to be used in subsequent greenhouse assays. Two separate media were included as antibiosis may be culture medium dependent. Five bacterial isolates that showed consistent inhibitory activity against *A. vitis* across all screens were identified as potential biological control agents. Three isolates were classified as *Bacillus* spp. and two were classified as *Pseudomonas* spp. Species within these genera have previously shown biological control activity against several plant pathogens. Simultaneous inoculation of *A. vitis* and each of the potential biological control agents identified in this study at a 1:1 ratio did not result in gall reduction compared to untreated controls. Further studies are currently being conducted.

138. Competition between *Plasmopara viticola* clade *aestivalis and* clade *riparia:* who can win the aggressiveness battle

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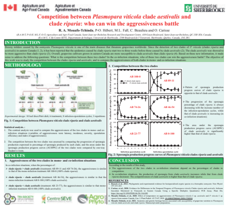

Since the evidence of the existence of two clades of *Plasmopara viticola* (clades *riparia* and *aestivalis*) in eastern Canada, it has been reported that epidemics caused by clade *riparia* start two to three weeks before those caused by clade *aestivalis*, however, clade *aestivalis* was more aggressive than clade *riparia*. The objective of this work was to study the competition between the clades *riparia* and *aestivalis,* and to compare the aggressiveness of both clades in mono- and co-infection situations. Solutions of sporangia from both clades were co-inoculated in six percentage combinations on leaf discs. Subsequently, the progression of sporangia production expressed as sporangia percentages (SP) was estimated after eight cycles of infection-sporulation. The aggressiveness of clades in mono-infection situations on leaf discs was then compared to that in co-infection situations. The results show that the percentage of sporangia produced by clade *aestivalis* increases with the infection-sporulation cycle, while that produced by clade *riparia* decreases. The aggressiveness of the clades *riparia* and *aestivalis* in co-infection situations were different from those in mono-infection situations and were strongly influenced by the SP of the clades in competition. These results suggest that *P. viticola* clade *aestivalis* is more competitive than clade *riparia* and that the management of downy mildew in eastern Canada should consider the percentages of each clade present in the vineyard. Even though these results raise new questions, they should be considered for the management of grape downy mildew.

Abstracts

139. Virulence structure of wheat powdery mildew population and effective resistance genes for Ontario in 2018 and 2019

A. G. XUE, S. LIM, Y. CHEN, G. HUMPHREYS, W. CAO, J. MENZIES, C. COWGER, H. LI AND M. SERAJAZARI. *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada (AAFC), 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; (J.M.) Morden Research and Development Centre, AAFC, 101 Route 100, Morden MB R6M 1Y5, Canada; (C.C.) USDA-ARS, Department of Entomology and Plant Pathology, North Carolina State University, Raleigh, NC 27695, USA; (H.L.) National Engineering Laboratory for Crop Molecular Breeding, Institute of Crop Sciences, Chinese Academy of Agricultural Sciences, Beijing 100081, China; (MS) Plant Agriculture, University of Guelph, Guelph, ON N1G 2W1, Canada.*

Powdery mildew caused by *Blumeria graminis* f. sp. *tritici* (Bgt) is a major disease of wheat (*Triticum aestivum*) in Ontario, which can cause up to 20% yield loss. The development of resistant commercial wheat cultivars is the most economical means of controlling this disease, but only if the resistance genes used are incompatible with the virulence phenotypes present in the pathogen population. The virulence structure of Bgt in Ontario was examined in 2018 and 2019. Of the 42 single colony isolates collected in Ontario greenhouses and commercial fields, 40 virulence phenotypes, assigned as VP1 to VP40, were identified on a set of 24 single-gene differential genotypes. Of the 24 resistance genes possessed by the differential genotypes, eight genes, namely, Pm1a, Pm1b, Pm1c, Pm12, Pm16, Pm21, Pm37, and MlAG12 were effective against all of the Bgt isolates. Four genes, Pm3d, Pm29, Pm34, and NCAG13, were mostly effective, with resistance reactions to more than 80% of the isolates. No significant differences in the numbers of virulence genes per isolate were found between the two years or between the greenhouse and field origins. The virulence frequencies of Bgt isolates for these effective and most effective genes were not significantly affected by the year of collection or their origin, suggesting that the Bgt population is relatively stable. The effective genes identified in this study may be deployed singly or used for gene pyramiding to develop powdery mildew-resistant cultivars in Ontario.

140. Genetic diversity of *Wheat streak mosaic virus* in the wheat growing region of Western Canada

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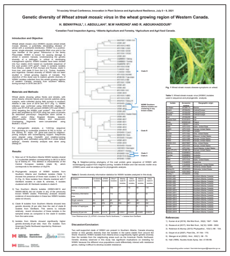

Wheat streak mosaic virus (WSMV) is a positive-sense, single-stranded, monopartite RNA virus and is the type member of the genus *Tritimovirus* in the family *Potyviridae*. WSMV is known for causing damage to wheat in western Canada, the most recent outbreak occurred in southern Alberta and Saskatchewan in 2016-17. Understanding the genetic diversity of a pathogen is critical in developing management options. WSMV isolates have been divided into four clades (A-D) based on nucleotide sequence of the coat protein (CP) gene. Clade A contains isolates from Mexico, clade B from Europe and Russia, clade C from Iran, and clade D from the U.S., Turkey, Australia, and Argentina. The objective of this study was to explore genetic diversity of WSMV isolates collected from the wheat growing regions of western Canada, primarily from southern Alberta, during 2016 - 2017. Phylogenetic analysis of 16 isolates and the isolates available in GenBank was performed using the 1,043-bp sequence corresponding to nucleotide positions 8,192 to 9,234 of the Sidney 81 strain coat protein gene using neighbour-joining analysis with bootstrapping support. Nine isolates clustered in clade B while five in clade D. Two isolates that did not cluster in known WSMV clades showed evidence of recombination. Among the local isolates investigated in this study, more polymorphic sites, parsimony informative sites, and increased diversity were observed in clade D isolates than clade B, suggesting more recent establishment of the virus in the latter. The observed diversity of WSMV could pose challenges to breeding durable resistance in wheat.

141. Factors affecting microspore-based doubled haploid production in winter wheat

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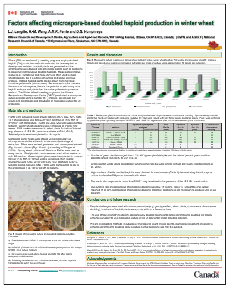

Wheat (*Triticum aestivum* L.) breeding programs often employ doubled haploid production methods to shorten the time required to develop new varieties. Haploid plants are generated and the chromosomes are then doubled with anti-mitotic agents such as colchicine to create fully homozygous doubled haploids. The maize pollen/embryo rescue technique is frequently used to make wheat haploids, but it is a time consuming and labour intensive process. Alternatively, haploid plants can be grown from individual immature pollen cells (microspores). Microspore culture has the potential to yield many more haploid embryos and plants than the maize pollen/embryo rescue method. The Winter Wheat breeding program at the Ottawa Research and Development Centre (ORDC) evaluated a microspore culture protocol using a number of F_1 crosses. The number of green plantlets per spike ranged from 49 plants to 1 plant and the ratio of green to albino haploid plantlets observed varied from 83% to 9% depending on genetic background. Putative spontaneous chromosome doubling of plants was 11% to

26%, also depending on genetic background. Hence, colchicine treatments are still required for chromosome doubling. Research is underway to attempt to improve chromosome doubling *in vitro*. Because hundreds of haploids can be produced with relatively less effort compared to the maize pollen/embryo rescue method, microspore culture should be a useful tool in the winter wheat breeding program.

142. Improving clubroot resistance in canola through CRISPR/Cas9 based genome editing technology

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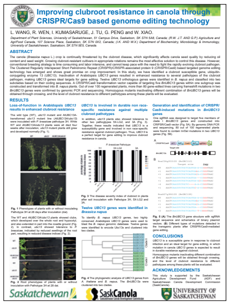

Improving clubroot resistance in canola through CRISPR/Cas9 based genome editing technology

L. WANG, R. WEN, I. KUMASARUGE, J. TU, G. PENG and W. XIAO.

Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada; (R.W. J.T. AND G.P.) Agriculture and AgriFood Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada; (I.K. AND W.X.) Department of Biochemistry, Microbiology & Immunology, University of Saskatchewan, Saskatoon, SK S7N 5E5, Canada.

ABSTRACT

RESULTS

Loss-of-function in Arabidopsis *UBC13* results in enhanced clubroot resistance

UBC13 is involved in durable non race-specific resistance against multiple clubroot pathotypes

Generation and identification of CRISPR/Cas9-induced mutations in *BnUBC13* genes

Twelve *UBC13* genes were identified in *Brassica napus*

CONCLUSIONS

ACKNOWLEDGEMENTS

The canola (*Brassica napus* L.) crop is continually threatened by the clubroot disease, which significantly affects canola seed quality by reducing oil content and seed weight. Growing clubroot-resistant cultivars in appropriate rotations remains the most effective solution to control this disease. However, conventional breeding strategy is time consuming and labor intensive, and cannot keep pace with the need to fight the rapidly evolving clubroot pathogen. The Clustered Regularly Interspaced Short Palindromic Repeat (CRISPR)/CRISPR-associated protein 9 (CRISPR/Cas9) based targeted genome editing technology has emerged and shows great promise on crop improvement. In this study, we have identified a clubroot susceptible gene, *ubiquitin-conjugating enzyme 13* (*UBC13*). Inactivation of Arabidopsis *UBC13* genes resulted in enhanced resistance to several pathotypes of the clubroot pathogen, making *UBC13* genes ideal targets for gene editing, Twelve *UBC13* orthologous genes were identified in *B. napus* and classified into two subgroups based on their coding sequences. A CRISPR/Cas9 transformation vector capable of targeting five *BnUBC13* genes within one subgroup was constructed and transformed into *B. napus* plants through an *Agrobacterium*-mediated canola transformation system. Out of over 100 regenerated plants, more than 80 gene-edited lines carrying frameshift mutations in four *BnUBC13* genes were confirmed by genomic PCR and sequencing. Homozygous mutants inactivating different combination of *BnUBC13* genes will be obtained through crossing, and the level of clubroot resistance to different pathotypes among these plants will be evaluated.

143. A *Wheat tandem kinase 1* (*Wtk1*) confers resistance to stripe rust as previously described as *Yr15*, *YrG303*, and *YrH52*

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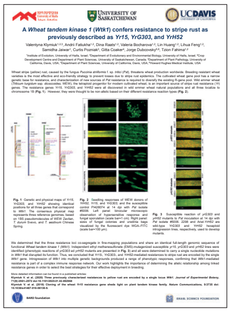

A *Wheat tandem kinase 1* (*Wtk1*) confers resistance to stripe rust as previously described as *Yr15*, *YrG303*, and *YrH52*

Valentyna Klymiuk[1,2,3], Andrii Fatiukha[1,2], Dina Raats[1,2], Valeria Bocharova[1,2], Lin Huang[1,2], Lihua Feng[1,2], Samidha Jaiwar[1], Curtis Pozniak[3], Gitta Coaker[4], Jorge Dubcovsky[5,6], Tzion Fahima[1,2]

[1]Institute of Evolution, University of Haifa, Israel; [2]Department of Evolutionary and Environmental Biology, University of Haifa, Israel; [3]Crop Development Centre and Department of Plant Sciences, University of Saskatchewan, Canada; [4]Department of Plant Pathology, University of California, Davis, USA; [5]Department of Plant Sciences, University of California, Davis, USA; [6]Howard Hughes Medical Institute, USA

Wheat stripe (yellow) rust, caused by the fungus *Puccinia striiformis* f. sp. *tritici* (*Pst*), is a disease that threatens wheat production around the globe. Breeding resistant wheat varieties is required to prevent losses due to stripe rust epidemics; this is accomplished using various sources of *Pst* resistance to widen and diversify the existing R-gene pool. Wild emmer wheat (*Triticum turgidum* ssp. *dicoccoides*), the undomesticated tetraploid progenitor for modern cultivated wheat, is an important source of stripe rust resistance (*Yr*) genes. The resistance genes named *Yr15*, *YrG303*, and *YrH52*, discovered in wild emmer wheat natural populations, all localize to chromosome 1B but were thought to be non-allelic based on their different resistance reaction types. Here we showed that these three resistance loci co-segregate in fine-mapping populations and share an identical full-length genomic sequence of functional *Wheat tandem kinase 1* (*Wtk1*). Independent ethyl methanesulfonate (EMS)-mutagenized susceptible *yr15*, *yrG303* and *yrH52* lines carried single nucleotide mutations in *Wtk1* that disrupted its function. Thus, we concluded that *Yr15*-, *YrG303*-, and *YrH52*-mediated resistances to stripe rust are encoded by the single *Wtk1* gene. Introgression of *Wtk1* into multiple genetic backgrounds produced a range of phenotypic responses, confirming that *Wtk1*-mediated resistance is part of a complex immune response network. Our work highlights the importance of determining the allelic relationship among linked resistance genes in order to select the best strategies for their effective deployment in breeding.

144. Identification and diagnosis of plant pathogenic nematodes

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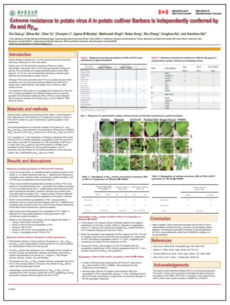
Abstract withdrawn

145. Extreme resistance to potato virus A in potato cultivar Barbara is independently conferred by *Ra* and Ry_{sto}

W. HUANG, B. NIE, Z. TU, C. LI, A. MURPHY, M. SINGH, B. SONG, S. ZHANG, C. XIE AND X. NIE. *Key Laboratory of Horticultural Plant Biology, Huazhong Agricultural University, Wuhan 430070, China; (A.M., X. N.) Fredericton Research and Development Centre, Agriculture and Agri-Food Canada, Fredericton, New Brunswick, Canada E3B 4Z7; (M.S.) Agricultural Certification Services, Fredericton, New Brunswick, E3B 8B7 Canada.*

Abstracts



Extreme resistance to potato virus A in potato cultivar Barbara is independently conferred by *Ra* and Ry_{sto}

Wei Huang[1], Bihua Nie[1], Zhen Tu[1], Chunyan Li[1], Agnes M Murphy[2], Mathuresh Singh[3], Botao Song[1], Shu Zhang[1], Conghua Xie[1], and Xianzhou Nie[2*]

Potato virus A (PVA) and potato virus Y (PVY), both belonging to the genus *Potyvirus* (family *Potyviridae*), are two of the most economically important viruses of potato worldwide. Host resistance offers the most effective means for the control and management of the viruses. In this study, 20 potato clones (cultivars) were screened for their resistance against PVA and PVY by mechanical and/or graft inoculation assay. Six clones, including Barbara, Jizhangshu 8, Longshu 7, Longshu 8, M6, and Solara, were found to be extremely resistant to both PVA and PVY; three clones (AC142, Eshu 3, and Shepody) were deemed to be extremely resistant to PVA but susceptible to PVY. To further reveal the inheritance of the extreme resistance (ER) against PVA, a tetraploid F_1 population of Barbara × F58050 and a tetraploid BC_1 population of BF145 (a PVA-resistant but PVY-susceptible progeny of Barbara × F58050) × F58050 were obtained and analyzed. Based on the phenotype of all progenies, two independent loci were found to control ER against PVA in Barbara: one (i.e., *Ry*) confers ER to both PVA and PVY, and the other (i.e., *Ra*) confers ER to PVA only. The deduced genotype of Barbara is *RyryryryRarararara*.

146. Genomic methylation levels appear adverse effect on total phenolic content between in vitro and greenhouse grown lingonberry (*Vaccinium vitis-idaea*)

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Abstract Withdrawn

147. Antimicrobial peptides display a potent activity against common fungal pathogens: A promising supplement in plant disease management

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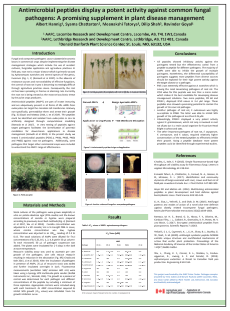

Antimicrobial peptides display a potent activity against common fungal pathogens: A promising supplement in plant disease management

Albert Hannig[1], Syama Chatterton[2], Meenakshi Tetorya[3], Dilip Shah[3], Ravinder Goyal[1]

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Plant disease management relies heavily on fungicides, especially where germplasm resistance is either weak or associated with unfavorable agronomic traits. Persistence application of fungicides often leads to insensitivity requiring a higher concentration for effectiveness, and a breakdown of protection needs a new formulation of fungicides. The evidences are emerging that fungicides negatively affect some of the beneficial microbial activity in soil, and the consequences of chemical residues in food and feed are yet to be fully determined. For climate preservation, there is a necessity to explore environmental-friendly alternatives. Antimicrobial peptides (AMPs) are an important component of innate immunity in living organisms that confers protection against biotic stresses. AMPs are short molecules (< 100 amino acids) which are highly potent at low concentrations against a wide range of pathogens. In this study, we assessed the antimicrobial activity of both the natural and synthetic AMPs against important fungal and oomycetes pathogens. An inhibitory concentration to reduce the pathogen growth by 50% (IC_{50}) and a minimum inhibitory concentration (MIC) for each peptide were determined through absorbance and resazurin-based cell viability assays. A direct incubation of AMPs with the pathogens resulted in the latter's reduced growth and the antimicrobial effect of an AMP was visible in multiple pathogens. A variation in an AMP's IC_{50} value suggested a different level of pathogen susceptibility. The AMPs with low IC_{50} values (<10uM) hold a great promise to develop them as biopesticides for foliar applications. Among the peptides tested, PD 30.1 and PN43 showed IC_{50} values less than 0.5uM against *F. graminearum.* The other peptides displayed high toxicity against *F. culmnorum.* A work is in progress to evaluate *in plantae* effectiveness of AMPs.

148. Genome Wide Association Studies (GWAS) of Root System Architecture in Barley (*Hordeum vulgare* L.)

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Plant root system is responsible for anchoring of plant in the soil as well as acquisition and absorption of water and nutrients for productivity. Genetic studies of barley root system architecture traits using seedling roots are scanty. Identification of single nucleotide polymorphisms (SNP) associated with root system architecture traits would enable the selection of barley genotypes with better root system that might help to improve barley productivity. A panel of 284 barley genotypes was phenotyped for seedling root architecture (RSA) traits using the germination paper-based moisture replacement system, image capture units, and root-image processing software. Mixed linear model was employed to determine marker-trait associations. We have identified 104 RSA QTL with effect size ranging from 5.8 to 12% across barley genome. Chromosome 2 had 64 QTL, six of which ranked among the most significant and had the largest effects. The results will greatly improve our understanding of the genetics of root system architecture traits in barley. In addition, SNPs associated with these traits could be applied in breeding programs for marker assisted and genomic selection of seedling root traits to improve overall barley productivity.

149. How do single and combined genes work in resistant breeding to northern corn leaf blight?

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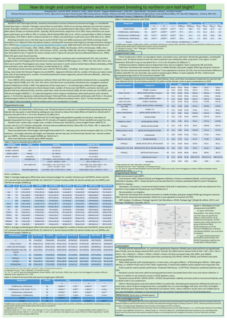

Breeding resistant corn (Zea mays L.) is the best way to control northern corn leaf blight. From 2006 to 2014, Htm1 and Htn1 were introgressed into susceptible inbred CO388, Ht1, Ht2, Ht3, Htm1, and Htn1 (Ht(s) were introgressed into polygenic (PG) resistant inbred CO428 and got PGHt(s). Both CO388 and CO428 families crossed with A619 family (A619, A619Ht1, A619Ht2, and A619Ht3) and other 7 testers, including T3 with partial resistance. From 2015 to 2017, three experiments were designed: to assess single and combined gene effects to three disease and four yield traits under artificial inoculation; to assess their effects under different inoculation times; and to find higher Yield and stability crosses and inbreds for corn production. Ht1, Ht2 and Ht3 reduced number of lesions per leaf (NLPL), Lesion size (LS), and percent leaf area affected (PLAA) >30%, Htm1 and Htn1 >20%. If both parents with resistant genes, (Htm1, Htn1)/(Ht1, Ht2, Ht3, Partial) and PGHt(s)/Ht(s) reduced NLPL, LS, and PLAA >50% and >39%, respectively. All single genes increased Yield, Kernel moisture, kernel number per ear and 100-kernel weight. Yield increased 7.5%, 21.1%, and 30.1% for females (Htm1 and Htn1), males (Ht1, Ht2, Ht3, and Partial), and their crosses, respectively. Additive action played a major role in most cases could be used to predict PLAA and yield. Linear regressions were found between four yield traits and PLAA. CO388 × A619 related resistant crosses had yield advantage >12% under twice inoculations. Three resistant crosses and four inbreds could be used in corn production.

150. Identification of Arabidopsis *Phospholipase A* knock-out mutants with increased susceptibility to *Plasmodiophora brassicae*

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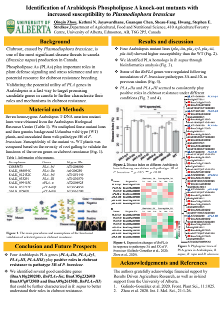

Clubroot, caused by the obligate parasite *Plasmodiophora brassicae*, is one of the most significant disease threats to canola (*Brassica napus*) production in Canada. The identification of novel genes that contribute to clubroot resistance is important for the sustainable management of this disease, as they may be used in the development of resistant canola cultivars. Phospholipase As (*PLAs*) play important roles in plant defense signaling and stress tolerance, and thus are attractive targets for crop breeding. However, since canola is an allopolyploid and has multiple copies of each *PLA* gene, it is time-consuming to test the functions of *PLAs* directly in this crop. In contrast, the model plant *Arabidopsis thaliana* has a simpler genetic background and only one copy of each PLA. Therefore, it would be reasonable and faster to validate the potential utility of *PLA* genes in Arabidopsis first. In this study, we identified seven homozygous T-DNA insertion *pla* knockout Arabidopsis mutants, and tested their performance following inoculation with *P. brassicae*. Five mutants (*pla1-IIα, pla1-Iγ3, pla1-III, spla2-a, pla-IIIβ, pla-IIIδ*) developed more severe clubroot than the wide-type, suggesting increased susceptibility to *P. brassicae*. The homologs of these *AtPLAs* in *B. napus* were identified through blast tools and phylogenic analysis. *BnPLAs* expression profiles were subsequently examined in transcriptomic datasets generated from canola infected by *P. brassicae*, and promising candidates will be selected for further characterization in canola.

151. Genotyping by sequencing analysis of *Fusarium poae* field populations affecting small grain cereals in Canada

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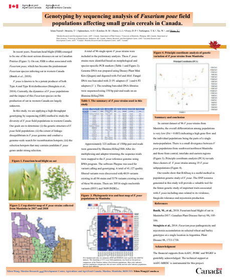

Fusarium head blight (FHB) is an important disease threatening the production of small grain cereals in Canada, reducing both the yield and quality of crops. Multiple species within the genus Fusarium cause mycotoxin contamination in FHB disease. *F. poae*, *F. graminearum*, and *F. sporotrichioides* are the most common species associated with FHB. In recent years, *F. poae* has become the predominant *Fusarium* species in commercial oat and barley fields in western Canada. Nevertheless, very little information is available on this pathogen's pathogenesis and genetic structure. To better understand the evolutionary processes affecting this pathogen, the restriction site-associated DNA sequencing and Illumina shotgun sequencing were used to conduct population genomics analyses using 198 Canadian *F. poae* isolate divided into 12 populations based on geographical origins and hosts specificity. The final filtered dataset included 2234 SNPs with a maximum of 2% missing data per SNP. The partitioning of the genetic variance within and among field populations using AMOVA revealed that 99.1 % of the total genetic variance was within field populations, and only 0.9 % was among populations. The corresponding overall Fixation index was 0.003, while pairwise differentiation between populations ranged from 0 to 0.033. These results indicate a high degree of gene flow and the individual populations in Canada being the parts of a single meta-population. We are currently utilizing these SNPs to study the structure of *F. poae* field populations in Canada, determine the extent of linkage disequilibrium, and identify hot spots in the *F.*

Abstracts

poae genome that may contain candidate genes under strong selection. Early detection of the potential genomic changes is critical to developed regional-scale management strategies for such an emerging FHB pathogen.

152. Applications of deep learning methods to genomic prediction in breeding wheat for fusarium head blight resistance

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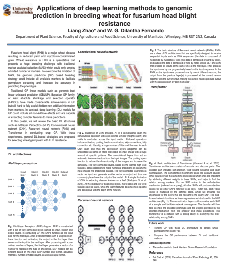

Fusarium head blight (FHB) is a major wheat disease resulting in reduced yield and mycotoxin-contaminated grain. *Fusarium graminearum*, by producing several trichothecene mycotoxins, is considered as the major etiological agent to wheat FHB. Wheat resistance to FHB is a quantitative trait which is controlled by many unique quantitative trait locus [QTLs; (Bai et al., 2018)]. Such a complex trait presents a huge breeding challenge with traditional marker-assisted selection (MAS) which could only employ a limited number of markers. To overcome the limitation of MAS, the genomic prediction (GP) based breeding strategy could include all available markers to facilitate germplasm screening and increase the accuracy in predicting phenotype. However, GP frequently faces statistical challenges given the unbalanced number between markers and plant individuals. Traditional GP linear models such as genomic best linear unbiased prediction (GBLUP), Bayesian GP family, or least absolute shrinkage and selection operator (LASSO) have made considerable achievements in GP but still hard to fully exploit hidden non-additive information from markers. In contrast, deep learning (DL) models for GP could include all non-additive effects and are capable of extracting complex features to make predictions. This is an interesting and promising strategy for polyploid plants. However, this method has not been widely applied in plant disease resistance identification, especially for wheat FHB. In this presentation, we will review the application of DL methods such as Convolutional neural network (CNN) and Transformers in conducting crop GP. With these experiences, a general DL-based strategy is proposed for selecting wheat germplasm with FHB resistance.

153. Potato mop-top virus, an emerging challenge to potato industry

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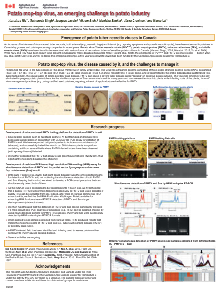

Potato mop-top virus (PMTV, genus *Pomovirus*, family *Virgaviridae*) is a soil-borne virus that causes a severe tuber disease called spraing, which is characterized by internal necrotic arcs or rings in infected potato tubers. The disease can result in significant economic losses to the potato industry when disease incidence becomes sufficiently high. Since its first discovery in North America in 2003, the virus has been reported in many potato production areas in USA and Canada. To unveil the occurrence of PMTV in Canada and to develop management strategies for the virus as well as other tuber necrotic viruses including tobacco rattle virus, alfalfa mosaic virus and potato virus Y strain NTN, a five-year study has been underway. An ongoing annual survey of potato tubers from Manitoba and New Brunswick suggests that PMTV is the primary virus responsible for virus-caused tuber necrotic diseases in both provinces. To facilitate the identification of PMTV-infested fields, a real-time PCR-based high resolution DNA melting (HRM) assay was developed for the simultaneous detection of PMTV and its protist vector, *Spongospora subterranea* f.sp. *subterranea* (Sss) in soil and for the identification of PMTV- and/or Sss-infested fields. Indeed, by using this method, several fields have been determined to be PMTV-infested, and one of them is being used for the trial of potato cultivar sensitivity to PMTV-induced spraing disease.

154. Sporulation potential of *Phytophthora ramorum* EU2 lineage on selected Canadian broadleaf and conifer tree species

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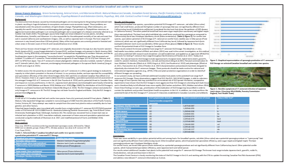

The invasive alien pathogen *Phytophthora ramorum* (Oomycetes) causes sudden oak death (SOD) in forests and Ramorum blight in nurseries, resulting in mortality of several forest species in western North America and Europe. Our previous investigation results based on the assessment of 33 Canadian trees, shrubs and landscape plants which were reported in the 7th SOD Science and Management Proceedings 2020, showed a large variation in aggressiveness and sporulation potential among the evaluated hosts. Since the sporulation potential of *P. ramorum* drives the epidemic of SOD, the objective of this study was to determine the most efficient inoculum reservoir of an isolate from the *P. ramorum* EU2 lineage on a selected sub-set of 11 tree species including red alder (*Alnus rubra*), bigleaf maple (*Acer macrophyllum*), California bay laurel (*Umbellularia californica*), sugar maple (*Acer saccharum)*, vine maple (*Acer circinatum*), Himalayan blackberry shrub (*Rubus armeniacus*), western hemlock (*Tsuga heterophylla*), western larch (*Larix occidentalis*), white spruce (*Picea glauca*), Sitka spruce (*Picea sitchensis*), and Japanese larch (*Larix kaempferi*). Detached leaves/needles of five conifer and six broadleaf species were inoculated with *P. ramorum* EU2 lineage mycelia isolated from a stream bait near an infected larch plantation in Scotland, UK. Of the 11 plants tested, red alder (*Alnus rubra*) had sporulation potential comparable to California bay laurel (*Umbellularia californica*) which drives the SOD epidemic in California forests. Sitka spruce (*Picea sitchensis*) and sugar maple (*Acer saccharum)* had moderate levels of sporulation. These results confirm the potential threat of the EU2 lineage of *P. ramorum* to Canadian flora.

155. A hydroponics based high throughput screening system for clubroot disease indexing

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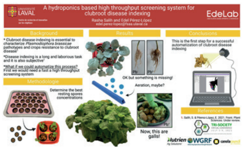
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A hydroponics based high throughput screening system for clubroot disease indexing

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EdeLab

Background

- Clubroot disease indexing is essential to characterize *Plasmodiophora brassicae* pathotypes and crops resistance to clubroot disease[1]
- Disease indexing is a long and laborious task and it is also subjective[1]
- What if we could automatize this process? First we would need a fast a high throughput screening system

Methodologie

Determine the best resting spores concentrations

Results

OK but something is missing!

Aeration, maybe?

Now, this are galls!

Conclusions

This is the first step for a successful automatization of clubroot disease indexing

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In recent years, clubroot has become one of the most devastating diseases affecting canola worldwide. Control of clubroot disease has proven to be very difficult to achieve. To this day, the best alternative is the use of resistant genotypes, but after one or two years of using certain clubroot resistant canola, resistance has been broken by different *P. brassicae* pathotypes. A very important step to identify which canola variety is the best for each field is the identification of the different pathotypes and how the plants respond to them. Pathotyping rely on the determination of disease index (DI) through a very laborious observational and subjective process that would benefit of digitalization. Selecting the appropriate growing conditions of the sample population is essential in selecting the suitable digital software. *P. brassicae* infection is conditioned by the transition of resting spores into motile spores, zoospores, which are chemotactically attracted by canola roots under water-saturated conditions. Therefore, a hydroponic system could provide the ideal condition to initiate and observe infections. Here we present the preliminary results of a hydroponics based high throughput screening system for clubroot disease indexing. We found that after 21 days post inoculation of Westar canola with *P. brassicae* field isolate pathotype 3H, 100 % of the plants showed large galls and the ratio shoot/root was significatively lower in the infected plants than in the mock-inoculated control. In this poster we will also present what are the next steps in our project to increase the efficiency of the system.

156. Assessment of western redcedar for susceptibility to root and butt rot diseases by controlled inoculation

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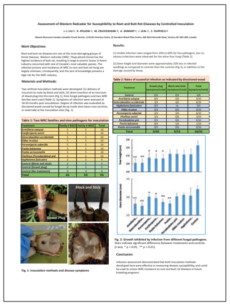
Assessment of Western Redcedar for Susceptibility to Root and Butt Rot Diseases by Controlled Inoculation

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Work Objectives:

Materials and Methods:

Table 1: Two WRC families and nine pathogens for inoculation

Fig. 1: Inoculation methods and disease symptoms

Results:

(1) Visible infection rates ranged from 10% to 60% for five pathogens, but no obvious infections were observed for the other four fungi (Table 2).

(2) Stem height and diameter were approximately 10% less in infected seedlings as compared to controls than the controls (Fig 2), in addition to the damage caused by decay.

Table 2: Rates of successful infection as indicated by discolored wood

Fig. 2: Growth inhibited by infection from different fungal pathogens. Stars indicate significant difference between treatments and controls (t-test, * p < 0.05, ** p < 0.01).

Conclusion:

Infection assessment demonstrated that both inoculation methods developed here were effective in measuring disease susceptibility, and could be used to screen WRC resistance to root and butt rot diseases in future breeding programs.

Root and butt rot diseases are one of the most damaging groups of forest diseases. Western redcedar (WRC; *Thuja plicata* Donn) has the highest incidence of butt rot resulting in large economic losses in one of Canada's most valuable tree species. The infection process and resistance of WRC to root and butt rot fungi are largely unknown; consequently, this presents a high risk for the WRC industry. To evaluate susceptibility of WRC to the diseases under greenhouse conditions, we developed two artificial inoculation methods using a block and stick to deliver inoculum to roots or an inoculum dowel plug directly inserted into the stem. Nine pathogenic fungi, including *Armillaria ostoyae, Coniferiporia weirii, Phellinus (Porodaedalea) pini, Heterobasidion occidentale, Postia balsamea, Postia sericeomollis, Perenniporia subacida, Obba rivulosa, and Hypholoma fasiculare* were used to inoculate two-year-old seedlings. Symptoms of infection were assessed at 18-20 months post inoculations. Symptoms of infection were indicated by discolored wood caused by fungal decay inside stem base cross-sections, or externally at the inoculation sites. Visual infection rates were 60% for *H. occidentale* and *P. subacida*, 30% for *C. weirii*, 20% for *A. ostoyae*, 10% for *P. balsamea*, and no obvious infection for the other four fungi. Furthermore, infected seedlings had stem height and stem diameter about 10% smaller than the controls, adding to the decay impacts. Infection assessment demonstrated that inoculation methods developed here were effective in measuring disease susceptibility, and could be used to screen WRC resistance to root and butt rot diseases in future breeding programs.

157. Fusarium head blight (FHB) and deoxynivalenol (DON) index for Ontario commercially grown winter wheat

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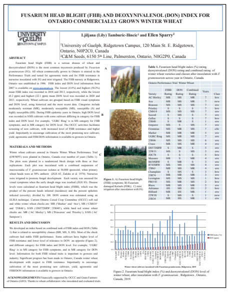
FUSARIUM HEAD BLIGHT (FHB) AND DEOXYNIVALENOL (DON) INDEX FOR ONTARIO COMMERCIALLY GROWN WINTER WHEAT

UNIVERSITY of GUELPH RIDGETOWN CAMPUS

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ABSTRACT

MATERIALS AND METHODS

RESULTS AND DISCUSSION

ACKNOWLEDGEMENTS Financially supported by OCCC and Grain Farmers of Ontario (GFO). Thanks to wheat collaborators who inoculated and evaluated trials.

Table 1. Fusarium head blight index (%) rating, deoxynivalenol (DON) rating and combined rating of winter wheat varieties and classes after inoculation with *F. graminearum* across year in Ontario, Canada.

Figure 1. A) Fusarium head blight (FHB) symptoms; B) Fusarium damaged Kernels (FDK); C) mist irrigation after inoculation with FG.

Figure 2. Fusarium head blight index (%) and deoxynivalenol (DON) level of winter wheat, after inoculation with *F. graminearum*, Ridgetown, Ontario, Canada, 2019.

Fusarium head blight (FHB) is a serious disease of wheat and deoxynivalenol (DON) is the most common mycotoxin produced by *Fusarium graminearum* (FG). All wheat commercially grown in Ontario is entered in the Performance Trials and tested for agronomic traits and for FHB resistance in nurseries inoculated with FG and mist irrigated. The FHB nursery at Ridgetown, Ontario was established in 1996. FHB index and DON level information from 2007 is available on www.gocereals.ca. The lowest (4.4%) and highest (50.2%) mean FHB index was recorded in 2018 and 2013, respectively, while the lowest (0.2 ppm) and highest (22.1 ppm) mean DON level was recorded in 2020 and 2013, respectively. Wheat cultivars are grouped based on FHB visual symptoms and DON level, using historical and the most recent data. Categories include moderately resistant (MR), moderately susceptible (MS), susceptible (S) and highly susceptible (HS). The Ontario Cereal Crop Committee (OCCC) checks are: MR ('Marker', 'AC Morley' and 'Ava'), MS ('CM614', '25R46', 'Princeton' and 'Priesley'), S/HS ('DS572SRW', '25R40' and 'AC Sampson'). During FHB epidemic years in Ontario, high DON level was recorded in S/HS cultivars with some cultivars differing in category for FHB index and DON level. For example, 'UGRC Ring' is in MS category for FHB symptoms, and in MR category for DON level. The OCCC activities facilitates screening of new cultivars, with increased level of FHB resistance and higher yield. Importantly to encourage cultivation of the most promising new cultivars, yield, agronomic and FHB/DON information is available to growers in Ontario.

158. Effectiveness of biofungicides to control several fungal diseases in vineyard

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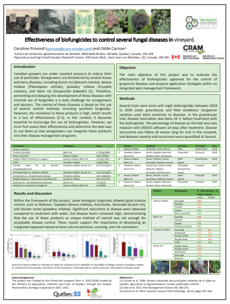

Effectiveness of biofungicides to control several fungal diseases in vineyard.

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Introduction

Canadian growers are under constant pressure to reduce their use of pesticides. Winegrowers are threatened by several leaves and berry diseases, including bunch rot (*Botrytis cinerea*), downy mildew (*Plasmopara viticola*), powdery mildew (*Erysiphe necator*), and black rot (*Guignardia bidwellii*) (1). Therefore, preventing and delaying the development of these diseases with minimal use of fungicides is a daily challenge for winegrowers and advisers. The control of these diseases is based on the use of several control methods, including synthetic fungicides. However, the resistance to these products is high, which results in a loss of effectiveness (2-3). In this context, it becomes essential to encourage the use of biofungicides. However, we must first assess their effectiveness and determine the best way to use them so that winegrowers can integrate these products into their disease management programs.

Objective

The main objective of this project was to evaluate the effectiveness of biofungicides approved for the control of grapevine diseases and propose application strategies within an integrated pest management framework.

Methods

Several trials were done with eight biofungicides between 2018 to 2020 under greenhouse and field conditions. Grapevine varieties used were sensitives to diseases. In the greenhouse trial, disease inoculation was done 24 h, before treatment with the biofungicide. The percentage of disease on the leaf area was measure with ASSESS software 14 days after treatment. Disease occurrence was fallow all season long for trial in the vineyard, and diseases severity and occurrence were quantified at harvest.

Results and discussion

Within the framework of this project, some biological fungicides allowed good disease control, such as Botector, Oxydate (downy mildew), Actinovate, Serenade (bunch rot), and Double nickel (powdery mildew). Significant reductions in disease were observed compared to treatment with water, but disease levels remained high, demonstrating that the use of these products as unique method of control was not enough for acceptable disease control. These results support the importance of developing an integrated approach based on best cultural practices, scouting, and risk estimation.

Acknowledgement
This project was funded by the Prime-Vert program (Part 4, 2013-2018) funded by the Ministry of Agriculture, Fisheries and Food of Quebec, through the Quebec Phytosanitary Strategy in Agriculture 2011- 2021.

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(3) Gossen et al. 2014. Canadian Journal Plant Pathology. 36 (3), pages 327-340.

Canadian growers are under constant pressure to reduce their use of pesticides. However, to ensure the industry's competitiveness, it is essential to secure yields by improving disease management. Winegrowers are threatened by several leaves and berry diseases, including bunch rot (*Botrytis cinerea*), downy mildew (*Plasmopara viticola*), powdery mildew (*Erysiphe necator*), and black rot (*Guignardia bidwellii*). Therefore, preventing and delaying the development of these diseases with minimal use of fungicides is a daily challenge for winegrowers and advisers. The control of these diseases is based on the use of several control methods, including synthetic fungicides. However, the resistance to these products is high, which results in a loss of effectiveness. In this context, it becomes essential to encourage the use of biofungicides. However, we must first assess their effectiveness and determine the best use strategy to provide winegrowers with precise information that will allow them to integrate these products into their disease control management. The main objective of this project was to evaluate the effectiveness of biofungicides approved for the control of grapevine diseases and propose application strategies within an integrated pest management framework. Within the framework of this project, some biological fungicides allowed good disease control, such as Botector, Oxidate, Actinovate, and Double nickel55. Significant reductions in disease were observed compared to treatment with water, but disease levels remained high, demonstrating that the use of these products as unique method of control was not enough for acceptable disease control. These results support the importance of developing an integrated approach based on best cultural practices, scouting, and risk estimation.

159. Impact of cluster leaf removal on grape disease pressure for cold-hardy hybrid cultivars under climatic conditions of eastern Canada

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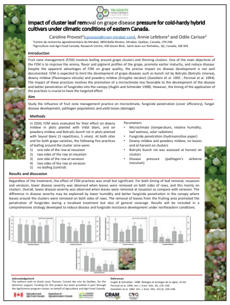

Impact of cluster leaf removal on grape disease pressure for cold-hardy hybrid cultivars under climatic conditions of eastern Canada.

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Introduction

Fruit zone management (FZM) involves leafing around grape clusters and thinning clusters. One of the main objectives of the FZM is to improve the aroma, flavor and pigment profiles of the grape, promote earlier maturity, and reduce disease. Despite the apparent advantages of FZM on grape quality, the precise impact on disease development is not well documented. FZM is expected to limit the development of grape diseases such as bunch rot by Botrytis (Botrytis cinerea), downy mildew (Plasmopara viticola) and powdery mildew (Erisyphe necator) (Zoecklein et al. 1992 ; Percival et al. 1994). The impact of these practices involves the promotion of a microclimate less favorable to the development of the disease and better penetration of fungicides into the canopy (Huglin and Schneider 1998). However, the timing of the application of the practices is crucial to have the targeted effect.

Aim

Study the influence of fruit zone management practice on microclimate, fungicide penetration (cover efficiency), fungal disease development, pathogen populations and yield losses (damage).

Methods

In 2020, FZM were evaluated for their effect on downy mildew in plots planted with Vidal blanc, and on powdery mildew and Botrytis bunch rot in plots planted with Seyval blanc (3 repetitions, 5 vines). At both sites and for both grape varieties, the following five practices of leafing around the cluster zone were:
1) one side of the row at nouaison
2) two sides of the row at nouaison
3) one side of the row at veraison
4) two sides of the row at veraison
5) no leafing (control)

Parameters:
- Microclimate (temperature, relative humidity, leaf wetness, solar radiation)
- Fungicide penetration (hydrosensitive paper)
- Downy mildew and powdery mildew, on leaves and at harvest on clusters
- Botrytis bunch rot was assessed at harvest on clusters
- Disease pressure (pathogen's airborne inoculum)

Results and discussion

Regardless of the treatment, the effect of FZM practices was small but significant. For both timing of leaf removal, nouaison and veraison, lower disease severity was observed when leaves were removed on both sides of rows, and this mainly on clusters. Overall, lower disease severity was observed when leaves were removed at nouaison as compare with veraison. The difference in disease severity may be explained by lower humidity and better fungicide penetration in the canopy where leaves around the clusters were removed on both sides of rows. The removal of leaves from the fruiting area promoted the penetration of fungicides during a localized treatment but also of general coverage. Results will be included in a comprehensive strategy developed to reduce disease and fungicide resistance development under northeastern conditions.

Acknowledgement
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There is a general agreement among scientists and grape specialists that proper canopy (CM) and fruit zone management (FZM) are essential practices to obtain good quality grapes. Fruit zone management involves leaf removal around the clusters. The ultimate objective of both CM and FZM is to improve grape aroma, flavour and pigment profiles, favour earlier maturity and reduce diseases. Practices of fruit zone management were evaluated for their effect on disease management during summer 2019 and 2020. The practices were leafing around the cluster zone on: 1) one side of the row at nouaison; 2) two sides of the row at nouaison; 3) one side of the row at veraison; 4) two sides of the row at veraison; 5) no leafing (control). Downy mildew, powdery mildew, and botrytis bunch rot were assessed weekly on leaves and at harvest on clusters. Regardless of the treatment, the effect of fruit zone management practices was small but significant. For both timing of leaf removal, nouaison and veraison, lower disease severity was observed when leaves were removed on both sides of rows. Overall, lowers disease severity was observed when leaves were removed at nouaison as compare with veraison. The difference in disease severity may be explained by lower humidity and better fungicide penetration in the canopy in sub-plots where leaves around the clusters were removed on both sides of rows at veraison. The removal of leaves from the fruiting area promotes the penetration of fungicides during a localized treatment but also of general coverage.

160. Assessment of compatibility of biofungicides in the development of a strategy for the control of diseases in vineyards

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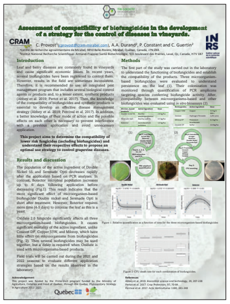

Assessment of compatibility of biofungicides in the development of a strategy for the control of diseases in vineyards.

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Introduction

Leaf and berry diseases are commonly found in vineyards and cause significant economic losses. In recent years, several biofungicides have been registered to control them. However, results in the field are sometimes inconsistent. Therefore, it is recommended to use an integrated pest management program that includes several biological control agents or products and, to a lesser extent, synthetic products (Abbey et al. 2019; Pertot et al. 2017). Then, the knowledge of the compatibility of biofungicides and synthetic products is essential to develop an effective disease management strategy (Abbey et al. 2019; Percival et al. 2017). In addition, a better knowledge of their mode of action and the possible effects on each other is necessary to prevent interference with a previous application and avoid unnecessary application.

This project aims to determine the compatibility of lower risk fungicides (including biofungicides) and understand their respective effects to propose an optimal use strategy to control grapevine diseases.

Methods

The first part of the study was carried out in the laboratory to understand the functioning of biofungicides and establish the compatibility of the products. Three microorganism-based biofungicides were evaluated to understand persistence on the leaf (1). Their colonization was monitored through quantification of PCR amplicons targeting species conferring biofungicide activity. After, compatibility between microorganisms-based and other biofungicides was evaluated using *in vitro* bioassays (2).

Results and discussion

The population of the active ingredient of Double Nickel 55 and Serenade Opti decreases rapidly after the application based on PCR analyses. In contrast, Botector microbial population increases up to 6 days following application before decreasing (Fig.1). This result indicates that the more significant effect of microorganism-based biofungicide Double nickel and Serenade Opti is short after treatment. However, Botector requires more time (4-5 days) to colonize the leaf as this is a yeast.

Oxidate 2.0 fungicide significantly affects all three microorganism-based biofungicides. It causes significant mortality of the active ingredient, unlike Cosavet DF, Copper 53W, and Milstop, which have little effect on microorganisms from biofungicides (Fig. 2). Then several biofungicides may be used together, but a delay is required when Oxidate is used with microorganisms-based products.

Field trials will be carried out during the 2021 and 2022 seasons to evaluate different application strategies based on the results observed in the laboratory.

Figure 1: Relative quantification as a function of time for the three microorganism-based biofungicides

Figure 2: CFU death rate for each combination of biofungicides.

Acknowledgement
This project was funded by the Prime-Vert program funded by the Ministry of Agriculture, Fisheries and Food of Quebec, through the Quebec Phytosanitary Strategy in Agriculture 2011- 2021.

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Pertot et al. 2017. Crop Protection, 97, 70-84.
Percival et al. 2017. Acta Horticulturae 1180, 241-248

Several leaf and berry diseases are present in vineyards and cause significant economic losses. In recent years, several biofungicides have been registered to control these diseases. However, the results in the field are sometimes inconsistent. Moreover, some aspects of their use are not well known, such as the compatibility of the different fungicides or the best strategy for using them. A better knowledge of their mode of action and the possible effects on each other is necessary to prevent interference with a previous application and avoid unnecessary application. This project aims to determine the compatibility of lower risk fungicides (including biofungicides) and understand their respective effects to propose an optimal use strategy to fight against grapevine diseases. The first part was carried out in the laboratory to understand the functioning of biofungicides and establish the compatibility of the products. The results show that the population of the active ingredient of Double Nickel 55 and Serenade Opti decreases rapidly after the application, whereas Botector microbial population increase up to 6 days following application, before decreasing. Oxidate 2.0 fungicide significantly affects all three biofungicides and causes significant mortality of the active ingredient, unlike Cosavet DF, Copper 53W, and Milstop, which have little effect on microorganisms from biofungicides. Secondly, field trials will be carried out during the 2021 and 2022 seasons to evaluate different application strategies based on the results observed in the laboratory.

161. Cotyledon infection is the primary pathway for *Leptosphaeria maculans* to cause blackleg of canola in western Canada

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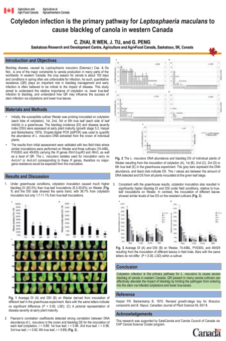

Blackleg disease, caused by *Leptosphaeria maculans*, is one of the major constraints to canola production worldwide. In western Canada, it has long been suspected that early infection is required for *L. maculans* to cause severe blackleg, because of a short crop season (~100 days) and often unfavorable spring conditions for infection. To test this hypothesis, the susceptible cultivar Westar was pricking inoculated on cotyledon, 1st, 2nd, 3rd or 6th true leaf in a greenhouse, and the blackleg disease incidence (DI) and severity (DSI) was assessed at early plant maturity. Blackleg DI originated from cotyledon inoculation (82%) was much higher than those from true leaves (6 - 25%), and DSI data also showed the same trend. Similar inoculations were performed on Westar and three common resistant cultivars (74-44BL, PV530G and 45H29) in two field trials. These resistant cultivars carry the *R* genes *Rlm3* and *Rlm1/LepR3*, as well as a level of quantitative resistance (QR). The *L. maculans* isolates used for inoculation carry no *AvrLm1* or *AvrLm3* corresponding to the *R* genes; therefore no major-gene resistance would be expected. Consistent with the results from greenhouse trial, cotyledon inoculation resulted in significantly higher blackleg DI and DSI than true-leaf inoculations on Westar. In contrast, the same inoculations showed no difference on any of the resistant cultivars. These findings show that cotyledon infection is the primary pathway for *L. maculans* to cause blackleg of canola in western Canada, but QR present in many canola cultivars can reduce the stem infection via infected leaves, alleviating the impact of blackleg.

162. Bioevaluation of seaweed extracts on the plant growth and resistance of tropical vegetables

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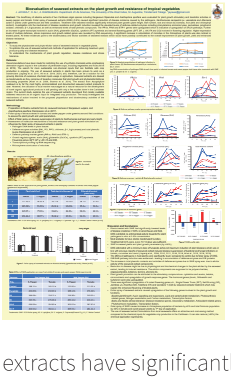

The bioefficacy of extract preparations from two Caribbean seaweed species (*Sargassum filipendula* and *Acathophora spicifera*) were evaluated in sweet pepper and tomato plants. Foliar spray application of algal extracts have significantly improved the growth and yield of plants under greenhouse and field conditions. The treated plants recorded higher chlorophyl contents and growth parameters. Gene expression analyses revealed the upregulated expression of genes involved in auxin (IAA), gibberellin (Ga2Ox), cytokinin (IPT) synthesis and the genes involved in flowering regulation (SFT, SP, J, AN, FA and CO). The treated plants were resistant to pathogen infections. This was noticeable through reduced disease severity levels by, *Xanthomonas campestris* pv. *vesicatoria* and *Alternaria solani* pathogens in tomato and sweet pepper plants under both greenhouse and field conditions. Elevated levels of defense-related enzymes including phenylalanine ammonia lyase, peroxidase, polyphenol oxidase, chitinase, and β-1,3-glucanase, as well as enhanced levels of total phenolic compounds were observed in the seaweed extract treated plants. The PR1a, PINII and ETR-1 genes were upregulated which is indicative of upregulation of SA/JA pathways. Significantly higher expression levels of multiple defense, stress responsive and growth-related genes was revealed in treated plants by RNA sequencing. A significant increase in colonization of microbes in the rhizosphere of plants was also noticed in treated plants. Multiple priming effects thus evoked by the seaweed extracts should have yielded in overall improved growth and productivity of plants and their enhanced resistance levels to pathogen infections.

163. Molecular Characterization of *Neopestalotiopsis* spp. affecting strawberry

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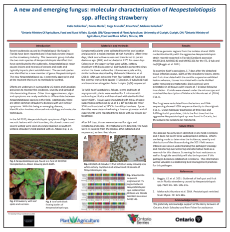

An aggressive strain of *Neopestalotiopsis* spp. was recently reported affecting strawberry (*Fragaria* x *ananassa* Duch.) in Florida and has now been detected in Ontario. In the fall of 2020, *Neopestalotiopsis* symptoms of light brown necrotic lesions with dark boarders, discolored crowns and severe wilting were seen at a single field location in southern Ontario strawberry *cv*. Albion. Black acervuli were seen on the foliage after incubation for three days at high humidity. The asexual spores were transferred to PDA and incubated at 22^{0}C for seven days. Colonies on the upper surface were white, cottony mycelium with black acervuli distributed in concentric rings and on the lower surface the colonies were pale white. DNA was extracted from four isolates of fungi and the internal transcribed spacer (ITS) region, β-tubulin, and translation elongation factor 1-alpha sequenced in both directions. All three genomic regions from the isolates shared 100% nucleotide identity with the aggressive *Neopestalotiopsis* strain recently reported in Florida. To fulfill Koch's postulates, foliage of strawberry were washed with 0.05% sodium hypochlorite for 2 min. and rinsed with sterile distilled water. Tissues were inoculated with spore suspensions of 1 x 10^6 conidia/ml and incubated at 22^{0}C in humidity chambers. After 5-7 days, 100% of the strawberry plants inoculated with the conidia suspension exhibited lesions whereas, tissues sprayed with sterile distilled water remained asymptomatic. The fungi were re-isolated from the lesions and DNA sequencing showed 100% sequence identity to the originals. Efforts should be made toward monitoring the occurrence and movement of this microbe.

164. Integration of cover crop programs in organic soils to improve soil health in the Holland/Bradford Marsh

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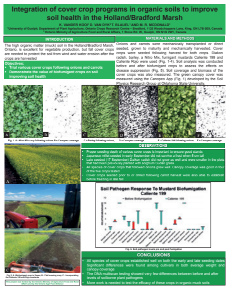

The Bradford-Holland Marsh has high organic matter soil (45-80%) that is ideal for vegetable production. The two main crops, onions and carrots, are harvested from August to November and there is a need for cover crops to protect the soil after harvest. The objectives of this project were to identify cover crops to follow onion and carrot harvest and to investigate biofumigant crops to improve soil health and reduce soilborne plant pathogens. Onions and carrots were mechanically transplanted or direct seeded, grown to maturity and mechanically harvested. Cover crops were seeded following harvest for both crops. Diakon radish, barley, a Nitro Mix, fumigant mustards Caliente 199 and Caliente Rojo were used. Soil analysis was conducted before and after biofumigant crops to assess the effects on plant pathogens. Soil coverage and biomass of the cover crops was measured. All species of cover crops that followed onions grew well. Canopy coverage was good for all except Caliente Rojo. In carrots, interseeded oats, radish and forage pea grew under and in-between carrot rows. Barley, seeded prior to, or drilled following carrot harvest, was also able to establish before freezing in late fall. In the biofumigant trial, all crops had good canopy coverage except for Caliente 199. A DNA multiscan showed few differences in the levels of soilborne plant pathogens between the two fumigation crops. Research is continuing to investigate full season cover crops on organic soils and identify good fall cover crops for use after onions and carrots.

165. Top ten plant parasitic nematodes of economic importance, threatening Prairie crops

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More than 4000 species of Plant Parasitic Nematodes (PPN's) have been described worldwide, responsible for crop losses between 8.8 to 14.6 %, equal to 100 to 157 billion USD annually, showing their potential threat to food security. The Canadian prairies with more than 32Mha of suitable land for agriculture, and 4M tones of Pulses, and the main Potato producer in Canada could potentially be subjected to several plant-parasitic nematodes. Vicinity with the North Dakota and Montana increasing this risk. Following is a short review on the most important species: 1) Soybean cyst nematode *Heterodera glycines*, on soybean, with the annual damage of $1 Billion to US agriculture. 2) Stem nematodes *Ditylenchus* spp, in Pulses and especially in fababean and pea, is an aggressive species with the economic threshold level of 0.8 eggs/g of soil, and complete crop failure at 64 eggs/g of soil in Europe. 3) Root-Knot Nematodes (*Meloidogyne* spp), a cosmopolitan species and the capability for producing complex disease and synergism with other pathogens. 4) Root Lesion Nematode (*Pratylenchus* spp), is a serious pathogen in field crops and fruit trees, with tolerance limit of 0.03 specimens/cm3 of soil, and yield losses of 58% at 2 specimens/cm^3 of soil in chickpea in Europe and the USA. 5-6). Cereal Cyst Nematode (CCN), *Heterodera trifolii* and *H. avenae*, in cereals and grains, with crop losses of $4 million in Europe and $70 million in Australia. 7-8) Potato Cyst Nematodes *Globodera pallida* and *G. rostocheinsis*, with the damage threshold of 1 to 2 eggs/g of soil. 9) Stubby Root Nematode *Thrichodorus* spp, and 10) Spiral nematodes *Helicotylenchus* spp in corn fields. Planning ahead regarding identification and control of PPNs is an essential component of sustainable crop production in Canadian agriculture.

166. Highlights from the 2020 Integrated Pest Management Program for muck vegetable crops in the Holland/Bradford Marsh

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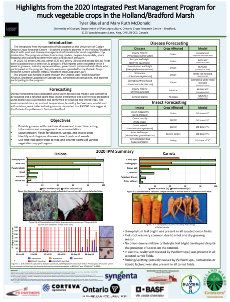

The Ontario Crops Research Centre – Bradford provides Integrated Pest Management services to vegetable growers in the Holland/Bradford Marsh. The main objective of the program is to provide growers with information about the risk of the major insect pests and diseases, so they can take timely action as needed. This is accomplished by: scouting growers' fields for diseases, weeds, and insect pests, providing disease and insect forecasting information, identifying and diagnosing diseases, insect pests and weeds, and implementing roto-rod spore traps to identify spores of vegetable crop pathogens. In 2020, 56 commercial onion, carrot, celery and potato fields were scouted twice a week for 21 growers. The forecasting models BOTCAST (for botrytis leaf blight of onion), DOWNCAST (for onion downy mildew), BREMCAST (for lettuce downy mildew), BSPCAST (for Stemphylium leaf blight of onion) and TOMCAST (for general leaf blights), along with models for white rot of onion and Sclerotinia white mold of carrot, were used to predict disease development. A harvest sample of 100 carrots and onions per field were assessed for below ground symptoms of diseases and insect damage. The forecasting models were generally useful for predicting blights and downy mildew development. Onion downy mildew spores were detected, and two fungicide applications were recommended in August. No downy mildew developed on onion in the Holland Marsh. Cavity spot and nematode/*Pythium* spp. forking were present in all scouted carrot fields. Stemphylium leaf blight (100% of fields) and pink root (96% of fields) were the most common onion diseases.

167. Nematicide efficacy for control of stem and bulb nematode (*Ditylenchus dipsaci*) in garlic (*Allium sativum*)

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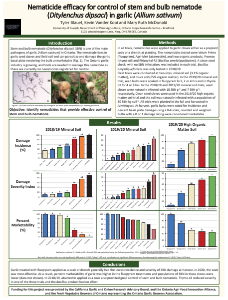

Nematicide efficacy for control of stem and bulb nematode (*Ditylenchus dipsaci*) in garlic (*Allium sativum*)

Tyler Blauel, Kevin Vander Kooi and Mary Ruth McDonald

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Introduction

Stem and bulb nematode (*Ditylenchus dipsaci*, SBN) is one of the main pathogens of garlic (*Allium sativum*) in Ontario. The nematode lives in garlic seed cloves and field soil and can parasitize and damage the garlic basal plate rendering the bulb unmarketable (Fig. 1). The Ontario garlic industry is growing, and tools are needed to manage this nematode as there are currently no nematicides registered for control.

Objective: Identify nematicides that provide effective control of stem and bulb nematode.

Methods

In all trials, nematicides were applied to garlic cloves either as a preplant soak or a drench at planting. The nematicides tested were Velum Prime (fluopyram), Agri-Mek (abamectin), and two organic products, Promax (thyme oil) and Rhizovital 42 (*Bacillus amyloliquefaciens*). A clean seed check, with no SBN infestation, was included in each trial. *Bacillus amyloliquefaciens* was only tested in 2018/19.

Field trials were conducted at two sites, mineral soil (3.1% organic matter), and muck soil (65% organic matter). In the 2019/20 mineral soil trial, seed bulbs were soaked in fluopyram fo 1, 2 or 4 hrs and in thyme oil for 4 or 8 hrs. In the 2018/19 and 2019/20 mineral soil trials, seed cloves were naturally infested with 18 SBN g^{-1} and 7 SBN g^{-1}, respectively. Clean seed cloves were used in the 2019/20 high organic matter soil trial and the soil was naturally infested with a population of 30 SBN kg $soil^{-1}$. All trials were planted in the fall and harvested in July/August. At harvest, garlic bulbs were rated for incidence and percent basal plate damage using a 0-4 scale, counted and weighed. Bulbs with a 0 or 1 damage rating were considered marketable.

Results

Conclusions

Garlic treated with fluopyram applied as a soak or drench generally had the lowest incidence and severity of SBN damage at harvest. In 2020, the soak was most effective. As a result, percent marketability of garlic was higher in the fluopyram treatments and populations of SBN in these cloves were lower (data not shown). In 2018/19, abamectin applied as a soak also provided good control of stem and bulb nematode. Thyme oil reduced severity in one of the three trials and the *Bacillus* product had no effect.

Funding for this project was provided by the California Garlic and Onion Research Advisory Board, and the Ontario Agri-Food Innovation Alliance, and the Fresh Vegetable Growers of Ontario representing the Ontario Garlic Growers Association.

Stem and bulb nematode (*Ditylenchus dipsaci*, SBN) is one of the main pathogens of garlic in Ontario. The Ontario garlic industry is growing, and tools are needed to manage this nematode as there are currently no nematicides registered for control. The objective of this research was to identify nematicides that provide effective control of stem and bulb nematode. The nematicides tested were Velum Prime (fluopyram), Agri-Mek (abamectin), and two organic products, Promax (thyme oil) and Rhizovital 42 (*Bacillus amyloliquefaciens*). A total of three trials were conducted, one in 2018/19 (mineral soil) and two in 2019/20 (high organic matter soil and mineral soil). Nematicides were applied either as a seed (clove) soak prior to planting in the fall, or a drench over the seed at planting. Garlic treated with fluopyram applied as a soak or drench generally had the lowest incidence and severity of SBN damage at harvest. In 2020, the soak was most effective. As a result, percent marketability of garlic was higher in the fluopyram treatments and populations of SBN in these cloves were lower. In 2018/19, abamectin applied as a soak also provided good control of stem and bulb nematode. Thyme oil reduced severity in one of the three trials and the *Bacillus* product had no effect. The garlic industry needs effective tools to manage SBN. Fluopyram applied as a soak or drench is a strong candidate for registration. Research is continuing to evaluate other chemical and biological nematicides that may have efficacy in controlling this nematode.

168. Potato disease and insect pests in Manitoba, 2020

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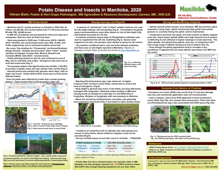

Potato Disease and Insects in Manitoba, 2020

Vikram Bisht. Potato & Hort Crops Pathologist, MB Agriculture & Resource Development, Carman, MB, R0G 0J0

Potato is a high value crop with significant disease and insect pest risks. The 2020 cropping season had a cool-moist start, slowing emergence; and partly responsible for high incidence of blackleg disease and poor emergence in some fields. The growing season was generally dry with extended warm periods; dry conditions continued to harvest. There were periods of consecutive days with ">28°C days with >20°C nights", which impacted potato yields and processing quality. Incidence of foliar diseases was lower than normal, but Verticillium wilt and black dot (*Colletotrichum coccodes*) diseases were extensive. Though *Phytophthora infestans* spores were trapped at one site in MB, there was no late blight disease reported. Colorado potato beetles continue to be problematic in select areas, possibly indicating resistance to the insecticides being used. Total aphid numbers trapped were significantly lower than normal. However, Green Peach Aphid numbers were higher, and risk for higher PVY in seed potato crops. Potato Mop Top Virus infection was noted in 4 of 7 samples tested, ranging from 1.6 to 18.6% incidence. European corn borer injury was report and did not warrant insecticide applications. Broad mites (*Polyphagotarsonemus latus)* were reported on potato for the first time in Canada. Rains and warm conditions in August maybe partly responsible for tuber infections by Pythium leak and Pink rot diseases in poorly drained spots in fields. A field trial comparing "Direct Planting" of potato in canola stubble vs "Traditional Planting" after cultivation showed no differences in yield or tuber quality, including surface diseases.

169. Boron (B) as an IPM tool for clubroot? Identification and potential utilization of B-insensitive lines of *Brassica napus*

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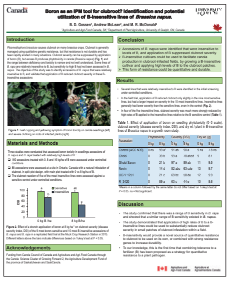

Boron as an IPM tool for clubroot? Identification and potential utilization of B-insensitive lines of *Brassica napus*.

B. D. Gossen[1], Andrew McLean[2], and M. R. McDonald[2]

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Introduction

Plasmodiophora brassicae causes clubroot on many brassica crops. Clubroot is generally managed using qualitative genetic resistance, but that resistance is not durable and has been rapidly eroded in many situations. Clubroot severity can be suppressed by application of boron (B), but excess B produces phytotoxicity in canola (*Brassica napus*) (**Fig. 1**) and the range between deficiency and toxicity is narrow and not well understood. Some lines of *B. rapa* are relatively insensitive to B, but sensitivity to high B had not been assessed in *B. napus*. The objective of this study was to identify accessions of *B. napus* that were relatively insensitive to B, and validate that application of B reduced clubroot severity in these B-insensitive accessions

Figure 1. Leaf cupping and yellowing symptom of boron toxicity on canola seedlings (left) and severe clubbing on roots of infected plants (right).

Materials and Methods

Three studies were conducted that assessed boron toxicity in seedlings accessions of *B. napus* and *B. rapa* treated with relatively high levels of B :

- ❑ 150 accessions treated with 0, 8 and 16 kg/ha of B were assessed under controlled conditions.
- ❑ 88 accessions were assessed at a site in Ontario, Canada with a natural infestation of clubroot, in split-plot design, with main plot treated with 0 vs 8 kg/ha of B.
- ❑ The clubroot reaction of five of the most insensitive lines were assessed against a sensitive control under controlled conditions.

Figure 2. Effect of a drench application of boron at 8 kg ha^{-1} on clubroot severity (disease severity index, DSI) of the 9 most boron-sensitive and 10 most B-insensitive accessions of *B. napus* and *B. rapa* in a replicated field trial at the Muck Crop Research Station in 2015. Different letters above the bars indicate differences based on Tukey's test at P < 0.05.

Acknowledgements

Funding from Canola Council of Canada and Agriculture and Agri-Food Canada through the Canola Science Cluster of Growing Forward 2, the Agriculture Development Fund of the province of Saskatchewan and SaskCanola.

Conclusion

- ➢ Accessions of *B. napus* were identified that were insensitive to levels of B, and application of B suppressed clubroot severity.
- ➢ B-insensitive cultivars could be used to facilitate canola production in clubroot-infested fields, by growing a B-insensitive cultivar and applying high levels of B to the clubroot patches.
- ➢ This form of resistance could be quantitative and durable.

Results

- Several lines that were relatively insensitive to B were identified in the initial screening under controlled conditions.
- In the field trial, application of B reduced clubroot only slightly in the nine most sensitive lines, but had a larger impact on severity in the 10 most insensitive lines. Insensitive lines generally had lower severity than the sensitive lines, even in the control (**Fig. 2**).
- In four of the five insensitive lines, clubroot severity was much more strongly reduced by high rates of B applied to the insensitive lines relative to the B-sensitive control (**Table 1**).

Table 1. Effect of application of boron on seedling phytotoxicity (0–3 scale), clubroot severity (disease severity index, DSI), and dry wt / plant in B-insensitive lines of *Brassica napus* in a growth room study.

Accession	Phytotoxicity		Severity (DSI)		Dry wt. (g)	
	0 kg	8 kg	0 kg	8 kg	0 kg	8 kg
Control (ASC N39)	0 ns	99 a[1]	91 ab	90 a	9 ns	7.8 ns
Ghobi	0	39 b	99 a	78 abcd	9	8.1
Ghobi Saron	0	21 b	97 a	89 ab	11	9.5
Nevin	0	14 d	82 abc	63 cde	13	9.7
UC77 1251	0	21 c	69 bc	58 de	12	9.9
R_3420	0	89 a	63 c	44 e	10	8.6

[1]Means in a column followed by the same letter do not differ based on Tukey's test at P = 0.05. ns = Not significant.

Discussion

- The study confirmed that there was a range of B sensitivity in *B. rapa* and showed that a similar range of B sensitivity existed in *B. napus*.
- The study demonstrated that application of high rates of B to a B-insensitive lines could be used to substantially reduce clubroot severity in small patches of clubroot infestation within a field.
- B-insensitivity would provide a novel source of quantitative resistance to clubroot to be used on its own, or combined with strong resistance genes to increase durability.
- To our knowledge, this is the first time that combining tolerance to a fertilizer (B) has been proposed as a strategy for quantitative resistance to a plant pathogen.

Clubroot (*Plasmodiophora brassica* Wor.) severity can be suppressed by application of boron (B), but excess B produces phytotoxicity in canola (*Brassica napus*). Some lines of *B. rapa* are relatively insensitive to B, but sensitivity in *B. napus* had not been assessed. Assessment of 150 accessions of *B. napus* and *B. rapa* treated with 0, 8 and 16 kg/ha of B under controlled conditions identified several lines that were relatively insensitive to B. Lines with sufficient seed and germination (88 accessions) were planted at a site in Ontario, Canada where there was a natural infestation of clubroot. The trial was arranged in a replicated split-plot design, where the main plot treatments were a low level (8 kg/ha) of B applied versus a non-treated control. Application of B reduced clubroot only slightly in the nine most sensitive lines, but had a larger impact on severity in the 10 least sensitive lines. Insensitive lines generally had lower severity than the sensitive lines, even in the control. Five of the most insensitive lines were assessed in combination with clubroot inoculation under controlled conditions. Clubroot severity was much more strongly reduced by high rates of B applied to the insensitive lines relative to the B-sensitive control. This indicated that lines of B. napus were available that were much less sensitive to applied B than standard canola cultivars in Canada. It also indicated that application of high rates of B applied to B-insensitive lines could dramatically reduce clubroot severity, regardless of pathotype. B-insensitive cultivars might ultimately be used to facilitate canola production in clubroot-infested fields, by growing a B-insensitive cultivar and applying high levels of B to the clubroot patches.

170. Spore survival of *Plasmodiophora brassicae* after liming and perennial grasses: Field trial 2018–2020

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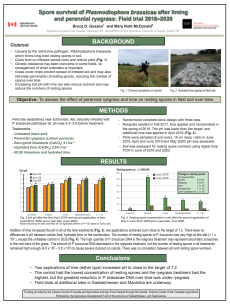

Clubroot (*Plasmodiophora brassica* Wor.) of canola is managed primarily with genetic resistance in Canada, but resistance has broken down in many fields. Treating infested patches of fields with lime to make soil less conducive for clubroot, and sowing grass crops to eliminate soil movement, are important tools for clubroot management. A study to examine the their effect on spore survival was initiated in a commercial field near Edmonton, AB on a clay-loam soil where severe clubroot developed on a resistant cultivar in 2016. Soil pH across the site ranged from 5.5–5.8. The treatments were: 1) perennial ryegrass (*Lolium perenne*), 2) zero-grind limestone applied @ 4 T/ha, 3) hydrated lime, equivalent based on reducing power, 4) a 50:05 mixture of lime and hydrated lime, and 5) a control. The grass was seeded in fall 2017, and lime was applied and incorporated in spring of 2018. Each plot was sampled (5 cores, 15-cm depth) in late June of 2018, late April and late June 2019 and mid-May 2020. The pH in the lime-treated plots did not reach the target of 7.2, so additional lime was applied and incorporated after sampling in April 2019. Spore concentration was initially assessed using qPCR, but that has been replaced with digital drop PCR because of better consistency and reproducibility. Spore concentration (based on copies of *P. brassicae* DNA) at the site is high (10^5 to 10^7 spores g^{-1}) and highly variable. To date, there is no clear pattern of response to treatment over time.

171. Canadian prairie canola yield trends from 2011 to 2020

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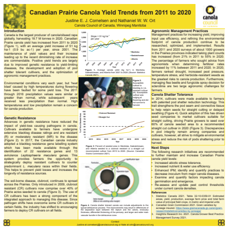

The average Canadian prairie canola (*Brassica napus* L.) yield has increased from 1867 to 2268 kg ha^{-1} from 2011 to 2020. This has been made possible in part because of an increase in genetic resistance to yield limiting diseases, the development and adoption of pod shatter tolerant cultivars, and the optimization of agronomic management practices. Developing genetic resistance to yield limiting diseases, like blackleg or clubroot, is a continuous effort because of their active shifts in pathogen virulence. Plant breeders and pathologists have and continue to work in collaboration to provide genetics that are resistant to current strains. The availability of resistant sources has strengthened integrated pest management to reduce the incidence and severity of diseases. The adoption of pod shatter tolerant cultivars has optimized canola production for direct harvesting, provided versatility in harvesting logistics, and has increased crop resilience to adverse environmental conditions. Agronomic management practices have been enhanced by adopting target seeding rates based on seed size, suitable fertilizer application practices, appropriate crop sequence, consulting established pest thresholds, and by reducing grain losses during harvest. As well, environmental conditions have affected overall disease development, yield, and the management practices deployed. The optimization of the forementioned within our control has led to increased canola production and profitability, long-term positive environmental sustainability, and ultimately, the continued competitiveness of the Canadian canola industry. Ongoing research, innovation, and collaboration among farmers, agronomists, and researchers is necessary for current canola production levels to be maintained and increased.

172. Determining the physiological basis of yield and yield stability in spring and winter wheat populations using the PlotCam

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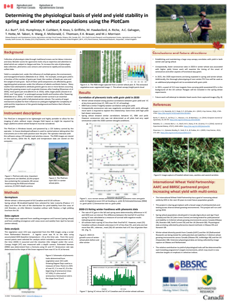

The International Wheat Yield Partnership (IWYP) has a goal of increasing wheat yields by 50% in the next 20 years. Meeting this goal will require the careful identification of yield related traits, optimization of these traits in agronomically important genetic backgrounds, and deployment of these improved varieties. For these strategies to realize an international impact, the gains made must be suitable for multiple wheat growing areas and diverse environments. IWYP provides the platform for synergies between national programs, in this case between Agriculture and Agri-Food Canada partners and the UK's Designing Future Wheat programme funded by BBSRC. This project aims to further the understanding of the extent to which the benefits conferred by traits and alleles in one of the partner countries can 'travel' to the other. Four spring wheat and three winter wheat testing sites in Canada and the UK are being used to examine yield stability over the four year project. Additionally, biomass accumulation data has been collected at the

Ottawa site via a hand-held field phenomics platform. The PlotCam platform collected image and sensor data on spring wheat and winter wheat populations once per week throughout the growing season to determine the physiological basis of the yield differences within the study populations. Data from 2019 and 2020 shows good evidence that high yielding cultivars have fast establishment, large biomass at heading and a slower senescence rate.

173. Variation in seed size in the perennial intermediate wheatgrass

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Variation in seed size in the perennial intermediate wheatgrass.

Seed size of intermediate wheatgrass (*Thinopyrum intermedium* (Host) Barkworth & D.R. Dewey) is variable within a single inflorescence, with inflorescence size variable within an individual plant. Understanding the underlying causes of this variability is important for its development as a crop. Trials at Brandon and Carman, Manitoba were established in 2019 with similar germplasm. Individual heads were collected immediately prior to harvest in 2020. Five heads plot^{-1} were collected from six plots (post-harvest treatments) replicate^{-1} totaling 120 inflorescences location^{-1}. Individual spikelets were excised, seeds removed, noting their position both within the spikelet and spike and later weighed. Analysis was carried out using PROC Mixed in SAS. Site interactions were found for spikelet number and florets spikelet^{-1} and the relationship of seed weight within spikelets. Drought in 2020 at both sites may have influenced these results. Carman produced a higher number of seeds head^{-1}, a lower number of spikelets inflorescence^{-1} but a higher number of seeds spikelet^{-1} and individual seed weight. Carman had a greater yield inflorescence^{-1} coupled with a higher inflorescence density in the field. Within spikelet differences for the sites indicated that seed size was not impacted by floret location for inflorescences harvested at Brandon, while at Carman, seeds from florets six and higher were significantly smaller. Obligate outcrossing coupled with inflorescence size differences provides a challenge in breeding for and realizing uniformity of seed size. Future research on the influences of tillering within the plant may assist in understanding the causes of this variation.

174. Can new sainfoin cultivars be profitably used for mixed stands with alfalfa and grass?

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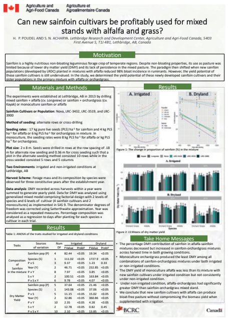
Can new sainfoin cultivars be profitably used for mixed stands with alfalfa and grass?

Sainfoin is a highly nutritious non-bloating leguminous forage crop of temperate regions. Despite non-bloating properties, its use as pasture was limited because of lower dry matter yield (DMY) and its lack of persistence in the mixed pasture. The paradigm then shifted when new sainfoin cultivars planted in mixtures with alfalfa reduced 98% bloat incidence in ruminants. However, the yield potential of these sainfoin cultivars is still undervalued. In the study described here, we determined the yield potential of these newly developed sainfoin cultivars and their sister populations in the primary mixture with alfalfa cv. AC BlueJ or orchardgrass cv. Kayak. The experiments were established by drilling the two crops in alternate rows or cross-drilling them under irrigated and non-irrigated conditions at Lethbridge, AB in 2013. Forage mass and its composition by species were observed for three constitutive years after the establishment year. Monoculture orchardgrass produced the least DMY among all combinations of sainfoin-orchardgrass mixtures under both irrigated or non-irrigated conditions and both planting schemes consistently over all three years. The DMY yield of monoculture alfalfa was less than its mixture with new sainfoin cultivars under irrigated condition but this did not happen consistently under non-irrigated condition. Under non-irrigated condition, alfalfa-orchardgrass yielded significantly greater than sainfoin-orchardgrass mixed stand. The percentage DMY contribution of sainfoin in alfalfa-sainfoin mixtures decreased but increased in sainfoin-orchardgrass mixtures across harvest time in both growing conditions. We conclude that new sainfoin cultivars with alfalfa can produce bloat-free pasture without compromising the biomass yield when supplemented with irrigation.

175. Evaluation of barley cultivar testing locations in Ontario

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In order to develop new cultivars, promising genotypes are evaluated for their performance each year at a number of test locations representing the mega-environment of the crop. In this study we used Ontario barley registration trial data from 2015 to 2020 and GGE biplot software to understand the barley mega-environment in Ontario and to evaluate the suitability of the test locations. The analysis showed that the barley test locations fall into two mega-environments, with a major mega-environment of five test locations and another mega-environment with one test location. Among the six test locations used for the barley registration trials, Palmerston, Ottawa and Osgoode were the most desirable test locations for the barley cultivar evaluation representing the Ontario mega-environment. This study also identified cultivars, AAC Ling and AAC Bell, with high yield and stability across Ontario. The finding from this study will be useful for the barley community in general, especially helping breeders to select the appropriate test locations for the evaluation of the advanced barley lines in the region.

176. Effect of Seeding Rate on Hulless Barley Production in Eastern Canada

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Hulless barley varieties are becoming more valuable due to higher levels of protein and digestible energy compared to hulled varieties. Although there is growing market potential for hulless barley, there is very little information on how cultural practices affect yield and quality in eastern Canada. A study was conducted over two years and four sites in eastern Canada (Charlottetown, PE; New Liskeard, ON; Normandin, PQ; and Ottawa, ON) to evaluate the responses of hulless and hulled barley varieties to various seeding rates (250, 350, 450, 550, 650, 750). The feed varieties tested included two 2-row hulless (AAC Starbuck and CDC Ascent), two 2-row hulled (AAC Ling and CH2720-1), and one each of a 6-row hulless (AAC Azimuth) and a 6-row hulled (AAC Bloomfield). Mixed models analysis with REML was used to measure the effects of variety (V), seeding rate (S) and V x S interactions. Polynomial contrasts were performed to measure differences between hulled vs. hulless varieties. There were significant effects of V and S on grain yield, plant height, thousand kernel weight, test weight, and grain protein. There were also significant contrasts between hulled vs. hulless on all factors except for thousand kernel weight. For the hulless varieties seeding at 450 – 550 seeds m^{-2} resulted in an increased grain yield whereas there was no significant yield increase for hulled varieties seeding at more than 350 seeds m^{-2}. Seeding rates for hulless barley should be at least 450 seeds m^{-2} to achieve the optimum grain yield in eastern Canada.

177. Functional analysis of exopolygalacturonase genes in Verticillium dahliae during interaction with potato

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Functional analysis of exopolygalacturonase genes in *Verticillium dahliae* during interaction with potato

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Introduction

Methodology

Results

Conclusion

Acknowledgements

Verticillium dahliae is one of the most destructive plant pathogens, with the capability of infecting plant species in more than 200 families worldwide. Previous subtractive hybridization/cDNA-AFLP revealed higher level of expression of an exopolygalacturonase (ExoPG) gene (VDAG_03463) in highly than in weakly aggressive *V. dahliae* isolates. We aimed to check the effect of this gene in the pathogeneicity of *V. dahliae*. ExoPG transcripts increased dramatically in the highly aggressive isolate compared to the weakly aggressive one when treated with potato leaf or stem extracts. We used a split-marker technique to knock-out this gene in *V. dahliae* and generated six mutants. No changes in the pathogenicity or ExoPG activity was observed in the mutants compared to the wildtype. To investigated more, we identified 8 polygalacturonase/pectinase-related genes in the genome of V. dahliae namely PGA, PGB, PGC, PGD, PEC1, PEC2, PEC3 and PEC4. Expression of PGA dramatically increased in the △exopg mutant treated with different potato extracts, compared to the wild type. Except for PGA gene, similar expression trends of the above-mentioned genes were observed in the △exopg mutant and weakly aggressive isolate when treated with different potato extracts. This indicates that other genes/pathways compensate the activity of the knocked out ExoPG gene in the △exopg mutant. This is the first report of protoplast-based split marker method for transformation of *V. dahliae*.

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