Welcome to the

88th Annual Meeting of the Canadian Phytopathological Society/La Societé Canadienne de Phytopathologie

and the

Annual Meeting of the Canadian Society of Agronomy/ La Societé Canadienne d'Agronomie

"CROP PRODUCTION & DISEASE MANAGEMENT - CULTIVATING IDEAS"

Program & Abstracts

Winnipeg, Manitoba, Canada

June 18-22, 2017

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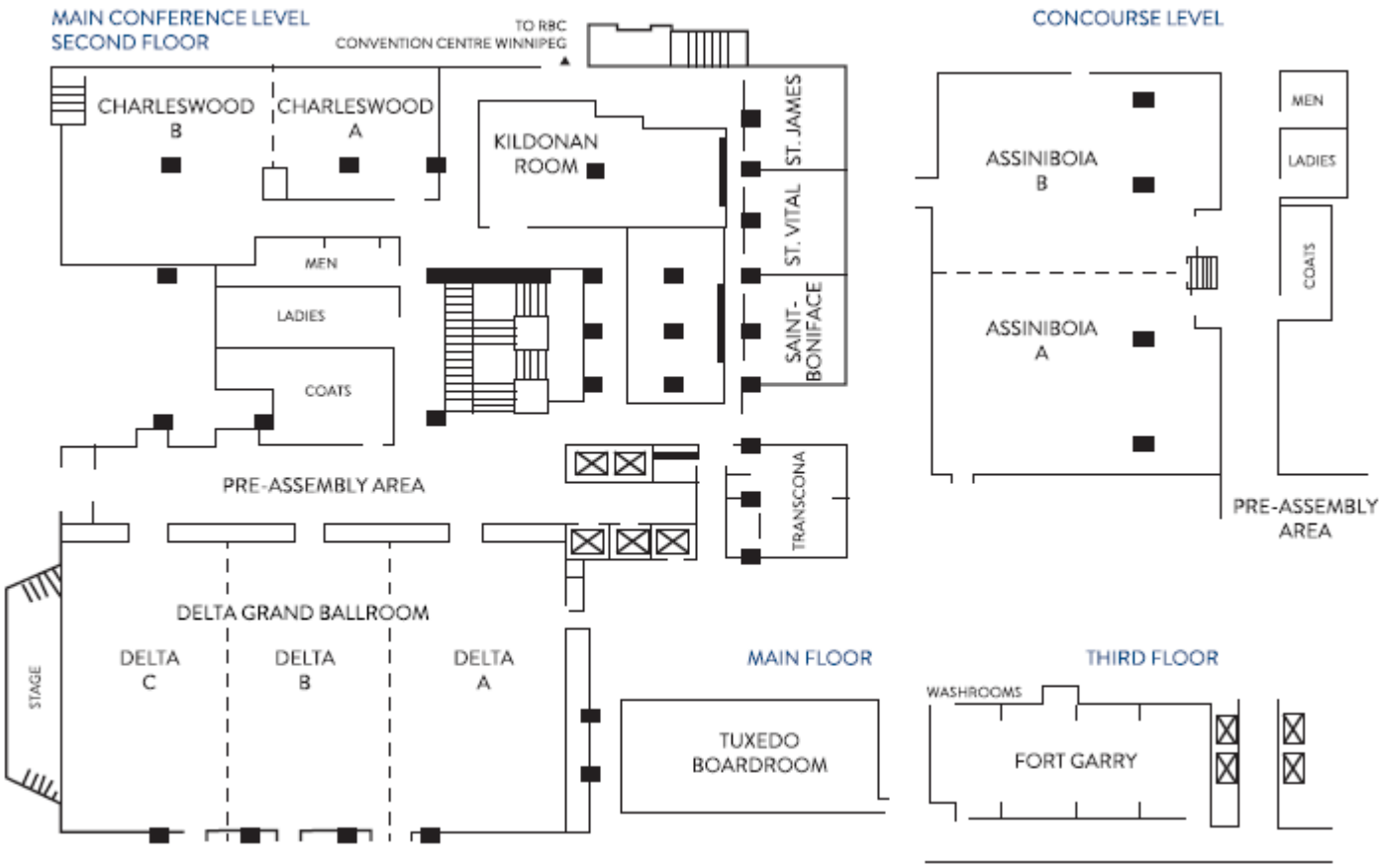
Facility Map



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Oral Presentation Sessions

Speakers are required to be at the designated room at least 15 minutes prior to when the oral session is scheduled to start. Please introduce yourself to the session chairperson and verify the agenda. Power Point presentations should be given to the computer supporting personnel at least 15 minutes prior to the start of the session.

Poster Sessions

Authors should identify their poster number listed in the program and display their poster at the specified site as soon as possible after their arrival. Posters will be on display in Ballroom A, which will be open on Sunday afternoon. Authors are required to attend their posters during the poster sessions scheduled Monday, June 19 from 16:30 to 18:30 (all student posters and even-numbered posters) and Tuesday, June 20 from 16:30 to 18:00 (odd-numbered posters). Posters should be removed by Wednesday, June 21 by 14:00.

Session Chairs

Chairs are required to be at the designated room at least 15 minutes prior to when the oral session is scheduled to start. Please introduce yourself to your co-chair and the speakers in your session. Please keep your session on time as all sessions are held concurrently (except the plenary). For contributed paper sessions, speakers are given 12 minutes for their presentation and three minutes for questions. In the interest of time, ask the audience to hold their applause until the end of a session and thank all speakers at that time.

Welcome to the 2017 joint meeting of the Canadian Phytopathological Society and the Canadian Society of Agronomy. We are pleased to be able to host all of you, and hope you enjoy the meeting and interactions with colleagues during your time in Winnipeg. The success of this meeting is dependent on the active participation of those attending the meeting. We encourage your enthusiastic participation in all the sessions and the informal discussions that will occur outside of the formal sessions.

The theme of this conference is 'Crop Production and Disease Management – Cultivating Ideas'. It represents the integrated nature of agronomy and plant pathology, and how we can use our differing knowledge and expertise to approach old issues and new opportunities for the benefit of Canadian and International agriculture. With this in mind, the local organizing committee has strived to develop a program that we hope everyone can benefit from. Many individuals from the CPS and CSA have contributed their time, effort and ideas to the planning and organizing of this meeting. We would like to thank them all for their contributions. It is very much appreciated.

We are grateful for the financial and in-kind contributions made in support of this conference by companies and government organizations listed on the sponsorship page. Their support is greatly appreciated, and indicates their commitment to agriculture in Canada.

On behalf of the local organizing committee, we wish you an informative and productive meeting. If time permits, we also wish you an enjoyable time visiting the local sites and activities offered in Winnipeg.

Sincerely

Fouad Daayf	Yvonne Lawley	Jim Menzies
Co-Chair	Co-Chair	Co-Chair

Pre-Conference					Field Tour
Sunday, June 18	**Monday, June 19**	**Tuesday June 20**		**Wednesday, June 21**	**Thursday, June 22**
	07:00–08:00 Breakfast (Ballroom BC)	07:00–08:00 Breakfast (Ballroom BC)		07:00–08:00 Breakfast (Ballroom BC)	
	08:00-08:15 Welcome Ceremonies	8:00-12:00 CPS Student Competition: Genetics & Resistance 2, Disease Management 1 (Ballroom BC)	8:00-10:00 CSA/CPS: Breeding & Genetics 1 (Charleswood B)	8:00-12:00 CPS Symposium: Disease Issues in Soybeans & Pulses (Ballroom BC)	8:00-12:00 CSA Symposium: Extending the Growing Season (Charleswood B)	08:00-08:20 Load bus (Delta Lobby)
	08:15–12:00 Plenary Session: Toxigenic Fusarium Species & Mycotoxins: Challenges & Perspective (Ballroom BC)					08:30-09:30 Travel to Carman, MB
			10:30-12:00 CPS: Epidemiology (Charleswood B)			09:30-12:30 University of Manitoba Ian N. Morrison Carman Research Farm (Carman, MB)
	12:00-13:00 Lunch (Ballroom BC)	12:00-14:00 Lunch and CPS Business Meeting (Ballroom BC)	12:00-14:00 Lunch and CSA Business Meeting (Charleswood B)	12:00-13:00 Lunch (Ballroom BC)		12:30-13:00 Travel to Morden, MB
13:00PM-16:00PM Workshop: Design Matters! Experimental Design & Statistics Workshop (Charleswood B)	13:00-15:00 CPS Student Competition: Genetics & Resistance 1 (Ballroom BC)	13:00-15:00 CSA Student Competition: Agronomy & Breeding (Charleswood B)		13:00-15:00 CPS: Disease Management 3 (Ballroom BC)	13:00-15:00 CPS: Genetics & Resistance 4 (Charleswood B)	13:00-15:00 Agriculture & Agri-Food Canada (Morden, MB)
		14:00-15:00 CPS Student Competition: Disease Management 2	14:00-15:00 CSA: Breeding & Genetics 2 (Charleswood)			
	15:30-16:30 CPS Student Competition: Genetics & Resistance 1 (Ballroom BC)	15:30-16:30 CSA: Agronomy (Charleswood B)	15:30-16:30 CPS/CSA Student Video Competition (Ballroom BC)	15:30-16:30 CPS: Disease Management (Ballroom BC)	15:30-16:30 CPS: Disease Management (Charleswood B)	15:00-16:15 Travel to Howden, MB
	16:30-18:30 Poster Session Student Competition & even-numbered posters (Ballroom A)		16:30-18:00 Poster Session Odd-numbered posters (Ballroom A)			16:15-18:00 Richardson International's Kelburn Farm (Howden, MB)
			18:00-22:00 Banquet and Awards Ceremony (Ballroom BC)			18:00-19:30 BBQ Dinner (Kelburn Farm)
19:00-22:00 Opening Reception (Ballroom AB)	19:00-22:00 Graduate Student Social *Graduate students only (Rudy's Eat & Drink, 375 Graham Ave)					17:30-20:00 Travel to Delta Hotel

***Registration and information desk hours:** Sunday, June 18th - 12:00 to 19:30

Monday, June 19th - 07:00 to 14:00

Tuesday, June 20th - during meals and coffee breaks

Wednesday, June 21st - during meals and coffee breaks

Sunday, June 18, 2017

12:00 to 19:30	**Registration**	Mezzanine
16:00 to 22:00	**Poster set-up**	Ballroom A

Workshops

Sponsored by Pest Surveillance Initiative
Charleswood B

13:00 to 16:00	**Design Matters! Experimental Design and Statistics workshop** hosted by Rob Gulden (University of Manitoba) and Alissa Kriss (Syngenta)
16:00 to 16:30	**Coffee Break**
16:30 to 17:30	**Scientific Writing workshop** hosted by Brent McCallum (AAFC), Tom Fetch (Assoc. Editor CJPP), Allison Paskins (Taylor and Francis), Zamir Punja (Editor CJPP)

Opening Reception

Ballroom AB

19:00 to 22:00	**Reception**

Monday, June 19, 2017

07:00 to 08:00	**Breakfast** Sponsored by BASF	Ballroom BC
07:00 to 14:00	**Registration**	Mezzanine
07:00 to 14:00	**Poster set-up**	Ballroom A
08:00 to 08:15	**Welcoming Ceremonies**	Ballroom BC

Joint CPS/CSA Plenary Session

Toxigenic Fusarium Species and Mycotoxins: Challenges and Perspective

Sponsored by Manitoba Agriculture
Chairs: Xiben Wang, Maria Antonia Henriquez
Ballroom BC

08:15	[FS1] **Fusarium mycotoxins: Current research at the USDA ARS Mycotoxin Prevention unit.** *Matthew Bakker, USDA Agricultural Research Service*	
08:45	[FS2] **A system approach to understand DON regulation in *Fusarium graminearum*.** *Gopal Subramaniam, Ottawa Research and Development Centre, AAFC*	
09:30	[FS3] **Wheat resistance to Fusarium head blight.** *Guihua Bai, USDA Agricultural Research Service, Kansas State University*	
10:00	**Coffee Break** Sponsored by BioChambers	Ballroom Foyer
10:30	[FS4] **Exploring G x E x M synergies to manage Fusarium head blight.** *Brian Beres, Lethbridge Research and Development Centre, AAFC*	
11:00	[FS5] **Insights into Fusarium-host interactions gained from crop and model species.** *Paul Nicholson, John Innes Centre, United Kingdom* ****CPS-BSPP Speaker Exchange Program Nominee**	
12:00	**Lunch**	Ballroom BC

CPS Contributed Paper Session (Student Competition*)

Genetics and Resistance 1

Chairs: Humin Xu, Austein McLoughlin (13:00 to 15:00)
Mark Belmonte, Michael Becker (15:30 to 16:30)
Ballroom BC

13:00	*[GR1] **Transcriptome analyses of canola (*Brassica napus*) treated with the plant growth promoting rhizobacterium *Pseudomonas chlororaphis* PA23 identifies differential expression of growth and defense related genes.** *Joey Wan, University of Manitoba*
13:15	*[GR2] **Investigating the cross kingdom biosynthesis of cytokinin in the *Ustilago maydis-Zea mays* pathosystem.** *Ibraheem Alimi, Trent University*
13:30	*[GR3] **Transcriptome profiling and laser microdissection identifies new regulators of resistance against blackleg disease of canola.** *Michael Becker, University of Manitoba*

13:45	*[GR4] **Interaction of Fusarium head blight resistance genes *Fhb1*, *Fhb2*, and *Fhb5* with fungicide application in hard red spring wheat.** *Gurcharn Singh Brar, University of Saskatchewan*	
14:00	*[GR5] **Identification, characterization and mapping of the seedling wheat leaf rust resistance gene in RL6071.** *Ming Zhe Che, Morden Research and Development Centre, AAFC*	
14:15	*[GR6] **The *Ustilago maydis* transcription factor *Zfp1* regulates the expression of effectors required for full pathogenesis, virulence, and anthocyanin production.** *Kitty Cheung, Trent University*	
14:30	*[GR7] **Genetic mapping of leaf rust resistance in the tetraploid wheat cross Strongfield/Blackbird.** *Xiangyu Pei, Morden Research and Development Centre, AAFC*	
14:45	*[GR8] **Development of molecular markers linked to *Leptosphaeria maculans* resistance gene *Rlm6* and inheritance of SCAR and CAPS markers in *B. napus* x *B. juncea* interspecific hybrids.** *Harunur Rashid, University of Manitoba*	
15:00	**Coffee Break** Sponsored by Cargill	Ballroom Foyer
15:30	*[GR9] **Effector triggered immunity vs non-host resistance against potato cyst nematodes, a transcriptomic analysis.** *Michael Sabeh, Saint-Jean-sur-Richelieu Research and Development Centre, AAFC*	
15:45	*[GR10] **Comprehensive investigation of gene transcript level change during teliospore germination in *Ustilago maydis*.** *Amanda Seto, Trent University*	
16:00	*[GR11] **Defense gene expression and metabolites accumulation in corn (*Zea mays* L.) in response to *Clavibacter michiganensis* subsp *nebraskensis*, the causal agent of Goss's Wilt.** *Alexander Shumilak, University of Manitoba*	
16:15	*[GR12] **The rachis node plays a structural and genetic role in Fusarium head blight resistance in Canadian winter wheat.** *Dustin Skrzenta, University of Manitoba*	

CSA Contributed Paper Session (*Student Competition)

Agronomy and Breeding 1

Chairs: Jennifer Mitchell-Fetch, Min Kang-Choi

Charleswood B

13:00	[AB1] **Management of injury by *Striacosta albicosta* (Lepidoptera: Noctuidae) and deoxynivalenol content in maize.** *Jocelyn Smith, University of Guelph*
13:15	*[AB2] **Genetic analysis of developmental traits contributing to enhanced winter survival in autumn-seeded rye (*Secale cereale* L.).** *Hirbod Bahrani, University of Saskatchewan*
13:30	*[AB3] **Characterization of sainfoin (*Onobrychis viciifolia* Scop.) accessions using agro-morphological and amplified fragment length polymorphism markers.** *Surendra Bhattarai, University of Saskatchewan*
13:45	*[AB4] **Cultural weed control decisions impact the competitiveness of *Glycine max* (L.) Merr. grown in the northern Great Plains.** *Jonathan Rosset, University of Manitoba*
14:00	*[AB5] **Assessing thermal indices for modeling grain corn phenological development on Canadian Prairies.** *Justice Zhanda, University of Manitoba*

14:15	*[AB6] **Effects of phosphorus sources on soil phosphatase activity, phosphorus availability and dry matter production of corn silage.** *Waqas Ali, Memorial University of Newfoundland*	
14:30	[AB7] **Effect of fall and spring applied urea and ESN on spring wheat production in northwestern Ontario.** *Tarlok Sahota, Thunder Bay Agricultural Research Station*	
14:45	[AB8] **Expanding the seeding window of winter wheat in Western Canada.** *Yvonne Lawley, University of Manitoba*	
15:00	**Coffee Break** Sponsored by Cargill	Ballroom Foyer

CSA Contributed Paper Session

Agronomy

Chairs: Brian Beres, Jonathan Rosset

Charleswood B

15:30	[AG1] **A funny thing happened on the way to…here.** *Shabtai Bittman, Agassiz Research and Development Centre, AAFC* ****Distinguished Agronomist Presentation**
16:15	[AG2] **Assessing existing information about greenhouse potting media organic content and microbial profile.** *Subashini Sivakumar, Van Luyk Greenhouses and Garden Centre*

Poster Session

Student Competition

Sponsored by Brewing and Malting Barley Research Institute

Ballroom A

16:30 to 18:30	**Poster Session** **Student Competition & even-numbered posters** *See list of poster titles by topic

Graduate Student Social

Sponsored by DL Seeds

Rudy's Eat & Drink, 375 Graham Ave

19:00	**Reception** **Quiz Competition** *Graduate students only

Tuesday, June 20, 2017

07:00 to 08:00	**Breakfast** Sponsored by SeCan	Ballroom BC

CPS Contributed Paper Session (Student Competition*)

Genetics and Resistance 2, Disease Management 1

Chairs: Vikram Bisht, Harunur Rashid

Ballroom BC

08:00	*[GR13] **Expression of selected *Phytophthora infestans*' RxLR effectors during infection of potato and tomato varieties.** *Hassna Alkher, University of Manitoba*
08:15	*[GR14] **RNA interference as a molecular fungicide targeting necrotrophic fungal pathogens *Sclerotinia sclerotiorum* and *Botrytis cinerea*.** *Nick Wytinck, University of Manitoba*
08:30	*[DM1] **Isochorismatase hydrolase (ICSH1) in *Verticillium dahliae* play roles in interacting with salicylate and jasmonate defense signaling in potato.** *Xiaohan Zhu, University of Manitoba*
08:45	*[DM2] **Biocontrol potential of *Trichoderma longibrachiatum* as an entomopathogenic fungi against *Bemisia tabaci*.** *Waheed Anwar, University of the Punjab, Pakistan*
09:00	*[DM3] **Pathogen complex on wasabi in British Columbia and evaluation of disease management options.** *Emily Betz, Simon Fraser University*
09:15	*[DM4] **Management of metalaxyl-m-resistant strains of the potato pink rot pathogen *Phytophthora erythroseptica* in field and storage.** *Bennett Crane, Charlottetown Research and Development Centre, AAFC*
09:30	*[DM5] **Root lesion nematode (*Pratylenchus penetrans*) mitigation through application of chitin and *Ascophyllum nodosum* extract in the soil prior to seeding red clover (*Trifolium pratense*) and birdsfoot trefoil (*Lotus corniculatus*).** *Zoshia Fraser, Saint Mary's University*
09:45	*[DM6] **Effects of fungicides in managing pasmo disease and seed yield in flax.** *Trisha Islam, University of Saskatchewan*
10:00	**Coffee Break** Sponsored by Crop Production Services — Ballroom Foyer
10:30	*[DM7] **RNA interference two ways: molecular fungicides and durable plants to control *Sclerotinia sclerotiorum*.** *Austein McLoughlin, University of Manitoba*
10:45	*[DM8] **Mitigation of stripe rust and leaf spot diseases in winter wheat in western Canada.** *Keiko Nabetani, University of Saskatchewan*
11:00	*[DM9] **Pathogen growth inhibition and disease suppression on cucumber (*Cucumis sativus* L.) and canola (*Brassica napus* L.) plants with Active Flower, a foliar nutrient spray containing boron.** *Li Ni, Simon Fraser University*
11:15	*[DM10] **Evaluation of weather-based forecasting models and cultivar resistance to manage leaf curl (*Colletotrichum fioriniae*) on celery crops in Ontario.** *Stephen Reynolds, University of Guelph*
11:30	*[DM11] **Determining the risk of Fusarium root rot on field pea by greenhouse soil bioassay and qPCR analysis.** *Samira Safari, University of Alberta*

11:45	*[DM12] **Effect of fungicide application timing on Fusarium head blight in durum wheat.** *Gursahib Singh, University of Saskatchewan*	
12:00 to 14:00	**Lunch**	
	CPS Business Meeting	Ballroom BC
	CSA Business Meeting	Charleswood B

CSA/CPS Contributed Paper Session

Breeding and Genetics

Chairs: Gavin Humphreys, Priscillar Wenyika

Charleswood B

08:00	[BG1] **Genotypic variations in root plasma membrane lipidome of silage corn grown under cool climatic production systems.** *Mumtaz Cheema, Memorial University of Newfoundland*	
08:15	[BG2] ***Aphanomyces* and *Phytophthora* root rot tolerance in alfalfa: Recurrent selection and marker development under stringent disease conditions.** *Patrice Audy, Quebec Research and Development Centre, AAFC*	
08:30	[BG3] **QTL mapping of seed hardness trait in common bean (*Phaseolus vulgaris*).** *Kulbir Sandhu, Morden Research and Development Centre, AAFC*	
08:45	[BG4] **Secretome analysis of *Clavibacter michiganensis* subsp. *nebraskensis*; the Goss's wilt bacterial pathogen of corn under induction with xylem sap.** *Atta Soliman, University of Manitoba*	
09:00	[BG5] **Studying early flowering flax mutants using genetics, physiology and genomics.** *Lester Young, University of Saskatchewan*	
09:15	[BG6] ***Sclerotinia sclerotiorum* disease severity on canola is influenced by the developmental age of the host's primary raceme.** *Matthew Denton-Giles, Curtin University, Australia*	
09:30	[BG7] **Transcriptome sequencing of a durum wheat population segregating for ergot resistance, to identify eQTL and enrich for SNPs.** *Ana Gordon, National Institute of Agricultural Botany, United Kingdom*	
09:45	[BG8] **Effects of long-term grazing on the yield, morphology and nutritive value of alfalfa (*Medicago sativa*).** *Bill Biligetu, University of Saskatchewan*	
10:00	**Coffee Break** Sponsored by Crop Production Services	Ballroom Foyer

CPS Contributed Paper Session **Epidemiology** Chairs: Rick Peters, Joey Wan Charleswood B	
10:30	[EP1] **Molecular identification of yeast species colonising grape fruits in Nova Scotia vineyards.** *Tharcisse Barasubiye, Ottawa Research and Development Centre, AAFC*
10:45	[EP2] **A brief history of INIAP and *Puccinia striiformis* in Ecuador.** *Charles W Barnes, Instituto Nacional de Investigaciones Agropecuarias, Ecuador*
11:00	[EP3] **How mineral oil impacts non-persistent Potato virus Y transmission.** *Sébastien Boquel, Fredericton Research and Development Centre, AAFC*
11:15	[EP4] **Predicting risk of pea root rot using molecular techniques to quantify inoculum of *Aphanomyces euteiches* in soil.** *Syama Chatterton, Lethbridge Research and Development Centre, AAFC*
11:30	[EP5] **Comprehensive survey of major grapevine (*Vitis vinifera* L.) viruses and their potential insect vectors in British Columbia.** *Sudarsana Poojari, Summerland Research and Development Centre, AAFC*
11:45	[EP6] **Foliar and root pathogens of *Cannabis sativa* L. (marihuana) in British Columbia.** *Zamir Punja, Simon Fraser University*
12:00 to 14:00	**Lunch**
	CPS Business Meeting — Ballroom BC
	CSA Business Meeting — Charleswood B

CPS Contributed Paper Session (Student Competition*) **Disease Management 2** Chairs: Barry Saville, Nick Wytinck Ballroom BC	
14:00	*[DM13] **Identification and utilization of target pathogenesis genes in *Sclerotinia sclerotiorum* through RNA sequencing and host-induced gene silencing.** *Philip Walker, University of Manitoba*
14:15	*[DM14] **Interactions between biocontrol agents and soil microbes: impact on pathogen growth and disease suppression.** *Andrew C. Wylie, Simon Fraser University*
14:30	*[DM15] **Applications of soil-applied fungicides to manage Phytophthora root rot on chili (*Solanum annum* L.) in Pakistan.** *Kiran Nawaz, University of the Punjab, Pakistan*
14:45	*[DM16] **Evaluating fungicidal activity of complex II inhibitors against late blight of potato.** *Sehrish Iftikhar, University of the Punjab, Pakistan*
15:00	**Coffee Break** Sponsored by Manitoba Corn Growers Association — Ballroom Foyer

CSA Contributed Paper Session **Agronomy and Breeding 2** Chairs: Ramona Mohr, Sean Asselin Charleswood B		
14:00	[AB9] **Comparative performance of annual and perennial forage legumes for forage production in northwestern Ontario.** *Tarlok Sahota, Thunder Bay Agricultural Research Station*	
14:15	[AB10] **Impact of selection for seed production in intermediate wheatgrass (*Thinopyrum intermedium*).** *Doug Cattani, University of Manitoba*	
14:30	[AB11] **Sugar beet response to rotation and conservation management in a 12-year irrigated study in southern Alberta.** *Francis Larney, Lethbridge Research & Development Centre, AAFC* ****CSA Best Paper Presentation**	
15:00	**Coffee Break** Sponsored by Manitoba Corn Growers Association	Ballroom Foyer

CPS/CSA Student Video Competition Chair: Gurcharn Brar Ballroom BC	
15:30 to 16:15	**Video Presentations**
	CPS Entries:
1	**Aphanomyces**. *Nimllash Thangam, University of Saskatchewan*
2	**Coffee rust.** *Alexandra Stinson, University of Guelph*
3	***Ditylenchus dipsaci*.** *Michael di Nardo, University of Guelph*
4	***Puccinia striiformis*.** *Sara Wyngaarden, University of Guelph*
5	**Wheat leaf rust.** *Mingzhe Che, Morden Research and Development Centre, AAFC*
6	**Ascochyta blight.** *Kun Lou, Keiko Nabetani, & Megan, University of Saskatchewan*
	CSA Entries:
1	**Cultural/Agronomic Control Methods for Ascochyta Blight in Pulses.** *Kun Lou, Keiko Nabetani, & Megan, University of Saskatchewan*
2	**Tillage Methods.** *Manpreet Kaur, University of Saskatchewan*
3	**Organic field pea and lentil cultivation methods.** *Oleksandr Alba, University of Sakatchewan*
4	**Demonstration on JoinMap software for genetic mapping studies.** *Christine Lee, Rob Brandt, & Rachel Whaley, University of Guelph*

Poster Session Ballroom A	
16:30 to 18:00	**Poster Session** **Odd-numbered posters** *See list of poster titles by topic

Banquet & Awards Ceremony Ballroom BC		
18:00	**Banquet & Awards Ceremony** Entertainment sponsored by Omex	Ballroom BC

Wednesday, June 21, 2017		
07:00 to 08:00	**Breakfast** Sponsored by Manitoba Pulse and Soybean Growers	Ballroom BC
07:00 to 14:00	**Poster Removal**	Ballroom A

CPS Symposium

Disease Issues in Soybeans and Pulses: Old Foes and New Challenges

Chairs: Fouad Daayf, Debbie McLaren

Ballroom BC

08:00	**Introduction.** *Fouad Daayf*	
08:15	[SP1] **Current and emerging nematode issues with soybean and pulses in Canada.** *Albert Tenuta, Ontario Ministry of Agriculture, Food and Rural Affairs*	
09:00	[SP2] **Management of *Phytophthora sojae* in soybean: a review and future perspectives.** *Anne Dorrance, Ohio State University*	
10:00	**Coffee Break** Sponsored by Novozymes	Ballroom Foyer
10:30	[SP3] **The long path to understanding a host-pathogen system: *Colletotrichum lentis* on lentil.** *Sabine Banniza, University of Saskatchewan*	
11:00	[SP4] ***Colletotrichum lentis* races on lentil and polymorphisms in the IGS region of ribosomal DNA related to pathogenicity.** *Lone Buchwaldt, Saskatoon Research and Development Centre, AAFC*	
12:00 to 13:00	**Lunch**	Delta B+C

CSA Symposium

Extending the Growing Season

Chair: Doug Cattani, Yvonne Lawley

Charleswood B

08:00	[EGS1] **Redesigning Canadian cropping systems for profitability, sustainability, and resilience.** *Joanne Thiessen Martens, University of Manitoba*	
08:30	[EGS2] **Winter cereals in Western Canada.** *Jamie Larsen, Lethbridge Research and Development Centre, AAFC*	
09:00	[EGS3] **Annual and perennial forages for fall/winter grazing.** *Emma McGeough, University of Manitoba*	
09:30	[EGS4] **Enhancing yields and environmental sustainability of biomass production systems by capitalizing on the extended growing periods.** *Naresh Thevathasan, University of Guelph*	
10:00	**Coffee Break** Sponsored by Novozymes	Ballroom Foyer
10:30	[EGS5] **Forage seed production and perennial grains.** *Doug Cattani, University of Manitoba*	

11:00	[EGS6] **Producer perspective and applications to extend the growing season.** *Ryan Boyd, SG&R Farms, Forrest, Manitoba*	
11:30	**Panel Discussion**	
12:00 to 13:00	**Lunch**	Delta B+C

CPS Contributed Paper Session

Disease Management 3

Chairs: Khalid Rashid, Philip Walker (13:00 to 15:00)
Holly Derksen, Alexander Shumilak (15:30 to 16:30)
Ballroom BC

13:00	[DM17] **Fungicide control of leaf mottle (*Septoria triseti* Speg.) and Fusarium seed infection of canary seed.** *Paulina Cholango-Martinez, University of Saskatchewan*	
13:15	[DM18] **Biocontrol agent *Streptomyces* combined with phosphite activate soybean defense mechanisms against *Phytophthora sojae*.** *Arbia Arfaoui, University of Manitoba*	
13:30	[DM19] **Phenazine-1-carboxylic acid contributes to the biocontrol of potato common scab through modulation of *Streptomyces scabies*' transcriptome.** *Tanya Arseneault, Saint-Jean-sur-Richelieu Research and Development Centre, AAFC*	
13:45	[DM20] **Chocolate spot disease and Lygus bugs degrade faba bean seed quality.** *Syama Chatterton, Lethbridge Research and Development Centre, AAFC*	
14:00	[DM21] **AeroNet: spore samplers in collecting fungal plant pathogens in the air and rain.** *Wen Chen, Ottawa Research and Development Centre, AAFC*	
14:15	[DM22] **Exogenous dsRNA application for control of Fusarium head blight.** *Shawn Clark, National Research Council Canada*	
14:30	[DM23] **Plant diagnostic research conducted by the Alberta Plant Health Lab.** *Jie Feng, Alberta Agriculture and Forestry*	
14:45	[DM24] **Epidemiology and management of white mold in dry bean by irrigation and plant architecture.** *Kazi Kader, Lethbridge Research and Development Centre, AAFC*	
15:00	**Coffee Break** Sponsored by WGRF	Ballroom Foyer
15:30	[DM25] **Assessing infection in wheat seeds *by Fusarium graminearum* using Biospeckle Laser Analysis, a novel application of the biospeckle technique.** *Darren Sutton, Simon Fraser University*	
15:45	[DM26] **Development of high throughput protocols for automated nucleic acid extraction and molecular detection of potato viral, fungal and bacterial pathogens on large scale.** *Huimin Xu, Canadian Food Inspection Agency*	
16:00	[DM27] **The rust species on impatiens (*Balsaminaceae*).** *Sarah Hambleton, Ottawa Research and Development Centre, AAFC*	
16:15	[DM28] **Update on Manitoba potato and horticultural crops disease and insect pests in 2016.** *Vikram Bisht, Manitoba Agriculture*	

CPS Contributed Paper Session

Genetics and Resistance 3

Chairs: Tharcisse Barasubiye, Dustin Skzerenta

Charleswood B

13:00	[GR15] **Integrated transcriptome and hormone profiling reveals the role of multiple phytohormone pathways in wheat resistance against Fusarium head blight.** *Lipu Wang, National Research Council Canada*
13:15	[GR16] **Gaining insight into biotrophic fungal carbon metabolism through characterization an *Ustilago maydis* xylitol dehydrogenase (*uxm1*).** *K.M. Goulet, Trent University*
13:30	[GR17] **Genome wide association studies (GWAS) of multiple disease resistance in spring barley.** *Sanjaya Gyawali, International Center for Agricultural Research in Dry Areas, Morocco*
13:45	[GR18] **Quantitative resistance to blackleg disease in three Canadian canola cultivars under elevated temperatures.** *Michelle Hubbard, Saskatchewan Research and Development Centre, AAFC*
14:00	[GR19] **Identification of immunity-related LRR-containing genes in *Cannabis sativa*.** *David Joly, Université de Moncton*
14:15	[GR20] **High resolution DNA melting (HRM) assay for detection of *Rx1* and *Rx2* for rapid high-throughput selection for extreme resistance to Potato virus X in potato.** *Xianzhou Nie, Fredericton Research and Development Centre, AAFC*
14:30	[GR21] **A previously unrecognized *Ustilago maydis* APSES protein has a role in pathogenic development.** *Barry Saville, Trent University*
14:45	[GR22] **Analysis of concomitant development of strawberry leaf spot and black seed disease caused by *Mycosphaerella fragariae*.** *Odile Carisse, Saint-Jean-sur-Richelieu Research and Development Centre, AAFC*
15:00	**Coffee Break** Sponsored by WGRF — Ballroom Foyer

CPS Contributed Paper Session

Disease Management 4

Chairs: Dilantha Fernando, Xiaohan Zhu

Charleswood B

15:30	[DM29] **Evaluation of products to control stem and bulb nematode on garlic.** *Mary Ruth Mcdonald, University of Guelph*
15:45	[DM30] **Pest risk assessment and its role in determining conditions for the importation and domestic movement of plant pathogens in Canada.** *Lindsay Vyvey, Canadian Food Inspection Agency*
16:00	[DM31] **The biocontrol agent *Pseudomonas chlororaphis* PA23 primes *Brassica napus* defense through distinct gene networks.** *Mark Belmonte, University of Manitoba*

16:15	[DM32] **A six-year study reveals the dynamics of avirulence allele profiles, blackleg incidence, and mating type alleles of *Leptosphaeria maculans* populations in canola in Manitoba, Canada.** *Dilantha Fernando, University of Manitoba*

Thank-you for attending the meeting and have a safe trip home!

Thursday, June 22, 2017

Agronomy and Pathology Field Tour

Sponsored by Agrium, Richardson International

*Pre-registration required

08:00 to 08:20	**Registraton and Load Bus from Delta Hotel Lobby**
08:30	**Bus departs and travel to Carman, MB**
09:30 to 12:30	**University of Manitoba Ian N. Morrison Carman Research Farm** Topics: Fusarium nursery, perennial grains breeding, soybean agronomy
12:30 to 13:00	**Bus departs to Morden, MB** **Box Lunch provided on bus**
13:00 to 15:00	**Morden Research and Development Centre, Agriculture and Agri-Food Canada** Topics: Wheat rust, Fusarium, pulse pathology and breeding
15:00 to 16:15	**Bus departs to Howden, MB**
16:15 to 18:00	**Richardson International's Kelburn Farm** Topics: On-Farm research, tillage systems research
18:00 to 19:30	**BBQ Dinner @ Kelburn Farm**
19:30 to 20:00	**Bus departs and travel back to Delta Hotel**

CPS/CSA Posters	
Genetics and Resistance	
P1	**Dispersal gradient of airborne *Botrytis cinerea* conidia.** O. CARISSE
P2	**Elucidation of canola disease resistance pathway against blackleg through characterization of *Arabidopsis thaliana* mutants.** R. M. CELOY, C. YANG, AND W.G. DILANTHA FERNANDO
P3	**Structural organization and haplotypes of rust resistance genes in flax.** S. RAVICHANDRAN, F. M. YOU, K. Y. RASHID, L. YOUNG, H. M. BOOKER and S. CLOUTIER
P4	CPS Student Competition. **Control of microRNA turnover contributes to plant immunity activated by flagelline**. R. AJMI, T. ABD EL RAHMAN and K. BOUARAB
P5	**Molecular characterization of Fusarium resistance from *Elymus repens* introgressed into bread wheat.** G FEDAK, W CAO, D WOLFE, D CHI AND A. XUE
P6	**Assessment of resistance to 'new' virulent pathotypes of *Plasmodiophora brassicae* in doubled haploid lines derived from *Brassica napus* cv. Mendel.** R. FREDUA-AGYEMAN, S. F. HWANG, S. E. STRELKOV, Q. ZHOU, H. AHMED, H. FU, I. AKTER, R. NYANDORO, G. TURNBULL AND D. FEINDEL
P7	**Mapping of the crown rust (*Puccinia coronata* Corda f. sp. *avenae* Eriks.) resistance gene *Pc45* in oat.** A. Z. KEBEDE, J. FRIESEN, J. G. MENZIES, J. W. MITCHELL FETCH, E. PACZOS-GRZĘDA, A. D. BEATTIE, and C. A. MCCARTNEY
P8	CPS Student Competition. **Improving genetic resistance to Fusarium head blight in durum and bread wheat.** G.S. BRAR, H.R. KUTCHER, P.K. SINGH, C.J. POZNIAK, AND P.J. HUCL
P9	**Mapping quantitative trait loci for Fusarium head blight resistance in Canada Western Red Spring wheat cultivar Carberry.** F. E. BOKORE, S. BERRAIES, R. D. CUTHBERT, R. E. KNOX, M. A. HENRIQUEZ, A. BURT, S. KUMAR, A. N'DIAYE, C. J. POZNIAK, Y. RUAN, A. G. SHARPE
P10	**Loss of function of chitin binding protein gene *CBPL* affects the pathogenicity of *Leptosphaeria maculans* the blackleg pathogen on canola.** F. LIU, C. SELIN, AND W. G. DILANTHA FERNANDO
P11	**Identification and screening of durable rust resistance-related metabolites in various wheat cultivars.** N. RAJAGOPALAN, Y. LU W. ZHANG, K. BOYLE, B. MCCALLUM, C. HIEBERT, E. REIMER, W. MCNABB, P. FOBERT, M. CUPERLOVICH-CULF AND M. C. LOEWEN
P12	**Possible roles for a cytochrome p450 and ABC transporter in deoxynivalenol tolerance in the biocontrol agent *Clonostachys rosea* strain ACM941.** Z. DEMISSIE AND M. C. LOEWEN
P13	CPS Student Competition. **Control of microRNA homeostasis and the establishment of effector-triggered immunity in *Arabidopsis thaliana*.**M.B.D.DIAM, T. ABD EL RAHMAN and K. BOUARAB
P14	**Leaf rust in Ontario: *Puccinia triticina* virulence and resistance genes identification in winter wheat.** B. D. MCCALLUM, L. TAMBURIC-ILINCIC, S. B. ROSA and A. TENUTA
P15	**Fusarium head blight resistance is enhanced by the wheat leaf rust resistance gene *Lr34*.** B.D. MCCALLUM, C.W. HIEBERT, J. THOMAS, and M.A. HENRIQUEZ
P16	CPS Student Competition. **Evaluation of Type II Resistance to Fusarium Head Blight in Canadian Winter Wheat.** M. KANG-CHOI, G. HUMPHREYS, S. CLOUTIER, W. CAO, A. XUE, AND A. NAVAB
P17	**Physiologic races of wheat leaf rust (*Puccinia triticina*) in Canada in 2016.** W. MCNABB, B.D. MCCALLUM, E. REIMER and A. XUE

P18	CPS Student Competition. **Fungal diversity across conventional, oasis and organic farming systems in arid areas of Oman.** ELHAM A. KAZEROONI and ABDULLAH M. AL-SADI
P19	**Genetic diversity of blackleg (*Leptosphaeria spp.*) isolates in Alberta**. E. PEREZ-LARA, R. FREDUA-AGEYMAN, S.-F. HWANG AND S. E. STRELKOV
P20	**Characterization of flax genotypes for resistance to *Oidium lini.*** KHALID Y. RASHID
P21	**Mapping QTL for *Fusarium* Head Blight Resistance in Canadian Spring Wheat AC Barrie.** DINUSHIKA THAMBUGALA, ANITA BRÛLÉ-BABEL, GEORGE FEDAK, MARIA ANTONIA HENRIQUEZ, ADAM FOSTER, RICHARD MARTIN, BRENT MCCALLUM, JEANNIE GILBERT, BARBARA BLACKWELL, DEAN SPANER, CURTIS POZNIAK, AMIDOU N'DIAYE and CURT MCCARTNEY
P22	CPS Student Competition. **Future Direction for Breeding Quantitative Disease Resistance in Barley at the Agriculture and Agri-Food Canada, Brandon Research and Development Centre.** JAMES R. TUCKER, ANA BADEA, COLIN W. HIEBERT, WILLIAM G. LEGGE, CURT A. MCCARTNEY and W. G. DILANTHA FERNANDO
P23	**Genome-wide association study for Fusarium wilt resistance in flax (*Linum usitatissimum* L.).** FRANK M. YOU, KHALID Y. RASHID, ZHEN YAO and SYLVIE CLOUTIER
P24	**Use of KASP assays for the analysis of *rpg4/Rpg5* gene complex for marker-assisted selection for Ug99 stem rust resistance in barley.** J. SANGHA, J. R. TUCKER, W. G. LEGGE AND A. BADEA
P25	CPS Student Competition. **The regulation of intrinsic signaling in *Brassica napus* defending against *Leptosphaeria maculans.*** C. YANG, AND W. G. DILANTHA FERNANDO
P26	CSA Student Competition. **Introduction of *Ac/Ds* Transposons into Oat Genome.** M. MAHMOUD, R. KAUR, and J. SINGH

Breeding

P27	**How many is too much: balancing utility with the cost of adding yield testing field sites in a wheat breeding program.** A. J. BURT, S. KUMAR, AND J. MITCHELL FETCH
P28	**Evaluation of soybean lines for resistance to iron deficiency chlorosis in southern Manitoba.** A. HOU and K.S. SANDHU
P29	CSA Student Competition. **Phenotyping of a Nepali spring wheat (*Triticum aestivum* L.) diversity panel for dark-adapted leaf epidermal conductance.** K. KHADKA, H. J. EARL, M. N. RAIZADA and A. NAVABI
P30	**Marker assisted wheat breeding for the Canadian prairies.** J. TOTH, S. PANDURANGAN, A. BURT, J. MITCHELL FETCH AND S. KUMAR
P31	**Principal Components Analysis facilitates selection of breeding lines with optimum trait combinations.** A. NAKHFOROOSH, C. MCCARTNEY, A. BEATTIE, S. KUMAR, A. BURT AND J. MITCHELL FETCH
P32	**Identification of pathogenicity factors involved in blackleg disease by *Leptosphaeria maculans* on canola.** C. SELIN AND W.G. DILANTHA FERNANDO
P33	**Crop management and the reduction of fusarium head blight in barley.** D. PAGEAU, S. RIOUX, A. VANASSE AND B. BLACKWELL

P34	CSA Student Competition. **Nitrogen Application Improves Photosynthetic Productivity, Leaf Chlorophyll Efficiency, and Yields of Contrasting Oat Genotypes under Salinity Conditions.** X. D. SONG, W. WU, B. L. MA, W. K. YAN, AND G. S. ZHOU
P35	**Integrated transcriptome and hormone profiling reveals the role of multiple phytohormone pathways in wheat resistance against Fusarium Head Blight.** L. WANG, L. JOHN, L. FOR-SEILLE, Z. LIU, T. FRANCIS, A. SURENDRA, Y. PAN, Y. LI, L. I. ZAHARIA, T. OUTLET AND P. R. FOBERT

Disease Management

P36	**First report of clubroot (*Plasmodiophora brassicae*) on canola in northern Ontario.** F. AL-DAOUD, M. MORAN, B.D. GOSSEN, AND M.R. MCDONALD
P37	**A shift in the pathotype of *Plasmodiophora brassicae* at a site in Ontario.** F. AL-DAOUD, B.D. GOSSEN, AND M.R. MCDONALD
P38	**The effect of selected mycorrhizae fungi on clubroot of canola.** A. SEDAGHATKISH, F. AL-DAOUD, S.H. LEE, J.J. ZWIAZEK, B. D. GOSSEN, AND M. R. MCDONALD
P39	CPS Student Competition. **Population dynamics survey of plant-parasitic nematode levels in southwestern Ontario tomato fields.** T. B. BLAUEL, M. J. CELETTI, M. R. MCDONALD AND K. S. JORDAN
P40	**Use of *Streptomyces sp*. in the biocontrol of *Rhizoctonia solani,* a root rot pathogen of soybean.** A. ARFAOUI, L. ADAM, F. DAAYF
P41	**Potential for biological control of potato late blight with *Pseudomonas chloroaphis* strain 189.** S. M. BOYETCHKO, P. AUDY, T. DUMONCEAUX, AND C. KIRBY
P42	**Biopesticides successfully supress bacterial spot disease caused by *Xanthomonas gardneri* in tomato.** MADANTHA.A.K. WIJESINGHE, TIM DUMONCEAUX AND SUSAN M. BOYETCHKO
P43	CPS Student Competition. **Does *glutathione-S-transferase 6* involve in canola disease defense against *Leptosphaeria maculans*?** K. R. E. PADMATHILAKE, M. F. BELMONTE, and W.G. DILANTHA FERNANDO
P44	**Development of southern stem canker disease on soybean seedlings in the greenhouse using a modified toothpick inoculation assay.** M. A. CAMPBELL, Z. LI, AND J. W. BUCK
P45	**Evaluation of field-based solutions to mitigate root rot of field pea.** S. CHATTERTON, R.S. ERICKSON, R. BOWNESS, B.D. GOSSEN, and M. W. HARDING
P46	**Fungicide efficacy against *Sclerotinia sclerotiorum* biofilms is improved by addition of trace elements.** M. W. HARDING, A. OMAR, B. BUZIAK AND J. FENG
P47	Field management practices have an effect on disease development in barley in Prince Edward Island. A. F. FOSTER, R. MATTERS AND R. A. MARTIN
P48	CPS Student Competition. **Analysis of NADPH oxidase family genes in *Verticillium dahliae* during interaction with potato.** X. ZHU, A. SOLIMAN, M. R. ISLAM, L. R. ADAM, F. DAAYF
P49	**Optimisation of suitable protocol to evaluate the pathogenicity of different *Fusarium* species affecting soybean in Manitoba.** Y. GHARBI, N. GARMA, M.A. HENRIQUEZ, X. WANG, L. ADAM, AND F. DAAYF

P50 **Effect of calcium cyanamide on clubroot (*Plasmodiophora brassicae*) of canola in a greenhouse study.** S. F. HWANG, H. U. AHMED, Q. ZHOU, H. FU, G. D. TURNBULL. AND S. E. STRELKOV

P51 **In-depth studies on Fusarium root rot of dry bean in Manitoba.** Y. M. KIM, M. A. HENRIQUEZ, D. L. MCLAREN, R. L. CONNER, K. F. CHANG, S. F. HWANG AND S. E. STRELKOV

P52 **Evaluating new seed-treatment chemicals to reduce early infection of blackleg on canola.** X. LIU AND G. PENG

P53 **Distribution of carrot cyst nematode in the Holland Marsh, Ontario, 2016.** M.R. MCDONALD, K. VANDER KOOI, D. VAN DYK, E. PONOMAREVA, F. SUN and Q. YU

P54 **Infection of canola cotyledons by *Leptosphaeria maculans* in relation to wounding and dew duration.** L. MCGREGOR and G. PENG

P55 **Meeting the challenges of carrot crown rot in Prince Edward Island.** R.D. PETERS, M.M. MACDONALD, H. LU, A. RYAN, S. ADAMS, J. DRISCOLL, A. MACPHAIL, D. GREGORY, B. CRANE, G. DYKERMAN, L. HALE AND G. WANG-PRUSKI

P56 **Assessment of strategies to enhance resistance against new Clubroot pathogens using current resources.** T. SONG, K, HORNADAY, N. TONU, F. YU, AND G. PENG

P57 **Three-dimensional coating of porous activated carbons with silver nanoparticles and its scale-up design for plant disease management in greenhouses.** YANG JIAN, XIUJIE LI, OLEKSANDRA SAVCHENKO and JIE CHEN

Agronomy

P58 CSA Student Competition. **Potential of biochar in reducing global warming potential and greenhouse gas intensities in corn silage cropping systems amended with different nitrogen sources.** W. ASHIQ, W. ALI, M. NADEEM, M. ZAEEM, S. M. GILLANI, J. WU, L. GALAGEDARA, V. KAVANAGH and M. A. CHEEMA

P59 **Haplotype analysis of loci associated with Fusarium head blight resistance in a collection of Brazilian spring wheat: An Update.** G. HUMPHREYS, L. LANGILLE, X. WANG, C. MCCARTNEY, S. KHANIZADEH and H. VOLDENG

P60 **Buckwheat (*Fagopyrum esculentum* Moench.) cultivar and seeding date response to Newfoundland growing conditions.** D.B. MCKENZIE, P.L. DIXON, C. NORONHA, AND K.N. HOBRECKER

P61 CSA Student Competition. **Plant density effects on N fixation by soybean and dry bean in southern Alberta.** T.T.N. THAI, F.J. LARNEY, J.E. THOMAS, M.S. BANDARA, D.G. PAULY, D.G. LE ROY

P62 **Effect of long-term phosphorus fertilizer management on phosphorus and cadmium concentration and yield of soybean.** R.M. MOHR, C.A. GRANT (ret'd), G.R. BARDELLA and D.N. FLATEN

P63 **Indian cup plant (*Silphium perfoliatum* L.): Promising results of a possible forage for the Canadian prairies.** M.P. SCHELLENBERG

P64 **Environmental correlates of creeping red fescue (*Festuca rubra* L. var. *rubra*) seed yield in Peace River region of Western Canada.** N. KHANAL, R. AZOOZ, J. OTANI AND H. W. KLEIN-GEBBINCK

P65 CSA Student Competition. **Relationship between rhizosphere soil acid phosphatase activities and**

	forage production in silage corn and soybean intercropping in cool climate. M. ZAEEM, M. NADEEM, W. ASHIQ, W. ALI, S.M. GILLANI, H. PHAM, V. KAVANAGH, S. ELAVARTHI, M.A. CHEEMA, L. GALAGEDARA, R. THOMAS
P66	**Phenotypic and Molecular Variation in Drought Tolerance of Jordanian Durum Wheat (*Triticum durum* Desf.) Landraces**. WESAM AL KHATEEB, ALA'A AL SHALABI, DANA SCHROEDER
P67	**Evaluation of western spring wheat varieties for their production potential in northwestern Ontario.** T. S. SAHOTA
P68	**Evaluation of Ontario and Manitoba winter wheat varieties for their production potential in northwestern Ontario.** T. S. SAHOTA

Epidemiology

P69	CPS Student Competition. **Comprehensive survey of soybean foliar diseases in Manitoba.** G. DIAZ-CRUZ AND B.J. CASSONE
P70	**Optimization of a TaqMan real-time PCR for detection of Goss's bacterial wilt pathogen in corn seeds.** A. SIDIBÉ, R. XU, F. DAAYF, A. SOLIMAN, L. ADAM, L. M. REID, T. BARASUBIYE AND J. T. TAMBONG
P71	**Collection and characterization of rust species infecting *Berberis* in Ecuador.** C. W. BARNES, M. E. ORDÓÑEZ, AND T. FETCH JR
P72	**Host range of *Phytophthora sansomeana* and the impact of inoculum density on disease severity, seedling emergence, and biomass of field pea.** K. F. CHANG, S. F. HWANG, H. U. AHMED, H. FU, Q. ZHOU, R. L. CONNER, D.L. M$_C$LAREN, S. E. STRELKOV AND G. D. TURNBULL
P73	CPS Student Competition. **Generation and characterization of *Fusarium graminearum* mutant overexpressing MAPK (Mgv1).** D. GONZÁLEZ-PEÑA FUNDORA, A. ERANTHODI, R. GOYAL, G. SUBRAMANIAM, C. RAMPITSCH, N. THAKOR AND N. A. FOROUD
P74	**Collection and characterization of species of *Berberis* in Argentina, Brazil, Chile, Ecuador, and Uruguay.** T. FETCH, S. HAMBLETON, M. S. CHAVES, J. MARTINELLI, G. B. P. DA SILVA, S. BORDIGNON, P. CAMPOS, R. MADARIANA, C. W. BARNES, M. E. ORDÓÑEZ, G. AZZIMONTI, AND S. GERMAN
P75	**Identification of strain-specific sequences in *Plasmodiophora brassicae*.** M. D. HOLTZ, S. F. HWANG AND S. E. STRELKOV
P76	**Development of high resolution melting (HRM) and TaqMan assays for *Plasmodiophora brassicae* strain identification.** M. D. HOLTZ, S. F. HWANG AND S. E. STRELKOV.
P77	CPS Student Competition. **Survey of *Pratylenchus neglectus* in Fields in Prairie Canada.** PRISCILLAR WENYIKA, FERNANDA GOUVEA-PEREIRA, and MARIO TENUTA
P78	**Quantitative PCR analysis of *Fusarium* species dynamics in Fusarium head blight of oat and barley.** M. BANIK, M. BEYENE AND X. WANG
P79	**Isolation and Identification of *Dickeya solani* from Hyacinth Bulbs Imported from the Netherlands.** X. LI, J. NIE, K. YUAN, H. XU, C. HUTTER, S. BRIÈRE, AND S.H. DE BOER
P80	CPS Student Competition. **Identification of *Fusarium* spp. and determination of chemotypes from bread and durum wheat samples collected during 2014 to 2016.** G. SINGH, A. BROWN AND H.R. KUTCHER

P81	**Priming effects of virulent *Plasmodiophora brassicae* strains on clubroot disease development during primary infection.** J. JIANG, R. FREDUA-AGYEMAN, S.-F. HWANG AND S. STRELKOV
P82	**Pathogenicity and plant defense response to a hypervirulent isolate of *Leptosphaeria maculans* induced by CRISPR/Cas system.** Z. ZOU, F. LIU, C. SELIN, and W.G. DILANTHA FERNANDO
P83	CPS Student Competition. **Telia production variability as a measure of sexual recombination in the *Puccinia striiformis* f. sp. *tritici* population of western Canada**. G.S. BRAR, K.LOU, S. ALI, AND H. R. KUTCHER
P84	**Interaction between spring wheat lines and deoxynivalenol (DON) chemotypes of *Fusarium graminearum***. K. HUDSON, M. SERAJAZARI, M. KAVIANI, AND A. NAVABI
P85	**Study on *Verticillium longisporum* of Canola for the First Reported Farm in North America.** A. AGARWAL and M. TENUTA
P86	**Virulence of isolates of *Claviceps purpurea* on eight different genotypes of wheat.** J.G. MENZIES, H.W. KLEIN-GEBBINCK, A. GORDON and D.M. O'SULLIVAN
P87	**Influence of cover crop residue management on the indigenous arbuscular mycorrhizal fungi, corn growth and yield.** MASAO HIGO
P88	**A potential biosensor for early detection of *Sclerotinia sclerotiorum* and *Leptosphaeria maculans* in canola**. X. LI, J. YANG, Y. HAO, X. YANG, & J. CHEN

ABSTRACTS - ORAL PRESENTATIONS (listed by topic)

Joint CPS/CSA Plenary Session

Toxigenic Fusarium Species and Mycotoxins: Challenges and Perspective

[FS1] *Fusarium* mycotoxins: Current research at the USDA ARS Mycotoxin Prevention unit. MATTHEW BAKKER, *Mycotoxin Prevention & Applied Microbiology, USDA Agricultural Research Service, 1815 N University St, Peoria, IL 61604*

Due to the health and economic costs of mycotoxins produced by *Fusarium* species, there is a compelling need for improved understanding of these fungi, from across diverse perspectives and disciplinary approaches. Current research at the USDA ARS Mycotoxin Prevention unit addresses *Fusarium* mycotoxins via research in chemistry, genomics and phylogenetics, fungal biology, plant-pathogen-environment interactions, and the phytobiome. **Chemistry**: We are active in screening isolates for toxin production to define the phylogenetic boundaries of trichothecene production, and in the identification of biotransformations that may limit the toxicity of trichothecenes. Acetylation of the C-3 oxygen helps protect Fusarium from the toxic effects of the trichothecenes during biosynthesis but toxins are deacetylated in infected plant tissue. Glycosyltransferases in plants can convert trichothecenes into less toxic glycosides. Microbial biotransformations of trichothecenes include acetylation, deacetylation, oxidation, de-epoxidation, epimerization, and glucosylation. **Genomics & phylogenetics**: We are using comparative genomic analyses to assess relationships among *Fusarium* species, to develop genetic markers to distinguish between species, and to determine genetic potential for production of mycotoxins and other secondary metabolites. The distribution of mycotoxin biosynthetic genes varies widely among *Fusarium* species, and has been shaped by vertical inheritance, gene loss, horizontal transfer, and gene duplication. Phylogenetic species delineation has resolved relationships among many taxa, and revealed the presence of additional taxa compared to classifications based on morphological and biological species concepts. **Fungal biology**: We are investigating the potential for reducing mycotoxin accumulation by manipulating *Fusarium* genetic regulatory mechanisms. We are testing RNA interference (RNAi) technology as a means of downregulating deoxynivalenol biosynthesis. **Plant-pathogen-environment**: Epidemiology of Fusarium head blight and accumulation of mycotoxins are directly related to climate. We have found that growth at elevated CO_2 concentrations alters the accumulation of wheat defense signaling phytohormones and pathogenesis-related (PR) gene transcript levels following *Fusarium* inoculation. **Phytobiome**: *Fusarium* species interact not only with plants, but also with a host of other organisms in the phytobiome. We are using amplicon sequencing to profile microbiomes associated with wheat and with *Fusarium*, with the expectation of revealing novel potential biocontrol organisms, or community-level characteristics that could impede pathogen success.

[FS2] A system approach to understand DON regulation in *Fusarium graminearum.* GOPAL SUBRAMANIAM, *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue; Ottawa, ON, K1A 0C6*

The mycotoxin deoxynivalenol (DON) produced by Fusarium spp. compromises plant host defenses and renders contaminated grains to be harmful to animals. Biosynthesis of DON involves integration of signalling pathways originating from myriad environmental conditions. Our understanding of DON biosynthesis has increased greatly in the last few years with accumulated knowledge from large scale genetics, genomics, and transcriptomics studies. However, most the information that has been gathered remains disconnected and only recently, efforts are underway to integrate by constructing gene expression networks, protein-protein interactions, etc. Thus, systems biology approaches offers an avenue to develop a comprehensive understanding of biological phenomena such as the biosynthesis of secondary metabolites.

[FS3] Wheat resistance to Fusarium head blight. GUIHUA BAI. *USDA Central Small Grain Genotyping Center, USDA/ARS/Hard Winter Wheat Genetics Research Unit, Manhattan KS 66506, USA*
Fusarium head blight (FHB), caused primarily by *Fusarium graminearum*, has rapidly become the most notorious wheat disease worldwide. Use of wheat resistance to FHB is the most effective and sustainable strategy to combat the disease. To date, more than 200 QTLs have been identified in diverse wheat populations, and *Fhb1* shows the highest level of resistance consistently in different genetic backgrounds. In spite of worldwide efforts to deploy *Fhb1* through wheat breeding, only a few cultivars currently used in production carry *Fhb1*. Recently *Fhb1* has been cloned and diagnostic markers have been developed, which will facilitate successful deployment of *Fhb1* in breeding. Using marker-assisted backcross, *Fhb1* has been successfully transferred into locally adapted cultivars that carry minor QTLs, and selected *Fhb1* lines in different backgrounds showed high levels of resistance. This approach may provide a quick solution to improvement of FHB resistance in commercial cultivars. In addition, gene editing that knocks down the susceptible allele of *Fhb1* in commercial cultivars may also improve wheat FHB resistance. However, most other QTLs identified to date show much smaller effects than *Fhb1*. These QTLs distribute in many locally adapted cultivars, and thus are important QTLs for FHB resistance improvement. Currently, diagnostic markers are still not available for most of these minor QTLs, therefore genomic selection may improve selection accuracy for these QTLs to create highly resistant cultivars.

[FS4] Exploring G x E x M synergies to manage Fusarium head blight in wheat. BRIAN BERES[1], ANITA BRULE-BABEL[2], ZESONG YE[2], ROBERT GRAF[1], T. KELLY TURKINGTON[3], MICHAEL HARDING[4], RANDY KUTCHER[5], AND DAVID HOOKER[6.]
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Fusarium head blight (FHB) is a key disease in wheat because of its production of mycotoxins (e.g., deoxynivalenol or DON) and direct detrimental effects on grain yield, quality, and marketability. Conditions most favorable for the development of FHB are high humidity, frequent rainfall and relatively warm night temperatures at heading, especially in regions where host crop residues are present. These risk factors have resulted in a significant westward expansion of FHB in the prairies, while favouring continued development in Ontario, Quebec, and the Maritimes. While cultivar selection is a key IPM strategy, a systems approach that couples genetics with management tactics is required. Thus, successful FHB mitigation is an ideal case study in Genotype (G) x Environment (E) x Management (M) interactions where more resistant cultivars (G) are grown in at risk regions (E), and require unique approaches to management (M) for sustainable wheat production. Given the few resistant cultivars, greater attention to management strategies is needed. The over-arching principle for FHB management is the manipulation of agronomic factors that allow the crop to complete critical developmental phases such as flowering, while doing so rapidly and uniformly, as a consequence of early sowing and increased seeding rates. These strategies and the adoption of practices involving proper fungicide selection, timing, and optimal application methods will lead to improved yield stability and quality in high risk environments. This paper will explore the potential synergies that exist for FHB mitigation when appropriate genetics are combined with an array of key agronomic strategies.

[FS5] Insights into Fusarium-host interactions gained from crop and model species. PAUL NICHOLSON, ANDREW STEED, RACHEL GODDARD, CHRISTOPHER BURT, BENJAMIN HALES, ANTOINE PERALDI, ELIZABETH BANKES JONES.
John Innes Centre, Norwich Research Park, Norwich NR4 7UH, UK
While most research into Fusarium head blight (FHB) is understandably focussed on resistance we have become interested in susceptibility. Investigations of wheat, barley and *Brachypodium distachyon* have highlighted the potential involvement of phytohormone signalling in both susceptibility and resistance to FHB. The relationships between particular pathways and susceptibility are not always clear-cut because of the hemi-biotrophic nature of the interaction between *Fusarium graminearum* and wheat. It appears that *F. graminearum* may be exploiting

certain pathways to prevent the plant from mounting an effective defence. This view is supported by the finding that isolates of *F. graminearum* are capable of producing some of the core phytohomones and these may be used by the pathogen to force/persuade the plant to maintain growth at the cost of mounting a full defence.

While the majority of wheat varieties lack the ability to prevent the spread of the fungus once it enters the spike, barley varieties have high levels of so-called Type 2 resistance and the fungus is generally restricted to infect individual spikelets. We examined barley chromosome addition/substitution lines of wheat to determine whether the addition of particular barley chromosomes could provide Type 2 resistance. The most potent effect, however, derived from the substitution of chromosome 4D suggesting that the lack of type 2 resistance in wheat is due to the presence of a susceptibility factor(s) rather than the absence of resistance factor(s).

While resistance to FHB and DON mycotoxin accumulation in agronomically adapted varieties can undoubtedly be enhanced by the introduction of resistance from various sources it is also possible that resistance can be increased through the elimination of susceptibility factors. The challenge in both cases is to provide robust FHB resistance without compromising other important agronomic characteristics required by breeders and growers.

CPS Symposium

Disease Issues in Soybeans and Pulses: Old Foes and New Challenges

[SP1] Current and Emerging Nematode Issues with Soybean and Pulses in Canada. ALBERT TENUTA. *Ontario Ministry of Agriculture, Food and Rural Affairs*, *Ridgetown, Ontario, Canada*

Soybean and pulses are some of the most economically important field crops grown in Canada and world-wide. But unfortunately, losses caused by both endemic and emerging nematode pests continues to be a major limitation towards sustainable production and producer profitability. New emerging soybean and pulse nematodes are potential invasive threats as they migrate to other geographical areas of Canada and elsewhere. For soybeans, soybean cyst nematode (SCN) remains the most important yield-limiting disease in soybeans. Unfortunately, yield loss is likely to increase in the future as SCN spreads to new soybean production areas in Prairie Canada as well as new aggressive SCN populations (HG-Types) develop in Ontario and Quebec which can feed and reproduce on the available sources of resistance to SCN. Establishment of SCN should follow the expansion of soybean acreage in Prairie Canada. Currently our surveys have not shown SCN to be in Manitoba. Its presence across the US border implies it soon will be established. Recent market access issues and its resolution for pulse exports due to the stem nematode, *Ditylenchus*, have also highlighted the importance of surveillance and identification programs in Canada. Emerging issues include the root lesion nematodes, *Pratylenchus penetrans* in Ontario and Quebec, *P. alleni* in Quebec and *P. neglectus* in Prairie Canada. In summary, early detection, awareness and implementation of appropriate control measures of these endemic and emerging diseases is critical to sustainable soybean and pulse production.

[SP2] Management of *Phytophthora sojae* in soybean: a review and future perspectives. A.E. DORRANCE. *Dept. of Plant Pathology, The Ohio State University-OARDC, 1680 Madison Ave., Wooster, OH 44691*

Phytophthora sojae Kaufmann & Gerdemann has been a yield limiting factor for soybean (*Glycine max* L.) in Ohio and other regions where soils are poorly drained for more than 60 years. Soybean is the primary host, although numerous *Lupinus* spp. have been called hosts based on artificial inoculations. More than 20 different major resistance (*Rps)* genes have been reported from sources from China, Japan, and South Korea; but few are deployed in cultivars. As in other host-pathogen systems with a gene-for-gene interaction, there are also numerous pathotypes (races) of *P. sojae*, with as few as 1 to more than 50 characterized within a single field. Due to high pathogen diversity and complexity in relation to pathotype, quantitative disease resistance (QDR) or partial resistance has become a priority and serves as the backbone for disease management in some production regions. However, QDR requires the use of seed treatments for early season protection in highly favorable environments. Current research efforts for the development of more durable management of this disease include the identification and characterization of novel *Rps* genes as well as markers and mechanisms that contribute to the expression of

QDR. There are at least two new seed treatment chemistries for *P. sojae* that will be available in addition to metalaxyl based fungicides. Finally, pathogen population structure both within and between production regions as well as variability within *Avr* loci of *P. sojae* are also elucidating potential new approaches to managing this disease.

[SP3] The long path to understanding a host-pathogen system: *Colletotrichum lentis* on lentil. S. BANNIZA
Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada
Among lentil diseases reported from around the world, anthracnose caused by the fungal ascomycete pathogen *Colletotrichum lentis* Damm is either not mentioned, or listed as a minor disease. In Canada, it was originally found in Manitoba in 1987 where most of the lentil acreage was grown at the time, and within three years was also detected in Saskatchewan as lentil production moved westward. , Since then, it has developed into the most important foliar lentil disease. Originally described as *C. truncatum* (Schwein.) Andrus & W.D. Moore, isolates from lentil were designated their own species in the destructivum clade in 2014. Two sexual incompatibility groups have been identified in the Canadian population, but both harbour *Mat 1-2* while lacking *Mat 1-1*, so sexual mating does not follow the classical ascomycete system of heterothallic species. Field data indicate that it primarily reproduces asexually, but readily mates in the laboratory, so may have facultative sexuality. The pathogen has a hemibiotrpophic life style with a brief biotrophic phase followed by necrotrophy. Two pathogenic races have been described and partial resistance to the less virulent race 1 was found in the cultivated lentil spaces. High levels of resistance to the virulent race 0 have only been identified in the related species *Lens ervoides*, and was introgressed into cultivated lentil. Using an ascospore-derived population developed from a cross between a race 1 and a race 0 isolate, one QTL for virulence was identified on one of 12 chromosomes.

[SP4] *Colletotrichum lentis* races on lentil and polymorphisms in the IGS region of ribosomal DNA related to pathogenicity. LONE BUCHWALDT, EDIS DZANANOVIC and JONATHAN DURKIN. *Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, 107 Science Place, Saskatoon, SK, S7N 0X2, Canada.*
The fungal pathogen *Colletotrichum lentis* Damm causes anthracnose of lentil (*Lens culinaris* L) in Canada, but is rarely reported elsewhere. In 2004, two races, Ct0 and Ct1, were characterized by inoculating differential lentil lines. Simultaneously, lines resistant to race Ct1 were identified after screening a world lentil collection. Subsequently, many lentil varieties were developed by the University of Saskatchewan with resistance to this race. In 2013, lines of *L. culinaris* with resistance to race Ct0 were published after multiple cycles of inoculation and selfing of resistant plants. Thus, resistance to Ct0 can now be crossed into Canadian varieties as with Ct1-resistance. In 2015, we discovered polymorphisms in the intergenic spacer (IGS) of ribosomal DNA consisting of 39 and 23 nucleotide (nt) repeats which differentiated the two *C. lentis* races. Length variations in the 39 nt repeat was used to survey isolates from lentil fields collected eleven years apart, and showed that the two races occurred at equal frequency before 1999, while race Ct0 dominated in 2010 most likely because Ct1-resistant varieties were grown in the intervening years. Interestingly, the 23 nt repeat has 10 conserved and 13 variable nucleotides in ten different variations, A-J. All Ct1 isolates have 17 repeats with identical order of A-J, while Ct0 isolates have either 14 or 19 repeats of a different order. We hypnotize that the IGS region has a molecular function, and are investigating whether the 23 nt repeat region synthesise race-specific RNA that interact differentially with receptors in the host plant.

CSA Symposium
Extending the Growing Season

[EGS1] Redesigning Canadian cropping systems for profitability, sustainability, and resilience. JOANNE THIESSEN MARTENS. *Department of Plant Science, University of Manitoba, Research Associate, Organic Production Agronomy*
Despite dramatic gains in crop genetics and the efficiency and precision of soil fertility management and crop protection, Canadian cropping systems continue to suffer the effects of pests and extreme weather and to cause unintended negative effects on the environment. Certain agricultural scientists are calling for a redesign of farming systems based on ecological processes and relationships, such as diversification, use of perennial plants, and crop-livestock integration. Extending the growing season through the use of perennial crops, or even cover crops or

winter annuals, allows for better use of available resources, including moisture, heat and photosynthetic potential, while reducing erosion potential and supporting soil biological activity. A holistic approach to farm system design, with attention to integrating the functions of diverse farm components, has the potential to improve Canadian crop production's environmental footprint while supporting long-term farm profitability and resilience.

[EGS2] Winter Cereals in Western Canada. R.J. LARSEN, B.L. BERES AND R.J. GRAF. *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada. 5403-1st Ave. S., Lethbridge, AB, Canada, T1J 4B1.*
Winter cereals provide distinct advantages over spring cereals. This includes capturing more moisture and sunlight from an extended growing period leading to higher grain and biomass yields. Further advantages include limiting weed pressure, soil erosion and exposure to multiple disease and insect pest which are regularly serious threats to spring cereal production. The story of winter cereals in western Canada is a marriage of the right agronomic practices with the right varieties. The agronomic system for winter cereals in western Canada is built around ensuring that the crop survives the winter. Critical to this system is uniform plant stands reaching the optimum growth stage to maximize cold tolerance and no-till production systems ensuring the maintenance of insulating snow cover through the utilization of stubble from the previous crop. The requirement for cold tolerant winter cereal varieties remains a focus for plant breeders; however, limited gains in cold tolerance have been realized in over 40 years. For wheat, major gains from a breeding perspective include the incorporation of robust disease resistance packages to ensure adaptation to growing conditions across the prairies, introduction of shorter, lodging resistant varieties, significant improvements in yield and the elevation of grain quality towards spring wheat levels. Fall rye and winter triticale lag in terms of similar levels of improvement; however, the recent introduction of hybrid rye to Canada and new high yielding triticale varieties targeted for grain, silage and double cropping means that the potential of winter cereals to be used to extend the growing season in Western Canada continues to be significant.

[EGS3] Annual and Perennial Forages for Fall/Winter Grazing. EMMA MCGEOUGH. *Department of Animal Science, University of Manitoba, Sustainable Grasslands/Livestock Production Systems*
Favoured for lower cost and labour requirements, extending the grazing season by maintaining beef cattle on pasture has been adopted by many producers on the Prairies. Grazing of stockpiled forages in the fall/winter following early season grazing reduces the need for mechanical harvesting and lowers manure management costs relative to feeding cattle in confinement. As the objective is low cost pasture-based, non-confined feeding, the identification of forages that can retain their nutritive value and support desired levels of animal productivity is essential. Stockpile grazing of perennial grass and legume species that retain nutritive value late in the growing season, alone or in combination, offers the potential for low input grazing. Additionally, annual forages, traditionally harvested as grain crops may also offer viable options to extend the grazing season for beef cattle.

[EGS4] Enhancing Yields and Environmental Sustainability of Biomass Production Systems by Capitalizing on the Extended Growing Periods. NARESH THEVATHASAN. *School of Environmental Sciences, University of Guelph, Guelph, ON. N1G 2W1*
In Canada, fossil fuel use can be reduced by growing biomass crops on lands that are not used for agricultural production, and enhance the capture of solar energy via photosynthetic pathways even beyond the conventional agricultural crops growing period. Biomass crops grown are perennials and once they are established the production systems can remain undisturbed for the next 15 to 21 years contributing to numerous environmental and socio-economic benefits.
Two major types of biomass crops are being promoted by BioFuelNet Canada and by the Canadian Wood Fibre Centre, NRCan. They are: herbaceous [switchgrass (*Panicum virgatum* L), miscanthus (*Miscanthus giganteus*)], and woody [poplar hybrids (*Populus* spp.), willow hybrids (*Salix* spp.)] biomass crops. Continuous and uninterrupted supply of biomass is important for all types of end-users including the emerging bio-auto products, heat energy for the northern First Nations, biofuels and biochemical industries. In this context, the University of Guelph, in collaboration with BioFuelNet Canada and the Canadian Wood Fibre Centre, NRCan has set-up long-term biomass crops research sites in the provinces of Alberta, Ontario and Nova Scotia. Sites were established in 2009 and in 2014

to study the yield responses of above indicated biomass crops in Canada with an aim to identify the best regions to grow these biomass crops.
Results, to-date, suggest that yields are significantly influenced by eco-climatic conditions in conjunction with nutrient cycling and soil carbon sequestration. The latter two are vital ecosystem processes contributing to sustainable biomass yields.

[EGS5] Forage Seed Production and Perennial Grains. DOUGLAS J. CATTANI AND SEAN R. ASSELIN**.** *Department of Plant Science, University of Manitoba, Winnipeg, Mb, Canada, R2T 2N2*
Production agriculture relies primarily on seeding of annual crops for food, feed, fuel and fibre in western Canada. Annual seeding and harvesting commonly leave land non-productive for a portion of the year. There is the potential for both soil and nutrient loss from this unused land base, and as important, we are missing the potential for photosynthesis. Capture of carbon in these off-season times may aid in carbon sequestration. Forage production (feed) relies on an animal market for its consumption. Forage seed production in Canada, seed for forage establishment, accounts for approximately 65,000 ha year^{-1}, and is almost exclusively located in western Canada. It is unlikely however that forage seed production area will dramatically increase due to limited markets. Perennial grains could greatly increase the land area dedicated to perennial seed production and provide alternative markets to forages and forage seed. Intermediate wheatgrass (*Thinopyrum intermedium* (Host) Bark. & Dewey) (Kernza^{TM}) is the perennial grain closest to release and some potential niche markets are currently emerging. Improvement has been made through selection for grain production on individual plants for characteristics that are likely of importance at field scale production. Agronomic packages for intermediate wheatgrass production are lacking, although forage seed production agronomy will guide this development. Agronomic benefits attributed both to perennial seed production and the inclusion of perennials in cropping systems will be greatly enhanced when the potential for perennial grain production (breeding and agronomy) is realized.

[EGS6] Producer perspective and application to extend the growing season. RYAN BOYD. *SG&R Farms, Forrest Manitoba*
Ryan Boyd is a family farmer who is passionate about soil health, forage efficient cattle and no-till cropping systems. Ryan operates a mixed farm just north of Forrest, Manitoba with his wife Sarah, daughter Piper, son Bingham, and parents Jim and Joanne Boyd. The farm focuses on integrating cattle and livestock to capitalize on the many synergies that exist between the two. The farm consists of approximately 300 black Angus beef cows, calving in June and a diverse crop rotation including spring and winter wheat, oats, canola, flax, peas, soybeans, corn, perennial forages and diverse annual forages for grazing and green feed. Several techniques are used to extend the growing season with the intent to make the most efficient use of available resources, including sunlight energy, water and nutrients.

CPS Contributed Paper Session (Student Competition*)
Genetics and Resistance

***[GR1] Transcriptome analyses of canola (*Brassica napus*) treated with the plant growth promoting rhizobacterium *Pseudomonas chlororaphis* PA23 identifies differential expression of growth and defense related genes.** J.C. WAN, M.G. BECKER, M.F. BELMONTE, T.R. DE KIEVIT, W.G.D FERNANDO. *Department of Biological Sciences, University of Manitoba, 66 Chancellors Circle, Winnipeg, MB, R3T 2N2, Canada;* (*J.C.W., M.G.B., M.F.B.*). (*T.R.D*) *Department of Microbiology, University of Manitoba, 66 Chancellors Circle, Winnipeg, MB, R3T 2N2, Canada. (W.G.D.F) Department of Plant Science, University of Manitoba, 66 Chancellors Circle, Winnipeg, MB, R3T 2N2, Canada*
The rhizosphere is a complex environment with a microbiome that contains bacterial and fungal species that promote plant growth. Recently, the use of microbes has become an emerging solution for improving productivity and sustainability of the agro-ecological landscape. However, the mechanisms underlying these intricate plant-microbe interactions are poorly characterized. *Pseudomonas chlororaphis* strain PA23 is a gram-negative

rhizobacterium endogenous to the soils of Western Canada. Canola seedlings treated with *P. chlororaphis* as a soil drench were larger in size with more developed root and shoot systems. We used a combination of RNA sequencing and computational biology to uncover the genes and gene ontology terms responsible for the remarkable growth phenotype. We show that treatment of canola with *P. chlororaphis* increased the expression of genes associated with photosynthesis, nutrient transport, and growth regulation. We also provide preliminary evidence that *P. chlororaphis* is capable of root colonization through the repression of host defense hormone signaling. Together, this study presents novel data into the global genetic and regulatory mechanisms responsible for improved plant performance and has applications for growing strategies using biological additives in Canada and abroad.

***[GR2] Investigating the Cross Kingdom Biosynthesis of Cytokinin in the *Ustilago maydis-Zea mays* Pathosystem** I. O. ALIMI, R. J. N. EMERY and B. J. SAVILLE. *Environmental and Life Sciences Graduate Program, Trent University, 1600 West Bank Drive, Peterborough, ON K9J 0G2, Canada; (R.J.N.E.) Biology Department, Trent University, 1600 West Bank Drive, Peterborough, ON K9J 0G2, Canada; and (B.J.S.) Forensic Science Program, Trent University, 1600 West Bank Drive, Peterborough, ON K9J 0G2, Canada*

Tumour formation in the *Ustilago maydis-Zea mays* pathosystem is a characteristic symptom of common smut of corn. During the development of these tumours, cytokinin levels are elevated. More specifically, the freebase *cis*-zeatin (cZ), riboside *cis*-zeatin (cZR), nucleotide *cis*-zeatin (cZRP) and O-glucoside *cis*-zeatins (cZROG) are elevated during infection. Although the level of these *cis*-zeatins are increased, the biosynthetic origins of these cytokinins have not been determined. Are they produced by the corn host or the fungus? Both can produce *cis*-zeatins when grown independently. To investigate this phenomenon, we identified the genes potentially involved in the biosynthesis of *cis*-zeatins, via the tRNA degradation pathway, in both organisms. Plant and fungal genes responsible for the common steps in the biosynthetic pathway had distinct sequences and this allowed us to determine the organism specific changes in transcript levels over the course of infection by using reverse transcription PCR (RT-PCR). The results are consistent with a *cis*-zeatin pool arising through the activity of host and pathogen enzymes. This led a model of the interaction in which, during early infection, the host attempts to modulate the levels of active cytokinins produced during infection by converting cZR to cZROG and cZRP; and then later during infection, the glucose modulation reverses, possibly due to pathogen glucosidase, causing the conversion of cZROG to cZR which would release glucose that could act as an additional carbon source for *U. maydis* during teliospore formation. Progress on experiments aimed at testing this model will be presented.

***[GR3] Transcriptome profiling and laser microdissection identifies new regulators of resistance against blackleg disease of canola.** M.G. BECKER, X. ZHANG, P.L. WALKER, W.D.G. FERNANDO, M.F. BELMONTE. *(M.G.B., P.L.W., J.W., M.F.B.); Department of Biological Sciences, University of Manitoba, 66 Chancellors Circle, Winnipeg, MB R3T 2N2, Canada. (X.Z., D.W.G.F) Department of Plant Science, University of Manitoba, 66 Chancellors Circle, Winnipeg, MB R3T 2N2, Canada.*

Leptosphaeria maculans, the causative agent of blackleg disease of canola, is a devastating fungal pathogen that affects the Canadian agriculture industry. Using RNA sequencing we identified 54 genes activated exclusively in resistant Canola cotyledons during defense against *L. maculans*. This includes receptors, transcription factors, and regulators of indole glucosinolate biosynthesis that were expressed specifically in resistant hosts across the first 11 days of infection. Arabidopsis plants carrying mutations in homologous genes were susceptible to blackleg infection, functionally validating RNA sequencing data and suggesting defense pathways against *L. maculans* are conserved between closely related plant species. Further, we identified spatial expression patterns directly at the host-pathogen interface by combining laser microdissection and gene expression profiling. Results suggest mobilization of cellular receptors and transcription factors in tissues directly exposed to invading pathogen at the RNA level. Additionally, changes in gene activity within several hundred microns from the infection site suggests development of antagonistic gradients of gene expression associated with salicylate and jasmonate signaling. Together, our research improves our understanding of blackleg resistance in the *Brassicaceae*, and provides a suite of new targets to bolster resistance in one of Canada's most valuable crops.

***[GR4] Interaction of Fusarium head blight resistance genes *Fhb1*, *Fhb2*, and *Fhb5* with fungicide application in hard red spring wheat.** G.S. BRAR, P.J. HUCL AND H.R. KUTCHER. *Crop Development Centre/Department of Plant Science, University of Saskatchewan, 51 Campus Dr., Saskatoon, SK S7N 5A8 Canada*

Fusarium head blight (FHB), caused by *Fusarium graminearum*, is one of the most devastating diseases of wheat in North America. There are many studies on integrated management of FHB combining host resistance and fungicide application, however, there are no studies of the interaction of fungicide with FHB resistance genes. The objective of this study was to assess the interaction of fungicide with three resistance genes: *Fhb1* (Type II resistance), *Fhb2* (Type II resistance), and *Fhb5* (Type I + some type II resistance). Two field experiments were conducted in 2016 in Saskatchewan consisting of six genotypes: CDC Go (moderately susceptible check), Carberry (moderately resistant check), and four near-isogenic lines (NILs) carrying *Fhb1*, *Fhb2*, *Fhb5*, and *Fhb1+Fhb2+Fhb5* in the CDC Go background. The Group 3 fungicide metconazole (Caramba®) was applied at the recommended 50% anthesis crop stage. There was no interaction of fungicide with the resistance genes for any trait measured. Both factors, resistance gene and fungicide application had an effect on disease incidence, FHB index, deoxynivalenol (DON) content, yield, test weight (TW), and thousand kernel weight (TKW), however, only resistance gene reduced disease severity. CDC Go had the highest FHB incidence, severity, and index; Carberry had the lowest, followed by the NIL carrying all three genes. Fungicide application reduced FHB index, FHB incidence, and DON, and improved yield, TW, and TKW, only in NILs carrying single genes. In most cases, fungicide application to the susceptible check did not reduce FHB index. The FHB index and DON content were positively correlated, however the FHB index was negatively correlated with TW, TKW, and yield.

***[GR5] Identification, characterization and mapping of the seedling wheat leaf rust resistance gene in RL6071.** M.Z. Che, B.D. McCallum, M. Boyce, C.A. McCartney and C.W. Hiebert. *(M.Z.C.; B.D.M.; C.A.M; C.W.H) Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Unit 100, Morden, MB, R6M 1Y5, Canada; (M.Z.C.) Department of Plant Pathology, China Agricultural University, Beijing, 100193, People's Republic of China; and (M.B) Global Edible Oil Solutions - Specialties, Cargill Ltd. Canada, 701 Central Ave. Aberdeen, SK, Canada, S0K 0A0.*

The emergence of a new predominant race of leaf rust, TDBG, in the 2004 Canadian virulence survey led to the identification of a second leaf rust resistance gene in the Thatcher-*Lr1* near-isogenic differential line, RL6003, in addition to *Lr1*. This gene, temporarily named *LrCen* produced an unusual mesothetic infection type and was mapped on 7AL. A gene with a very similar infection type was found in the stem and leaf rust susceptible line RL6071 (Prelude/8*Marquis*2/3/ Prelude//Prelude /8*Marquis). Using 116 KU168-2/RL6071 double haploid lines we mapped this gene in RL6071 (temporarily named *LrMar* because of the genetic similarity of RL6071 with Marquis) on 7BL, between markers barc182 and barc50, with linkage distances of 1.8 and 0.9cM, respectively. As *Lr14a/Lr14b*, *LrBi16* and *LrFun* were also mapped on 7BL, these four genes were compared by SSR markers close to each gene, and differential reaction to 16-45-3 TSBS. Results suggested that *LrMar* was a different gene from *Lr14a*, *LrBi16* or *LrFun*. To explore the relationship among *LrMar*, *LrCen* and *Lr20* since they shared a similar infection type, we tested cfa2240 (close to *LrCen* on 7AL) and barc182 and barc50 (close to *LrMar* on 7BL) on lines with each gene. These markers would indicate which lines are likely to carry *LrMar* or *LrCen*. Fourty-five selected Canadian wheat cultivars were tested with barc182 and cfa2240, eight lines were positive for the allele size indicative of *LrMar* and eight lines were positive for *LrCen*, which suggested that the two genes were distributed at a low frequency throughout Canadian germplasm. A number of Canadian wheat lines had a mesothetic response to TDBG, but were not positive for the alleles of neither barc182 nor cfa2240 associated with resistance. The TDBG resistance in the Tc-*Lr20* NIL segregated independently of cfa2240 so was not *LrCen*, and also segregated independent of a molecular marker for *Lr20*, this resistance could be due to *LrMar* or a similar type of gene.

***[GR6] The *Ustilago maydis* transcription factor Zfp1 regulates the expression of effectors required for full pathogenesis, virulence, and anthocyanin production.** H.Y.K. CHEUNG, M.E. DONALDSON, K.L. SPENCE, J.L.O. FETSCH, M.C. HARRISON AND B.J. SAVILLE. *(M.E.D., B.J.S) Environmental and Life Sciences Graduate Program, Trent University, Peterborough, ON, K9J 7B8, Canada; (K.L.S.) Department of Population Medicine, Ontario Veterinary*

College, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada; *and (M.E.D, B.J.S, J.L.O.F., M.C.H) Forensic Science Program, Trent University, Peterborough, ON, K9J 7B8, Canada*
As a biotrophic plant pathogen, *Ustilago maydis* D.C. Corda secretes effectors to establish and maintain a relationship with the host, *Zea mays*. One such effector, *tin2*, induces host anthocyanin production to facilitate fungal penetration of host cells. The molecular functions of *tin2,* and other effectors, have been characterized, but there is limited knowledge of how effector gene expression is controlled. We identified a *U. maydis* transcription factor, Zfp1 that, when deleted, altered transcript levels of 1870 genes, several encoding predicted or confirmed effectors. Notably, 83 predicted effectors, including *tin2*, were found to be down-regulated. The reduced pathogenesis and arrested virulence exhibited by infection with *zfp1* deletion (Δ*zfp1*) strains is consistent with this altered expression of effector genes. Conspicuously Δ*zfp1* infected seedlings produced little to no anthocyanin, and hyphal growth of Δ*zfp1*strains was localized to the epidermis with attenuated hyphal branching, which are consistent with deregulation of *tin2*. When a *zfp1* deletion strain was complemented using wild-type *zfp1*, *tin2* transcript levels were restored to near wild-type levels, and pathogenesis and virulence were partially restored. The partial complementation suggests Zfp1 may have a binding partner or interact with other factors to regulate pathogenesis and virulence. Complementation of the *zfp1* deletion strain with wild-type *tin2* partially restored pathogenesis and virulence and fully reestablished anthocyanin production, indicating that some Δ*zfp1* phenotypes result from altered *tin2* regulation. It also indicates that Tin2 acts downstream of Zfp1. We conclude that Zfp1 contributes to *U. maydis* pathogenesis, virulence, and anthocyanin production by regulating effector gene expression.

***[GR7] Genetic mapping of leaf rust resistance in the tetraploid wheat cross Strongfield/Blackbird.** X. PEI[12*], B. D. MCCALLUM[1], C. W. HIEBERT[1], C. A. MCCARTNEY[1], A. BRÛLÉ-BABEL[2], R. KNOX[3], Y. RUAN[3], C. J. POZNIAK[4]. *[1] Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB R6M 1Y5, Canada [2] Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB R3T 2N2, Canada [3] Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, 1 Airport Road, Swift Current, SK S9H 3X2 Canada [4] Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada [*]Correspondence: curt.mccartney@agr.gc.ca or peix@myumanitoba.ca*
Leaf rust, caused by *Puccinia triticina* Eriks. (*Pt*), is an economically important disease of wheat worldwide. Deploying wheat cultivars with effective leaf rust resistance (Lr) genes is an efficient method for disease management. The genetic basis of leaf rust resistance was studied using a doubled haploid (DH) population of the cross Strongfield/Blackbird. Strongfield is a widely grown Canadian durum wheat variety (*Tritucum turgidum* var. *durum* L.; genome AABB), which is highly resistant to *Pt* in Canada. Blackbird (*Triticum carthlicum*; genome AABB) is susceptible to *Pt* at the seedling stage but may possess adult plant resistance to leaf rust. The population was previously genotyped with SSR markers and the 90K wheat Infinium SNP array. Based on QTL analysis of leaf rust reaction from an inoculated field nursery in 2016, one resistance gene was found on chromosome 1B in Blackbird and another was found on chromosome 3AS in Strongfield. This population was then screened for leaf rust resistance with multiple races at the seedling stage indoors; Blackbird was susceptible while Strongfield was resistant. One leaf rust resistance gene was identified on chromosome 3AS based upon seedling inoculation data and 90K wheat Infinium SNP genotype results. Specific KASP markers will be designed for marker-assisted selection based on the linkage map.

***[GR8] Development of molecular markers linked to Leptosphaeria maculans resistance gene Rlm6 and inheritance of SCAR and CAPS markers in B. napus x B. juncea interspecific hybrids.** M. HARUNUR RASHID, ZHONGWEI ZOU AND W.G. DILANTHA FERNANDO. *Department of Plant Science, University of Manitoba, Winnipeg, MB, R3T 2N2 Canada*
Canola/rapeseed (*Brassica napus*) is an economically important oilseeds crop in China, Canada Europe and Australia. It serves as a host to a number of major fungal pathogens including *Leptosphaeria maculans*, the causal agent of blackleg disease, which causes significant yield loss. *B. juncea*, carrying the B-genome, has shown high levels of resistance to blackleg disease and is a promising source for the development of resistant *B. napus* varieties. To

determine the resistance genes carried by the *B. juncea* cultivar 'Forge', pathogenicity tests were carried out using a differential set of *L. maculans* isolates. This study revealed that the 'Forge' cultivar carried a single dominant *Rlm6* resistance gene. To transfer the *Rlm6* resistance gene from *B. juncea* into *B. napus*, an interspecific cross between *B. napus* 'Topas DH16516' and *B. juncea* 'Forge' was performed followed by the development of F_2 and F_3 generations. In addition, Sequence Characterized Amplified Regions (SCAR) and Cleaved Amplified Polymorphic Sequence (CAPS) markers linked to *L. maculans* resistance gene *Rlm6* were also developed. The segregation of SCAR and CAPS markers linked to *Rlm6* in F_2 and F_3 progeny were confirmed by PCR genotyping. Genotyping SCAR markers suggested that approximately 52% of F_2 and 28% of F_3 plants carried *Rlm6*, indicating a distortion of the expected segregation ratio for the dominant markers. More importantly, segregation of CAPS marker and phenotype for the blackleg disease severity in F_2 plants have an acceptable fit ratio of 3:1 in resistant versus susceptible plants, respectively, supporting the assumption that genetic control of resistance is by a single dominant gene.

***[GR9] Effector triggered immunity vs non-host resistance against potato cyst nematodes, a transcriptomic analysis.** M. SABEH, E. LORD, M. ST-ARNAUD AND B. MIMEE. *Saint-Jean-sur-Richelieu Research and Development Center, Agriculture and Agri-Food Canada, 430 boulevard Gouin, Saint-Jean-sur-Richelieu (QC) J3B 3E6; (M.S. and M.S-A.) Biodiversity Center, University of Montreal and Montreal Botanical Garden, 4101 Sherbrooke East, Montréal (QC) H1X 2B2.*
The potato cyst nematodes *Globodera rostochiensis* and *G. pallida,* are major plant parasitic nematodes affecting Solanaceous species including potato, tomato, and eggplant. They are quarantine organisms in Canada and many other countries. These nematode species have developed specialized proteins called effectors to outwit plant defenses. Some plants as a result evolved resistance based on the recognition of these effectors, which was again overcome by virulent nematode pathotypes. RNA sequencing of different *Globodera* species and pathotypes at the parasitic stage was used to identify sequence variations and differentially expressed genes. *G. rostochiensis* and *G. pallida* were directly compared to *G. tabacum* and *G. mexicana* because of the difference in their primary host and genetic similarities. Pathotypes of *G. rostochiensis* were also compared to understand their ability to parasitize different potato genotypes. These analyses revealed 22 genes unique to potato infecting species, *G. rostochiensis* and *G. pallida*, including 10 that have a signal peptide but no transmembrane domain suggesting they are secreted and potentially implicated in pathogenicity. These analyses also highlighted genes, including the RBP-1 and RBP-4 effector genes, as being significantly more expressed as well as having sequence variation which show very strong evidence of being associated with pathogenicity in the same two species. *G. rostochiensis* pathotype analysis showed members of the SPRYSEC effector family strongly associated with avirulence to the H1 resistance gene, deployed in commercially available resistant potato.

[GR10] Comprehensive investigation of gene transcript level change during teliospore germination in *Ustilago maydis. A.M. SETO, M.E. DONALDSON AND B.J. SAVILLE. *Environmental and Life Sciences Graduate Program, Trent University, 2140 East Bank Drive, Peterborough, ON, K9L 0G2, Canada; (B.J.S.) Forensic Science Program, Trent University, 2140 East Bank Drive, DNA Building, Peterborough, ON, K9L 0G2, Canada*
The fungal plant pathogen *Ustilago maydis* D.C. Corda is dispersed as thick-walled teliospores, which are dispersed, germinate, complete meiosis, and initiate new rounds of infection. Teliospore germination is asynchronous and this is a challenge when identifying changes in gene expression. This challenge was overcome by performing RNA-seq on dormant *U. maydis* teliospores and teliospores induced to germinate for 9 and 18 hours. RNAs in the teliospore may be at a higher or lower level than in the haploid or dikaryon cultures. Starting from either of these two levels, nine distinct patterns in transcript level change were identified during teliospore germination. The existence of these 18 patterns suggested transcriptional and post-transcriptional control of gene expression during teliospore development and germination. Gene ontology (GO) term enrichment analyses were performed to identify the biological categories that are represented in each pattern. This provided insight into the biological processes that are changing during teliospore germination. Reverse transcriptase quantitative PCR (RT-qPCR) was performed, to assess the existence of the transcript level changes indicated by RNA-seq, in a biological replicate of teliospores that have been induced to germinate. The results of RNA-seq, RT-qPCR and GO enrichment analysis will be presented, and

summarized in a model of gene expression/biological function control during teliospore development and germination. This model can be used to direct future investigations into the biological processes associated with teliospore germination in the smut fungi.

***[GR11] Defense gene expression and metabolites accumulation in corn (*Zea mays* L.) in response to *Clavibacter michiganensis* subsp *nebraskensis*, the causal agent of Goss's Wilt.** A. B. SHUMILAK[1], A. SOLIMAN[1, 3], L. R. ADAM[1], J. T. TAMBONG[2], L. M. REID[2], AND F. DAAYF[1]. *[1]Department of Plant Science, University of Manitoba, 222 Agriculture Building, 66 Dafoe Road, Winnipeg, MB Canada R3T 2N2; [2]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Central Experimental Farm Ottawa, ON Canada, K1A 0C6; [3]Department of Genetics, Faculty of Agriculture, University of Tanta, Egypt*

Goss's wilt is a growing concern for corn growers in Manitoba, Canada. Little is known about the genetic interaction between corn and the bacterial pathogen, *Clavibacter michiganensis* subsp *nebraskensis* (CMN). The objective of this study is to understand at the molecular level, how corn can defend against CMN. Two lines of corn screened as susceptible (CO447) and tolerant (CO450) to Goss's wilt, respectively, were inoculated with CMN isolates that possess different aggressiveness levels. The highly aggressive CMN isolate (CMN14-5-1) produced severe symptoms on CO447, which quickly developed water soaked lesions, and then rapidly developed into necrotic lesions. However, symptoms on CO450 exhibited chlorosis, freckling, and necrosis that did not progress beyond the initial 6 days after inoculation, with the same isolates. Similar results were observed with the less aggressive CMN isolate (DOAB232), though symptoms were less severe. Area under disease progress curve values were estimated for both lesion length and disease severity, which yielded significant differences amongst treatments. Analysis of the expression of 31 genes associated with plant defense was performed on plants challenged with each CMN isolate. Three genes, *respiratory burst oxidase homolog protein D* (rbohD), *ras-related protein 7* (Rab7), and *1-deoxy-D-xylulose-5-phosphate synthase* (DXS) were upregulated only in CO450. One gene, *jasmonate-zim-domain protein 20* (jaz20), was upregulated only in CO447. The results of phenolic extractions from corn leaves inoculated with CMN, and analyzed using HPLC equipped with UV-PDA and fluorescent detectors, will be discussed. There is potential of developing cultivars with higher resistance to CMN, and this research can be a foundation for it.

***[GR12] The rachis node plays a structural and genetic role in Fusarium Head Blight resistance in Canadian winter wheat.** D.S. SKRZENTA, M.G. BECKER, L. HE, B.D. MCCALLUM, C.A. MCCARTNEY, T. OUELLET, F.M. YOU, H.S. RANDHAWA, M.F. BELMONTE AND M.A. HENRIQUEZ. *(D.S.S., M.G.B., M.F.B.) Department of Biological Sciences, University of Manitoba, 66 Chancellors Circle, Winnipeg, MB R3T 2N2, Canada; (L.H., B.D.M., C.A.M., F.M.Y., M.A.H.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB R6M 1Y5, Canada; (T.O.) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Ave, Ottawa, ON, K1A 0C6, Canada; (H.S.R.) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 – 1st Avenue South, PO Box 3000, Lethbridge, AB, T1J 4B1, Canada.*

Fusarium Head Blight (FHB) of wheat, caused by *F. graminearum*, results in yield losses and downgrading of infested grain by mycotoxins. Currently, FHB management is limited and few sources of resistance have been identified. While we are starting to gain a better understanding of the pathosystem, we know little about the cellular and genetic activity underlying susceptibility and tolerance to this pathogen. A Histological examination by confocal microscopy was performed on three Canadian winter wheat lines; susceptible, moderate resistant and resistant. These varieties were point inoculated in the floret with a highly pathogenic *F. graminearum* isolate isolated from Manitoban winter wheat. Cellular analyses showed *F. graminearum* infection behaved differently between these varieties; As predicted the spread and severity of infection was minimal in the resistant line, moderate in the moderate resistant line and severe in the susceptible line. Colonization of *F. graminearum* was detected 48hpi and travelled up and downward from the point of inoculation. However, in the resistant line there were no visible symptoms on the spikelet(s) above or below the inoculated floret. It was found the spread of infection to other spikelets appears to be inhibited by a structure called the rachis node implying this tissue plays a role in wheat-FHB resistance. We then profiled gene activity in the node and found genes associated with the plant defense response

highly expressed in this tissue. Together, data reveal the rachis node plays an important structural and genetic role in the control of Fusarium Head Blight in Canadian winter wheat.

***[GR13] Expression of selected *Phytophthora infestans'* RxLR effectors during infection of potato and tomato varieties**. H. A. ALKHER. L. ADAM AND F. DAAYF. *Department of Plant science, university of Manitoba, 222 Agriculture Building, 66 Dafoe Road, Winnipeg, MB R3T 2N2, Canada.*
Late blight is a devastating disease of potato and tomato worldwide; it's caused by the hemibiotrophic oomycete *Phytophthora infestans* deBary. In major potato/tomato growing regions, the disease causes significant crop losses leading to billions of dollars expenses. The frequent variations in *P. infestans* strains in the United States and Canada are making late blight management more challenging, with the newest strains being very aggressive on tomato in comparison to potato. To achieve beter control of late blight, it is important to understand the pathogenicity factors that lead to the high aggressiveness of some *P. infestans* isolates on potato and/or tomato. Among seven RxLR effectors, we evaluated the expression of PITG-12737-2 in six *P. infestans* isolates during their interaction with potato cultivars Kennebec (moderately resistant) and Russet Burbank (susceptible) and with tomato hybrids Ultra sweet (moderately resistant) and Sun rise (susceptible). Infected plant tissues were collected at 1, 2, 3 and 6 days post-inoculation. Quantitative real-time PCR results showed that PITG-12737-2 was the most expressed gene among the tested effector genes. Higher expression of this gene was observed at 3 and 6 dpi in infected tomato hybrids compared to potato cultivars. These results correlate with a previous cross-pathogenicity study, where isolates of genotype US-24 caused more symptoms on tomato than potato. Our finding suggests that PITG-12737-2 could be one of the pathogenicity factors that play a role in facilitating *P. infestans*' infection process while colonizing the host plant.

***[GR14] RNA interference as a molecular fungicide targeting necrotrophic fungal pathogens *Sclerotinia Sclerotiorum* and *Botrytis cinerea*.** N. WYTINCK, A. G. MCLOUGHLIN, I. J. GIRARD, M.F. BELMONTE, AND S. WHYARD *Department of Biological Sciences, 50 Sifton Road, University of Manitoba, MB, R3T 2N2, Canada*
Necrotrophic fungal phytopathogens, such as *Sclerotinia sclerotiorum and Botrytis cinerea,* devastate a wide range of crop species. These fungi are capable of infecting more than 500 different plant species worldwide, including economically significant crops such as canola, pulses and fruits. In particular, canola, which contributes 27 billion dollars to the Canadian economy annually, is especially susceptible to infection from necrotrophic fungi. Control practices currently used by producers predominantly include the use of broad spectrum fungicides which are becoming increasingly ineffective because of the development of resistance in addition to the damage they cause to beneficial species and the environment. A novel, species specific, and effective solution is therefore needed to control these evermore difficult pests. Through the use of RNA interference, an innate cellular defense, we can drastically reduce fungal pathogenesis by targeting specific transcripts through careful design of double stranded RNA molecules (dsRNA). Through a rigorous bioinformatics pipeline, our lab has already identified dsRNAs in *Sclerotinia* that have proven effectively limited fungal growth *in planta* in canola by as much as 85%. Using a similar methodology, this technology has proved to be effective against other fungal pathogens through both *in planta* assays and quantitative real time PCR. In particular, we have shown up to a 75% reduction in lesion size using *Botrytis cinerea in planta* assays. Ultimately, using leading-edge technology in molecular biology, we developed molecular, species specific fungicides that will be of utility to both producers and researchers in Canada and abroad.

[GR15] Integrated transcriptome and hormone profiling reveals the role of multiple phytohormone pathways in wheat resistance against Fusarium Head Blight. L. WANG, L. JOHN, L. FORSEILLE, Z. LIU, T. FRANCIS, A. SURENDRA, Y. PAN, Y. LI, L. I. ZAHARIA, T. OUTLET AND P. R. FOBERT. *(L.W., L.F., T.F., L.I.Z., P.R.F.) National Research Council Canada, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada; (L.W., L.J.) Department of Plant Science, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada; (Z.L., A.S., Y.P., Y.L.) National Research Council Canada, 1200 Montreal Rd, Ottawa, ON K1A 0R6, Canada; (T. O.) Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, 960 Carling Ave, Ottawa, ON T1J 4B1, Canada; (P.R.F.) National Research Council Canada, 100 Sussex Drive, Ottawa, ON K1N 5A2, Canada*

Fusarium head blight (FHB or scab) caused by *Fusarium* spp. is a destructive disease of wheat. Since most existing FHB resistance is tightly associated with other undesirable agronomic traits, breeding commercial wheat cultivars that combine desired agronomic traits and a high level of FHB resistance remains a challenge. A better understanding of the molecular mechanisms of FHB resistance will help to design more efficient and precise breeding strategies. In this study, we compared the resistant variety 'Sumai3' with three regionally adapted Canadian variety using multiple molecular tools and assays. After macroscopic and microscopic disease evaluation, we determined the relative Type II FHB resistance level of four varieties and found that the *Fusarium graminearum* (*Fg*) infection process displayed substantial temporal differences among organs, with the rachis playing a critical role to prevent *Fg* spread in the spike. Based on this result, large scale organ-specific RNAseq and hormone profiling experiments were performed on the varieties after *Fg* infection. From this analysis, we attempted to describe the roles of several plant hormones during the interaction with *Fg*, including salicylic acid (SA), jasmonic acid (JA), ethylene (ET), auxin and abscisic acid (ABA). We found that SA and JA played predominantly positive roles in FHB resistance, whereas auxin and ABA were associated with susceptibility. Interestingly, our analyses suggest that ET played a dual role during interaction with *Fg.* In addition, we highlighted the importance of phenylpropanoid related secondary metabolites in rachis-based FHB resistance.

[GR16] Gaining insight into biotrophic fungal carbon metabolism through characterization an *Ustilago maydis* xylitol dehydrogenase (*uxm1*). K.M. GOULET, E.R.M. STORFIE AND B.J. SAVILLE. *(B.J.S.) Environmental and Life Sciences Graduate Program, Trent University, 2140 East Bank Drive, Peterborough, ON K9L 0G2 Canada; and (B.J.S.; E.R.M.S) Forensic Science Program, Trent University, 2140 East Bank Drive, Peterborough, ON K9L 0G2, Canada*

Ustilago maydis, the causal agent of 'common smut of corn', is used as a model to investigate basidiomycete biotrophic pathogenesis. In this fungus, the deletion of *UMAG_02150* (*uxm1*) altered pathogenesis, stimulating us to investigate its function. Comparative sequence analyses revealed that it encodes a protein with similarity to xylitol dehydrogenase (XDH), an enzyme involved D-xylose metabolism (XDH converts xylitol to D-xylulose) via the pentose catabolism pathway. The *uxm1* solopathogen deletion strains (Δ*uxm1*) were unable to grow on media containing D-xylose as a sole carbon source, which indicated these mutated cells are inhibited in their ability to process this sugar. Growth of the Δ*uxm1 U. maydis* strain was restored on medium containing D-xylulose as the sole carbon source, which supported the hypothesis that *uxm1* encodes a XDH. Further confirmation of this came from complementing the Δ*uxm1* mutant with a previously-characterized XDH gene from *Aspergillus oryzae* (*xdhA*). The *A. oryzae* gene was synthesized using *U. maydis* optimized codons, and was ectopically inserted into a Δ*uxm1* mutant strain. Expressing *xdhA* in the deletion cells resulted in restored growth on D-xylose medium. Together, these data provide strong evidence that *uxm1* encodes a xylitol dehydrogenase, which is the first characterized enzyme in the *U. maydis* pentose catabolism pathway. This confirmation of gene function suggested that the impaired pathogenesis resulting from deletion of *uxm1* resulted from a requirement for *U. maydis* to utilize D-xylose during infection of corn. The results of pathogenesis assays that assess this role will be presented along with the characterization data.

[GR17] Genome wide association studies (GWAS) of multiple disease resistance in spring barley. [1,2]SANJAYA GYAWALI, [1,3]REDA AMEZROU, [4]SHIOMAN CHAO, [5]SUBHASH CHAND BHARDWAJ, [6]ROBERT BRUEGGEMAN, [2]W.G. DILANTHA FERNANDO, AND [1]RAMESH PAL SINGH VERMA. *[1]International Center for Agricultural Research in Dry Areas (ICARDA), BIGM Program, Morocco; [2]Present Address: Department of Plant Sciences, University of Manitoba, Winnipeg, Canada; [3]Present address: FAO, West Africa and Sub-Saharan Regions; [4]USDA, ARS, Fargo, ND, USA; [5]Indian Institute of Wheat and Barley Research (IIWBR), Indian Council of Agricultural Research (ICAR), India; [6]North Dakota State University, Fargo, ND, USA*

A world collection of barley genotypes (*n*=336) called association mapping 2014 (AM-2014) was collected to study multiple disease resistance (stripe rust [PSH], leaf rust [LR], stem rust [SR], net form of net blotch [NFNB], spot form of net blotch [SFNB], and spot blotch [SB]) and mapping QTL in India, Morocco, and USA. The AM-2014 was genotyped with 9K markers using iSelect Illumina Inifinium SNP in USDA, ND. Phenotyping of resistance to multiple diseases was carried out at seedling and adult plant stages. Seedling resistance was assayed in controlled conditions

by challenging with virulent isolates of PSH, LR, SR, NFNB, SFNB, and SB while evaluation of resistance at adult stages were carried out under field conditions. Population structure (Q) was investigated using Structure and multivariate approaches while Kinship matrix (K) was generated using SNP markers. Genome wide association study (GWAS) was carried out in TASSEL software using MLM model (MLM+Q+K). The significant markers were corrected for false discovery rate (FDR) at $P<0.05$. Barley genotypes showed multiple disease resistance to PSH, LR, SR, NFNB, SFNB, and SB and furnished important genetic resources for breeding programs across the globe. Six resistance QTL were detected in 2H, 3H, 4H, 5H, 6H, and 7H chromosomes against PSH races M, 24, Q, 57, and 7S0 in India at the seedling stage. At adult stage, five resistance QTL were detected against PSH in the field. For LR, seven QTL, for seedling resistance, were mapped in 3H, 4H, 5H, and 7H chromosomes. For SR, three QTL were detected in 2H, 3H and 7H chromosomes. Several novel QTL were detected for resistance to NFNB, SFNB and SB at seedling and adult plant stages in 2015 and 2016. Gene annotation showed several biotic and abiotic stress tolerance genes were associated with resistance to foliar diseases in barley. The Fusarium Head Blight (FHB) resistance mapping in AM-2014 and AM-2017 panels using virulent isolates originating from the Canadian prairies is in progress at the University of Manitoba. The information generated in these studies should help barley breeders and researchers to enhance selection efficiency using marker assisted selections in the future.

[GR18] Quantitative resistance to blackleg disease in three Canadian canola cultivars under elevated temperatures. M. HUBBARD AND G. PENG. *Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, 107 Science Place, Saskatoon, SK S7N 0X2, Canada*
Blackleg disease, caused by *Leptosphaeria maculans* (Desmaz.) Ces. & De Not, is a serious threat to canola production in the Canadian prairies. While major resistance (*R*) genes (qualitative resistance) can provide effective protection, this type of resistance can be rapidly overcome by shifts in pathogen populations. Quantitative resistance (QR) has the potential to provide a more durable, if less complete, protection. However, the effectiveness of QR can vary widely in the field. It has long been suspected that elevated temperatures can reduce the effectiveness of QR. To better understand this impact, we assessed the infection development of blackleg in three Canadian canola (*Brassica napus* L.) cultivars (CCC1, CCC2 and CCC4) carrying QR, with and without a weeklong heat treatment with 7-hour of daily exposure to 32°C at the early flowering stage under controlled-environment conditions. The impact of elevated temperatures on the susceptibility of canola cultivars to blackleg was compared with that of 22°C day-time high temperature. A susceptible cultivar, 'Westar', was used as a control in both temperature treatments. Elevated temperatures increased blackleg symptoms in the absence of QR and enhanced the effectiveness of QR in the three commercial cultivars tested. CCC1, CCC2 and CCC4 had strong, moderate and weak QR at lower temperatures, respectively. However, at higher temperatures, all three cultivars displayed strong QR relative to 'Westar'. Our findings suggest that the QR gene(s) carried by CCC1, and QR in general, are promising tools for the control of blackleg when warmer temperatures occur after canola has flowered.

[GR19] Identification of immunity-related LRR-containing genes in *Cannabis sativa*. N. PÉPIN AND D.L. JOLY. *Université de Moncton, 18 avenue Antonine-Maillet, Moncton, NB E1A 3E9, Canada.*
Cannabis sativa L. is a multi-purpose plant that has been domesticated for its bast fiber in the stem, its seed of high nutritional value and its appealing medicinal properties. However, its cultivation faces important phytosanitary problems mainly due to diseases like powdery mildew (caused by various fungal species), gray mold (*Botrytis cinerea* Pers.), and white mold (*Sclerotinia sclerotiorum* (Lib.) de Bary). Here, we used genomic and transcriptomic data from *C. sativa* to search for proteins that encode conserved domains related to plant immunity, including: CC (Coiled-Coil), TIR (Toll/Interleukin-1 Receptor), NBS (Nucleotide-Binding Site), LRR (Leucine-Rich Repeat), etc. We identified several immunity-related gene candidates in *C. sativa* which have the typical architecture of Receptor-Like kinase (RLKs) and Receptor-Like Proteins (RLPs) candidates involved in PAMP-Triggered Immunity (PTI), or resistance gene (*R* genes) candidates involved in Effector-Triggered Immunity (ETI). Candidates were characterized based on conserved protein motifs, gene duplication events, chromosomal locations, phylogenetic relationships and gene expression analysis. Gene expression profiling using existing RNA-seq data revealed the expression of these genes in a wide range of tissues, and an additional RNA-seq dataset of *C. sativa* leaves infected with powdery mildew is

currently being analyzed. This study will provide insight into the evolution of immune receptors in the *C. sativa* genome, which may aid efforts to further characterize the function of these predicted genes and develop disease-resistant cultivars.

[GR20] High resolution DNA melting (HRM) assay for detection of *Rx1* and *Rx2* for rapid high-throughput selection for extreme resistance to *Potato virus X* in potato. XIANZHOU NIE, VIRGINIA DICKISON, SYDNEY BROOKS, MATHURESH SINGH, AND AGNES MURPHY. *Fredericton Research and Development Centre, Agriculture and Agri-Food Canada, 850 Lincoln Road, Fredericton, NB E3B 4Z7, Canada; (M.S.) Agricultural Certification Services, Fredericton, NB E3B 8B7, Canada; and (S.B.) Department of Biochemistry and Microbiology, University of Victoria, Victoria, BC V8P 5C2, Canada*
Potato selections are regularly assessed for their response to *Potato virus X* (PVX) infection prior to their release by AAFC's potato breeding program. Extreme resistance (ER) to PVX has been detected in many potato breeding clones and advanced selections. Assessment of the existing PCR-gel electrophoresis based methods for detection of *Rx1* and *Rx2*, the genes that independently control ER to PVX, indicated that the 5Rx1F/5Rx1R primer pair led to reliable detection of *Rx1*. However, the methodology is time consuming and it does not differentiate the absence of *Rx1* from a failed PCR reaction. A newly designed primer pair that targets both *Rx1* and *rx1* produced an amplicon for both alleles. When the primer pair is combined with 5Rx1F/5Rx1R, respective amplicons, although not distinguishable in regular agarose gel electrophoresis, were produced. When subjected to a high resolution DNA melting (HRM) assay, two distinct melting profiles for *Rx1* and *Rx1*/*rx1*, respectively, were detected. The efficacy of the HRM assay was validated in potato cultivars/clones with known phenotypes, indicating its potential for high-throughput selection of potato carrying *Rx1*. HRM assays of over 600 progeny from 12 crosses involving various parents correctly detected the presence or absence of *Rx1* in each progeny, allowing accurate prediction of the phenotype. Progeny that tested positive for *Rx1* by HRM exhibited ER to PVX whereas progeny that tested negative for *Rx1* were susceptible to PVX infection. The genotype of each parent and the possible presence of *Nx* in two *Rx1*-possessing parents will also be discussed.

[GR21] A previously unrecognized *Ustilago maydis* APSES protein has a role in pathogenic development. JUSTIN MEADE, MARK SEEGOBIN, MICHAEL E. DONALDSON AND BARRY J. SAVILLE. *Environmental and Life Sciences Graduate Program, Trent University, 1600 West Bank Drive, Peterborough, ON K9J 0G2, Canada; and (B.J.S.) Forensic Science Program, Trent University, 1600 West Bank Drive, Peterborough, ON K9J 0G2, Canada*
Ustilago maydis D.C. Corda is a well-established model for investigating basidiomycete biotrophic pathogenesis. This fungus requires interaction with *Zea mays* for sexual reproduction and teliospore development. The resistant teliospores are critical for disease spread, and understanding the control of their development may reveal new means of disease management. We are investigating teliospore formation and germination by identifying genes expressed during these developmental transitions. In doing so, we identified a previously unrecognized APSES domain transcription factor UMAG_04778. The fungal specific APSES family of transcription factors contain a highly-conserved helix-loop-helix DNA binding domain and are generally involved in controlling morphological transitions. There are five APSES proteins encoded in the *U. maydis* genome including Ust1, which was previously shown to regulate dimorphism, virulence, and sporulation. However, only UMAG_04778, was found to have increased transcript levels during pathogenic development and in the teliospore, but undetected transcript levels in haploid cells. UMAG_04778 deletion did not inhibit plate mating or filamentous growth; however, it led to decreased leaf tumour formation, and virulence, as well as dramatically reduced teliospore formation during infections by both solopathogenic haploid and dikaryon strains. Constitutive expression of UMAG_04778 in solopathogenic strains led to the pigmentation of colonies grown on PDA and to the pigmentation, rounding, increased volume and rupture of cells grown in PDB. The gene expression pattern and mutant phenotypes led us to hypothesize that UMAG_04778 has a role in regulating morphological transitions leading to teliospore development in *U. maydis*. Data on characterization of this gene's function will be presented.

[GR22] Analysis of concomitant development of strawberry leaf spot and black seed disease caused by *Mycosphaerella fragariae*. O. CARISSE AND V. MCNEALIS. *Agriculture and Agri-Food Canada, 430 Gouin Blvd., St-Jean-sur-Richelieu, Quebec, Canada J3B 3E6; Department of Mathematics and Statistics, Université de Montréal, André-Aisenstadt Building, PO Box 6128, Centre-ville Station, Montréal, Quebec, Canada H3C 3J7*
Mycosphaerella fragariae is responsible for dual strawberry diseases: common leaf spot (CLS) and black seed disease (BSD). In June bearing strawberry productions, CLS can be present during the planting year as well as during the production years causing reduced vigor, yield and winter survival. During production years, BSD can cause black lesions surrounding strawberry seeds reducing the market values of the fruits. The objective of this study was to characterize the relationships between CLS and BSD. Data on number of lesions per leaflets, number of black seeds per berry and percent diseased berries were collected in experimental and commercial sites from 2000 to 2011 at 50 farm-years. First, logistic regression was used to model the relationship between black seed disease severity in its binary data form (presence or absence of black seeds) and number of lesions per leaflet 7, 14, 21, and 28 days before bloom. Secondly, linear regression was used to model the relationship between black seed disease severity, incidence (expressed as percentage of diseased berries) and number of lesions per leaflet 7, 14, 21, and 28 days before bloom. For both analyses, the accuracy of predictions increased with decreasing delay between CLS assessments and bloom. Nevertheless, based on these analyses, a threshold of 10-15 lesions per leaflet, 1 to 2 weeks before bloom could be used to eliminate unnecessary fungicide applications and to combine the risk of black seed disease and gray mold when making decisions related to fungicide applications during the pre-bloom and bloom periods.

CSA Contributed Paper Session (*Student Competition)
Agronomy and Breeding

[AB1] Management of injury by *Striacosta albicosta* (Lepidoptera: Noctuidae) and deoxynivalenol content in maize. J.L. SMITH[1], V. LIMAY-RIOS, D. C. HOOKER, and A.W. SCHAAFSMA. *Department of Plant Agriculture, Ridgetown Campus, University of Guelph, 120 Main St. E., Ridgetown ON, Canada N0P 2C0*
Western bean cutworm, *Striacosta albicosta* Smith (Lepidoptera, Noctuidae) has become a key ear-feeding maize pest in Ontario, Canada that is challenging to control due to tolerance to commonly used transgenic *Bacillus thuringiensis* (Bt) events. Infection by *Fusarium graminearum* Schwabe frequently occurs in Ontario resulting in mycotoxin contamination of maize grain, particularly deoxynivalenol (DON). The objectives of this study were to evaluate the impact of injury by *S. albicosta* on mycotoxin accumulation and to evaluate Bt-maize events, alone, or in combination with insecticides and fungicides for control of *S. albicosta* injury and DON accumulation. A positive response was found between DON, injury, and risk of *F. graminearum* infection during the silking period. The Vip3A event provided superior protection from *S. albicosta* injury over insecticide treatment of non-Bt or Cry1F hybrids. Injury reduction was similar among pyrethroid and diamide insecticides, applied alone or pre-mixed at early VT or R1 stages. Lower DON concentrations were observed with chlorantraniliprole tank-mixed with prothioconazole during VT/R1 or with chlorantraniliprole + £-cyhalothrin at early VT followed by prothiconazole at R1. A combined insecticide/fungicide treatment applied at silk emergence is the most effective management approach in regions with frequent incidence of this pest complex in the absence of *F. graminearum*-tolerant maize hybrids expressing high-dose insecticidal proteins against *S. albicosta*.

***[AB2] Genetic analysis of developmental traits contributing to enhanced winter survival in autumn-seeded rye (*Secale cereale* L.).** H. BAHRANI, M. BÅGA, J. LARSEN*, R.N. CHIBBAR. *Department of Plant Science, University of Saskatchewan, Saskatoon, SK, S7N 5A8, Canada; * Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, T1J 4B1, Canada.*
Over-wintering plants prepare for winter by accumulating frost tolerance during a cold acclimation period in the fall. This process confers much higher frost resistance in rye cultivars (LT50=-33°C) than winter wheat (LT50=-23°C) and translates into higher winter survival for winter rye. It has been very challenging to transfer the rye winter hardiness character to wheat by breeding. A few of the rye cold hardiness genes are known, but a more complete picture of

the complex cold tolerance regulon in rye is needed. Based on previous studies, we hypothesize that winter field survival is largely dependent on the developmental program of the plant. To study winter field survival in rye a set of 96 cultivars with varying winter hardiness were planted in the fall of 2015 and 2016 at Saskatoon (very harsh winter), Vauxhall, AB (harsh winter) and Lethbridge, AB (mild winter) to determine winter survival frequencies. The number of plants that survived the winter were determined. Several developmental traits tolerance associated with frost tolerance were assessed by greenhouse studies. Results from the genotyping by sequencing analyses were used to identify marker-trait associations for the plant developmental traits. Successful completion of this research will identify the genomic regions/genes contributing to high winter hardiness in rye.

***[AB3] Characterization of sainfoin (*Onobrychis viciifolia* Scop.) accessions using agro-morphological and amplified fragment length polymorphism markers.** S. BHATTARAI, B. COULMAN AND B. BILIGETU, DEPARTMENT OF PLANT SCIENCES, UNIVERSITY OF SASKATCHEWAN. *51 Campus Drive, Saskatoon, Saskatchewan, S7N 5A8, Canada.*
Sainfoin (*Onobrychis viciifolia* Scop.) is a palatable, bloat-free perennial legume for grazing animal. It is widely distributed in northern temperate regions of the world. Though sainfoin has valuable characteristics, this species is an under-developed forage legume with limited genetic information available. The objective of this study was to evaluate agro-morphological characteristics and genetic diversity of 38 sainfoin accessions representing 20 countries. A field nursery was established in 2014 at Saskatoon, SK, Canada using randomized complete block design with four replications. Genetic diversity was estimated using amplified fragment length polymorphism (AFLP) markers. Analysis of variance revealed significant ($P<0.05$) variations among the accessions for winter survival, plant height, days to flower, stem number, dry matter yield, regrowth, seed yield, and 1000-seed weight in 2015 and 2016. Using phenotypic data, 31 sainfoin accessions were grouped into three main clusters. An analysis of molecular variance revealed that a large proportion of genetic variability (84%) resides within-population. A number of promising accessions were identified which could be used to develop synthetic cultivars with high forage yield, and improved persistence and nutritive value.

***[AB4] Cultural weed control decisions impact the competitiveness of *Glycine max* (L.) Merr. grown in the northern Great Plains.** J. D. ROSSET, *Department of Plant Science, University of Manitoba, Winnipeg, MB, R3T 2N2*
Manitoba is located at the northern fringe of the North American soybean (*Glycine max* (L.) Merr.) growing region. The development of short-season soybean varieties has enabled producers in Manitoba and eastern Saskatchewan to adopt the crop for primary production. Soybean production in the prairie region has doubled in the last half decade, and current production recommendations have been adopted from the warmer long-season soybean growing regions of Ontario and the USA. Soybean production in these areas has contributed to the selection of herbicide-resistant (HR) weed biotypes. As part of a responsible, integrated weed management strategy, soybean production in the prairie region must adopt good agronomic practices to reduce selection pressure for HR weeds. Narrow row widths, high population densities and competitive varieties may be used as cultural weed management tools to interfere with weeds and thus reduce selection pressure of HR biotypes. This study evaluated the influence of row width (19 cm vs. 76 cm), population density (0.75, 1, and 1.5 times the recommended target density) and cultivar (erect, intermediate, and bushy) on the critical weed free period (CWFP) (i.e. the duration which a crop must be kept weed free to reach maximum yield potential) of soybean grown in the northern Great Plains region. Data from three experimental sites revealed that using narrow row widths or competitive cultivars can shorten the duration of the CWFP, while low population densities can lengthen the CWFP of soybean grown in the northern Great Plains region.

***[AB5] Assessing Thermal Indices for Modeling Grain Corn Phenological Development on the Prairies.** J. ZHANDA, P. R. BULLOCK, F. ZVOMUYA, Y. LAWLEY, L. M. REID AND D. FLATEN**.** *University of Manitoba, Faculty of Agricultural and Food Sciences, Winnipeg, Manitoba, R3T 2N2,Canada;and (L.M.R) Ottawa Research and Development Centre, Agriculture and Agri-food Canada, Ottawa, Ontario, K1A 0C6, Canada*
Grain corn (*Zea mays*) production on the Canadian Prairies is delayed by limited seasonal heat unit accumulation. However, agroclimatic studies have shown some positive trends in heat unit accumulation in recent decades,

increasing the feasibility of corn grain production in cooler regions such as the Prairies. A two year study was initiated in 2015 at six sites in Manitoba and two sites in Alberta to quantify heat unit requirements of five corn hybrids with different maturity ratings and to identify a thermal index with a consistent accumulated value from planting to maturity. The indices assessed included the corn heat unit (CHU), growing degree days with a base temperature of 10^{o}C, modified growing degree days with a base temperature of 10^{o}C and maximum temperature of 30^{o}C, general thermal index (GTI) and days after planting. Corn phenology from emergence to silking was monitored by time-lapse cameras. Physiological maturity (R6) was defined by the presence of a black layer at the tip of the corn kernels. Automated weather stations recorded hourly and daily weather conditions including air temperature. There were no significant differences in heat unit accumulation among the five hybrids, despite their differences in CHU rating and regardless of the index used. There was an inverse relationship between cold nights and CHU. Overall, the hybrids required more CHU to reach R6 than their rated values. The cumulative heat at R6 for all thermal indices across all locations had a coefficient of variation <10%, with GTI having the lowest (<5%) regardless of the hybrid. Although not statistically significant, the GTI was the most consistent and accurate heat unit especially at the R6 stage. Cold overnight temperatures on the Canadian Prairies are speculated to slow corn phenological development on subsequent days and thus increase the amount of heat required for corn to reach R6. However, in this study, an increased number of cold nights decreased the amount of CHU accumulated by all hybrids from planting to maturity.

***[AB6] Effects of phosphorus sources on soil phosphatase activity, phosphorus availability and dry matter production of corn silage.** W. ALI, W. ASHIQ, M. NADEEM, M. ZAEEM, S. M. GILLANI, V. KAVANAGH, R. THOMAS, A. UNC AND M. A. CHEEMA. *(W.A., W.A., M.N., M.Z., S.M.G., A.U., R.T., M.A.C.) School of Science and Environment, Grenfell Campus, Memorial University of Newfoundland, Corner Brook, NL, A2H 5G4, Canada; (M.N.) COMSATS Institute of Information Technology, Vehari, 61100, Pakistan; (V.K.) Department of Fisheries, and Land Resources, Pasadena, NL, A0L 1K0, Canada*

Insufficient or unavailable soil phosphorus (P) is a key limitation for crop productivity. Dairy manure (DM) adds nutrients to soil, enhances soil phosphatase activity (SPA), and generally stimulates exoenzymatic hydrolytic activities of microbial decomposers of organic matter. Most P added to soil with inorganic fertilizers is rapidly fixed, leading to decreased phosphatase activity, and thus decreasing availability of P to plants. However, DM applications can favor an increase in P availability by enhancing biological activity through provision of easily available carbon sources and by improving soil physicochemical parameters. We carried out a field experiment at Pynn's Brook Research Station, Pasadena, Newfoundland, on a podzol to; 1) determine the effect of different P sources on soil phosphatase activity and soil P availability, 2) explore the production potential of several corn silage genotypes with different P sources, and 3) examine the correlation matrix between SPA, available P, and dry biomass production. Experimental treatments were P sources; [P_0, (control); P_1, DM with high P concentration; P_2, DM with low P concentration; P_3, Inorganic P] and five corn silage genotypes. Results showed that, compared to control, P_1 treatment enhanced SPA by 18.91%, available P by 60.11%, and dry biomass production by 28.13%. Higher dry biomass (21.94 Mg ha^{-1}) produced by the Yukon R genotype under P_1 treatment was correlated with greater SPA and soil available P. We thus found a strong positive correlation between SPA and soil available P, and corn silage biomass production.

[AB7] Effect of fall and spring applied urea and ESN on spring wheat production in northwestern Ontario. T. S. SAHOTA. *Thunder Bay Agricultural Research Station, 435 James St. S, Thunder Bay, Ontario, Canada P7E 6S7 (e-mail: tarloksahota@tbaytel.net)*

Spring wheat is an important cash crop in NWO with short growing season. Fall application of N could help seeding early in spring. Fall applied urea may lead to high N losses. ESN could be an alternative to urea; though in cold springs it may be too slow to release N. Part substitution of N from urea with ESN could be better than urea alone. A field experiment, with 9 treatments (a no N check, and N @ 80 kg ha^{-1} from urea, ESN and urea + ESN (3:1/and 1;1 on N basis) – applied in the fall and spring), was conducted in completely randomized block design, replicated four times, during 2014-'16 at Thunder Bay, Ontario. Application of N irrespective of its source and time of application significantly improved the grain and straw yield and grain protein content. Results from N treatments varied with the

years. In 2016, when 209 mm rainfall occurred in June, spring applied ESN gave 1.24 Mg ha^{-1} extra grain and 0.92 Mg ha^{-1} higher straw yield than urea. Pooled analysis over 3 years, indicated that highest grain (4.46 Mg ha^{-1}; 14. 6 % protein) and straw (5.52 Mg ha^{-1}) yields were obtained with spring application of urea + ESN (3:1on N basis) @ 80 kg N ha^{-1}. Overall, grain yields from spring and fall applied N were similar. Grain protein content was highest (15.3 %) with spring applied ESN @ 80 kg N ha^{-1}.

[AB8] Expanding the seeding window of winter wheat in Western Canada. Y. LAWLEY, *Department of Plant Science, University of Manitoba, 222 Agriculture Building, Winnipeg, MB, R3T 2N2 yvonne.lawley@umanitoba.ca*
Seeding date is one of the key management steps to growing a successful winter wheat crop in Western Canada. Several factors are now limiting the ability of farmers to plant winter wheat within the optimum seeding window. These factors include continuous cropping, limited use of summer fallow, selection of longer season varieties, and the introduction of new late maturing crops, such as soybean and corn. A study was initiated in 2013 at 13 sites across the Canadian Prairies (Manitoba, Saskatchewan, Alberta) to re-evaluate the seeding window of winter wheat in light of the recent release of more cold tolerant varieties as well as the introduction of fungicide seed treatments. Winter wheat (cv. Flourish) was planted on five fall planting dates (Sept 1, Sept 15, Oct 1, Oct 15, and Nov 1) in the fall of 2013, 2014, and 2015. At each planting date, winter wheat treated with a fungicide seed treatment (*Tebuconazole* and *Prothioconazole*) was compared to an untreated control. Weather was less restrictive during late planting dates in all years than initially anticipated. The November 1 dormant seeding treatment (+ or – 4 days) could be planted in 24 out of 29 sites years during the study period. Yield trends were most consistent in Manitoba with yields generally declining with later planting and the highest relative yields occurring when planting winter wheat between Sept 1 and Sept 15. In Alberta and Saskatchewan, yield trends were variable with yields for some site years increasing while others were decreasing with later planting. Seed treatment increased spring plant stand and grain yield relative the an untreated check when averaged over all planting dates at 8 out of 27 site years. Most of the site years with seed treatment benefits occurred in Manitoba.

[AB9] Comparative performance of annual and perennial forage legumes for forage production in northwestern Ontario. T. S. SAHOTA. *Thunder Bay Agricultural Research Station, 435 James St. S, Thunder Bay, Ontario, Canada P7E 6S7 (e-mail: tarloksahota@tbaytel.net)*
Alternate forage legumes could compensate production losses due to winter kill of alfalfa. An experiment in completely randomized block design with 15 treatments (alfalfa, berseem clover, at standard seed rates, fenugreek @ 15, 30 and 45 kg ha^{-1}, galega @ 25, 35 and 45 kg ha^{-1}, galega/and alfalfa mixtures with berseem @ 6.5 and 13 kg ha^{-1}, and alfalfa red clover mixture), replicated four times, was initiated at Thunder Bay in 2011. Results, averaged over 2012-'14, indicated that galega seeded @ 25 kg ha^{-1} produced the highest dry matter yield of 5.6 Mg ha^{-1} yr^{-1} (~20 % higher than alfalfa). Increasing seed rate of galega from 25 to 45 kg ha^{-1} didn't help in increasing its yield. First cut protein content in galega @ 25 kg seed ha^{-1} (26.1 %) was higher than that in alfalfa (22 %). In the 2nd cut, protein content in galega at different seed rates was either similar or somewhat better than alfalfa. Galega had higher RFV than alfalfa. Calcium, sodium and boron seemed to be lower, but copper, zinc, iron and manganese were higher in galega than that in alfalfa. Intercropping alfalfa and galega with berseem improved the forage dry matter yield in the initial years only. Fenugreek yield was significantly lower than other legumes. In 2016, galega @ 35 kg ha^{-1} recorded 2.02 Mg ha^{-1} higher yield than its seeding @ 25 kg kg ha^{-1} and 3.07 Mg ha^{-1} higher yield than alfalfa. Fifteen farmers in Ontario would be seeding galega for the first time in 2017 in 1000 acres!

[AB10] Impact of selection for seed production in intermediate wheatgrass (*Thinopyrum intermedium*). D.J. CATTANI AND S.R. ASSELIN. *Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB, R2T 2N2 (D.J.C. and S.R.A.).*
Selection for perennial seed production should move the selected population away from non-selected populations. As selection based upon seed production in an herbaceous perennial may influence other important traits such as persistence, it is important to understand the impact of selection on overall plant phenology and phenotype. Two sources of intermediate wheatgrass (IWG) germplasm, USDA-GRIN (GRIN) and The Land Institute (TLI) were accessed

and planted out (≈ 4,500) at Carman MB in 2011. After a severe spring frost eliminated >60% of the materials, a total of 100 hundred surviving plants (75 TLI, 25 GRIN) were selected for detailed phenological and yield component measurements in 2012, 2013 and 2014. Principal component analysis (PCA) and discriminant analysis of principal components (DAPC) were carried out to compare the two populations over the three years of seed productivity. PCA indicated days to first flower differentiated between years while populations were best identified using DAPC where flowering, yield and components of yield contributed to the differentiation between the two sources. Yield and its components showed progress under selection for TLI versus GRIN materials. Due to the obligate outcrossing nature of IWG, some progeny of selected materials were found to regress to within the range of the GRIN accessions. Selection has improved yield and harvest index in the TLI materials. Two GRIN accessions were found to be similar to much of the TLI material, and were from germplasm of forage cultivars.

[AB11] Sugar beet response to rotation and conservation management in a 12-year irrigated study in southern Alberta. F.J. LARNEY, J.J. NITSCHELM, P.J. REGITNIG, D.C. PEARSON, R.E. BLACKSHAW AND N.Z. LUPWAYI. *Agriculture and Agri-Food Canada, Lethbridge Research & Development Centre, 5403 1st Avenue South, Lethbridge, AB T1J 4B1, Canada*; (*J.J.N.) Alberta Agriculture and Forestry, 5401 1st Avenue South, Lethbridge, AB T1J 4V6, Canada;* (*P.J.R.) Lantic Inc. (Rogers Sugar Ltd.), 5405 64th Street, Taber, AB T1G 2C4, Canada*

Sugar beet (*Beta vulgaris* L.) has a long history as an option for irrigated crop rotations in southern Alberta. A 12-yr (2000–2011) study compared conservation (CONS) and conventional (CONV) management for sugar beet in 4- to 6-yr rotations which also included dry bean (*Phaseolus vulgaris* L.), potato (*Solanum tuberosum* L.), and soft white spring wheat (*Triticum aestivum* L.). Oat (*Avena sativa* L.) and timothy (*Phleum pratense* L.) were included in the longest 6-yr rotation. Conservation management incorporated reduced tillage, cover crops, feedlot manure compost addition, and solid-seeded dry bean. Compared with a 4-yr CONV rotation (52.2 Mg ha^{-1}), sugar beet root yield (averaged over the second 6 yr of the study, 2006–2011) was significantly higher, by 11%, on 4- and 5-yr CONS rotations (57.7–57.9 Mg ha^{-1}), and by 8% on a 6-yr CONS rotation (56.1 Mg ha^{-1}). Sugar beet impurity parameters were significantly affected by rotation in, at most, 3 of 12 yr. However, averaged over the final 6 yr of the study (2006–2011), a significantly higher K concentration (impurity) was found with CONS (2108 mg kg^{-1}) vs. CONV (1958 mg kg^{-1}) management. Integrating CONS management practices into sugar beet rotations led to significant yield benefits while effects on sugar beet quality were minimal.

CSA Contributed Paper Session
Agronomy

[AG1] DISTINGUISHED AGRONOMIST PRESENTION: A funny thing happened on the way to…here. SHABTAI BITTMAN. *Agassiz Research and Development Centre, Agriculture and Agri-Food Canada.*

[AG2] Assessing existing information about greenhouse Potting media organic content and microbial profile. S. SIVAKUMAR. *Van Luyk Greenhouses and garden Centre*

In the greenhouse industry, various types of growing media are used for growing and maintaining plants in containers or in the ground. Growing media components can have a significant impact on plant health and pest problems. Disease management in the greenhouse is challenged by the source of plant material, the greenhouse environment and the options available to effectively deal with pest management. Fertilizer and pesticide usage in the greenhouse could be better managed through optimizing growing media properties and handling. This has the added economic benefit of reducing input costs through potential savings in crop inputs while contributing to less potential waste. Growing media or soil is a dynamic, complex mixture of diverse physical, chemical and biological properties that influences plant health, pest problems and thus forms the basis for sustainable agriculture. Vast majority of organic and inorganic growing media properties are still not well described, despite being extensively used in the industry. Growing media characteristics (physical components such as peat or bark and chemical composition such as the pH) can have a significant impact on plant production and are influenced by external input (e.g. irrigation and fertilizer application) and environmental conditions (e.g. storing temperature). Farmers would be

better able to manipulate the properties of their growing media to carryout sustainable greenhouse production if these properties were known in advance. Optimal handling practices for growing media in the greenhouse industry are not well described. This fundamental information about growing media will assist greenhouse operators in maintaining their farming operations environmentally friendly.

CPS Contributed Paper Session (Student Competition*)
Disease Management

***[DM1] Isochorismatase hydrolase (ICSH1) in *Verticillium dahliae* play roles in interacting with salicylate and jasmonate defense signaling in potato.** X. ZHU[1], A. SOLIMAN[1,2], M. R. ISLAM[3], L. R. ADAM[1], F. DAAYF[1]* [1] *Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada,* [2] *Department of Genetics, Faculty of Agriculture, University of Tanta, Tanta, Egypt,* [3] *Department of Plant Pathology, Bangladesh Agricultural University, Mymensingh, Bangladesh*

Verticillium dahliae is the primary cause of Verticillium Wilt in potato. In a prior proteomic study, we detected Isochorismatase Hydrolase (ICSH1) in a highly aggressive isolate of *V. dahliae* but not in a weakly aggressive one. Results showed that the *in vitro* expression of the *VdICSH1* gene increased more in response to root extracts than to leaf or stem extracts. Moreover, during the infection, it was drastically up-regulated in the highly, versus the weakly, aggressive isolate. We generated dysfunctional mutants of *VdICSH1* from the highly aggressive *V. dahliae* isolate by Agrobacterium-mediated gene insertion. The pathogenicity analysis of both wild type and mutants proved that *VdICSH1* is required for full virulence on potato. Members of the isochorismatase gene family convert isochorismate into other components. Therefore, we had hypothesized that *VdICSH1* would reduce salicylic acid (SA)-mediated signaling and related plant defenses in potato. Quantification of SA and jasmonic acid (JA) accumulations in susceptible potato cultivars inoculated with *vdicsh1* mutant and wild type strain using HPLC-PDA-Fluorescence and UPLC-MSMS, revealed that at early stages of infection, a higher accumulation of bound-SA in the leaves in response to the mutant compared to the wild type was noticed. This indicated that *VdICSH1* does interfere with SA synthesis in potato. In addition, potato roots and stems accumulated more SA and less JA at early *V. dahliae* infection stage, whereas potato leaves accumulated both SA and JA. This suggests that early potato defense responses against *V. dahliae* occurs more via the SA signaling pathway in the roots and stems, and via both SA and JA signaling pathways in the leaves at later stages of infection.

***[DM2] Biocontrol Potential of *Trichoderma longibrachiatum* as an Entomopathogenic Fungi against *Bemisia tabaci*.** ANWAR, K. NAWAZ, M.S. HAIDER, A.A. SHAHID AND S. IFTIKHAR. *Institute of Agricultural Sciences, University of the Punjab, 54590 Lahore, Pakistan; (A. A.) Center of Excellence in Molecular Biology, University of the Punjab, 54590 Lahore, Pakistan*

Bemisia tabaci (Gennadius) is a complex insect species, including many cryptic species or biotypes. Whitefly causes damage to many ornamental and horticultural crops through directly feeding on phloem sap, resulting in sooty mould. Biological control has emerged as one of the most important methods for the management of soil-borne plant pathogens. Among the natural enemies of insects different entomopathogenic fungi are mostly used as biological control of the pest. The purpose of this research was to find indigenous insect-associated fungi and their virulence against *Bemisia tabaci.* A detailed survey of cotton fields in sample collection was conducted during July and August 2013 from the central mixed zone of Punjab, Pakistan. For the isolation of *T. longibrachiatum*, sabouraud dextrose peptone yeast extract agar (SDAY) media was used and morphological characterization of isolated *T. longibrachiatum* was studied using different dichotomous keys. Molecular Identification of the pathogen was confirmed by amplifying the internal transcribed spacer region and Blastn analysis showed 100% homology with already reported sequences on the database. For these bioassays, two conidial concentrations 4×10^8/mL & 4×10^4/mL of *T. longibrachiatum* was sprayed in clip cages for nymph and adult *B. tabaci* respectively under controlled environmental conditions. The pathogenicity of *T. longibrachiatum* was tested on nymph and adult whitefly to check mortality. Mortality of *B. tabaci* at nymphal and adult stages was observed after 24-hour intervals. Percentage mortality of nymphs treated with 4×10^4/mL conidia of *T. longibrachiatum* was 20, 24, 36 and 40% after 48, 72, 96,

72, and 96, 120 and 144 hours respectively. However, no considerable difference was recorded in percentage mortality of whitefly after 120 and 144 hours. *Trichoderma longibrachiatum* showed maximum activity on nymphal stages of whitefly as compared to adult stages. The present findings indicated that *T. longibrachiatum* is an entomopathogenic fungus against *B. tabaci* and many species of *Trichoderma* were already reported as an antagonistc organism against a wide range of bacterial and fungal pathogens.

***[DM3] Pathogen complex on wasabi in British Columbia and evaluation of disease management options.** E.C. BETZ AND Z.K. PUNJA. *Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada*

Wasabi (*Wasabia japonica* (Miq.) Matsumura) is a greenhouse crop grown under high humidity conditions, which provide an ideal environment for pathogen development. During a survey of five British Columbia greenhouses conducted in the summer of 2016, a range of disease symptoms were observed, which included powdery mildew, leaf spot, root rot, rhizome rot, and petiole blight. Some of the prevalent microbes isolated included *Verticillium isaacii* Inderb., Bostock, Davis & Subbarao, *Leptosphaeria biglobosa* Shoemaker & H. Brun, *Pythium intermedium* de Bary, *Pythium irregulare* Buisman, and *Fusarium avenaceum* (Fr.) Sacc. An assessment of the effects of *Trichoderma harzianum* Rifai strain T-22 from Rootshield® Plus WP, *Streptomyces lydicus* De Boer, Dietz, Silver & Savage strain WYEC 108 from Actinovate® SP, and *Bacillus subtilis* (Ehrenberg) Cohn strain QST 713 from Rhapsody® ASO™ against pathogen growth was made on Luria Broth, Potato Dextrose and V8-juice agars. In addition, Cueva® Copper Fungicide, and Regalia® Biofungicide were also evaluated. Plates were inoculated with the biocontrol agent and left to incubate 24 h before the addition of the pathogen. Pathogen growth was measured 5 days later and compared to control plates on which no treatment was added. All three biological organisms had inhibitory effects on pathogen growth in culture, with *S. lydicus* and *B. subtilis* demonstrating clear pathogen inhibition and *T. harzianum* outcompeting the pathogens for space on the media. Neither Cueva nor Regalia had a visible inhibitory effect in culture. Assessment of these biocontrol products for disease control on wasabi plants is underway.

***[DM4] Management of metalaxyl-m-resistant strains of the potato pink rot pathogen *Phytophthora erythroseptica* in field and storage.** B. CRANE, R.D. PETERS, L.M. KAWCHUK, L. HALE, A. FOSTER, C. LACROIX, A. MILLS, K.A. DRAKE, D. GREGORY, I. MACDONALD, K. MACDONALD, A. MACPHAIL, AND M.M. CLARK. *Agriculture and Agri-Food Canada, Charlottetown Research and Development Centre, Charlottetown, PE C1A 4N6 Canada; (L.M.K) Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre, Lethbridge, AB T1J 4B1 Canada; (L.H, C.L) University of Prince Edward Island, Charlottetown, PE C1A 4P3 Canada; (M.M.C) Government of Prince Edward Island, Charlottetown, PE C1A 7N3 Canada*

Phytophthora erythroseptica is the causal agent of pink rot of potato which results in a wet rot and complete tuber breakdown causing significant yield losses under field and storage conditions. Traditionally, the pathogen has been managed with metalaxyl-m based products (Ridomil Gold®), however, in recent years, metalaxyl-m-resistant isolates have been recovered in the United States and Atlantic Canada, signifying a need for alternative management strategies. A national survey was established to determine the distribution of metalaxyl-m-resistant strains in Canada and trials were conducted to assess the efficacy of alternative fungicides to inhibit infection under field and storage conditions. The national survey revealed a high proportion of metalaxyl-m-resistant isolates in pathogen populations from the Maritime Provinces and recovered metalaxyl-m-resistant strains for the first time from Ontario, Manitoba, and Alberta. Inoculated field and storage trials evaluated the efficacy of treatments of Phostrol™, Orondis®, Presidio®, and Serenade SOIL® to inhibit pink rot. In-furrow applications of Orondis® or Presidio®, or foliar applications of Phostrol™ provided significant suppression of pink rot relative to inoculated controls. Applications of Orondis®, Presidio®, or Phostrol™ to daughter tubers one hour after inoculation also provided significant suppression of pink rot under storage conditions. These results suggest that there are promising new potential management strategies to control metalaxyl-m-resistant strains of *P. erythroseptica* which are increasing in frequency across Canada. Continued surveys to track metalaxyl-m resistance and the on-going development of new control strategies will aid producers with pink rot management and help mitigate fungicide resistance development in *P. erythroseptica*.

***[DM5] Root lesion nematode (*Pratylenchus penetrans*) mitigation through application of chitin and *Ascophyllum nodosum* extract in the soil prior to seeding red clover (*Trifolium pratense*) and birdsfoot trefoil (*Lotus corniculatus*).** Z. L. FRASER, Y. A. PAPADOPOULOS, Z. DONG, J. DUYNISVELD, C. E. GALLANT, T. FORGE, B. LEES, AND S. A. E. FILLMORE. *Saint Mary's University 923 Robie Street, Halifax, NS, Canada B3H 3C3; (Y.A.P) Agriculture & Agri-Food Canada, Faculty of Agriculture, Dalhousie University; (J.D). Agriculture and Agri-Food Canada, Atlantic Food and Horticulture Research Centre, Nappan, NS, Canada B0L 1C0; (C.E.G.) Cherry Valley, PEI, Canada C0A 2E0; (T.F.) Agriculture & Agri-Food Canada, Summerland Research and Development Centre, Summerland, BC, Canada V0M 1A0; (B.L. and S.A.E.F.) Agriculture & Agri-food Canada, Atlantic Food and Horticulture Research Centre, Main St., Kentville, NS, Canada B4N 1J5.*
Traditional mitigation strategies for root lesion nematodes (RLN) are typically ineffective and include application of nematicides and crop rotation. This research assessed the effect of a soil drench with chitin or *Ascophyllum nodosum* extract (ANE) on RLN infection and also compared levels of RLN infection among cultivars of birdsfoot trefoil (*Lotus corniculatus*) and red clover (*Trifolium pratense*). Two experimental cultivars of red clover were used, TRC12-156 selected for high isoflavones and TRC12-157 selected for low isoflavones, along with two commercially available birdsfoot trefoil cultivars, AC Langille and Leo. Legumes were seeded into nematode-infested soil with a population of 19 RLN/ g dry soil and treated by soil drench with 3000ppm ANE, 350ppm chitin or water, and grown in a growth chamber. After 19 weeks, nematodes were extracted from roots using the modified Baermann funnel method. Following, a seven-day incubation nematode suspensions were examined and roots were dried and weighed. The ANE and chitin treatments both resulted in significantly smaller numbers of RLN/g dry root than the water control; ANE had the lowest RLN populations at 5185 RLN/g dry root, a 30% reduction relative to water (7424RLN/g). Red clover cultivars (3877/g) had lower concentrations of RLN than birdsfoot trefoil cultivars (11276/g) in both treated and untreated soil. One cultivar of red clover, TRC12-156, had particularly low RLN populations with 2088RLN/g; a 63% decrease compared to TRC12-157 (5666/g). These results indicate the potential for new RLN mitigation strategies through application of novel soil treatments and also selection of forage species and cultivar.

***[DM6] Effects of fungicides in managing pasmo disease and seed yield in flax.** T. ISLAM, C. VERA, J. SLASKI, R. MOHR, K.Y. RASHID AND H.R. KUTCHER. *Department of Plant Sciences/Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada; (C.V.) Agriculture and Agri-Food Canada (AAFC), Melfort, SK, Canada; (J.S.) Alberta Innovates, Vegreville, AB, Canada; (R.M.) AAFC, Brandon, MB, Canada; (K.R.) AAFC, Morden, MB, Canada*
Pasmo disease of flax, caused by *Septoria linicola* (Speg.) Garassini, is commonly observed in western Canada every year. It reduces both the quality and quantity of flax. The main objectives of this study were to determine the impact of fungicide products and application timings on pasmo in flax in terms of seed yield and quality at Brandon, MB; Melfort, SK; Saskatoon, SK; and Vegreville, AB from 2014 to 2016. Three fungicides, Headline® (pyraclostrobin, 100 g a.i. ha^{-1}), Xemium® (fluxapyroxad, 51 g a.i. ha^{-1}) and Priaxor® (50.1 g fluxapyroxad ha^{-1} and 99.9 g pyraclostrobin ha^{-1}) were applied to flax at early-flower, mid-flower and at both stages. Priaxor and Headline were the very most effective in to reducing pasmo disease severity at most of the sites. Priaxor and Headline reduced pasmo disease severity by 40% and 38%, respectively, while reduction due to Xemium was 20% compared with the untreated control. There was no difference between early and mid-flower fungicide applications for disease severity. Fungicide applications at both flowering stages reduced disease severity slightly more than at early or mid-flowering stage. Combined data analysis of all site years indicated that application of fungicides improved the seed yield over the control. Priaxor increased the yield by 26% in comparison with the control. followed by Headline at 19%. Although Xemium was less effective at reducing pasmo severity, it still resulted in an 18% yield increase over the untreated control. No differences were observed between the effects of early and mid-flower fungicide applications for seed yield.

[DM7] RNA interference two ways: molecular fungicides and durable plants to control *Sclerotinia sclerotiorum. A. G. MCLOUGHLIN, N. WYTINCK, P. WALKER, M. F. BELMONTE, S. WHYARD AND D. FERNANDO. *Department of*

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Infecting over 450 plant species, sclerotinia stem rot (white mold, *Sclerotinia sclerotiorum*) substantially threatens Canadian canola, which contributes over 26 billion dollars to the economy. Traditionally, *Sclerotinia* control involved the use of broad-spectrum fungicides, which are neither economical or effective. Crop rotations, which are also used, fail due to the promiscuous host range of *Sclerotinia* and the formation of durable, melanized resting structures called sclerotia, which persist in the soil for up to 10 years. Consequently, there is an urgent need for novel species-specific methods to mitigate *Sclerotinia*. Our novel strategy exploits the inherent cellular defense process known as RNA interference (RNAi) by employing *in vitro* or *in planta* synthesized double stranded RNAs (dsRNA). Upon encountering the designer molecules, the cell processes the dsRNA to specifically target homologous transcripts. Using a comprehensive bioinformatics pipeline, *Sclerotinia* genes were identified and *Sclerotinia*-specific dsRNA molecules were synthesized. Target gene knockdown was confirmed and quantified using quantitative real-time PCR from RNA isolated from fungal liquid cultures. Using a petal inoculation method that mimicked aggressive infection conditions, over 70 dsRNA molecules were evaluated. Lesion size was significantly reduced on mature leaf tissues by up to 85%. To protect plants throughout their lifecycle, we developed constitutively expressing dsRNA expressing *Arabidopsis thaliana*. When challenged with *Sclerotinia*, transgenic RNAi plants reduced lesion size up 75% when compared to wild-type controls. Taken together, we have developed two novel solutions to combat this devastating fungus: a species-specific molecular fungicide capable of controlling fungal infection on the leaf surface and transgenic RNAi plants protected throughout the lifecycle.

***[DM8] Mitigation of stripe rust and leaf spot diseases in winter wheat in western Canada.** K. NABETANI, J. M. LOBO, B. L. BERES, K. COLES, R. ABOUKHADDOUR, T.K. TURKINGTON, W.E. MAY and H. R. KUTCHER. *Department of Plant Sciences, 51 Campus Drive, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada; (B.L.B., K.C., R.A.) Agriculture and Agri-Food Canada (AAFC) Lethbridge Research and Development Centre, 5403 1st Ave South, Lethbridge, AB T1J 4B1; (T.K.T.) AAFC Lacombe Research and Development Centre, 6000 C&E Trail, Lacombe, AB T4L 1W1, Canada; (W.E.M.) AAFC Indian Head Research Farm, P.O. Box 760, R.R. #1 Government Road, Indian Head, SK S0G 2K0, Canada*
Stripe rust disease of wheat, caused by *Puccinia striiformis* f. sp. *tritici* Eriks. is prevalent throughout western Canada. This study was conducted to evaluate disease impact on winter wheat at Lethbridge and Lacombe, AB and Saskatoon and Indian Head, SK. The effects of fungicide (combination of metconazole and pyraclostrobin) on stripe rust and leaf spot severity, and yield and quality of winter wheat were observed after fungicide application at three timings. Four cultivars varying in disease resistance, 'AC Bellatrix,' 'Moats,' 'Radiant,' and 'CDC Osprey' were seeded in the 2015/2016 crop season. Fungicide was applied in the fall, spring, or both fall and spring to each cultivar and effects were compared with unsprayed checks. Under high stripe rust pressure, severity on susceptible cultivars, 'AC Bellatrix' and 'CDC Osprey,' and severity of leaf spot on these cultivars and 'Radiant,' were reduced by a single application in spring or applications in fall and spring. Stripe rust severity was reduced from 78% to less than 5% on 'AC Bellatrix.' Yield increased by nearly 30%, and quality was also improved this cultivar. 'Radiant' was more susceptible to leaf spot than other cultivars, but had low stripe rust severity and the benefit of fungicide depended on location. 'Moats,' which is highly resistant to stripe rust, did not benefit from fungicide application. Stripe rust and leaf spot susceptible cultivars were effectively controlled with spring fungicide application while fall application alone appeared ineffective for disease control. The dual application in spring and fall did not offer additional benefits.

***[DM9] Pathogen growth inhibition and disease suppression on cucumber (*Cucumis sativus L.*) and canola (*Brassica napus L.*) plants with Active Flower, a foliar nutrient spray containing boron.** L. NI AND Z. K. PUNJA. *Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC, V5A 1S6, Canada*
Greenhouse cucumber (*Cucumis sativus L.*) and canola (*Brassica napus L.*) are grown extensively in Canada and fungal diseases are a major limiting factor during commercial production of these crops. The effectiveness of Active Flower™ (AF), a fertilizer containing 3.0% boron (B) plus 8:4:12 of N:P:K in reducing the severity of several diseases

was evaluated in this study. Six fungi were selected based on their importance as plant pathogens, and included *Sclerotinia sclerotiorum, Botrytis cinerea, Pythium dissoticum, Fusarium oxysporum, Phoma lingam* and *Thielaviopsis basicola*. They were grown in potato dextrose broth (PDB) with 4 concentrations (0, 1, 3 and 5 ml per L) of AF. Growth inhibition was observed at rates of 1 and 3 ml/ L, with the most pronounced effect seen at 3-5 ml/L. These concentrations were applied to cucumber 'Tasty Green' and canola 'Westar' grown under greenhouse conditions. Four applications were made at weekly intervals, and pathogen inoculation was made after the third application. Cucumber plants inoculated with *Pythium* and *Fusarium* and treated with AF had higher dry weights compared to the water control, with 3 ml/L giving the greatest increase. The number of powdery mildew (*Podosphaera xanthii*) colonies on cucumber leaves was significantly reduced by AF at 3 and 5 ml/L when applied at the onset of infection. On canola plants, AF at 1, 3 and 5 ml/L increased dry weight and reduced disease development on leaves due to *Sclerotinia* and *Phoma*. Preliminary experiments showed that phenolic content, chlorophyll, B and N levels in foliage receiving AF were significantly increased.

***[DM10] Evaluation of weather-based forecasting models and cultivar resistance to manage leaf curl (*Colletotrichum fioriniae*) on celery crops in Ontario.** S. REYNOLDS, M. J. CELETTI, K. JORDAN, M. R. MCDONALD. *Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada; (M.J.C.) Ontario Ministry of Agriculture, Food and Rural Affairs, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada*

Colletotrichum fioriniae ((Marcelino & Gouli) R.G. Shivas & Y.P. Tan) causes leaf curl on celery in Ontario. The disease renders the crop unmarketable when lesions develop along the stalk and when crown rot develops. The objectives of this study were to: (i) evaluate disease forecasting programs to reduce the number of fungicide sprays while maintaining disease control, and (ii) to screen for cultivar resistance. For the forecasting trial, the fungicide Quadris Flowable (azoxystrobin 25%) was alternated with Switch 62.5WG (cyprodinil 37.5% and fludioxonil 25.0%) and were applied on cv. 'TZ 6200'. Spray timings were determined using: TOMCAST with a threshold of 15 disease severity value, and BOTCAST at a cumulative disease severity index of 21. A weekly calendar spray and a no-spray control were included. Disease management was achieved using TOMCAST, with five fungicide applications compared with the seven sprays applied on a calendar spray basis. BOTCAST prompted only one spray and disease severity was equivalent to that of the no-spray control. The percent of marketable weight was >98% for TOMCAST and the calendar spray, while BOTCAST and the no-spray control had <70%. For the cultivar trial, twelve cultivars were evaluated for resistance to *C. fioriniae*. Cultivars 'TZ 9075', 'TZ 6010', 'Hadrian', and 'Merengo' were the least susceptible with a percent marketable yield greater than 70%, while 'TZ 9779' was the most susceptible with percent marketable yield less than 20%. Cultivar selection and TOMCAST can be incorporated into the integrated pest management program to manage celery leaf curl in Ontario.

***[DM11] Determining the risk of Fusarium root rot on field pea by greenhouse soil bioassay and qPCR analysis.** S. SAFARI, L. HALL and S. CHATTERTON. *Faculty of Agricultural, Life & Environmental Sciences, University of Alberta, Edmonton, AB, Canada, T6G 2P5; (S.S., S.C) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge AB, Canada T1J 4B1*

Field avoidance is one of the most recommended management options to minimize impact of pea root rot pathogens. Field indexing tools commonly used to quantify pathogens in fields are real time PCR (qPCR) for pathogen quantification or greenhouse bioassays. The objective of this study was to determine the efficiency of these tools for predicting *Fusarium* root rot risk. Field surveys were conducted in 14 commercial pea fields across Alberta to collect soil and root samples. Overall, 140 soil and root samples were collected from 10 sites in each field. Root samples were rated for severity and used for PCR analysis to determine causal organisms. To determine minimum inoculum potential, field soils were serially diluted, planted to peas in a greenhouse, and root rot severity measured by visual assessment. Significant difference in disease severity was observed when the proportion of field soils was below 10% but there was no significant difference between plants grown in soil collected from symptomatic and asymptomatic sites in a field. Results showed low correlation between DNA quantities of *Fusarium avenaceum* or *F. solani* in the soil and disease severity. This could be due to low pathogen DNA recovery from soil

samples and/or presence of PCR inhibitors in soil DNA extracts. To improve the accuracy of estimation, soil DNA will tested using droplet digital PCR which is not affected by PCR inhibitors. The results obtained from the disease severity assessments of the fields soil and quantification of *F. avenaceum* and *F. solani* DNA from soil will be compared to determine the efficiency of these methods in predicting disease risk in pea fields.

***[DM12] Effect of fungicide application timing on fusarium head blight in durum wheat.** G. SINGH[1*], G. HNATOWICH[2], J. WEBER[3], G. ISSAH[3], W. MAY[4] AND H.R. KUTCHER[1] . *[1]Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada. [2]Irrigation Crop Diversification Corporation (ICDC), Box 609, Outlook, SK S0L 2N0, Canada. [3]Western Applied Research Corporation (WARC), Box 89, Scott, SK S0K 4A0, Canada. [4]Agriculture and Agri-Food Canada, Research Farm - Indian Head, Box 760, SK S0G 2K0, Canada*
Fusarium head blight (FHB) is one of the most important diseases of wheat in Canada. Presently farmers rely on the current recommendation to apply fungicide at 50% anthesis (BBCH 65) to manage the disease. Field experiments were conducted at Saskatoon, Indian Head, Scott and Outlook in 2016 to assess the effect of fungicide application timing and seeding rates on durum wheat affected by FHB. Seven treatments of metconazole fungicide 'Caramba®' were applied to two seeding rate treatments: 400 seeds/m^2 and 75 seeds/m^2. The fungicide treatments consisted of an untreated check (no fungicide), a treated check (fungicide application at all stages), and applications at: BBCH 59 (heading), BBCH 61 (early anthesis), BBCH 65 (50% anthesis), BBCH 69 (late anthesis) and a treatment with two applications: BBCH 61 followed by BBCH 73 (soft dough). Evaluated parameters were: FHB index (IND), DON, fusarium damaged kernels (FDK), protein and yield. Seeding rate influenced all parameters, higher seeding rate had higher IND and yield while lower level of FDK, DON and protein as compared to lower seeding rate. All fungicide application treatments led to lower IND, DON and FDK than the untreated check. The treatment with two fungicide applications had the lowest FHB index and FDK; however, the BBCH 61 and BBCH 65 treatment had the highest yield. All fungicide treatment expects BBCH 59 had similar effect on DON levels. These are preliminary results from year one of a multiple site-year study.

***[DM13] Identification and utilization of target pathogenesis genes in *Sclerotinia sclerotiorum* through RNA sequencing and host-induced gene silencing.** P.L. WALKER, A. MCLOUGHLIN, N. WYTINCK, M.G. BECKER, I.J. GIRARD, S. WHYARD, M.F. BELMONTE. *Department of Biological Sciences, University of Manitoba, 50 Sifton Road, Winnipeg, MB R3T 2N2, Canada.*
White stem mold in canola (*Brassica napus*) is caused by the fungal pathogen *Sclerotinia sclerotiorum* and is responsible for significant losses in crop yield across the globe. With advances in high-throughput transcriptomics and computational biology our understanding of the canola-sclerotinia pathosystem is improving; however, currently no resistant canola cultivars are available and control relies on crop management. Using high-throughput RNA sequencing coupled with a comprehensive bioinformatics approach we have identified target genes expressed in *S. sclerotiorum* pathogenesis. These genes were targeted for knock down in the fungus using host-induced gene silencing through the RNA interference pathway. RNAi is a regulatory mechanism widely conserved in eukaryotes that knocks down gene expression in response to intracellular double-stranded RNA (dsRNA). Generation of transgenic plants expressing dsRNA can activate RNAi pathways in invading fungi and affect its ability to successfully infect host tissues. Infection assays using a *S. sclerotiorum* ascospore inoculum were performed on transgenic *Arabidopsis* targeting the SS1G_08281 gene involved in oxalic acid production, results demonstrated a 74% reduction in leaf lesion size compared to wild-type *Arabidopsis.* We will discuss our method of target gene identification and the utility of host-induced gene silencing as a preventative strategy against white stem mold in canola.

***[DM14] Interactions between biocontrol agents and soil microbes: impact on pathogen growth and disease suppression.** A. C. WYLIE AND Z. K. PUNJA. *Simon Fraser University, Department of Biological Sciences, 8888 University Drive, Burnaby, BC V5A 1S6, Canada*
Biological control of plant diseases is of particular importance in intensive organic greenhouse vegetable production where pesticides are not permitted. In these production systems, growers use microbially-diverse substrates

including composts as a medium for plant growth. The impact of a microbially-rich substrate on the efficacy of an inundatively applied biocontrol agent has not been previously studied i.e. is it additive, neutral, or negative with respect to disease suppression? Using several different vermicomposts incorporated into sterilized substrate, we assessed pathogen suppression *in vitro* and disease suppression on cucumber plants. In addition, the effects of two biocontrol agents -*Bacillus subtilis* strain QST 713 (Rhapsody) and *Clonostachys rosea* f. *catenulata* (*Gliocladium catenulatum*) strain J1446 (Prestop), against the pathogens *Fusarium oxysporum* f. sp. *radicis-cucumerinum* (Forc), and *Rhizoctonia solani* on cucumber and radish, respectively, were evaluated. We found a range of synergistic and antagonistic responses, depending on the host, pathogen, and biocontrol agent. For example, *C. rosea* alone provided better control of Forc growth *in vitro* and more consistent disease suppression in cucumber growth experiments compared to vermicompost alone, and when combined they showed a synergistic effect. Neutral to negative effects were found for *B. subtilis* alone and combined with vermicompost in this Forc system. Vermicompost microbes had neutral to synergistic effects with *C. rosea* in growth trials using the radish/*R. solani* model. The methods developed herein could be used as a preliminary screen for biological control organisms for their efficacy in microbially-rich environments.

***[DM15] Applications of Soil-Applied Fungicides to Manage *Phytophthora* Root Rot on Chili (*Solanum annum* L.) in Pakistan.** K. NAWAZ, A. A. SHAHID, S. IFTIKHAR, W. ANWAR AND M.N. SUBHANI. *Institute of Agricultural Sciences, University of the Punjab, 54590 Lahore, Pakistan; (A. A.) Center of Excellence in Molecular Biology, University of the Punjab, 54590 Lahore, Pakistan*

Chili (*Solanum annum* L.) attacks by many fungal pathogens, including members of Oomycetes which are responsible for root rot in the worldwide. Fungal pathogens cause economic losses in different chili growing areas of the Pakistan. Most of the plant tissues, including roots, crowns, fruit, and leaves, are vulnerable to *P. capsici*. It is very difficult to manage the *Phytophthora* root rot of chili as different commercial varieties are extremely susceptible to *P. capsici*. The causal agent of the disease was isolated on corn meal agar (CMA), and identified on a morphological basis by using available taxonomic keys. The pathogen was also confirmed on the molecular basis through the internal transcribed spacer region. The Blastn results showed 100% homology with already reported sequences of *P. capsici* in NCBI database. Most of the farmers have conventionally relied on foliar fungicide applications to control *Phytophthora* root rot in spite of their incomplete effectiveness. In this study, *in vitro* plate assay, seed soaking and foliar applications of 6 fungicides were evaluated against root rot of chili. *In vitro* assay revealed that significant inhibition of linear growth was obtained with Triflumizole at 7.0%, followed by Thiophanate methyl (8.9%), Etridiazole (6.0%), Propamocarb (5.9%) and 7.5% with Mefenoxam and Iprodione for *P. capsici*. The promising treatments of *in vitro* plate bioassay were evaluated in pot experiments under controlled conditions in the greenhouse. All fungicides were applied after at 6-day intervals. Results of pot experiment showed that all treatments considerably inhibited the percentage of *P. capsici* root rot incidence. In addition, application of seed soaking with all six fungicides combined with the foliar spray of the same components showed the significant reduction in root rot incidence. The combine treatments of all fungicides as *in vitro* bioassay, seed soaking followed by foliar spray is considered non-harmful control methods which have advantages and limitation. Hence, these applications proved effective and harmless for the management of soil-borne plant pathogens.

***[DM16] Evaluating Fungicidal Activity of Complex II Inhibitors against Late Blight of Potato .** S. IFTIKHAR, A. A. SHAHID, K. NAWAZ AND W. ANWAR**.** *Institute of Agricultural Sciences, University of the Punjab, 54590 Lahore, Pakistan; (A. A.) Center of Excellence in Molecular Biology, University of the Punjab, 54590 Lahore, Pakistan*

Respiratory inhibitors are among the fungicides most widely used for disease control on crops. Modern agriculture depends on efficient tools for controlling fungal diseases that can have a strong impact on yield and quality. Potato late blight is the most significant and damaging disease of potato worldwide. The oomycete pathogen *Phytophthora infestans*, causal agent of late blight, is widely known emerging plant pathogens. New broad spectrum foliar fungicides against complex II were designed using pharmacophore modeling and structure based virtual screening. The enzyme links the carboxcylic acid cycle and the cellular respiration by catalyzing the oxidation of succinate to

fumarate. The focus of the research work was on finding compounds with high intrinsic activity against *P. infestans.* The fungus was identified using morphological and molecular characteristics. Fungicidal activity of twelve novel active ingredients targeted against complex II was evaluated for the effect on mycelial growth and spore germination of the fungi using poisoned agar assay. In mycelial growth assay, compounds C6 and C2 were highly active against *P. infestans* while compound C10 showed second highest antifungal activity. In the case of spore germination assay, compounds C1 and C6 were most effective. All the other compounds displayed intermediate inhibitory activity against *P. infestans* as compared to commercially available fungicide. This study showed that compound C1, C2, C6 and C10 resulted in the decrease in mycelial growth and spore germination. The complex II inhibitors identified in this work can be recommended as active ingredients for fungicides against *P. infestans*.

[DM17] Fungicide control of leaf mottle (*Septoria triseti* Speg.) and fusarium seed infection of canary seed. L. P. CHOLANGO-MARTINEZ, H. R. KUTCHER, P. J. HUCL and W.E. MAY. *Crop Development Centre/Department of Plant Science, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada/ Indian Head Research Farm, Indian Head, SK S0G 2K0.*

Canary seed (*Phalaris canariensis* L.) is an annual grass originating from the Mediterranean. This crop is used mainly for feeding caged birds, although it has been approved recently as a novel food for human consumption. Saskatchewan produces >90% of the Canadian production, with an annual seeded area of approximately 100,000 ha. Leaf mottle disease caused by *Septoria triseti* Speg., and fusarium seed infection caused by *Fusarium graminearum* species complex are believed to impact yield of this crop. Triazole and strobilurin fungicides are used to control leaf diseases and fusarium head blight of other cereals, but their effects are unknown on canary seed. This project assessed the effect of fungicide application timing on leaf mottle severity, incidence of fusarium seed infection and impact on yield. Two field experiments were established in 2014 and 2015 at Saskatoon and Indian Head; Saskatchewan using the canary seed cultivar 'Keet' (susceptible) and the genotype 'PI 251274' (moderately resistant). Fungicide treatments included three products: prothioconazole + tebuconazole (Prosaro ®), pyraclostrobin + metconazole (Twinline®), and propiconazole (Bumper ®), which were sprayed at two crop growth stages: flag leaf or head emergence. Sprayed treatments had lower leaf mottle severity and fusarium seed infection, but not at all site-years. Fungicide application at flag leaf stage reduced leaf mottle and at head emergence reduced fusarium seed infection. Prothioconazole + tebuconazole occasionally reduced leaf mottle and fusarium seed infection; however, fungicide application provided little yield benefit.

[DM18] Biocontrol agent *Streptomyces* combined with phosphite activate soybean defense mechanisms against *Phytophthora sojae.* A. ARFAOUI, L. ADAM, F. DAAYF. *Department of Plant Science, Faculty of Agricultural and Food Sciences, University of Manitoba, Winnipeg, Canada.*

Phytophthora sojae (*P. sojae*) is a soil-borne pathogen causing root rot disease in soybean plants. The use of selected bacteria, such as *Streptomyces*, is a promising strategy for managing *Phytophthora* root rot of soybeans. Phosphite (Phi) compounds are salts derived from phosphorous acid and were previously shown to protect plants against certain pathogens. We explored the beneficial effect of the endophytic bacterium *Streptomyces gelobus* (S11) in combination with phosphite in terms of reducing *P. sojae* disease development in soybeans and the molecular mechanisms behind such effects. Both S11 and phosphite inhibited the growth of *P. Sojae in vitro* on PDA agar plates and pre-treatment of soybeans with S11 and/or phosphite reduced the disease severity. Quantification of *P. sojae's* DNA in soybean roots by Real-Time PCR, indicated that the growth of *P. sojae* was restricted in presence of *Streptomyces* and/or phosphite. Also, both treatments affected the activation of stress hormones and related defense genes in soybean plants. *Streptomyces* in combination with phosphite may constitute an efficient complementary strategy to protect soybeans from *P. sojae*.

[DM19] Phenazine-1-carboxylic acid contributes to the biocontrol of potato common scab through modulation of *Streptomyces scabies'* transcriptome. T. ARSENEAULT, R. ROQUIGNY, A. NOVINSCAK, C. GOYER AND M. FILION. *Saint-Jean-sur-Richelieu Research and Development Centre, Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu, QC, Canada, J3B 3E6, (R.R., A.N., M.F.) Université de Moncton, Department of Biology, Moncton, NB,*

Canada, E1A 3E9, (C.G.) Fredericton Research and Development Centre, Agriculture and Agri-Food Canada, Fredericton, NB, Canada, E3B 4Z7.
Potato common scab, mainly caused by the bacterial pathogen *Streptomyces scabies (Ss)*, is an economically important disease for which there are no efficient control measures. Pot and field experiments have determined that *Pseudomonas fluorescens* LBUM223 is able to reduce disease symptoms through its production of the antimicrobial compound phenazine-1-carboxylic acid (PCA). Several potential mechanisms of biocontrol were investigated: 1) reduction of *Ss* soil populations, 2) induction of plant defense responses and 3) alteration of virulence gene expression in *Ss*. Results showed that the reduction in scab symptoms was not associated with reduced *Ss* soil populations nor changes in plant defense gene expression, but coincided with a reduced expression of *txtA*, an essential gene for the production of *Ss'* major pathogenicity and virulence factor, thaxtomin A. To further characterize this effect, *in vitro* RNA-seq analyses were conducted to determine how PCA affects *Ss*' entire transcriptome. Following exposure to wildtype LBUM223 or purified PCA, reduced mycelium and spore formation in *Ss* was observed, and 12%-14% of all genes were differentially expressed. Among these, we noted a strong down-regulation of the *cfa* biosynthetic cluster, which produces a virulence factor resembling coronatine. The specific implication of PCA is made clear when treatment with an isogenic PCA-deficient mutant of LBUM223 only up-regulated 0.13% of genes in the pathogen. This demonstrates that these concentrations of PCA cause important physiological changes in *Ss*, likely leading to biocontrol through mechanisms such as reduced virulence and differentiation, and increased oxidative stress, rather than reduced pathogen populations through toxicity.

[DM20] Chocolate spot disease and Lygus bugs degrade faba bean seed quality. S. KAUR, J. THOMAS, S. MEERS, S. CHATTERTON, and H.A. CARCAMO. *Department of Biological Sciences, University of Lethbridge, Lethbridge AB, Canada T1K 3M4; (S.K., S.C., H.A.C.) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge AB, Canada T1J 4B1; (S.M.) Crop Diversification Centre South, Alberta Ministry of Agriculture and Forestry, Brooks AB, Canada T1R 1E6*
Insect pests and pathogens can affect agricultural crops independently or through their interactions. In the Prairies, faba bean seeds are often damaged by lygus bugs (LB) and chocolate spot disease (CSD), caused by *Botrytis* sp. CSD becomes evident at the crop flowering stage, which is also when LB are present and feeding on flowers and developing pods. Therefore, it is hypothesized that concomitant presence of these pests in the field may increase seed damage severity and further reduce quality. Field and greenhouse studies were conducted to determine: (i) geographic and spatial (within canopy) distribution of CSD and LB in central and southern Alberta; (ii) association of CSD and LB abundance and; (iii) the effect of CSD and LB on faba bean seed severity (as a measure of seed quality loss). Significant effect of LB abundance on the seed damage confirms their role in lowering seed quality through feeding that result in necrotic spots and hull perforations. Conversely, no significant effect of CSD on seed severity was found. However, *Botrytis* sp. was frequently isolated from seeds but infestation levels were not significantly correlated to Lygus abundance. Therefore, results suggest that while LB affects the seed quality by feeding damage, *Botrytis* sp. have the potential to affect faba bean seed quality by infesting the seeds. It also suggests that different management strategies will be needed to keep the insect population and disease progression under check. Greenhouse studies to further explore the interaction between *Botrytis* sp. infection and Lygus feeding on the pod are underway.

[DM21] AeroNet: spore samplers in collecting fungal plant pathogens in the air and rain. W. CHEN, S. HAMBLETON, K. A. SEIFERT, C. A. LÉVESQUE, O. CARISSE, M. S. DIARRA, R. D. PETERS, C. LOWE, J. T. CHAPADOS. *Ottawa Research & Development Centre, Science & Technology Branch, Agriculture and Agri-Food Canada, 960 Carling Ave., Ottawa, ON, K1A 0C6, Canada[1] (O.C.) Saint-Jean-sur-Richelieu Research & Development Centre, Science & Technology Branch, Agriculture and Agri-Food Canada, 430 Gouin Boulevard, Saint-Jean-sur-Richelieu, Quebec, J3B 3E6, Canada[2] (M.S.D.) Guelph Research and Development Centre, Science & Technology Branch, Agriculture and Agri-Food Canada, 93 Stone Road West, Guelph, Ontario, N1G 5C9, Canada[3]; (R.D.P.) Charlottetown Research & Development Centre, Science & Technology Branch, Agriculture and Agri-Food Canada, 440 University Avenue, Charlottetown, Prince Edward Island, C1A 4N6, Canada*

Spore samplers are widely used in pathogen-surveillance but not so much for monitoring the composition of aeromycobiota. The composition of fungal community from air and rain samples collected using three different spore samplers in summers 2010 and 2011 was exhaustively characterized based on the Internal Transcribed Spacer (ITS) metabarcodes generated by High-Throughput Sequencing (HTS). Diverse spatial and temporal distribution patterns in the aeromycobiota were observed at the Canadian west and east coasts. The aeromycobiota diversity was found higher during the cooler, wetter summer and showed a positive correlation with the speed and northward direction of the wind. The relative abundance and/or richness of some fungal taxa were significantly different based on ITS1 or ITS2 sequencing data; e.g. those of *Epicoccum* and *Ganoderma spp*, were significantly higher in ITS1; but those of *Botrytis* and *Fusarium* spp were significantly higher in ITS2. In addition, singificant differences were observed beteween samplers for their ability to collecte pathogenic plant fungi. For instance, *Cladosporium* spp., *Drechslera* spp. and *Entyloma* spp. were mainly collected with the air samplers; while *Fusarium* spp., *Microdochium* spp. and *Ustilago* spp. were recovered more frequently with the rain samplers. The usefulness and collection preference of spore samplers in recovering fungal pathogens in air and rain were addressed to provide guidelines in selecting optimal samplers for taxa of concerns. AeroNet, a nationalwide spore-sampling network, combined with HTS and well-designed sampling strategies, may contribute significantly to the national biovigillance network for protecting plants of agricultural and enconomic importance in Canada.

[DM22] Exogenous dsRNA application for control of fusarium head blight. ENWU LIU and SHAWN CLARK. *National Research Council Canada, 110 Gymnasium Place, Saskatoon, SK, Canada, S7N 0W9*
Fusarium head blight (FHB) is a devastating disease affecting both yield and quality of wheat grain in Canada and around the world. While FHB-resistant cultivars are available, the mechanism of resistance remains poorly understood and the transfer of strong resistance into elite varieties remains a challenge. Expression of RNAi constructs in plants can also lead to the silencing of genes in closely associated organisms such as pathogenic fungi in a phenomenon known as host induced gene silencing (HIGS). This strategy can provide strong resistance to a number of prominent pathogens including *Fusarium graminearum.* While this approach holds great promise, it requires the use of genetically modified crops. The commercial implementation of transgenic RNAi wheat is currently not possible due to challenges with regulatory approval and perceived value in international trade markets. The goal of this research is to determine if exogenous application of double-stranded (dsRNA) can serve as an effective method of control of Fusarium Head Blight (FHB) in wheat. We have tested the application of exogenous double stranded RNA targeting a fusarium chitin synthase both as a soil drench and foliar application. Both treatments had a significant impact on fusarium head blight symptoms compared to plants treated with control RNA. Quantitative PCR of target *F. graminearum* genes during wheat infection confirmed silencing of fungal transcripts via dsRNA applied to the wheat plant.

[DM23] Plant Diagnostic Research Conducted by the Alberta Plant Health Lab. J. FENG, K. ZUZAK, Y. YANG, D. RENNIE, K. ZAHR, AND D. FEINDEL. *Alberta Plant Health Lab, Alberta Agriculture and Forestry, Edmonton, AB T5Y 6H3, Canada*
To provide authoritative, commercially-unavailable plant diagnostic services in Alberta, Alberta Agriculture and Forestry established the Alberta Plant Health Lab (APHL) at the Crop Diversification Centre North, Edmonton, Alberta. The lab became fully functional in 2016 and currently conducts diagnostic analyses of all plant diseases encountered across the province. Currently, all services provided by the APHL are free of charge. Besides diagnostic testing, the APHL also provides DNA barcoding service on weed, insect and microbes including fungi, oomycetes and bacteria. Diagnostics-related research has been extensively conducted in the APHL including 1) descriptions of plant pests new to Alberta or Canada, 2) optimization of diagnostic techniques such as sample preparation and DNA extraction, 3) standardization of existing and new PCR-based diagnostic protocols, 4) development of genetic makers and PCR primers for diagnosis of important or potentially important plant diseases such as clubroot (*Plasmodiophora brassicae* Woronin) and Verticillium wilt (*Verticillium longisporum* (C. Stark) Karapapa, Bainbr. & Heale) of canola, 5) identification of fungal pathogenicity-related genes that can be used for diagnosis and 6) investigation of molecular

mechanisms of new virulence generation in populations of plant pathogens such as *P. brassicae* (clubroot) and *Leptosphaeria maculans* (Sowerby) P. Karst (blackleg) on canola.

[**DM24] Epidemiology and management of white mold in dry bean by irrigation and plant architecture.** K. A. KADER, P. M. BALASUBRAMANIAN AND S. CHATTERTON. *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5401 – 1st Avenue South, Lethbridge, AB T1J 4B1, Canada*
In the semi-arid region of southern Alberta, dry bean (*Phaeseolus vulgaris* L.) is grown under irrigation. White mold (WM) caused by the fungus *Sclerotinia sclerotiorum* (lib.) de Bary is a major constraint to dry bean production. High irrigation levels to maximize dry bean yield potential can also influence WM development by creating conducive environmental conditions such as high soil moisture and leaf wetness, and cool soil temperatures. Field experiments were conducted during 2015 and 2016 at AAFC-Lethbridge to determine the effect of irrigation and cultivars on WM epidemiology and management. Three levels of irrigation (high, medium and low) and five cultivars with three different architectures (determinate upright bush, indeterminate semi-upright and indeterminate prostrate) were arranged in a split-plot randomized block design. Sensors and data loggers were established to monitor micro-climate data, such as soil moisture within top 5-cm, leaf wetness and soil temperature under the canopy. Canopy porosity, lodging, flower infection and WM disease severity were also measured. Pearson's correlation coefficient revealed significant relationship of WM severity with soil moisture, leaf wetness and soil temperature. Lodging was positively correlated with WM severity while the relationship was negative for canopy porosity with the disease. Flower infection was highly correlated with WM severity and explained maximum variability. Overall, significantly lower disease was observed in medium and low irrigation plots, but yield was highest in medium irrigation plots. Thus, reduced level of irrigation (medium) and accelerated development of lodging resistant cultivars would be useful for WM management in Alberta.

[DM25] Assessing infection in wheat seeds by *Fusarium graminearum* using Biospeckle Laser Analysis, a novel application of the biospeckle technique. D. B. SUTTON AND Z. K. PUNJA. *Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC, V5A 1S6, Canada*
Fusarium head blight is a major fungal disease on cereal grains worldwide, reducing crop yields and contaminating harvested grains with mycotoxins. Infection is frequently latent and scab symptoms may be non-apparent in diseased seeds. In this study, *F. graminearum* infection in red spring wheat seeds was studied using Biospeckle Laser Analysis, a laser light technique that measures the light scattering activity, known as biospeckle activity (BA), on the specimen surface. Each measurement produces a biospeckle pattern (BP) that is an image representing the BA in the field of view. Dissected seeds were inoculated with a spore suspension of *F. graminearum*, placed in a humid chamber, and BA was measured sequentially over 48 hr using a prototype sensor and compared to the uninoculated control. Results indicated that the germ BA of inoculated seeds was significantly reduced over time compared to healthy control seeds. Infection of whole seeds was then studied using mycelium of *F. graminearum* as inoculum. Observations over 48 hr indicated that while the BA from healthy seeds increased with time, reflecting biological activity, the BA in infected seeds peaked at 36 hr. When the mycotoxin deoxynivalenol (DON) was added to seeds at 20 µg/mL, the BA was suppressed compared to healthy control seeds. These results indicate that Biospeckle Laser Analysis may be a promising method to monitor seed response to infection by measuring cellular activity via light scattering activity on the seed surface. In addition, moderately-resistant and moderately-susceptible breeding lines were compared to susceptible red spring wheat. Significantly lower disease indices, computed from BA time-response curves, were observed in moderately-resistant seeds and moderately-susceptible seeds compared to susceptible seeds ($p < 0.05$).

[DM26] Development of high throughput protocols for automated nucleic acid extraction and molecular detection of potato viral, fungal and bacterial pathogens on large scale. H. XU, L. WARD, X. LI, J. NIE, S. CODY AND M. ANNETT. *Canadian Food Inspection Agency, Charlottetown Laboratory, 93 Mt. Edward Rd., Charlottetown, PE, C1A 5T1. Email: huimin.xu@inspection.gc.ca*

Numerous fungi, bacteria and viruses can infect potato and cause various diseases, many of which are regulated in Canada for protecting potato production. Potato nuclear stock and seed tubers must be indexed for regulated pests and certified for use in Canada and for export. Imported potato germplasm and other types of potatoes must be subjected to quarantine and surveillance testing, respectively. Disease surveys are often conducted for understanding pest status in Canada for appropriate phytosanitory actions. In order to perform these tests, the diagnostic laboratories have to develop and implement reliable and cost-effective diagnostic procedures with the capacity to screen massive samples within a short period of time. Here we report the development of high throughput testing process for automated nucleic acid (NA) extraction based on the use of magnetic beads, automated liquid dispensation, PCR/RT-PCR (multiplex, 96 well plate based) and capillary analysis of PCR amplicons. Potato viral, bacterial and fungal species were used in the evaluation. Standard procedures were developed, validated and employed for screening over 3000 field samples (leaves, tubers). Over 30% of the test samples were verified using conventional testing procedures including NA extraction based on organic solvent, PCR, RT-PCR and agarose gel electrophoresis. In comparison with the conventional molecular procedures, the high throughput testing retained the same level of sensitivity and specificity and improved the repeatability and reproducibility. The high throughput testing procedures significantly reduced the hand-on testing time and overall turnaround testing time that is extremely important for seed potato trade and for taking regulatory and phytosanitory actions.

[DM27] The rust species on *Impatiens* (Balsaminaceae). S. HAMBLETON, Q. EGGERTSON and S.A. REDHEAD. *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6*
Impatiens L. is a large genus of herbaceous plants with many horticultural forms. The Database of Vascular Plants of Canada lists 5 native and 3 introduced species. The invasive Himalayan balsam (*I. glandulifera* Royle), originally from Asia and introduced widely as a garden ornamental, has escaped cultivation in eight Canadian provinces and is crowding out native vegetation. The rust that infects *I. glanduliferae*, a variety of *Puccinia komarovii* Tranzschel ex P. Syd. & Syd, was developed as a biological control agent in the United Kingdom and released for field trials in 2014. The risk assessment studies were based on collections from Asia and DNA sequences were also generated for collections from the Czech Republic of *P. argentata* (Schultz) G. Winter. To date, there are no publicly available sequences for the rusts occurring on *Impatiens* from Canada. To address this gap in reference databases, 20 specimens selected from accessions in the National Mycological Herbarium (DAOM) were sampled for ITS2/28S sequences, including five *P. komarovii* from Europe or Russia and three *P. argentata* from Japan or Canada. The rest were from North America and filed as *P. impatientis-elymi* Arthur or *P. recondita* Roberge ex Desm. The ITS2 sequences were effective for differentiating four species and *P. argentata* from Japan was distinct from the Canadian collections. There are nomenclatural issues to be resolved for *P. impatientis-elymi*, also known as *P. rubigo-vera var. impatientis* (Arthur) Mains in the *P. recondita* complex, but the DNA evidence supports Arthur's original concept.

[DM28] Update on Manitoba potato and horticultural crops disease and insect pests in 2016. V. BISHT AND M. PRADHAN. *Primary Agriculture Branch, Manitoba Agriculture, 65, 3rd Avenue NE, Carman, Manitoba. R0G 0J0, Canada; (M.P.) Crop Diagnostics Centre, 201- 545 University Crescent, Winnipeg, R3T 5S6, Canada*
Conditions in 2016 crop season allowed for early planting and later harvest, resulting in record productivity in many crops. However, frequent rains during the season (110-150% of normal precipitation in potato and vegetable crops areas) and warm conditions (100 to 114% of normal) created disease favorable conditions. Late blight (LB) was reported in mid-July, when the LB forecast model used in Manitoba had shown high LB risk. The disease spread to potato and tomato crops throughout Manitoba by end of season, and caused significant losses to tomato crop. All *Phytophthora infestans* isolates tested were US#23; later collected isolates showed less sensitivity to metalaxyl than earlier ones. European corn borer (ECB) trapping showed widespread occurrence in the province, but lower numbers compared to 2015. The ECB injury creates ports for bacterial entry, which can increase stem rots in many fields. Blackleg disease (*Pectobacterium* spp.) was quite wide spread due to frequent precipitation. Aphid populations trapped in seed potato fields were low, except one field where surge occurred near end of season. For the first time, potato psyllids (PPs) were trapped in 3 separate locations; one field showing PPs in three separate weeks. All PPs

tested negative for the zebra chip pathogen, *Candidatus* Liberibacter solanacearum. Root maggot (*Delia* spp.) damage to rutabaga was significant; and even hybrids (resistant in Ontario) were severely damaged. Blackrot (*Xanthomonas campestris*) of cauliflower was severe again in 2016. Though observed at low levels in previous years, the black canker (*Itersonilia perplexans*) of parsnip caused noticeable losses.

[DM29] Evaluation of products to control stem and bulb nematode on garlic. M.R. MCDONALD, K. VANDER KOOI AND M. J. CELETTI. *Dept. of Plant Agriculture, Univ. of Guelph, Guelph, ON, Canada, N1G 2W1, Canada; (MRM, KV) Ontario Ministry of Agriculture, Food and Rural Affairs, Guelph, ON, Canada (MC)*
The stem and bulb nematode, *Ditylencus dipsaci* (Kuehn) Filipjev, is a threat to garlic production in many parts of the world. It is spread in infected cloves used as seed. Heavy infestations cause the bulbs to rot and can reduce marketable yield to zero. Field trials were conducted at two sites in Ontario, Canada, to evaluate products for control of stem and bulb nematode. The trials were established on mineral soil and high organic matter (muck) soil in the fall of 2015 and assessed in July, 2016. Naturally-infested garlic cloves (226 nematodes g^{-1} dried clove), cv. Music, were used in both trials. At the muck site, seed was soaked for four hours in solutions of Velum Prime (fluopyram), Agri-Mek EC and SC (abamectin) and Nimitz (flufensulfone). Velum Prime and Nimitz were also applied as a soil drench at planting and a granular formulation of Nimitz was also applied at seeding. After emergence in the spring, Nimitz EC was applied as a drench and another treatment was three sprays of Movento (spirotetramat). At the mineral soil site, 3 rates of Velum Prime (0.6, 1.25 and 2.5 g L^{-1}) as a 2 or 4 hour soak, were evaluated. At the muck soil site, Velum Prime as a soak was most effective. Agri-Mek as a soak also reduced incidence and severity compared to the check. At the mineral soil site, soaking for 2 or 4 hours, with any rate of Velum Prime, effectively reduced damage and nematodes populations in harvested bulbs.

[DM30] Pest risk assessment and its role in determining conditions for the importation and domestic movement of plant pathogens in Canada. L. VYVEY. *Canadian Food Inspection Agency, 1400 Merivale Road, Ottawa, ON K1A 0Y9*
The Canadian Food Inspection Agency (CFIA) is the National Plant Protection Organization (NPPO) of Canada, and is responsible for regulatory functions relating to protecting Canada's plant resource base from potentially harmful pests. Pest Risk Assessment (PRA) provides the scientific foundation for identifying threats to the health of plants in Canada's agriculture and forestry sectors, and also in the natural environment. PRA processes investigate key questions in determining the risk posed by a plant pathogen, including the likelihood of entry, likelihood of establishment, potential for spread within Canada, and the potential economic and environmental consequences of introduction. The CFIA aims to prevent the entry of organisms that pose an unacceptable risk to plant health in Canada, including plant pathogens. However, there are times when importing a plant pathogen can be valuable, such as for scientific research. Therefore, the CFIA has developed risk management measures that allow for the importation of plant pathogens for specific purposes, including research. In order to determine appropriate conditions for importation, reviews of individual plant pathogens are completed following PRA principles. This presentation will focus on the components of a PRA, and how PRA principles are used in the review of import permit applications for plant pathogens.

[DM31] The biocontrol agent *Pseudomonas chlororaphis* PA23 primes *Brassica napus* defense through distinct gene networks. KELLY A. DUKE[1], MICHAEL G. BECKER[2], IAN J. GIRARD[2], JENNA L. MILLAR[2], W. G. DILANTHA FERNANDO[3], MARK F. BELMONTE[2], AND TERESA R. DE KIEVIT[1]. *[1]Department of Microbiology, University of Manitoba, Winnipeg, MB R3T 2N2, Canada; [2]Department of Biological Sciences, University of Manitoba, Winnipeg, MB R3T 2N2, Canada; [3]Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada.*
The biological control agent *Pseudomonas chlororaphis* PA23 is capable of protecting *Brassica napus* (canola) from the necrotrophic fungus *Sclerotinia sclerotiorum* via direct antagonism. While we have elucidated bacterial genes and gene products responsible biocontrol, little is known about how the host plant responds to bacterial priming on the leaf surface, including global changes in gene activity in the presence and absence of *S. sclerotiorum*. Application of PA23 to the aerial surfaces of canola plants reduced the number of *S. sclerotiorum* lesion-forming petals by 91.1%.

RNA sequencing of the host pathogen interface showed that pretreatment with PA23 reduced the number of genes upregulated in response to *S. sclerotiorum* by 16-fold. By itself, PA23 activated unique defense networks indicative of defense priming. Genes encoding MAMP-triggered immunity receptors detecting flagellin and peptidoglycan were downregulated in PA23 only-treated plants, consistent with post-stimulus desensitization. Downstream, we observed reactive oxygen species (ROS) production involving low levels of H_2O_2 and overexpression of genes associated with glycerol-3-phosphate (G3P)-mediated systemic acquired resistance (SAR). Leaf chloroplasts exhibited increased thylakoid membrane structures and chlorophyll content, while lipid metabolic processes were upregulated. In addition to directly antagonizing *S. sclerotiorum*, PA23 primes the plant defense response through induction of unique local and systemic defense networks. This study provides novel insight into the effects of biocontrol agents applied to the plant phyllosphere. Understanding these interactions will aid in the development of biocontrol systems as an alternative to chemical pesticides for protection of important crop systems.

[DM32] A six-year study reveals the dynamics of avirulence allele profiles, blackleg incidence, and mating type alleles of *Leptosphaeria maculans* populations in canola in Manitoba, Canada. W. G. DILANTHA FERNANDO, XUEHUA ZHANG, CARRIE SELIN, ZHONGWEI ZOU, PAULA S. PARKS, M. HARUNUR RASHID, K. RASANIE E. PADMATHILAKE, LIHUA RONG, CUNCHUN YANG, SAKARIA H. LIBAN, BELAGHIHALLI N. GNANESH, SHUANGLONG HUANG, DEBRA L. MCLAREN, AND ANASTASIA KUBINEC. *Department of Plant Science, University of Manitoba, Winnipeg, MB, R3T 2N2, Canada (W.G.D.F); Agriculture and Agri-Food Canada, Brandon Research and Development Centre, Brandon, MB, R7A 5Y3, Canada (D.L.M); Crops Branch – Industry Development, Manitoba Agriculture, Carman, MB, R0G 0J0, Canada (A.K).*
Blackleg, caused by *Leptosphaeria maculans*, is the most serious disease of canola (*Brassica napus*, oilseed rape) worldwide. Although the disease was well controlled through resistance, in recent years blackleg has emerged as a threat to canola cultivation in Canada. This is mainly due to selection pressure exerted on the pathogen population with tight rotations with canola leading to the breakdown of resistance. This study evaluated blackleg incidence, the avirulence allele, and mating type distributions of *L. maculans* isolates collected from grower fields in Manitoba, Canada from 2010 to 2015. A total of 964 *L. maculans* isolates was collected for analysis and the presence of 12 avirulence alleles were identified using differential canola cultivar cotyledon inoculations assays (pathogenicity) and/or PCR assays specific for each allele. *AvrLm2*, *AvrLm4*, *AvrLm5, AvrLm6*, *AvrLm7*, *AvrLm11* and *AvrLmS* were detected at frequencies ranging from 97% to 33%, where the *AvrLm1*, *AvrLm3, AvrLm9*, *AvrLepR1*, and *AvrLepR2* alleles were the least abundant. When the race structure was examined, a total of 170 races were identified from the 964 isolates, with three major races, *AvrLm-2-4-5-6-7-11, AvrLm-2-4-5-6-7-11-S*, and Avr-1-4-5-6-7-11-(S) accounting for 15%, 10%, and 6% of the total fungal population respectively. The distribution of the mating type alleles (*MAT1-1* and *MAT1-2*) indicated that sexual reproduction was not inhibited in any of the nine Manitoba regions in any of the years *L. maculans* isolates were collected. The information derived is helpful in mitigating resistance breakdown, for disease resistance breeding and in implementing innovative methods of blackleg management such as R-gene rotations.

CSA/CPS Contributed Paper Session
Breeding and Genetics

[BG1] Genotypic variations in root plasma membrane lipidome of silage corn grown under cool climatic production systems. M. CHEEMA, M. NADEEM, H. PHAM, R. THOMAS, L. GALAGEDARA, V. KAVANAGH. *(M.C., M.N., H.P., R.T., L.G.) School of Science and the Environment, Grenfell Campus, Memorial University of Newfoundland, Corner Brook, A2H 5G4, Canada; (M.N.) Department of Environmental Sciences, COMSATS Institute of Information Technology, Vehari 61100, Pakistan; and (V.K.) Agriculture Production and Research, Department of Fisheries and Land Resources, Pasadena, Newfoundland, Canada*
Root membrane lipids play major roles in plant signaling, growth, development and adaptation to varying climatic conditions. The present study was conducted to determine genotypic variation in silage corn root membrane lipid profiling, and its potential impact on agronomic traits. To our best knowledge, this is the first study reporting

genotypic variations in root lipidome in silage corn genotypes in a cool climate production system. A field research trial was conducted at Pynn's Brook Research Station Pasadena, Newfoundland, Canada. Five silage corn genotypes (Fusion-RR, Yukon-R, A4177G3-RIB, DKC23-17RIB, DKC26-28RIB) were seeded in a completely randomized design with four replications per treatment. Root samples were randomly collected from each treatment before final harvest and lipid profile was assessed using ultra high performance liquid chromatography coupled to a high resolution Orbitrap mass spectrometer. Three lipid classes were noted in silage corn roots profile that included phospholipids (PA, PC, PE, PG, PI, LPA, LPC, LPE), glycolipids (DGDG), and sphingolipids (HexCer). Phospholipids was found to be a major lipid class (74 nmol%), irrespective of genotypes. Phosphatidic acid (PA) was the principal phospholipid class (approximately 45 nmole%), and was highly correlated with superior agronomic performance (leaf area, plant height and biomass production). It can be concluded that PA is an emerging secondary signaling lipid under cold stress and higher PA in root lipidome could be used as a potential indicator or biomarker in selecting superior silage corn genotypes with enhanced adaptation in cool climatic conditions.

[BG2] *Aphanomyces* and *Phytophthora* root rot tolerance in alfalfa: recurrent selection and marker development under stringent disease conditions. P. AUDY, S. ROCHER AND A. CLAESSENS. *Quebec Research and Development Centre, Agriculture and Agri-Food Canada, Québec, QC G1V 2J3, Canada*
Aphanomyces euteiches (Ae) and *Phytophthora medicaginis* (Pm) are two major pathogens causing the decline of established stands of alfalfa in northern production areas particularly in wet and poorly drained soils. Marker-assisted selection could help accelerate the introgression of resistance genes in germplasm of high agronomic value. In this study, alfalfa cultivars were used for marker selection linked to *Aphanomyces* root rot (ARR) or to *Phytophthora* root rot (PRR) superior tolerance. For each cultivar, 1500 seedlings were challenged with a mixture of four Ae or Pm pathogenic isolates. The best 100 ARR- or PRR-tolerant phenotypes were selected and DNA was extracted from each plant individually (first cycle of the recurrent selection; ARR1 and PRR1). Pooled DNA samples (50 genotypes per pool sample) for each population were generated and used for a bulk segregant analysis of DNA polymorphisms using the SRAP (sequence related amplified polymorphism) technique. Polymorphic fragments associated with tolerance to ARR or PRR tolerance were identified within each genetic background. A second cycle of recurrent selection was completed with seeds resulting from crosses of the best 100 genotypes of the first round of selection (ARR2 and PRR2). A third cycle was completed for PRR tolerance (PRR3) and is in progress for ARR tolerance (ARR3). In the case of PRR tolerance, we improved the initial alfalfa populations from sensitive (S, 0-5% resistant plants) to highly resistant (HR, >50% resistant plants) after three cycles of recurrent selection. The same progression was observed with ARR tolerance but to a lesser extent.

[BG3] QTL mapping of seed hardness trait in common bean (*Phaseolus vulgaris*). K.S. SANDHU[1*], F.M. YOU[1], R.L. CONNER[1], P.M. BALASUBRAMANIAN[2] AND A. HOU[1]. *Agriculture and Agri-Food Canada – [1]Morden Research and Development Centre; [2]Lethbridge Research and Development Centre*
The seed hardness trait has a profound negative impact on cooking time and canning quality in dry beans. This study aims to identify the genetic factors associated with this trait, and develop associated molecular markers to better understand and tag this trait. A recombinant inbred line (RIL) population was derived from a cross between hard- and soft-seeded black bean parents H68-4 and BK04-001, respectively. Ninety-two RILs and parents were grown at two locations in southern Manitoba during the years 2014-16, and under greenhouse conditions. Seeds from both the field and greenhouse grown RIL populations were tested for seed hardness traits. The hydration coefficient and stone seed count were estimated by soaking the seeds overnight at room temperature. For mapping of genomic regions contributing to the trait, the RIL population was also genotyped using genotype by sequencing (GBS) approach. The QTL mapping revealed that in addition to the major QTL on chromosome 7 at a genomic location previously reported to affect the trait, novel QTLs with significant effects were also detected on chromosome 1 and 2. This study demonstrated that multiple genetic factors are involved in the control of this complex trait.

[BG4] Secretome analysis of *Clavibacter michiganensis* subsp. *nebraskensis*; the Goss's wilt bacterial pathogen of corn under induction with xylem sap. A. SOLIMAN, C. RAMPITSCH AND F. DAAYF. *Department of Plant Science,*

University of Manitoba, Winnipeg, Manitoba, R3T 2N2; (A.S) Department of Genetics, Faculty of Agriculture, University of Tanta, Egypt; (C.R) Agriculture and Agri-Food Canada, Morden, Manitoba, R6M 1Y5; (F.D) Department of Plant Science, University of Manitoba, Winnipeg, Manitoba, R3T 2N2

The host specificity of *Clavibacter michiganensis* subspecies is still not fully understood, as different subspecies may colonize different hosts without developing disease. Our goal in this research was to investigate changes in the secretome profile of *Clavibacter michiganensis* subsp. *nebraskensis* (Cmn) under induction with corn (host) or tomato (non-host) xylem sap. Two Cmn isolates; Cmn14-5-1 and DOAB232 that possess high and low level of aggressiveness, respectively were induced with xylem sap of corn (CXS) or tomato (TXS). Secreted proteins in the supernatant were extracted and digested with trypsin. Tryptic peptides were injected into LC-ESI- MS/MS, and then MS spectra were searched on the Mascot engine against Cmn and maize databases. In CXS, the highly aggressive Cmn isolate, Cmn 14-5-1 produced higher levels of cell wall degrading enzymes such as cellulase (CelA), endoglucanase and numerous hydrolases. High levels of protein degrading enzymes such as serine peptidase, aminopeptidase, and metallopeptidase that can suppress plant defense proteins were also produced by Cmn 14-5-1. Catalase and carbonic anhydrase proteins, ROS scavengers, showed high abundance in the Cmn14-5-1 isolate in comparison to DOAB232 which may provide some protection against plant ROS during the interaction. Generally, DOAB232 had a weak response to CXS and even weaker to TXS induction. Protein abundance of Cmn14-5-1 secretome under induction with TXS was higher than those of DOAB232. The secretome of the CXS with either isolate showed unique proteins that facilitate molecule transport and signalling such as peptidyle ABC transporters and other hydrolases proteins. The study shed some light on the possible pathogenicity factors of Cmn in corn.

[BG5] Studying early flowering flax mutants using genetics, physiology, genomics and epigenetics. L.W. YOUNG, M.A. HOUSE, R. RAGUPATHY, A. VASUDEVAN, S.J. ROBINSON, H.M. BOOKER. *Department of Plant Sciences, 51 Campus Drive, University of Saskatchewan, Saskatoon, SK, S7H 5A8*

Flax requires 90-110 days to reach maturity in the Canadian Prairies, limiting the northern-most latitudes that flax may be grown. A focus of the Flax Breeding Program at the Crop Development Center, University of Saskatchewan is development of Northern Adapted flax cultivars better suited for production in the Northern prairies. Earlier flowering is a trait of interest under study which can be correlated to earlier maturity.

We are using physiology, genetics and molecular biology approaches to study three early flowering mutants derived from cultivar “Royal,” registered in 1939. In growth chambers RE1, RE2 and RE3, “Royal” and CDC Bethune require 42, 35, 47, 51 and 52 days to reach flowering, respectively. The mutant lines are much less photoperiod sensitive than “Royal” or other Canadian cultivars and RE2 and RE3 mature earlier. The early flowering trait has been introgressed into other lines via crossing, and appears to be independent of the shorter plant, height exhibited in “Royal” and the RE lines

Each of the RE lines are selections from “Royal” that was mutated using 5-azacytidine, a compound that reduces DNA methylation. The resulting epigenetic mutations are heritable and penetrant where the trait has been stably inherited over 10 generations. We are currently studying the genetics of the early flowering trait using segregating populations derived from crosses between the RE and Royal parents. We will use Next Generation Sequencing of both genomic DNA and bisulphite converted DNA to identify SNPs and epigenetic marks associated with loci controlling this valuable phenotypic variation.

[BG6] *Sclerotinia sclerotiorum* disease severity on canola is influenced by the developmental age of the host’s primary raceme. M. DENTON-GILES, M. C. DERBYSHIRE, Y. KHENTRY, I. G. KAMPHUIS. *Centre for Crop and Disease Management, Curtin University, 210 Kent Street, Bentley, Western Australia, 6102*, *Australia*

Sclerotinia sclerotiorum (Lib.) de Bary is an economically important fungal pathogen of Canola (*Brassica napus* L.). Significant yield loss occurs in Canola following the establishment of *S. sclerotiorum* on the primary raceme. Observations made during routine stem infection assays led us to test the hypothesis that the virulence of *S. sclerotiorum* on Canola is enhanced on mature racemes. We conducted a time of sowing (TOS) experiment by sowing seed of cultivar ‘Charlton’ at 7 day intervals over a three week period. Plants were propagated in a temperature controlled glasshouse under natural light, with a controlled watering schedule. The developmental

stage of each raceme was documented, by measuring primary raceme height (mm) every 7 days. Eighteen, 17, 16 and 15 week old racemes (WOR) were collectively inoculated with *S. sclerotiorum* using 5 mm agar plugs. Weekly lesion length measurements (mm) were conducted for 28 days. Lesions that developed on mature racemes (18 WOR) were significantly larger than lesions on the most immature racemes (15 WOR) (Tukey's HSD $P < 0.05$). Following natural raceme desiccation, total sclerotia were extracted and weighed. Mature racemes (18 WOR) developed 16 fold more sclerotia than younger racemes ($P < 0.001$). Together these data suggest that older, mature racemes are more easily infected by *S. sclerotiorum,* resulting in a greater mass of sclerotial development. We hypothesize that changes in the source-sink relationship within the plant may contribute to the differences observed.

[BG7] Transcriptome sequencing of a durum wheat population segregating for ergot resistance, to identify eQTL and enrich for SNPs. A. GORDON, M. SGORI, N. EREFUL, C. A. MCCARTNEY, C. HIEBERT, R. KNOX, J. MENZIES, D. O'SULLIVAN, L BOYD. *National Institute of Agricultural Botany (NIAB), Bingham Laboratory, Huntingdon Road, Cambridge, CB3 0LE, United Kingdom (A.G., M.S., N.E., L.B.); Agriculture and Agri-Food Canada, Morden Research and Development Centre, 101 Route 100, Morden, Manitoba, R6M 1Y5, Canada (C.A.M., C.H., J.M.); Agriculture and Agri-Food Canada, Swift Current Research and Development Centre, Box 1030, Swift Current, Saskatchewan, S9H 3X2, Canada (R.K.); School of Agriculture, Policy and Development, University of Reading, Whiteknights Campus, Reading, RG6 6UR, United Kingdom (D.O.S.)*

Ergot, caused by the ascomycete *Claviceps purpurea* (Fr.) Tul., is an important disease of wheat in Canada and the UK. Ergots contain toxic alkaloids, which can cause severe health problems if ingested. The durum wheat line 9260B-173A, identified as a source of ergot resistance (Menzies 2004), was studied in an 'AC Avonlea'/9260B-173A recombinant inbred line (RIL), and further doubled haploid (DH) population. Genotyping was performed with the wheat iSelect 90K single nucleotide polymorphism (SNP) array (Wang et al. 2014) and with KASP SNP assays. Linkage maps were developed for the population and QTL analysis conducted. A major QTL on chromosome 2A reduced honeydew production, reduced sclerotia size and weight, and percentage infected florets.

In a reciprocal UK experiment, RNA samples were taken from plants 2 days after inoculation with a Canadian Claviceps isolate EL-2. 10 lines were chosen for their phenotypic extremes for honeydew and sclerotia along with parents 'Avonlea' and 9260B-173A. Illumina 100bp sequencing was performed and mapped onto IWGSC Chinese Spring genome. Differential expression analysis was performed to identify wheat genes up- and down- regulated at this crucial point in the infection process, and will give insights in the biology of the interaction. Additionally a further set of SNP-based KASP markers were developed from the RNA-Seq data, from genes that were predicted to lie within the QTL regions and were tested on the population. Of the markers developed, a high proportion subsequently mapped into the QTL regions acting to validate the approach and enrich the genetic linkage map.

[BG8] Effects of long-term grazing on the yield, morphology and nutritive value of alfalfa (*Medicago sativa)*. BILL BILIGETU, JACQUELINE TOEWS, BRUCE COULMAN. *Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan, S7N 5A8, Canada.*

Understanding morphological traits of alfalfa populations in response to long-term grazing is important for selecting plants for grazing tolerance. The objective of this study was to characterize morphological and nutritional traits of 13 alfalfa populations with a 25-yr grazing history. Plants of the 13 alfalfa populations were grown in greenhouse at the University of Saskatchewan using a randomized complete block design with four replications. Plant height, forage dry matter yield, regrowth yield, and crude protein concentration were significantly different ($P<0.001$) among the populations, but fiber concentrations (acid detergent and neutral detergent fiber) were similar. Resistance (%) to *verticillium* wilt varied ($P=0.0028$) among the 13 alfalfa populations. There are similar growth trends in forage dry matter yield and heights of alfalfa plants derived from the same soil zones. Based on our preliminary results, the populations of Pike Lake and Arcola SK are suitable for development of a locally adapted alfalfa population in Saskatchewan.

CPS Contributed Paper Session
Epidemiology

[EP1] Molecular identification of yeast species colonising grape fruits in Nova Scotia vineyards. T. BARASUBIYE, L. FAN, AND C. DOUCETTE. *(T.B.), Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; (L.F., & C.D.) Kentville Research and Development Centre, Agriculture and Agri-Food Canada, 32 Main St., Kentville, NS B4N 1J5, Canada*
The diversity of yeasts involved in wine fermentation can impact the wine parameters such as pH, alcohol level, viscosity, color, flavor, and aroma. The goal of this study was to isolate and identify naturally occurring yeasts associated with vineyards in Nova Scotia. Grape cultivars of L'Acadie, Riesling, New York Muscat, and Pinot Noir were sampled at multiple vineyard sites within the Annapolis Valley of Nova Scotia. Two sub-samples of approximately 25g each of grapes were blended. Serial diluted samples were surface plated on potato dextrose agar supplemented with 0.1g/L of chloramphenicol and incubated at 25°C for 72 hours. Yeasts were isolated and then purified on YM agar. The internal transcribed spacer (ITS), the D1/D2 domains of the nuclear 28S rRNA gene and the second largest subunit of RNA polymerase II were sequenced for 60 isolates. Sequencing data have allowed to recognize the 12 following yeast species: *Hanseniaspora uvarum* (Niehaus) Shehata, Mrak & Phaff; *Saccharomyces bayanus* Sacc.; *Saccharomycopsis crataegensis* Kurtzman & Wick.; *Pichia kluyveri* Bedford; *Aureobasidium pullulans* (de Bary & Löwenthal) G. Arnaud; *Sporidiobolus pararoseus* Fell & Tallman; *Rhodotorula glutinis* (Fresen.) F.C. Harrison; *Filobasidium magnum* (Lodder & Kreger-van Rij) X.Z. Liu, F.Y. Bai, M. Groenew. & Boekhout. *Rhodotorula mucilaginosa* (A. Jörg.) F.C. Harrison; *Bullera alba* (W.F. Hanna) Derx; *Papiliotrema flavescens* (Saito) X.Z. Liu, F.Y. Bai, M. Groenew. & Boekhout; and *Naganishia diffluens* (Zach) X.Z. Liu, F.Y. Bai, M. Groenew. & Boekhout. This study represents the first attempt to determine yeast species colonising grape fruits in vineyards in Nova Scotia.

[EP2] A brief history of INIAP and *Puccinia striiformis* in Ecuador. C.W. BARNES, J. GARÓFALO, D. CAMPAÑA, AND J. NOROÑA. *Instituto Nacional de Investigaciones Agropecuarias, Estación Experimental Santa Catalina, Programa Cereales, Panamericana Sur Km 1, Sector Cutuglahua, Pichincha, Ecuador*

The National Agricultural Research Institute (INIAP-Instituto Nacional de Investigaciones Agropecuarias) was established in 1961 at the public farm previously used by the National Wheat Commission of Ecuador. Its importance in wheat research was recognized by a group of international researches led by Dr. Norman Borlaug, who designated the INIAP Santa Catalina station as the headquarters for High Altitude Wheat Research in 1966. During this time wheat production was at its peak, but has steadily declined since. *Puccinia striiformis* on wheat (Pst) and barley (Psh) are the most common diseases in the important cereal growing areas of Ecuador. However, *P. triticina* can be more common in some provinces, and *P. graminis* can be found on several susceptible lines in various parts of the country. While race identification has not been a common practice, Pst differentials have been sown at the Santa Catalina station most years from 2007 to present. Differential lines with Yr10, Yr15, and Yr17 have been consistently resistant to natural populations, while lines with Yr1, Yr7, and Yr9 have always been susceptible during this time frame. Infection levels on Yr2, Yr3, Yr6, Yr8, Yr24, and Yr27 have been very erratic between years. In 2015, 63 *P. striiformis* samples on wheat and barley were analyzed for race identification. Eighty-two percent of the identified races have never been reported, resulting in potentially 20 new races of *P. striiformis* in Ecuador.

[EP3] How mineral oil impacts non-persistent *Potato virus Y* transmission. S. BOQUEL AND X. NIE. *Fredericton Research and Development Centre, Agriculture and Agri-Food Canada, 850 Lincoln Road, Fredericton, NB E3B 4Z7, Canada; and (S.B.) SIPRE – Comité Nord, Rue des Champs Potez, 62217 Achicourt, France*
Potato virus Y (PVY) is an important concern in Canada. It is transmitted from plant to plant exclusively by aphids in a non-persistent manner and can result in significant economic losses to producers. To date, a weekly application of mineral oil is the only reliable method to reduce the spread of PVY in potato seed production, but its mode of action is still poorly understood. Understanding the mechanism of inhibition of PVY infection by mineral oil is a key component in accurately advising seed potato growers on how to efficiently use mineral oil.

Experiments on PVY acquisition by aphids were not able to explain the mode of action of mineral oil. However, a strong reduction of PVY transmission by aphids as well as PVY quantity in leaves was observed under field conditions in plants that were treated with mineral oil compared to untreated plants. These results suggest that the mode of action of mineral oil is mainly linked to the effect on the interaction between PVY and the potato host plant. Therefore, we are actively investigating the impact of mineral oil on the replication and accumulation of the virus within the plant. Results obtained this year suggest that mineral oil reduces the number of plants that become infected. The number of leaves becoming infected is also reduced but the leaves that do become infected have a greater quantity of virus. This suggests that mineral oil is limiting virus colonization within the plant by constraining the virus to a few leaves.

[EP4] Predicting risk of pea root rot using molecular techniques to quantify inoculum of *Aphanomyces euteiches* in soil. S. CHATTERTON, A. ERICKSON, R. BOWNESS, M. W. HARDING, B. GOSSEN, D. L. MCLAREN AND S. BANNIZA.
Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre, Lethbridge, AB T1J 4B1, Canada. (R. B) Lacombe Research Centre, Alberta Agriculture and Forestry, 6000 C E Trail, Lacombe, AB T4L 1W1, Canada (M.W.H) Crop Diversification Centre South, Alberta Agriculture and Forestry, 301 Horticultural Station Road East, Brooks, AB T1R 1E6, Canada; (B.D.G.) Saskatoon Research and Development Centre, AAFC, 107 Science Place, Saskatoon, SK S7N 0X2, Canada; (D.L.M.) Brandon Research and Development Centre, AAFC, 2701 Grand Valley Road, Brandon, MB R7A 5Y3, Canada. (S.B.) Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada
Root rot of field pea causes severe yield losses across the Canadian prairies, where 1.5 million hectares of peas are grown annually. Recent surveys in Alberta, Saskatchewan and Manitoba revealed that 40 - 60 % of fields were positive for *Aphanomyces euteiches*, while 80-90 % were also infested with *Fusarium spp*. Pathogenicity tests indicated that while *A. euteiches* was the most damaging, *Fusarium avenaceum* and *Fusarium solani* were also highly pathogenic to pea. To assess risk of Aphanomyces root rot prior to planting peas, the relationship of oospore concentrations of *A. euteiches* to DNA quantification and disease severity was first determined in greenhouse trials. At the same time, inoculum potential of field soils was evaluated using greenhouse bioassays, quantitative PCR and digital droplet PCR. The inoculum potential was then compared to the observed root rot severity in pea crops grown in the corresponding fields. Although there was a linear relationship between oospore concentration, disease severity and DNA quantification, the limit of detection of oospores from soil was too high (100 oospores/ g soil) to accurately quantify oospores in field soils at damaging levels. As a result, greenhouse bioassays were the most accurate predictor of field disease levels. The number of false negative field soil samples was high (>50%) using real-time quantitative PCR, but was slightly improved using digital droplet PCR. To improve accuracy of molecular quantification, a process to concentrate oospores from soil prior to DNA extraction is under development. Droplet digital PCR techniques are also being refined for simultaneous quantification of *A. euteiches*, *F. avenaceum* and *F. solani* for prediction of the inoculum potential of the pea root rot complex.

[EP5] Comprehensive survey of major grapevine (*Vitis vinifera* L.) viruses and their potential insect vectors in British Columbia. S. POOJARI, J. BOULE, N. DELURY, M. ROTT, A-M SCHMIDT, T.D. LOWERY AND J.R. ÚUBEZ-TORRES.
Agriculture and Agri-Food Canada, Summerland Research and development Centre, Summerland, British Columbia V0H 1Z0, Canada; (M.R. and A-M. S.) Sidney Laboratory, Canadian Food Inspection Agency, North Saanich, British Columbia, Canada
Grapevine leafroll disease and Grapevine red blotch disease, associated with grapevine leafroll associated viruses (GLRaVs) and *grapevine red blotch virus* (GRBV) are reported to be widespread and pose economic constraints for grapevine (*Vitis vinifera* L.) production in North America. Through large-scale surveys during 2014-2016 growing seasons, a total of 3,054 composite five-vine samples were collected from six grape-growing regions of British Columbia representing 153 *V. vinifera* and three interspecific hybrid vineyard blocks. Samples were tested for the presence of *Grapevine leafroll-associated virus* 1 (GLRaV-1), GLRaV-2, GLRaV-3, GLRaV-4. ELISA and RT-PCR based diagnostic test results using virus-specific primers revealed GLRaV-3 to be the most widespread (23.5%) followed by GLRaV-2 (6.9%), GLRaV-1 (2.9%), and GLRaV-4 (2.1%). Similarly, PCR-based diagnostics for a total of 2,000 composite

five-vine samples tested for the presence of GRBV resulted in 1.6% positives indicating the low incidence of GRBV in BC vineyards. Significant differences were observed in the relative incidence of GLRaVs among regions and age of vines in established vineyards. Surveys during 2014 and 2015 growing seasons for potential insect vectors revealed the presence of *Pseudococcus maritimus*, *Parthenolecanium corni* and other *Pulvinaria* spp. in BC vineyards. Spatio-temporal distribution of GLRaV-3 in four vineyard blocks during 2013-2016 growing seasons indicated rate disease spread up to 19%. Our results stress the need to develop and implement sustainable virus management practices for BC vineyards.

[EP6] Foliar and root pathogens of *Cannabis sativa* L. (marihuana) in British Columbia. Z.K. PUNJA AND G. RODRIGUEZ. *Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada; and (G.R.) Agrima Botanicals Corporation, 260-22529 Lougheed Highway, Maple Ridge, BC V2X 0T5, Canada*
An increase in the cultivation of *Cannabis sativa* (marihuana) plants in Canada is associated with increased incidence and severity of various diseases, many of which have not been previously reported. In this study, hydroponically-grown *C. sativa* were sampled over a 4-year period (2013-2017) to determine the prevalence of foliar and root pathogens. Following isolation, pathogenicity studies were conducted to establish the extent of disease symptoms caused by the recovered microbes. Browning and rotting of roots was shown to be caused by *Pythium dissotocum* Drechsler and *P. myriotylum* Drechsler. In addition, *Fusarium oxysporum* Schlecht. emend. Snyder & Hansen and *F. solani* (Mart.) Sacc. were also isolated from symptomatic roots, which upon reinoculation onto healthy plants, caused stunting, yellowing and wilting. The potential for spread of *F. oxysporum* through the hydroponic system was confirmed by its detection in the recirculating nutrient solution. A rot of the flower buds was associated with *Botrytis cinerea* Pers., which caused Botrytis bud rot. In addition, the pathogenicity of *Penicillium olsonii* Bainer & Sartory, and to a lesser extent, *P. copticola* Houbraken, Frisvad & Samson, which were also recovered from diseased flower buds, is reported for the first time, causing Penicillium bud rot. These species were also present on dried flower buds destined for sale. Powdery mildew was found to be caused by *Golovinomyces* (*Erysiphe*) *cichoracearum* sensu Salmon. The pathogen was detected on vegetatively propagated cuttings. The management of these pathogens on *C. sativa* will require the implementation of sanitation methods, biological control agents, and chemical products adopted from greenhouse vegetable production, as well as the use of pathogen-free propagation materials. Breeding for disease resistance should also become a priority.

ABSTRACTS - POSTERS

Genetics and Resistance

[P1] Dispersal gradient of airborne *Botrytis cinerea* conidia. O. CARISSE. *Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu Research and Development Centre, Saint-Jean-sur-Richelieu, Quebec, Canada.*
During the last decades, our knowledge on Botrytis aerobiology has increased. The availability of sensitive and accurate DNA-based assays for detection and quantification of *Botrytis* spp. have improved our ability to monitor *Botrytis* populations. However, little is known about conidia dispersal. Gregory (1973) suggested that most spores of plant pathogens do not disperse beyond the field in which they were produced. In order to improve monitoring of airborne inoculum, dispersal of airborne conidia and incidence of Botrytis fruit rot were monitored at two raspberry plantings, in sprayed (dispersal) and unsprayed field plots, respectively, during three successive years together with meteorological data. The Concentrations of conidia were monitored using a Burkard volumetric sampler and rotating-arms samplers.The number of *B. cinerea* conidia in air samples was determined with a real-time qPCR assay. Dispersal of airborne conidia was assessed at 0.5, 1.0, 1.5, 3, and 6 m from point source inoculum with samplers placed at 0.45, 0.90, and 1.35 m from the ground. The coefficient of correlation between the volumetric and rotating-arms samplers placed at 45, 90, and 135 cm from the ground was significant; and a diurnal pattern of conidial release was observed. During the pre-bloom and bloom period, conidia dispersal gradient (log conidia/m^3 vs distance in m) showed significant flattering at a distance of more than 2 m from the inoculum source. However, near or at harvest no significant dispersal gradients were observed. Correlation between fruit rot incidence and weekly mean airborne conidia concentration was significant and positive.

[P2] Elucidation of canola disease resistance pathway against blackleg through characterization of *Arabidopsis thaliana* mutants. R. M. CELOY, C. YANG, AND W.G. DILANTHA FERNANDO. *Department of Plant Science, 66 Dafoe Road, Room 222 Agriculture Building, University of Manitoba, Winnipeg, MB R3T 2N2, Canada*
Blackleg is an important fungal disease in oilseed rape (canola, *Brassica napus*) caused by *Leptosphaeria maculans.* This plant disease causes serious stem canker resulting in substantial yield loss to canola farmers worldwide. The importance of canola ensued to a collaborative global research network in decoding the genetic resistance against the blackleg disease. Results of various studies proposed the involvement of receptors and phytohormone signaling in canola – blackleg pathosystem. In this study, it is our aim to elucidate the canola – blackleg interaction through the characterization of *Arabidopsis thaliana* mutants against blackleg by studying receptors and phytohormone signaling. Time course experiments were performed onto *A. thaliana* wild type and apoplastic-related mutant plants [suppressor of BIR1 1(sobir1), non race-specific disease resistance 1 (ndr1), required for MLA12 resistance 1/non race-specific disease resistance 1 (rar1ndr1), peroxidase 34 (prx34), antisense French bean oxidative burst peroxidase 1.1 (as*FBP1.1*), respiratory burst oxidase homologue F (rbohF), respiratory burst oxidase homologue D (rbohD)] that were inoculated with *L. maculans* isolate #41-2 (carrying *AvrLm2*, *AvrLm4*, *AvrLm6*, *AvrLm7*, and *AvrLmS*. Accumulations of super oxide and hydrogen peroxide, lesion sizes, and stem canker were assessed. Phenotyping results indicate that the receptors SOBIR1 and NDR1, and the reactive oxygen species (ROS) producers PRX33, PRX34, RBOHD, and RBOHF are potentially involved in the apoplastic response against blackleg. Likewise, stem lesions were observed onto sobir1, ndr1, asFBP1.1, and rbohD mutant plants wherewith severe lesion is shown by the latter. Transcriptome and metabolic analyses are currently being processed on the above-mentioned experiments.

[P3] Structural organization and haplotypes of rust resistance genes in flax. S. RAVICHANDRAN, F. M. YOU, K. Y. RASHID, L. YOUNG, H. M. BOOKER and S. CLOUTIER. *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; (F.M.Y. & K.Y.R) Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden , MB R6M 1Y5, Canada; (L.Y & H.M.B) Crop Development Centre, Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada*

Flax (*Linum usitatissimum* L.) and flax rust, caused by the fungal pathogen *Melampsora lini*, were the basis of the pathosystem studied by Dr. H. Flor when he hypothesized the gene-for-gene concept in the 1950's. Since then, five rust resistance loci named *K*, *L*, *M*, *N* and *P*, have been identified to contain race-specific rust resistance genes. The *L* locus harbors a single gene with at least 12 alleles while *M*, *N* and *P* have tandemly duplicated genes, in addition to multiple allelic forms. With the exception of locus *K*, DNA sequences for some allelic forms have been defined but a comprehensive understanding of all loci and their genetic diversity are still lacking. First, we performed a structural analysis of the four known loci to illustrate their evolution through duplication mechanisms. Second, a set of 30 differential lines each containing different alleles of the five genes was sequenced using Illumina short reads to a coverage of ~28×. Reads homologous to each of the rust resistance genes were extracted and *de novo* assembled. Here, we report on the *L* allelic series which is highly polymorphic, displaying multiple indels and single nucleotide polymorphisms. Comparisons with previously published sequences indicated several discrepancies in DNA sequence. The present analysis will clarify sequence identity and enhance our knowledge of the diversity and functionality of flax rust resistance genes.

[P4] CPS Student Competition. **Control of microRNA turnover contributes to plant immunity activated by flagelline.** R. AJMI, T. ABD EL RAHMAN and K. BOUARAB. *SEVE, Department of Biology, Sherbrooke university, 2500, boulevard de l'université, Sherbrooke (Québec) CANADA J1K2R1*

Despite the lack of a circulating immune system and the sessile state, plants are not easy hosts and passive organisms. In fact, during a continuous co-evolution with a wide range of pathogens, plants have developed an effective and a specific immune system. PAMPs triggered immunity (PTI) represents the first lane of defense in plant immunity. Although it is based on the recognition of the pathogen molecular pattern (PAMPs) by the pattern recognition receptors (PRRs), this basal immune response depends on different biological phenomenon such as the accumulation of microARN (miRNA). These small non-coding RNAs play a crucial role in the PTI pathway and so does their regulation. Small RNA degrading nucleases (SDN) are essential regulators of miRNA homeostasis by controlling their degradation. Our results showed that SDNs control salicylic acid signaling pathway activated by the Flagelline PAMP. We also showed that SDNs are required for local resistance mediated by flagelline against the virulent bacteria *Pseudomonas Syringae* pv tomato DC3000. Therefore, SDN proteins appear to be a regulatory hub for an optimal immune response.

[P5] Molecular characterization of Fusarium resistance from *Elymus repens* introgressed into bread wheat. G FEDAK, W CAO, D WOLFE, D CHI AND A. XUE. *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa, ON, K1A 0C6 Canada*

A cross was made of *Elymus repens* into wheat cultivar Crocus and BC progeny were advanced to BC1 F7 by single seed descent. Sixteen lines were selected based on agronomic performance and evaluated in a FHB epiphytotic nursery. Eight lines with resistance to FHB were selected. GISH analysis revealed many complex chromosome numbers and recombination in the derived lines. The least complex recombinant line was P1142-3-1 with 42 chromosomes with one pair of chromosomes showing telomeric recombinants on both arms. This wheat chromosome was identified as 3D by applying several SSR markers from every arm of every wheat linkage group and noting those that provided no signal. Lines with single telomeric recombinants were produced by additional backcrosses to Crocus and inoculated with FHB spores. It was found that the resistance was contributed by the recombinant on the long arm of chromosome 3D. These lines have minimal linkage drag and should be amenable to applications in breeding for disease resistance.

[P6] Assessment of resistance to 'new' virulent pathotypes of *Plasmodiophora brassicae* in doubled haploid lines derived from *Brassica napus* cv. Mendel. [1]R. FREDUA-AGYEMAN, [1]S. F. HWANG, [2]S. E. STRELKOV, [1]Q. ZHOU, [1]H. AHMED, [1]H. FU, [1]I. AKTER, [1]R. NYANDORO, [1]G. TURNBULL AND [1]D. FEINDEL.[1]*Crop Diversification Center North, Alberta Agriculture and Forestry, Edmonton, AB, T5Y 6H3; and* [2] *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada.*

Resistance derived from the *Brassica napus* L. cultivar 'Mendel' has been overcome in some fields in Alberta, Canada, by the emergence of 'new' strains of *Plasmodiophora brassicae* Woronin. The objective of this study was to assess clubroot resistance in 57 doubled haploid lines derived from 'Mendel' which were identified as resistant to *P. brassicae* single-spore pathotype 3. The lines were evaluated against 15 field populations representing 'new' pathotypes of *P. brassicae* and five single-spore isolates representing the 'old' pathotypes 2, 3, 5, 6 and 8. Clubroot development was assessed 42 days after inoculation and expressed as a disease severity index (DSI, 0 - 100%). The results revealed that the number of resistant (DSI ≤ 30%), moderately resistant (30% < DSI ≤ 50%) and susceptible (DSI > 50%) DH lines inoculated with the 'old' pathotypes were 40 resistant, 11 moderately resistant and 6 susceptible, respectively. With respect to the 'new' pathotypes, none of the lines were resistant or moderately resistant to pathotype 5x (L-G1, L-G2, L-G3 and D-G3) while three were moderately resistant and 54 were susceptible to pathotypes Club 1 to K. Using the mean DSI induced by the 'old' pathotypes (approx. 13.50%) as the baseline, clubroot severity increased by 300 - 600% when inoculated with the 'new' pathotypes. The findings suggest that 'Mendel' resistance has been almost completely overcome by the 'new' *P. brassicae* strains.

[P7] Mapping of the crown rust (*Puccinia coronata* Corda f. sp. *avenae* Eriks.) resistance gene *Pc45* in oat. A. Z. KEBEDE, J. FRIESEN, J. G. MENZIES, J. W. MITCHELL FETCH, E. PACZOS-GRZĘDA, A. D. BEATTIE, and C. A. MCCARTNEY. *Morden Research and Development Center, Agriculture and Agri-Food Canada, 101 route 100 Morden, MB R6M 1Y5, Canada; (J.F.) University of Manitoba, 1590 Chancellor Drive, Winnipeg, MB R3T4B9, Canada; (JWMF) Brandon Research and Development Center, Agriculture and Agri_Food Canada, 2701 Grand Valley Rd, Brandon, MB R7C 1A1, Canada; (EPG) Institute of Plant Genetics, Breeding and Biotechnology, University of Life Sciences, Akademicka 15, 20-950 Lublin, Poland; (ADB) Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada*
The development and effective deployment of crown rust resistant oat cultivars requires the identification, phenotypic and molecular characterization of available resistance genes. An earlier linkage mapping study identified a seedling crown rust resistance gene, temporarily designated as *PcKM* in the oat cultivars Kame and Morton. This gene was mapped to Chromosome 12D of the oat chromosome-anchored linkage map. In addition, Kompetitive Allele Specific PCR (KASP) markers closely linked to this gene were developed. It was postulated that *PcKM* was *Pc45* based upon haplotype analysis of *PcKM*-linked SNPs and comparison of the individual *P. coronata* races to which *PcKM* and *Pc45* confer resistance. To further investigate whether *PcKM* and *Pc45* are the same gene, a *Pc45* differential line was mapped in crosses involving two susceptible checks, AC Morgan and Kasztan. Seedlings of F_2 progeny and $F_{2:3}$ families generated from the crosses were inoculated with crown rust isolate *CR258* (race NTGG) in the greenhouse at the single leaf stage. Seedling ITs and KASP markers were used to create linkage maps. Results show that the IT segregation ratio for F_2 progeny (3:1) and $F_{2:3}$ families (1:2:1) of the two populations follow a single gene inheritance pattern as expected. Interestingly, the KASP markers identified to be linked with *PcKM* gene were also linked with *Pc45* gene confirming that the two genes were actually the same or very closely linked to each other.

[P8] CPS Student Competition. **Improving genetic resistance to Fusarium head blight in durum and bread wheat.** G.S. BRAR, H.R. KUTCHER, P.K. SINGH, C.J. POZNIAK, AND P.J. HUCL. *Crop Development Centre/Department of Plant Science, University of Saskatchewan, 51 Campus Dr., Saskatoon, SK S7N 5A8 Canada; (PKS) Wheat Pathology, Global Wheat Program, International Maize and Wheat Improvement Centre, El Batan, Mexico*
Fusarium head blight (FHB) of wheat, predominantly caused by *Fusarium graminearum*, is a potentially devastating disease. In addition to yield loss, production of trichothecene mycotoxins (primarily deoxynivalenol) affects grain quality making it unfit for consumption. So far only a few partially resistant wheat varieties in the primary wheat gene pool are available from China and Brazil. Sumai 3, Wuhan1 and Frontana are some of the most widely used donor parents from which to transfer resistance. Durum wheat is more susceptible to FHB than bread wheat and relatively little research has been conducted to improve resistance. Introgression of resistance from bread wheat to durum poses challenges. New sources of FHB resistance need to be characterized and exploited, not only to prevent resistance breakdown, but to enrich the genetic basis of durable resistance in modern wheat cultivars. One way to

do this is wide hybridization using intergeneric and interspecific lines. Genes *Fhb3*, *Fhb6* and *Fhb7* were derived from the wheat related grasses *Leymus racemosus*, *Elymus tsukushiensis*, and *Thinopyrum ponticum*, respectively. Thus, intergeneric lines can be very effective in developing wheat introgression or translocation lines with improved traits. We discuss gene mapping strategies from wheat breeding populations developed from BGRC3487 (*T. turgidum* L. subsp. *dicoccum*), a domesticated landrace and 00Ar134-1, an intergeneric spring wheat line, as resistant parents.

[P9] Mapping quantitative trait loci for Fusarium head blight resistance in Canada Western Red Spring wheat cultivar Carberry. F. E. BOKORE, S. BERRAIES, R. D. CUTHBERT, R. E. KNOX, M. A. HENRIQUEZ, A. BURT, S. KUMAR, A. N'DIAYE, C. J. POZNIAK, Y. RUAN, A. G. SHARPE. *(F.E.B., S.B., R.D.C., R.E.K., Y.R.) Swift Current Research and Development Center, Agriculture and Agri-Food Canada, Box 1030, Swift Current, SK, S9H 3X2, Canada;(M.A.H.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB, R6M 1Y5, Canada;(A.B., S.K.) Brandon Research and Development Centre, Agriculture and Agri-Food Canada, 2701 Grand Valley Road, Brandon, MB, R7A 5Y3, Canada;(A.N., C.J.P.) Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, S7N 5A8, Canada; (A.G.S.) National Research Council of Canada, 110 Gymnasium Place, Saskatoon, SK, S7N 0W9, Canada*

Fusarium head blight (FHB) is a major disease of wheat causing losses in grain yield and quality. Growing resistant cultivars is one of the best ways to manage the disease. This research was conducted to identify single nucleotide polymorphism (SNP) markers associated with quantitative trait loci (QTL) controlling FHB resistance in a moderately resistant Canadian spring wheat cultivar, Carberry. A population of 180 lines from a Carberry by Vesper cross was phenotyped for FHB incidence and severity at Morden, MB in 2015 and 2016, Bratt's Lake, SK in 2015 and Brandon, MB in 2016. The lines were genotyped with the 90K iSelect SNP genotyping assay (Illumina Inc., San Diego, CA) and the chromosomal positions of loci and SNP markers associated with FHB resistance were identified with multiple QTL analysis using MapQTL.6®. The distribution of incidence and severity were continuous. Transgressive segregant lines more resistant than Carberry were observed indicating both parents contributed to resistance. Carberry contributed the resistance QTL on chromosomes 1A, 3B and 4B for FHB incidence and severity, and Vesper contributed the resistance QTL on 2B for FHB incidence and 6B for FHB severity. The QTL on 1A and 3B were detected in all environments, the 4B QTL in two environments and the 2B and 6B QTL each in one environment. The 1A QTL explained phenotypic variation approaching 13 % in FHB severity and the 3B QTL up to 22.7 %. These findings will help to understand the resistance in Carberry and develop markers for marker assisted selection.

[P10] Loss of function of chitin binding protein gene *CBPL* affects the pathogenicity of *Leptosphaeria maculans* the blackleg pathogen on canola. F. LIU, C. SELIN, AND W. G. DILANTHA FERNANDO; *Department of Plant Science, University of Manitoba, Winnipeg, MB, R3T 2N2.*

Blackleg, caused by *Leptosphaeria maculans* (*L. maculans*), is one of the most devastating diseases on canola (*Brassica napus* L.) and causes large amount of economic loss worldwide. During the co-evolution of plants and pathogens, plants have evolved diverse mechanisms against pathogens. Plant chitinase, as an antimicrobial compound is one of these mechanisms. Chitin, the major structural component of the fungal cell wall, can be targeted by plant chitinases, which forms part of the host defense response. Here, we report the loss function of a *L. maculans* gene *CBPL* (*chitin binding protein-like gene*), encoding a chitin binding protein with a chitin binding domain on the N terminal. Expression of *CBPL* could be detected in infected cotyledons of canola, indicating the secretory feature of CBPL protein. CRISPR-Cas9 system was used to knock out *CBPL* gene in *L. maculans* isolate JN3. Agrobacterium-mediated transformation was used for delivering CRISPR-Cas9 system into *L. maculans*, and one isolate *cbpl-1* showing a 13bp deletion was obtained. Decreased pathogenicity on different canola cultivars was detected when isolate *cbpl-1* was tested on two cultivars, 1135 and Westar (both showing susceptible to isolate JN3), indicating that *CBPL* may play an important role in the infection process of *L. maculans*. Research is presently being conducted to confirm the function of *CBPL* gene in pathogenicity mechanisms. Our results demonstrate the

effectiveness of the CRISPR-Cas9 system for gene editing in *L. maculans*, thereby an additional evidence as a useful tool for understanding gene functions.

[P11] Identification and screening of durable rust resistance-related metabolites in various wheat cultivars. N. RAJAGOPALAN, Y. LU W. ZHANG, K. BOYLE, B. MCCALLUM, C. HIEBERT, E. REIMER, W. MCNABB, P. FOBERT, M. CUPERLOVICH-CULF AND M. C. LOEWEN**.** *Aquatic and Crop Resources Development, National Research Council of Canada, 110 Gymnasium Place, Saskatoon, SK, S7N 0W9 Canada; (B.M., C.H., E.R., W.M.) Agriculture and Agri-Food Canada, 101 Route 100, Unit 100, Morden, Manitoba, R6M 1Y5, Canada; (P.F. and M.C.L.) Aquatic and Crop Resources Development, National Research Council of Canada, 100 Sussex Drive, Ottawa, ON, K1A 0R6, Canada; and (M.C.-C.) Information and Communication Technology, National Research Council of Canada, 1200 Montreal Road, Ottawa, ON K1A 0R6, Canada.*
For almost a century, the gene *Lr34* has conferred durable resistance against fungal rust diseases, making it one of the most important resistance genes in wheat. Recently, we showed that the LR34Sus homolog of the protein (which does not provide disease resistance) may be an importer of chlorophyll catabolite compounds, while others have shown that close relatives of these compounds accumulate in the flag leaves of *Lr34* containing plants. We are expanding on these findings toward a broader evaluation of metabolites linked to resistance. Toward this we report here a comparative study of the metabolite makeup of the flag leaves of a collection of germplasm, using LC-MS technology. Wheat lines including Thatcher and Thatcher Lr34 as well as a variety of other near isogenic lines with various resistance genes presented individually or stacked with each other, as well as select sister pairs (+/- Lr34) arising from a Sumai3 x Thatcher cross. From these data we have identified a single unique novel metabolite (P6) that uniquely accumulates to higher levels in plants carrying *Lr34* and see some preliminary evidence of additional metabolic separation in broader metabolomics analyses.

[P12] Possible roles for a cytochrome p450 and ABC transporter in deoxynivalenol tolerance in the biocontrol agent *Clonostachys rosea* strain ACM941. Z. DEMISSIE AND M. C. LOEWEN *Aquatic and Crop Resources Development Portfolio, National Research Council of Canada, 100 Sussex Drive, Ottawa, ON, K1A 0R6, Canada.* *Clonostachys rosea* strain ACM941 is a fungal bio-control agent developed and patented in Canada against the FHB disease causative agent *Fusarium graminearum*. Although the molecular and biochemical basis of its tolerance are yet to be resolved, one peculiar feature of *C. rosea* is its ability to tolerate high level of the *Fusarium* mycotoxin deoxynivalenol (DON). Based on available EST databases arising from mycotoxin treated *C. rosea* strain IK726, a cytochrome p450 and two ABC-transporter homologs (abcg5 and abcg29) identified as potential targets of interest in *C. rosea* strain ACM941. The transcriptional activities of the abcg29 were not significantly affected by treatments with either DON or spent *F. graminearum* growth media. In contrast, the Fg3639 spent media did result in up-regulation of abcg5, and the cytochrome p450 homolog was transcriptionally up-regulated by both DON and Fg3639 growth media. Furthermore, yeast cells transformed with the p450 showed improved growth characteristics compared to control yeast in the presence of DON. Together these data imply potential roles in DON tolerance for the cytochrome p450 and the abcg5 homologs. We are in the process of testing the abcg5 in a recombinant yeast system and determining the reaction catalyzed by the CYP450 toward understanding their roles in *C. rosea*'s antagonistic property against Fg3639.

[P13] CPS Student Competition. **Control of microRNA homeostasis and the establishment of effector-triggered immunity in *Arabidopsis thaliana*.** M.B.D.DIAM, T. ABD EL RAHMAN and K. BOUARAB. *SEVE, Department of Biology, University of Sherbrooke,2500, boulevard de l'universite Sherbrooke (Quebec), CANADA J1K2R1*
Plants have developed an effective immune system that is triggered when they recognize effectors secreted by pathogens; this defense pathway is called effector-triggered immunity (ETI). The resistance protein RPS5 senses the bacterial Type-III effector AvrPphB to activate ETI. Small RNAs, including microRNAs, play important roles in numerous aspects of eukaryotes development and host-microbe interactions. MicroRNAs turnover was shown to be properly controlled by Small RNA-Degrading Nucleases (SDNs) to ensure normal development; the possibility that this turnover plays crucial roles in plant immunity remains unknown. Here, we showed that SDNs are required for

ETI induced by AvrPphB in *Arabidopsis thaliana*. We also showed that SDNs are important for AvrPphB-triggered resistance in *A. thaliana* against *Pseudomonas syringae pv tomato* DC3000 expressing the effector AvrPphB. These data highlight the importance of microRNAs turnover as a critical step in the establishment of plant immunity.

[P14] Leaf rust in Ontario: *Puccinia triticina* virulence and resistance genes identification in winter wheat. B. D. MCCALLUM[1,] L. TAMBURIC-ILINCIC[2], S. B. ROSA[2] and A. TENUTA[3]. [1]*Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100 Morden, MB, Canada, R6M1Y5;* [2]*Department of Plant Agriculture, University of Guelph, Ridgetown Campus, 120 Main Street E., Ridgetown, ON, Canada, N0P 2C0,* [3]*OMAFRA, 120 Main Street E., Ridgetown, ON, Canada N0P 2C0.*
Leaf rust is caused by the fungal pathogen *Puccinia triticina* Eriks. The disease is common and can cause significant economic losses, especially on susceptible wheat cultivars under favorable environmental conditions. Annual surveys for *P. triticina* have been conducted in Canada annually since 1931 to determine the frequency of virulence to resistance genes and to monitor changes in the pathogen population. The aim of this study was to understand the recent shifts in *P. triticina* population in Ontario and to identify the resistance genes in a doubled-haploid population between Ontario winter wheat cultivars 'Vienna' (moderately susceptible) and '25R47' (moderately resistant). Virulence of the *P. triticina* population collected in Ontario from 1987 to 2015 was analyzed using 17 standard differential lines, showing high diversity in the *Puccinia* populations. In 2015, for the first time, virulence was found on *Lr21* in Ontario. Virulence of *Lr9, Lr16, Lr24, Lr26* and *Lr18* was varied by year, from non-virulence to 36%, 50%, 84.2%, 83.3%, respectively. The 'Vienna'/'25R47' population was evaluated once in the greenhouse and in the field at Centralia in 2011 and Ridgetown in 2011 and 2012. There were at least four seedling resistance genes segregating in this population after artificial inoculation with BBBD, TDBG, TBBG and MBDS races, and *Lr24* and *LrCen* were identified as possible resistance genes. A QTL on chromosome 1B was significantly associated with leaf rust resistance for combined field environments and explained up to 30% of the variation.

[P15] Fusarium head blight resistance is enhanced by the wheat leaf rust resistance gene *Lr34*. B.D. MCCALLUM, C.W. HIEBERT, J. THOMAS, and M.A. HENRIQUEZ. *Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Unit 100, Morden, MB, R6M 1Y5, Canada.*
The leaf rust resistance gene *Lr34* provides resistance to stripe rust, stem rust, powdery mildew and other diseases. We investigated the effect of *Lr34* on Fusarium head blight (FHB) using 21 pairs of near isogenic F_3 sister lines from the cross Sumai*6/Thatcher. One of each pair of sister lines contained the resistant allele for *Lr34,* while the other line had the susceptible allele; otherwise the sister lines were similar to Sumai 3, which has a high level of resistance to FHB. These lines were evaluated in inoculated and irrigated nurseries each year from 2012 to 2016. The lines were rated for visual FHB Index each year and harvested grains were assayed for DON content in 2014, 2015, and 2016. In each year, FHB severity was lower for the lines with the resistant allele than those with the susceptible allele as determined by the FHB Index and DON content. In most pairs of sister lines the line with the resistant allele was more resistant than the line with the susceptible allele. It appears that *Lr34* enhances FHB resistance in the highly resistant Sumai 3 background.

[P16] CPS Student Competition. **Evaluation of Type II Resistance to Fusarium Head Blight in Canadian Winter Wheat.** M. KANG-CHOI, G. HUMPHREYS, S. CLOUTIER, W. CAO, A. XUE, AND A. NAVABI. *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Ave, Ottawa, ON K1A 0C6, Canada; (A.N.) Department of Plant Agriculture, University of Guelph, 50 Stone Road E., Guelph, ON N1G 2W1 Canada*
Fusarium head blight (FHB) is a destructive disease that reduces grain yield and end-use quality of wheat. The common causal agent of FHB disease in Canada is *Fusarium graminearum*, which produces mycotoxin deoxynivalenol (DON). Toxin accumulation in grains and the processed products is a serious concern for human and animal health. The Canadian winter wheat varieties, 'AC Morley' and 'Emerson', are rated in the field as moderately resistant and resistant, respectively. A previous greenhouse experiment that evaluated type II resistance to FHB, showed that both 'AC Morley' and 'Emerson' were susceptible at 21-days post inoculation (DPI). In the present study, a doubled haploid (DH) population developed from the cross 'AC Morley' x 'Emerson' was tested for type II

resistance in the greenhouse. Single floret inoculation was performed at 50% flowering stage and the inoculated plants were incubated in the misting chamber for 48 hr. Initial symptoms were visible after 48 hr to 72 hr. The level of disease spread was rated at 7, 10, 14, 17, and 21 DPI. Disease rating and disease progress curve for the population, along with morphological characteristics observed, such as awnedness, head density, anther extrusion and plant height, will be presented. The greenhouse experiment will be repeated in winter 2018, and the field screening of this DH population for FHB resistance will be conducted at three locations (Ottawa and Elora, ON and Yangzhou, China) in 2017 and 2018.

[P17] Physiologic races of wheat leaf rust (*Puccinia triticina*) in Canada in 2016. W. MCNABB, B.D. MCCALLUM, E. REIMER and A. XUE. *Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB R6M 1Y5, Canada; and (A.X.) Ottawa Research and Development Centre, AAFC, KW Neatby Bldg., 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada*
Collections of 277 leaf rust (*Puccinia triticina* Eriks.) samples were obtained from spring and winter wheat cultivars grown in research plots and commercial fields throughout Manitoba, Saskatchewan and Ontario in 2016 to assess the virulence profile of the pathogen population. These samples produced 255 single pustule isolates which were inoculated onto a set of 16 differential isolines at the seedling stage. There was a high level of diversity with 72 virulence pathotypes identified. The most common pathotype was MNPS which comprised 15.7% of the isolates and was found more commonly on winter wheat than spring wheat cultivars. This pathotype was not detected from 2000-2014 and appeared at very low levels in 2015. The other common pathotypes were MBDS (14.5%) and MPPS (7.1%). A notable decline in virulence was seen on *Lr2a* and a slight decline in virulence on *Lr9* and *Lr21* in comparison with previous years. An increase of virulence was observed on *Lr16*, *Lr17* and *Lr24*. A set of 79 isolates representing each of the virulence pathotypes was tested on an additional 12 wheat lines at the seedling stage and on five lines with adult plant resistance genes. On the expanded differential set no isolates were virulent on *Lr19* and *Lr52* and only one isolate overcame the resistance of *Lr29*. On adult plant differentials, no virulence was found for *Lr22a* and very few isolates were virulent on *Lr35* which follows the trend from previous years.

[P18] CPS Student Competition. **Fungal diversity across conventional, oasis and organic farming systems in arid areas of Oman.** ELHAM A. KAZEROONI and ABDULLAH M. AL-SADI. *Department of Crop Sciences, College of Agricultural and Marine Sciences, Sultan Qaboos University, PO Box 34,Al-Khod 123, Oman*
This study examined fungal diversity in conventional, oasis and organic farms in arid areas of Oman. Fungal diversity was assessed using pyrosequencing and culture-based techniques from crops of date palm, acid lime, mango, cucumber and tomato. Pyrosequencing revealed that fungal diversity was variable among different farming systems as well as among different crops within the same farm. Fungal diversity was high in organic farms compared to other farms. In addition, the rhizosphere of date palms had more fungi compared to other crops. Ascomycota was the dominant phylum in most of the soil samples. The other common phyla were *Microsporidia*, *Chytridiomycota* and *Basidiomycota*. Classes *Dothideomycetes*, "Teresporidia", *Sordariomycetes* and *Eurotiomycetes* and fungal genera *Systenostrema*, *Hypocrea, Cladosporium* and *Oidium* dominated soils from all samples. Principle component analysis revealed that fungal diversity was affected by the farming system as well as the type of crops grown. Pyrosequencing was more efficient (4-6 times) than culture based techniques for estimating fungal diversity. Our study indicated that differential levels of fungal diversity are associated with different farming systems and crops, and effects of cultural practices, plant species, soil type and other factors on fungal diversity are discussed.

[P19] Genetic diversity of blackleg (*Leptosphaeria spp.*) isolates in Alberta. [1] E. PEREZ-LARA, [2] R. FREDUA-AGEYMAN, [2] S.-F. HWANG AND [1] S. E. STRELKOV. *[1] Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada T6G 2P5; [2] Crop Diversification Center North, Alberta Agriculture and Forestry, Edmonton, AB, T5Y 6H3.*
Blackleg can be a devastating disease of *Brassica napus* L. (rapeseed/canola) and occurs in most countries where this crop is grown. The disease is caused by the *Leptosphaeria maculans - L. biglobosa* complex. In Alberta, blackleg disease has been reported in more than 70% of fields surveyed. The objective of this study was to evaluate the

extent of genetic diversity in *L. maculans* and *L. biglobosa* populations in the province. Canola stem tissues showing symptoms of blackleg were collected from 110 fields visited in 2016. Single-spore isolation was carried out on samples from each field and one isolate per field was randomly selected for DNA extraction. PCR amplification with *L. maculans* and *L. biglobosa*-specific DNA markers and with inter-simple sequence repeat (ISSR) markers and suggested that all of the isolates analyzed from the 110 fields were *L. maculans*, with no isolates of *L. biglobosa* identified in 2016. Significant genetic diversity existed among the *L. maculans* isolates, indicating the potential for different virulence phenotypes on host plants.

[P20] Characterization of flax genotypes for resistance to *Oidium lini.* KHALID Y. RASHID***.*** *Agriculture and Agri-Food Canada, Morden Research and Development Centre, 101 Route 100, Morden, Manitoba, Canada R6M 1Y5.*
Powdery mildew caused by the fungus *Oidium lini* Skoric, is a major disease affecting flax (*Linum usitatissimum* L) worldwide. This disease was first identified in Canada in 1997, and the incidence and severity have been on the rise in Canada, causing major reductions in yield and quality of the seed and fibre. This research aimed at characterizing the resistance in flax. Commercial flax cultivars and 100s of flax genotypes including the flax core collection and improved breeding lines have been tested under natural inoculum pressure in the field, and to a local isolate of powdery mildew under controlled growth cabinet conditions. Results showed a moderate level of resistance in most Canadian flax cultivars, a wide range of reactions in the core collection and breeding lines, and high level of resistance in some breeding lines with a high correlation between the field and the controlled indoor testing. Resistant breeding lines are potentially useful in breeding higher level of resistance in future flax cultivars for mitigating the risk from this disease.

[P21] Mapping QTL for *Fusarium* Head Blight Resistance in Canadian Spring Wheat AC Barrie. DINUSHIKA THAMBUGALA, ANITA BRÛLÉ-BABEL, GEORGE FEDAK, MARIA ANTONIA HENRIQUEZ, ADAM FOSTER, RICHARD MARTIN, BRENT MCCALLUM, JEANNIE GILBERT, BARBARA BLACKWELL, DEAN SPANER, CURTIS POZNIAK, AMIDOU N'DIAYE and CURT MCCARTNEY. *Morden Research and Development Centre, Agriculture and Agri-Food Canada, Morden, MB, Canada, R6M 1Y5; (A.B.B.) Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada, R3T 2N2; (G.F.) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa, ON, Canada, K1A 0C6; (M.A.H.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, Morden, MB, Canada, R6M 1Y5; (A.F.) Charlottetown Research and Development Centre, Agriculture and Agri-Food Canada, Charlottetown, PEI, Canada, C1A 4N6; (R.M.) Charlottetown Research and Development Centre, Agriculture and Agri-Food Canada, Charlottetown, PEI, Canada, C1A 4N6; (B.M.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, Morden, MB, Canada, R6M 1Y5; (J.G.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, Morden, MB, Canada, R6M 1Y5; (B.B.) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa, ON, Canada, K1A 0C6; (D.S.) Faculty of Agricultural, Life & Environmental Sciences, University of Alberta, Edmonton, AB, Canada, T6G 2P5; (C.P.) Crop Development Centre, University of Saskatchewan, Saskatoon, SK, Canada, S7N 5A8; (A.N.D.) Crop Development Centre, University of Saskatchewan, Saskatoon, SK, Canada, S7N 5A8; and (C.M.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, Morden, MB, Canada, R6M 1Y5*
Breeding for resistance to *Fusarium* head blight (FHB) in Canadian spring wheat is hampered by the poor understanding of genetics of resistance, particularly native FHB resistance. Here we dissected the genetic basis of FHB resistance in the Canadian spring wheat variety AC Barrie. AC Barrie is a hard red spring wheat variety that possesses an intermediate level of FHB resistance, while Cutler is a susceptible spring wheat. A recombinant inbred line (RIL) population from the cross AC Barrie/Cutler was evaluated for FHB resistance in eight environments over 2013 and 2014. A total of 212 RILs were used for constituting a genetic linkage map and mapping QTL for deoxynivalenol (DON) accumulation and disease-related morphological traits (plant height, anthesis date and FHB Visual Rating Index). Genotyping was performed with the Illumina iSelect 90K SNP wheat chip. Major QTL for FHB resistance from AC Barrie were mapped on chromosomes 3B and 6B at the expected locations of *Fhb1* and *Fhb2*. Plant height locus *Rht-D1* was identified on 4D, and *Rht8* and *Ppd-D1* loci co-located on chromosome arm 2DS. An additional FHB resistance QTL from AC Barrie mapped to the same region as Nyubai on 3BS, near the centromere (3BSc). AC Barrie has a unique haplotype at *Fhb1*, *Fhb2*, and 3BSc relative to known resistance sources such as

Sumai-3, Wuhan-1, and Nyubai. A DH population of the cross AC Barrie/Reeder is also being studied. This study provides insight into the genetic basis of FHB resistance in Canadian spring wheat variety AC Barrie.

[P22] CPS Student Competition. **Future Direction for Breeding Quantitative Disease Resistance in Barley at the Agriculture and Agri-Food Canada, Brandon Research and Development Centre.** JAMES R. TUCKER, ANA BADEA, COLIN W. HIEBERT, WILLIAM G. LEGGE, CURT A. MCCARTNEY and W. G. DILANTHA FERNANDO. *Brandon Research and Development Centre (BRDC), Agriculture and Agri-Food Canada (AAFC), 2701 Grand Valley Rd., R.R. 3, Brandon, MB R7A 5Y3, Canada; (C.W.H., C.A.M.) Morden Research and Development Centre, AAFC, 101 Route 100, Morden, MB R6M 1Y5, Canada; (J.R.T., W.G.D.F.) Department of Plant Science, University of Manitoba, 222 Agriculture Building, Winnipeg, MB R3T 2N2, Canada*
Development of resistance to pathogens is a major objective for plant breeders. While quantitative resistance (polygenic) is generally considered to be more durable than major gene resistance, breeding for quantitative traits is considerably more challenging. Traditional breeding has involved discovery proceeded by incremental incorporation of multiple quantitative trait loci (QTL) over time. Additive accumulation of QTLs can result in a high level of resistance; however the process is slow and laborious due to the requirements of phenotypic testing. New genotyping technologies are now available that could hasten the breeding process. Currently, a 50K Illumina Infinium® iSelect® HTS custom genotyping assay (developed by the James Hutton Institute, Scotland, UK with single nucleotide polymorphisms (SNPs) identified using a diverse collection of international barley germplasm) is being evaluated for generating genomic estimated breeding values (GEBV's) for prediction of Fusarium head blight (FHB) and deoxynivalenol (DON) content in two-row barley. If successful, this breeding method could also be employed for developing adult-plant resistance for other important diseases in barley such as stem rust and spot blotch. Preliminary results indicate that 50K SNP markers are generally applicable to Canadian barley germplasm, and this technology should be useful for high-throughput genotyping. Future testing will evaluate applicability for use in genomic selection in the AAFC-BRDC barley breeding program. This research represents a new collaboration and common effort among AAFC-Brandon, AAFC-Morden and the University of Manitoba.

[P23] Genome-wide association study for Fusarium wilt resistance in flax (*Linum usitatissimum* L.). FRANK M. YOU[1*], KHALID Y. RASHID[1], ZHEN YAO[1] and SYLVIE CLOUTIER[2*]. *[1]Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, Manitoba R6M 1Y5, Canada, and [2]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, Ontario K1A 0C6, Canada*
Fusarium wilt is a disease of flax that is caused by the fungus *Fusarium oxysporum* f. sp. lini (Bolley) Snyd. & Hans. The fungus infects the roots and blocks the vascular system causing wilt and death that result in severe yield loss. To identify genes and markers associated with wilt resistance, the core collection of 407 flax accessions was re-sequenced with the Illumina platform and evaluated for wilt resistance in the flax wilt nursery at Morden, Manitoba between 2011 and 2014. A total of 1,773,632 SNPs were identified. A genome-wide associated study was performed using the general linear model with TASSEL. Based on the data from three years, 49 putative quantitative trait loci (QTL) were located near resistance gene analogs (RGAs) on all 15 chromosomes. Thirty seven QTL were located within a distance of 1.5 MB to NBS-coding genes and nine QTL were as close as within 0.1 Mb. One QTL was validated by a previously identified SSR marker. These QTL explained 7-12% of phenotypic variation of wilt resistance and were additive. The results provide useful resources for genomics-assisted breeding in flax.

[P24] Use of KASP assays for the analysis of *rpg4*/*Rpg5* gene complex for marker-assisted selection for Ug99 stem rust resistance in barley. J. SANGHA, J. R. TUCKER, W. G. LEGGE AND A. BADEA*. *Brandon Research and Development Centre, Agriculture and Agri-Food Canada, 2701 Grand Valley Road, Brandon, MB R7A 5Y3, Canada*
The highly virulent stem rust *Puccinia graminis* f. sp. *tritici* race TTKSK (aka isolate Ug99) has emerged as a potentially serious threat to global wheat and barley production. Sources of resistance in barley are limited and only a few cultivated and wild barley accessions have been found resistant to TTKSK. Three of these resistant lines were developed at Agriculture and Agri-Food Canada's Brandon Research and Development Centre, Brandon, Manitoba. One of these lines, TR02272 is derived from the backcross (BC-6) of AC Metcalfe cultivar with Q21861as the donor parent of *rpg4*/*Rpg5* gene complex. This line is being used to introgress stem rust resistance into barley germplasm

along with a few other lines through molecular marker-assisted backcrosses and doubled haploid production. Several molecular markers for Kompetitive Allele Specific PCR (KASP) assays linked to this gene complex were designed based on the information reported by Arora et al. (2013) and publicly available sequences at NCBI. The assays target the single nucleotide polymorphisms (SNPs) corresponding to the amino acids at 205, 217, and 1287. This approach increased the accuracy and automated the screening process by eliminating the time-consuming analysis of PCR products by gel electrophoresis or the need to sequence the rare mutations. These KASP assays combined with a simplified and economical DNA extraction protocol provide barley researchers a rapid, cost-efficient, and reliable method of screening for Ug99 stem rust resistance.

[P25] CPS Student Competition. **The regulation of intrinsic signaling in *Brassica napus* defending against *Leptosphaeria maculans.*** C. YANG, AND W. G. DILANTHA FERNANDO. *Department of Plant Science, Faculty of Agriculture and Food Science, University of Manitoba, 66 Dafoe Road, Winnipeg, Manitoba, R3T 2N2, Canada*
Gene-for-gene interaction is triggered by the recognition between R proteins from host and Avr effectors from pathogen. The interaction between host R proteins and pathogenic effectors initiates set of localized and rapid signaling cascades called hypersensitive response (HR). This response subsequently induces several signaling pathways including oxidative burst, hormonal biosynthesis/signaling and programmed cell death (PCD). In this study, the general objective is to explore the crucial factors in *Brassica napus – Leptosphaeria maculans* pathosystem. The cultivars Surpass400 and 01-23-2-1 exhibited the HR phenotype while the cultivar Westar showed susceptibility. RT-qPCR results suggest that the early activation (3 dpi) of salicylic acid (SA) signaling was related to the initiation of the processes resulting to HR. The abundance of ethylene (ET) responsive genes coincides with SA signaling, suggesting co-expression between SA and ET signaling in the resistant cultivars. Histological staining showed that the cultivars with HR induced the localized oxidative burst to hinder early hyphal development (3 dpi to 5 dpi). This was supported by hydrogen peroxide accumulation, lignification and localized cell death. Moreover, the co-inoculation between *L. maculans*/*L. biglobosa* mixed inoculum and the aminotriazole (AT) treatment (a catalase inhibitor) exhibited smaller leaf lesions in the susceptible cultivar Westar. These results agree with the findings that the early induction of cellular signaling in basal defense is the key to induce HR.

[P26] CSA Student Competition. **Introduction of *Ac/Ds* Transposons into Oat Genome** M. MAHMOUD, R. KAUR, and J. SINGH, *Plant Science Department, 21 111 Rue Lakeshore, McGill University, Quebec, H9X 3V9, Canada*
Oat (*Avena sativa*.L.) is one of the most important cereals for animal feed, human food and industrial production worldwide, due to its unique nutrition components. However, because of oat's complex hexaploid genome and redundancy coupled with limited knowledge of oat germplasm impeding further improvement in oat cultivars. Thus, there is an urgent need to provide modern functional genomic approach to characterize the oat genome. Here, we employed Ac/Ds transposon-based reverse genetics approach for activation gene tagging for the first time in oat. Highly regenerative callus derived from mature oat seeds, cultivar (Park), were bombardment, or co-bombardment by various *Ac/Ds* genes constructs, using PDS-1000 /He Biolistic gun. Our biochemical and molecular analyses indicate successful introduction of *Ac/Ds* elements in the oat cultivar. A total of 20 unique transformation events were generated. Individual single copy *Ac* and *Ds* lines are being hybridized for the development of a genetic population for the identification of unique transposed *Ds* mutants.

Breeding

[P27] How many is too much: balancing utility with the cost of adding yield testing field sites in a wheat breeding program. A. J. BURT, S. KUMAR, AND J. MITCHELL FETCH. *Brandon Research and Development Centre, Agriculture and Agri-Food Canada, 2701 Grand Valley Rd, Brandon, MB, Canada, R7A 5Y3*Plant breeding is the scientific application of genetic principles to improve plants for human benefit. Successful breeding programs continuously invest in efficiency both attempting to increase genetic gain and to balance budgets. The Canadian Western Red Spring (CWRS) wheat breeding program for the northern prairies develops germplasm with early maturity and high yield for the Peace River Valley and Parkland region of Western Canada. Data produced in multi-location testing is

used to estimate yields and to select superior genotypes, as well as to account for genotype by environment interactions and to provide an estimate of yield stability. A breeding program must balance the need for additional yield test locations with logistics and available resources. In recent years, the cost of privately contracted yield trials has increased and represents a larger proportion of the total program budget. Historical data from several years of advanced yield trials were used to build site regression models. The results of these models are used to discuss the value and cost effectiveness of privately contracted yield trials. In addition to increasing statistical power these sites may improve the representation of the target region. However, the marginal value and cost effectiveness of privately contracted trial sites decrease with the total number of sites in the study.

[P28] Evaluation of soybean lines for resistance to iron deficiency chlororsis in southern Manitoba. A. HOU and K.S. SANDHU. *Agriculture and Agri-Food Canada – Morden Research and Development Centre*
Soybean iron deficiency chlorosis (IDC) is an economically important and common abiotic disease affecting soybean and production and often causes severe yield losses. Growing IDC resistant varieties is the best management practice to reduce yield loss under severe conditions. In an effort to screen for resistant soybean materials, one hundred and sixty lines were evaluated under field conditions at Emerson in southern Manitoba. Significant differences were observed among the genotypes; however, substantial errors were also caused by the heterogeneous field conditions. In order to evaluate soybean materials uniformly and reliably, a protocol was also established using calcareous soil and hydroponic conditions in a controlled environment. The same soybean lines that were tested under field conditions were evaluated again using the hydroponic conditions. While a large number of soybean lines that showed resistance in the field conditions were determined to be susceptible or moderately resistant under hydroponic testing, eight lines were confirmed as highly resistant to IDC. The resistant materials selected in the process will be used for crossing for early-maturing variety development and genetic analysis. The protocol established can be used for future screening of soybean breeding materials for resistance to IDC at our research centre.

[P29] CSA Student Competition. Phenotyping of a Nepali spring wheat (*Triticum aestivum* L.) diversity panel for dark-adapted leaf epidermal conductance. K. KHADKA, H. J. EARL, M. N. RAIZADA and A. NAVABI. *Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1, Canada*
Rapidly changing global climate has largely influenced wheat (*Triticum aestivum* L.) production in recent years. More specifically, wheat production is predicted to be more severely affected in developing countries due to the consequences of climate change, drought being one of such phenomenon, which affects wheat yield negatively. Physiological approaches to breeding crops have been emphasized in recent years to identify genotypes exhibiting drought tolerance, but few screening methods for such traits have been developed which are practically applicable to large number of genotypes. We attempted to phenotype a diversity panel of 320 spring wheat genotypes, the Nepali Wheat Diversity Panel (NWDP), for dark-adapted leaf epidermal conductance (g_{dark}), considered to be a surrogate for water use efficiency (WUE). We measured the g_{dark} of the penultimate leaf of 21 day old seedlings grown under growth room conditions. Details of the phenotyping protocol and the results will be presented.

[P30] Marker assisted wheat breeding for the Canadian prairies. J. TOTH, S. PANDURANGAN, A. BURT, J. MITCHELL FETCH AND S. KUMAR. *Cereal Genomics, Brandon Research and Development Centre, Agriculture and Agri-Food Canada, 2701 Grand Valley Road, Brandon, MB R7A 5Y3, Canada*
Bread wheat (*Triticum aestivum* L.) is an important crop and export commodity for Canada. Increased global population, demand for quality grains, and rapidly evolving pathogens have necessitated the need to breed high yielding disease resistant wheat cultivars. Significant gains in breeding efficiency can be made through advances in wheat genetics and genomics. Identification of genes and quantitative trait loci for economically important traits and associated molecular markers have the potential to improve selection efficiency in breeding programs. Marker assisted selection enriches desirable allelic frequency, complements phenotypic data, and allows gene stacking. An important class of molecular markers for high-throughput marker assisted selection are Kompetitive Allele Specific Polymerase chain reaction (KASP) markers, based on single nucleotide polymorphisms. KASP markers have been

developed for various genes and quantitative trait loci that confer resistance to leaf rust, stripe rust, stem rust, fusarium head blight, loose smut, common bunt, leaf spot, wheat blossom midge and wheat stem sawfly. KASP markers are also available for wheat grain and flour protein content and characteristics. Agronomic traits such as vernalization, day length sensitivity, and height can also be selected based on KASP markers. We present a list of validated KASP markers to improve selection efficiency in Canadian breading programs.

[P31] Principal Components Analysis facilitates selection of breeding lines with optimum trait combinations. A. NAKHFOROOSH, C. MCCARTNEY, A. BEATTIE, S. KUMAR, A. BURT AND J. MITCHELL FETCH. *Brandon Research & Development Centre, Agriculture and Agri-Food Canada, 2701 Grand Valley Road, Brandon, MB R7A 5Y3, Canada; (C.M.) Morden Research & Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Unit 100, Morden MB R6M 1Y5, Canada; and (A.B.) Crop Development Centre, University of Saskatchewan, College of Agriculture and Bioresources 51 Campus Drive, Saskatoon SK S7N 5A8, Canada*

The primary goal of many plant breeding programs is to develop new varieties with an optimized combination of traits. However, in many cases there is an inherent trade-off when combining traits (e.g. yield and β-Glucan in oat). We assessed the suitability of using principal components analysis (PCA) to select the best lines carrying several desired traits when they do not combine well. A cross was made to incorporate the high β-Glucan content from 'CDC Morrison' into the high-yielding 'AC Morgan' background. A population of 191 recombinant inbred lines (RILs, F6:F9), along with the parents and three check lines, was planted at Brandon, MB in 2016 in an alpha-lattice design with three replications. The agronomic traits (seed yield, plant height, maturity and lodging) were measured in the field, and the quality traits (β-Glucan content, plumpness and test weight) were subsequently determined on RIL composites using standard methods. Agronomic traits varied significantly among investigated lines and checks. Seed yield and β-Glucan were not correlated in analysis of trait averages across replications, however, a significant and negative correlation was observed between plumpness and β-Glucan (r= -0.14, P = 0.052). Principal Components Analysis revealed how selection for yield and β-Glucan leads to trade-offs. These results showed the usefulness of PCA by visualization of traits and lines in biplots in order to identify the best lines in a segregating population when traits are negatively associated.

[P32] Identification of pathogenicity factors involved in blackleg disease by *Leptosphaeria maculans* on canola. C. SELIN, AND W. G. DILANTHA FERNANDO. *Department of Plant Science, University of Manitoba, Winnipeg, MB R3T 2N2, Canada*

Blackleg, caused by the fungal pathogen *Leptosphaeria maculans*, is one of the most devastating diseases of canola in Canada. Understanding the role and key functions of pathogenicity factors in disease and host interactions is extremely important as it may provide new possible insights into managing the disease. To elucidate the role and function of pathogenicity genes involved in disease, gene disruption mutants in the JN3 *L. maculans* isolate were generated through *Agrobacterium tumefaciens*-mediated random insertional mutagenesis (ATMT). Two rounds of ATMT, using *A. tumefaciens* Agl-1 (pKHt), generated an initial 115 *L. maculans* mutants that displayed a positive PCR product for the hygromycin cassette carried in the T-DNA. As indicated by Southern hybridization, only 80 of these mutants demonstrated a single T-DNA insertion within the genome. Interestingly, some of the mutants display very visible phenotypic changes. For example, 4 of the mutant isolates display an inability to produce pycnidiospores, while 2 mutants displayed reduced levels of pycnidiospore production, indicating that asexual reproduction may be affected in these mutants. To determine if sexual reproduction is also affected in these mutants, mating type of the JN3 isolate is being determined and mating assays with the corresponding mating type partner will be carried out. In addition, some mutants exhibited different pigmentation when growing on V8 plates and show slight reduction in growth compared to the parental JN3 isolate. Presently, growth, sporulation, and germination assays are being conducted along with pathogenicity assays to assess virulence towards *Brassica napus* (Westar).

[P33] Crop management and the reduction of fusarium head blight in barley. D. PAGEAU, S. RIOUX, A. VANASSE AND B. BLACKWELL. *Research farm, Agriculture and Agri-Food Canada, 1468 St-Cyrille, Normandin QC G8M 4K3 Canada; (S.R.) Centre de recherche sur les grains, Quebec QC G1P 3W8 Canada; (A.V.) Département de phytologie,*

Université Laval, Quebec QC G1V 0A6 Canada; and (B.W.) Agriculture and Agri-Food Canada, 960 Carling avenue, Ottawa ON K1A 0C6 Canada

Fusarium head blight (FHB) associated with the presence of *Fusarium graminearum* is becoming a problem in barley (*Hordeum vulgare*) production in Eastern Canada. In addition to reducing grain yields, the fungus produces a toxin (deoxynivalenol or DON) which can reduce feed intake, decrease performance and affect the health of livestock. A study was conducted in 2014 and 2015 at three locations in Quebec to evaluate the contribution of three different methods and their combinations to reduce FHB. Those methods were: (1) rotation with a soybean crop the year prior to the cereal compared with cereal as the previous crop; (2) use of the partially resistant cultivar 'Chambly' vs. the use of the susceptible cultivar 'Oceanik' and, (3) use of a fungicide (Prosaro 250) vs. no fungicide treatment. The results showed that, in general, the combination of two or three control methods is more efficient to reduce DON content in grain than the use of a single method. The rotation with soybean tends to be less effective at reducing DON content than the use of a resistant cultivar or the application of a fungicide. However, the triple combination gave the best results in reducing DON content in barley.

[P34] CSA Student Competition. Nitrogen Application Improves Photosynthetic Productivity, Leaf Chlorophyll Efficiency, and Yields of Contrasting Oat Genotypes under Salinity Conditions. X. D. SONG, W. WU, B. L. MA, W. K. YAN, AND G. S. ZHOU. *Agriculture and Agri-Food Canada, Ottawa Research and Development Centre, 960 Carling Avenue Ottawa, ON, K1A 0C6;(X.D.S. AND G.S.Z.) Key Lab of Crop Genetics and Physiology of Jiangsu Province, Yangzhou University, 12 East of Wenhui Road Yangzhou, Jiangsu Province, China.*

Salinity is one of the major environmental stresses that adversely affect plant growth and metabolism. Agronomic practices such as nitrogen (N) management have been considered as a critical strategy to alleviate this stress and increase crop production. This study aims to determine the role of various N applications in crop yield formation and its associated physiological mechanisms under two saline conditions. Two oat genotypes, 6-SA120097 (salt tolerance) and 153-ND121147 (salt sensitive), subjected to medium saline (100 Mm) in comparison with non-saline conditions under four levels of N (0, 0.5, 1.5 and 2.5 g/pot), were grown under the controlled greenhouse conditions. The N treatments were applied as basal fertilizer (30% of N), and at tillering (30% of N), booting (20% of N) and flowering (20% of N) stages. Photosynthetic gas exchange rate, photosystem II (PSII) photochemistry, chlorophyll readings, electrolyte leakage of flag leaves during the grain-filling stage, as well as yield and yield components were determined. Under the non-saline conditions, N application increased ($p < 0.05$) leaf net photosynthetic rate, maximum photochemical quantum yield and effective photochemical quantum yield of PSII. High rates of N treatment also ameliorated the inhibition effect of saline stress on leaf photosynthetic parameters. Irrespective of N treatments and saline conditions, the salt-tolerant genotype displayed a higher net photosynthetic rate, maximum photochemical quantum yield, and effective photochemical quantum yield of PSII with low electrolyte leakage, as compared to those of the salt-sensitive genotypes. This study implies that use of salt-tolerant cultivars with appropriate N management can be recommended as a promising strategy for alleviating the adverse effects of salt stress on crop physiological parameters and crop yield.

[P35] Integrated transcriptome and hormone profiling reveals the role of multiple phytohormone pathways in wheat resistance against Fusarium Head Blight. L. WANG, L. JOHN, L. FORSEILLE, Z. LIU, T. FRANCIS, A. SURENDRA, Y. PAN, Y. LI, L. I. ZAHARIA, T. OUTLET AND P. R. FOBERT. *(L.W., L.F., T.F., L.I.Z., P.R.F.) National Research Council Canada, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada; (L.W., L.J.) Department of Plant Science, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada; (Z.L., A.S., Y.P., Y.L.) National Research Council Canada, 1200 Montreal Rd, Ottawa, ON K1A 0R6, Canada; (T. O.) Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, 960 Carling Ave, Ottawa, ON T1J 4B1, Canada; (P.R.F.) National Research Council Canada, 100 Sussex Drive, Ottawa, ON K1N 5A2, Canada*

Fusarium head blight (FHB or scab) caused by *Fusarium* spp. is a destructive disease of wheat. Since most existing FHB resistance is tightly associated with other undesirable agronomic traits, breeding commercial wheat cultivars that combine desired agronomic traits and a high level of FHB resistance remains a challenge. A better

understanding of the molecular mechanisms of FHB resistance will help to design more efficient and precise breeding strategies. In this study, we compared the resistant variety 'Sumai3' with three regionally adapted Canadian variety using multiple molecular tools and assays. After macroscopic and microscopic disease evaluation, we determined the relative Type II FHB resistance level of four varieties and found that the *Fusarium graminearum* (*Fg*) infection process displayed substantial temporal differences among organs, with the rachis playing a critical role to prevent *Fg* spread in the spike. Based on this result, large scale organ-specific RNAseq and hormone profiling experiments were performed on the varieties after *Fg* infection. From this analysis, we attempted to describe the roles of several plant hormones during the interaction with *Fg*, including salicylic acid (SA), jasmonic acid (JA), ethylene (ET), auxin and abscisic acid (ABA). We found that SA and JA played predominantly positive roles in FHB resistance, whereas auxin and ABA were associated with susceptibility. Interestingly, our analyses suggest that ET played a dual role during interaction with *Fg.* In addition, we highlighted the importance of phenylpropanoid related secondary metabolites in rachis-based FHB resistance.

Disease Management

[P36] First report of clubroot (*Plasmodiophora brassicae*) on canola in northern Ontario. F. AL-DAOUD, M. MORAN, B.D. GOSSEN, AND M.R. MCDONALD. *Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1, Canada; (M.M.) Ontario Ministry of Agriculture, Food, and Rural Affairs, Stratford, ON N5A 6S5, Canada; (B.D.G.) Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, Saskatoon, SK, S7N 0X2, Canada.* Clubroot, caused by *Plasmodiophora brassicae* Woronin, is endemic on Brassica vegetables in many regions of Ontario. It has not been a major concern to canola (*Brassica napus* L.) growers because the most common pathotype in Ontario (pathotype 6, Williams' system) is not highly aggressive on most canola cultivars. Also, clubroot has not previously been reported in northern Ontario. In 2016, clubroot was found on canola in a field near Verner, Ontario, and a subsequent survey found P. brassicae DNA in soil of 11 of 95 fields that had been planted with canola, including 7 fields in northern Ontario. The pathotype from the Verner site was determined as follows. The inoculum was increased by growing a susceptible host (Shanghai pak choy cv. 'Mei Qing Choi', *Brassica rapa* var. *chinensis*) in field soil from the site for 6 weeks under controlled conditions. The resulting clubs were harvested and cultivars that comprise Williams' differential set were inoculated one week after seeding. Four replicates were used with 11-12 plants per experimental unit. Plants were rated for clubroot symptoms using a 0-3 scale at 6 weeks after inoculation, and a disease severity index (DSI) was calculated. A host was resistant if DSI ± 95% confidence interval < 50%; otherwise it was susceptible. The pathotype of *P. brassicae* in Verner was pathotype 2, which was previously identified on rutabaga in Ontario in the 1970's. It is also the pathotype identified on canola in Quebec, but it has not yet been found on canola in western Canada.

[P37] A shift in the pathotype of *Plasmodiophora brassicae* at a site in Ontario. F. AL-DAOUD, B.D. GOSSEN, AND M.R. MCDONALD. *Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1, Canada; (B.D.G.) Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, Saskatoon, SK, S7N 0X2, Canada.* *Plasmodiophora brassicae* Woronin causes clubroot disease on Brassica crops worldwide. Genetic resistance is the principal strategy for clubroot management, but resistance has often been overcome by the emergence of new pathotypes. Pathotype 6 is the predominant pathotype in Ontario. Changes over time in the pathotype at the Muck Crops Research Station in King, Ontario, were assessed following observation of changes in the disease reaction of previously resistant canola (*Brassica napus* L.) cultivars. Clubbed roots of the susceptible canola line ACS-N39 were collected from field trials in 2011 and 2014, and inoculum was increased on a susceptible host. The cultivars that comprise Williams' differential set were inoculated under controlled conditions at about one week after seeding (four replicates, 10-12 plants per experimental unit). Plants were rated for clubroot symptoms using a 0-3 scale at 6 weeks after inoculation, and a disease severity index (DSI) was calculated. A host was resistant if DSI ± 95% confidence interval < 50; otherwise it was susceptible. This assessment identified the collections as pathotype 6 in 2011 and pathotype 2 in 2014. This apparent pathotype shift was associated with changes in the Brassica crops grown at this site. Prior to 2009, clubroot experiments at this site were performed exclusively on susceptible

cultivars. After 2009, most studies included resistant or moderately resistant lines. Assessment of *P. brassicae* collections from this site in 2016 is underway to characterize any subsequent changes in pathotype.

[P38] The effect of selected mycorrhizae fungi on clubroot of canola. A. SEDAGHATKISH, F. AL-DAOUD, S.H. LEE, J.J. ZWIAZEK, B. D. GOSSEN, AND M. R. MCDONALD. *Department of Plant Agriculture, University of Guelph, 50 Stone Rd E, Guelph, ON N1G 2W1, Canada; (S.L. and J.J.Z) Department of Renewable Resources, University of Alberta, Edmonton, AB, T6G 2E3, Canada; (BDG) Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*
In previous studies with commercial biocontrol agents, clubroot (caused by *Plasmodiophora brassicae* Woronin) severity was reduced under controlled conditions, but only occasionally reduced in the field. The current study investigated suppression of clubroot symptoms on canola (*Brassica napus* L.) using the mycorrhizae fungi *Piriformospora indica* Verma, *Glomus intraradices* Schenk and Smith (AGTIV, Premier Tech), or a mixture of endo and ectomycorrhizal species in a commercial formulation (Root Rescue) in growth room studies that were replicated and repeated. *Brassicae* species rarely develop mycorrhizal associations, but the research was initiated because it was known that *P. indica* can colonize the roots of some Brassica crops and promote growth and stress tolerance, and that *P. indica* can induce disease resistance in other plants. Microscopic observation showed that canola roots were colonized by *P. indica* and some of the fungi in Root Rescue, but not by *G. intraradices.* Clubroot severity index (DSI) was slightly reduced in canola plants treated with *P. indica* (60% DSI as compared to 79% DSI in the untreated check) when plants were inoculated with 5×10^5 resting spores mL^{-1}, but not in plants inoculated with 5×10^4 or 5×10^6 resting spores mL^{-1}. There were no differences among treatments in shoot fresh and dry weights. The reason that symptoms were not reduced at the lowest inoculum concentration for *P. brassicae* is not known. Colonization by *P. indica* may protect roots from infection, stimulate root growth, or induce resistance to clubroot by modifying plant metabolism.

[P39] CPS Student Competition. **Population dynamics survey of plant-parasitic nematode levels in southwestern Ontario tomato fields.** T. B. BLAUEL, M. J. CELETTI, M. R. MCDONALD AND K. S. JORDAN. *Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, Ontario, N1G 2W1, Canada; and (M.C.) Ontario Ministry of Agriculture, Food and Rural Affairs, 1 Stone Road West, Guelph, ON N1G 4Y2, Canada*
Plant-parasitic nematodes (PPN) are damaging soil-borne pests with a wide host range, including tomatoes. Tomatoes are high value crops in southwestern Ontario; however, the extent of PPN populations in Ontario tomato fields is currently unknown. Northern root-knot (*Meloidogyne hapla* Chitwood) and root-lesion nematodes (*Pratylenchus penetrans* Cobb) are the most concerning in tomatoes due to their known destructiveness. The objective of this study was to examine the population dynamics of PPN in southwestern Ontario tomato fields over different seasons and different growing regions. To determine the population dynamics of PPN, 3 to 5 soil samples/field were collected throughout the growing season from 50 tomato fields located in Essex, Chatham-Kent, and Norfolk counties over 2016-2017. Root tissue samples were collected once per field in 2016. Nematodes were extracted from soil using the sugar centrifugal flotation method and from roots using the shaker method. All PPN were counted and morphologically identified to genus. In 2016, populations of stunt nematodes significantly increased and lance nematodes significantly decreased; all other nematode populations did not change throughout the season. The fields sampled in Chatham-Kent and Essex County had significantly more total PPN than fields in Norfolk County. Norfolk County tended to have higher populations of root-knot nematode, whereas Chatham-Kent County had higher root-lesion populations. Nematode population levels did not surpass currently available thresholds except in one of the fields surveyed.

[P40] Use of *Streptomyces sp*. in the biocontrol of *Rhizoctonia solani,* a root rot pathogen of soybean. A. ARFAOUI, L. ADAM, F. DAAYF. *Department of Plant Science, Faculty of Agricultural and Food Sciences, University of Manitoba, Winnipeg, Canada.*
Several soilborne diseases routinely damage soybeans in production areas in Canada. *Rhizoctonia solani* (*R. solani*) is a soil-borne pathogen which causes root rot disease in soybean plants. Due to the lack of fungicides for effective

management of this disease, alternative techniques such as biological control, are required. A promising bacterium (S11), identified as *Streptomyces* based on morphological and molecular traits, was tested as a potential biocontrol agent of *Rhizoctonia solani*. *In vitro* assays on PDA plates, indicated that this isolate was able to inhibit the radial growth of multiple *Rhizoctonia* groups. Pathogenicity testing on soybean plants also indicated that this bacterium provided a certain level of protection against *Rhizoctonia*. Based on these results, *Streptomyces* could have a potential role in integrative management strategies for several soybean diseases.

[P41] Potential for biological control of potato late blight with *Pseudomonas chloroaphis* strain 189. S. M. BOYETCHKO, P. AUDY, T. DUMONCEAUX, AND C. KIRBY. *Saskatoon Research and Development Centre, Saskatoon, SK, S7N 0X2 Canada; (P.A.) Soils and Crops Research and Development Centre, Québec, QC G1V 2J3 Canada; (C.K.) Charlottetown Research and Development Centre, Charlottetown PE, C1A 4N6 Canada*
Late blight caused by *Phytophthora infestans* (Mont.) de Bary is a highly aggressive disease of potato (*Solanum tuberosum* L.). Management of late blight currently requires repeated application of synthetic fungicides each growing season. *Pseudomonas chloroaphis* strain 189 effectively reduces disease caused by several genotypes of *P. infestans*, including one of the most common genotypes presently in Canada, US-23. Tests were conducted to assess the effect of spray application of *P. chloroaphis* strain 189 onto potato plants infected with selected genotypes (US-23, US-8, and CA-09) of *P. infestans*. Spray application of the biopesticide occurred: i) 2 days before inoculation with the pathogen, ii) same day as pathogen, or iii) 4 days + 6 days after inoculation. Disease severity was based on % diseased tissue using a 0-10 rating scale. Spraying before inoculation with the pathogen did not significantly reduce disease severity. The disease severity reached 91%, and was not significantly different from the potato inoculated with only the pathogen. One spray application was required to control all three genotypes. US-8 was more aggressive than US-23 and CA-09, and required a second spray application to provide further disease reduction. The efficacy of *P. chloroaphis* strain 189 was also compared to three commercial biopesticides (Serenade®, Rhapsody® and Actinovate®) and mancozeb synthetic fungicide. Strain 189 provided similar efficacy to mancozeb (i.e. at least 90% disease control) but the commercial biopesticides did not reduce disease, which reached almost 100% disease severity. *Pseudomonas chloroaphis* is considered a potential candidate for management of potato late blight.

[P42] Biopesticides successfully supress bacterial spot disease caused by *Xanthomonas gardneri* in tomato. MADANTHA.A.K. WIJESINGHE, TIM DUMONCEAUX AND SUSAN M. BOYETCHKO. *Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK, S7N 0X2*
Bacterial spot disease is a serious problem worldwide in tomato cultivation without successful control measures to date. A series of growth chamber experiments were conducted to assess the efficacy of a formulated biopesticide Neo-Boost and a biological control agent *Bacillus* amyloliquefaciens against *Xanthomonas gardneri*. The disease incidence was lowered by 65.6% and 70.9% due to the application of Neo-Boost and *B. amyloliquefaciens*, respectively. Quantitative PCR showed a reduction of *X. gardneri* gene copy number due to application of the biopesticides at two days after challenging the plants. In addition, thebiopesticides increased plant biomass, nutrient absorption and induced flowering in tomato plants. A strong positive correlation was observed between *X. gardneri* gene copy number and disease severity. Negative correlations were seen between disease severity, plant dry weight, plant nutrient absorption, and number of flowers at 50% flowering. Application of biopesticides increased the production of plant defense enzymes peroxidase, superoxide dismutase and polyphenol oxidase. Neo-Boost and *B. amyloliquefaciens* were proven to be efficient in controlling tomato bacterial spot disease and inducing systemic resistance in tomato plants.

[P43] CPS Student Competition. **Does *glutathione-S-transferase 6* involve in canola disease defense against *Leptosphaeria maculans*?** K. R. E. PADMATHILAKE, M. F. BELMONTE, and W.G. DILANTHA FERNANDO. *Department of Plant Science, University of Manitoba, Winnipeg, MB R3T2N2, Canada; (M.F.B) Department of Biological Sciences, University of Manitoba, Winnipeg, MB R3T2N2, Canada*
Blackleg disease caused by *Leptosphaeria maculans* remains a significant threat to canola (*Brassica napus*) cultivation. Searching for genes to counter *L. maculans* infection is important in resistance cultivar development.

Since RNAseq studies showed *glutathione-S-transferase6 (GST6)* was highly expressed after *L. maculans* infection we anticipated GST6 could play an essential role in plant defense against this pathogen. GSTs represent a family of multifunctional enzymes involve in detoxification and oxidative stress tolerance. To determine the involvement of *GST6* in defense against *L. maculans,* a *GST6* knockdown mutant of Arabidopsis along with wild type Col-0 were inoculated with a *L. maculans* isolate 'D3'. Histological staining results at 14 days after inoculation (dai) showed more H_2O_2 production and cell death in *gst6* leaves compared to wild type. For the inoculation assay performed using *L. maculans* isolate 'D10', *B. napus* cv. 'Goeland' with *Rlm9* and cv. 'Westar' were used as the resistant and susceptible cultivars, respectively. The induction of *GST6* at different time points was analysed by real-time qPCR. In both susceptible and resistant cultivars, *GST6* expression was upregulated from seven dai as the pathogen established and increased the lesions in cotyledons which was not seen in control. The results support *GST6* involves in defense process in *B. napus* against *L. maculans.* The next steps would be to study *GST6* expression in other Avr-R gene interactions in the same pathosystem as well as in different pathosystems; and to study how this enzyme involves in the defense mechanism.

[P44] Development of southern stem canker disease on soybean seedlings in the greenhouse using a modified toothpick inoculation assay. M. A. CAMPBELL, Z. LI, AND J. W. BUCK. *Institute of Plant Breeding, Genetics, and Genomics/Department of Crop and Soil Sciences, University of Georgia, Athens, GA, United States 30602; and (J.W.B) Department of Plant Pathology, University of Georgia, Griffin, GA, United States 30223*
Southern soybean stem canker caused by *Diaporthe aspalathi* has caused major soybean losses for growers in the Southeast U.S. The most effective disease management tool for growers is the use of stem canker resistant soybean varieties. A fast, reliable greenhouse assay for stem canker would help develop resistant soybean varieties. An existing toothpick assay was modified to include culturing *D. aspalathi* on oxgall agar on toothpicks pre-soaked in oxgall liquid medium. Inoculation was performed on 3 week-old seedlings between cotyledons and the first trifoliate leaf, inoculation sites were sealed with petroleum jelly, and seedlings were incubated in humidity chambers for 72 h. Stem canker disease was highly consistent on susceptible lines four weeks post-inoculation and was not observed on soybean lines with known stem canker resistance genes *(Rdm)*. High levels of disease (≥98.3%) were observed with cultivars Braxton, Davis, and Centennial thought to have resistance in field studies. Isolates of *D. aspalathi* were observed to differ in virulence. This modified greenhouse assay will assist in the efforts for breeding stem canker resistance and better understanding the differences in disease phenotypes for some cultivars.

[P45] Evaluation of field-based solutions to mitigate root rot of field pea. S. CHATTERTON, R.S. ERICKSON, R. BOWNESS, B.D. GOSSEN, and M. W. HARDING. *Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre, Lethbridge, AB T1J 4B1, Canada. (R. B) Lacombe Research Centre, Alberta Agriculture and Forestry, 6000 C E Trail, Lacombe, AB T4L 1W1, Canada; (B.D.G.) Saskatoon Research and Development Centre, AAFC, 107 Science Place, Saskatoon, SK S7N 0X2, Canada; (M.W.H) Crop Diversification Centre South, Alberta Agriculture and Forestry, 301 Horticultural Station Road East, Brooks, AB T1R 1E6, Canada*
Aphanomyces root rot, caused by *Aphanomyces euteiches* Drechs., was first detected in pea (*Pisum sativum* L.) fields in Saskatchewan and Alberta in 2012 and 2013, respectively, and has caused significant crop loss in both provinces. Currently, extending the cropping interval between susceptible crops and avoiding infested fields are the only root rot management recommendations. To evaluate potential in-season management options, field trials were conducted in 8 locations over 2 years to determine the effect of a) cultivar tolerances; b) seed treatments; c) soil amendments with calcium, Edge or Treflan; and d) foliar-applied chemical (Phostrol). Trial sites were chosen based on natural inoculum of *A. euteiches*, *Fusarium* spp. or both. Emergence, root rot incidence and severity, shoot health and yield were recorded. The experimental design was randomized, complete block with 4 to 6 replicates and data were analyzed using SAS (PROC Mixed). All cultivars were equally and highly susceptible to root rot. Some seed treatment products provided early season suppression of root rots, but did not result in significant yield differences. None of the chemical products tested reduced root rot or significantly improved yields. Although none of the products tested improved yields, average yields across all treatments varied from 0 to >4,000 kg/ha at different locations, indicating the variability and difficulty in assessing the impact of root rots on pea yields. Future trials are

planned to evaluate the effect of stacking multiple products, as well as varying product rates and application timing, on root rot and pea yield.

[P46] Fungicide efficacy against *Sclerotinia sclerotiorum* biofilms is improved by addition of trace elements. M. W. HARDING, A. OMAR, B. BUZIAK AND J. FENG. *Alberta Agriculture and Forestry, Crop Diversification Centre South, 301 Horticultural Stn Rd E, Brooks Alberta T1R 1E6; (A.O, B.B.) Innovotech Inc. Suite 101 – 2011 94th St, Edmonton, Alberta T6N 1H1; (J.F.) Alberta Agriculture and Forestry, Crop Diversification Centre North, 17507 Fort Rd NW, Edmonton, Alberta T5Y 6H3*.
Sclerotinia sclerotiorum (Lib.) de Bary is a pathogen of many field and horticultural crops grown in Canada. Fungicides are important tools for management of *S. sclerotiorum*, however adequate disease control may not always be provided by a fungicide application. This study looked at the effects of trace elements (Ag, Bo, Ca, Cu, Mn, Zn) on the efficacy of six fungicides registered for control of *S. sclerotiorum*. The fungicides were prepared at three concentrations and mixed separately with each micronutrient at one of three concentrations for a total of 324 treatment combinations. The fungus was grown as a biofilm on pegs using the MBEC® Assay and performed in triplicate. Biofilm survival was quantified by detection of live cells using a Resazurin cell viability assay. Quantification was done using a microplate reader at 570, 595 and 630 nm before and after the fungicide treatment, and compared with untreated growth and sterility control wells. Most fungicides had improved efficacy when combined with one of the trace elements. For example, boscalid treatments were more efficacious when Ag was added, while ciprodinyl and fluazinam were improved when Cu was added. In some instances the efficacy increased more than five times. These results suggest that improvements in fungicide efficacy may be afforded by the addition of trace elements. While the mechanism is not known, the effect is similar to that seen with metallic complexes of antibiotic drugs

[P47] Field management practices have an effect on disease development in barley in Prince Edward Island. A. F. FOSTER, R. MATTERS AND R. A. MARTIN. *Charlottetown Research and Development Centre, Agriculture and Agri-Food Canada, 440 University Ave., Charlottetown, PE C1A 4N6, Canada*
There are many challenges to growing barley in Atlantic Canada. Wet and cool weather in summer contributes to high pressure from a number of economically important diseases such as *Fusarium* head blight (*Gibberella zeae* (Schwein.) Petch, (1936) anamorph: *Fusarium graminearum*), powdery mildew (*Blumeria graminis* f. sp. *hordei* (DC.) Speer (1975)), scald (*Rhynchosporium secalis* (Oudem) Davis) and netblotch (*Pyrenophora teres* Drechs (1923)). Trials were run from 2014-16 at the Harrington Research Farm, Prince Edward Island (PEI) to test different parameters of disease management. Factors tested were foliar fungicide application timing, the timing of planting and the source of seed of different barley cultivars. Application of different registered foliar fungicides showed consistent responses on the different cultivars bred for eastern and western Canadian environments, but the fungicides did produce a variety of responses for disease control and yield. Spray timing and planting timing also had significant influence over agronomic responses. Late planting during 3rd week of May resulted in significantly higher yield than early planting (1st week of May), but negligible differences in disease severity were observed. Western cultivars showed differences in disease and agronomic properties when grown from seed produced in Alberta compared to seed grown in PEI, Plants grown from seeds of western cultivars produced in PEI had significantly less netblotch than plants grown from seeds produced in western Canada, but yield was significantly higher in plants from western-produced seed. These results provide information to improve disease management practices for producers in Atlantic Canada.

[P48] CPS Student Competition. **Analysis of NADPH oxidase family genes in *Verticillium dahliae* during interaction with potato.** X. ZHU[1], A. SOLIMAN[1,2], M. R. ISLAM[3], L. R. ADAM[1], F. DAAYF[1] *[1] Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada, [2] Department of Genetics, Faculty of Agriculture, University of Tanta, Tanta, Egypt, [3] Department of Plant Pathology, Bangladesh Agricultural University, Mymensingh, Bangladesh*
Both animals and plants produce ROS and induce “oxidative bursts” against pathogens. However, in fungi, ROS also play an important role in cellular differentiation and fruiting body formation. NADPH oxidase (Nox) homologues, which are involved in ROS production, are present in different kinds of multicellular organisms including plants,

animals and fungi, but not in unicellular organisms. In *Verticillium dahliae*'s genome, three types of Nox genes have been identified, NoxA, NoxB, and NoxC. We compared *in vitro* the expression of NoxA, NoxB, and NoxC genes in highly and weakly aggressive isolates of *V. dahliae* elicited with different potato extracts. NoxA expression increased more in the weakly than in the highly aggressive isolate in response to potato leaf extracts, whereas NoxC expression increased more in the highly than in the weakly aggressive isolate in response to leaf and stem extracts. After inoculation of detached leaves from a susceptible potato cultivar with these two *V. dahliae* isolates, the tested genes except NoxC, were dramatically up-regulated in the highly aggressive isolate, compared to the weakly aggressive one. Pathogenicity analysis of NoxA, NoxB, and NoxC mutants generated from the highly aggressive *V. dahliae* isolate, showed that mutants of NoxA and NoxB, have significantly reduced aggressiveness, indicating that both genes play import roles in *V. dahliae*'s pathogenicity on potato.

[P49] Optimisation of suitable protocol to evaluate the pathogenicity of different *Fusarium* species affecting soybean in Manitoba. Y. GHARBI[1], N. GARMA[1], M.A. HENRIQUEZ[2], X. WANG[2], L. ADAM[1], AND F. DAAYF[1].
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Different *Fusarium* species are associated with root rot disease in soybeans. However, published soil infestation methods have limitations in the expression of disease. Our objective was to compare the efficacy of different inoculation protocols for generating root rot caused by *Fusarium graminearum*, *Fusarium avenaceum*, and *Fusarium poae* collected from cereals and pulses. Root dipping of seedlings in conidia suspension, soil spiked with conidia suspension and soil inoculated with agar plugs containing mycelia were used for inoculation. The cultivar TH32004R2Y was evaluated at V3 growth stage for plant height, root length and weight; root rot was estimated visually on a percent scale ranging from 0 to 9. Soil spiked with conidia suspension of *F. graminearum* produced the greatest root rot severity (40%), followed by root dipping in conidia suspension of *F. graminearum* (23%), whereas soil infested with agar plugs containing mycelia resulted in less than 10% root rot. Root rot for control plants was less than 5%. Soil spiked with conidia suspension reduced plant height, root length and weight compared to the other two methods ($P<0.05$). However, *F. avenaceum* and *F. poae* were less aggressive than *F. graminearum* with disease severity ranging between 15% and 25%. Pathogen colonization was assessed using conventional PCR. The number of positive samples detected by PCR was always higher than that detected by pathogen isolation, which indicates that *Fusarium* isolates colonize soybean roots without inducing rot disease symptoms. Overall, our study suggests that soil spiking with conidia suspension is more effective for producing seedling root rot.

[P50] Effect of calcium cyanamide on clubroot (*Plasmodiophora brassicae*) of canola in a greenhouse study. S. F. HWANG, H. U. AHMED, Q. ZHOU, H. FU, G. D. TURNBULL. AND S. E. STRELKOV, *Crop Diversification Centre North, Alberta Agriculture and Forestry, Edmonton, AB T5Y 6H3, Canada; (S.E.S.) Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada*
Clubroot, caused by *Plasmodiophora brassicae* Woronin, has become a serious threat to canola (*Brassica napus* L.) production in western Canada. Extensive studies have shown that calcium cyanamide ($CaCN_2$) and its degradation products calcium and nitrate are associated with reductions in the severity of clubroot of Brassica crops. Experiments were conducted under greenhouse conditions to evaluate the effect of calcium cyanamide on seedling emergence, plant growth parameters, gall weight, and clubroot severity of canola at inoculum concentrations of 1×10^3 to 1×10^5 spores mL^{-1} soil. Calcium cyanamide reduced gall weight and clubroot severity compared with the non-treated control. Treatment with this product, however, also reduced seedling emergence, plant height and plant biomass compared with the non-treated control, and the reduction of these parameters was greater at higher application rates. Clubroot severity levels were similar across inoculum concentrations ranging from 1×10^3 to 1×10^5 spores mL^{-1} soil. These results suggest that calcium cyanamide has the potential to reduce or prevent clubroot development when *P. brassicae* resting spore populations are relatively low.

[P51] In-depth studies on Fusarium root rot of dry bean in Manitoba. Y. M. KIM, M. A. HENRIQUEZ, D. L. MCLAREN, R. L. CONNER, K. F. CHANG, S. F. HWANG AND S. E. STRELKOV. *(Y.M.K., D.L.M.) Brandon Research and Development Centre, Agriculture and Agri-Food Canada (AAFC), 2701 Grand Valley Road, Brandon, MB R7A 5Y3, Canada; (M.A.H, R.L.C) Morden Research and Development Centre, AAFC, 101 Route 100, Unit 100 Morden, MB R6M 1Y5, Canada; (K.F.C., S.F.H.) Crop Diversification Centre North, Alberta Agriculture and Forestry, 17507 Fort Road N.W., Edmonton, AB T5Y 6H3, Canada; and (S.E.S) Department of Agricultural, Food and Nutritional Science, 410 Agriculture/Forestry Centre, University of Alberta, Edmonton, AB T6G 2P5, Canada*
Fusarium root rot of bean is a serious soil-borne disease and occurs in most bean-growing regions worldwide. In Manitoba, it has occurred in over 95% of commercial dry bean crops for the past decade based on data from annual crop surveys. In order to monitor changes in pathogen populations over time and create pathogen profiles, in-depth studies on root rot pathogen identification were conducted each year for two years (2011 and 2016) in three different commercial dry bean crops from the major production areas in Manitoba. A total of 1920 single spore isolates were obtained and pathogen species were identified based on their morphological characteristics on selection media and through microscopic examination. Identification of *Fusarium* spp. was confirmed by DNA sequencing using the ribosomal intergenic spacer (IGS), the translation elongation factor 1 alpha (EF1-α) gene, and the internal transcribed spacer (ITS) region. A set of *Fusarium* spp. from 2011 were screened for pathogenicity on the cultivar Envoy. An important finding from this research was the identification of *Fusarium cuneirostrum* causing root rot in dry beans. The identification of additional *Fusarium* spp. known to be associated with root rot of rotational crops stresses the need to acquire more information on dry bean root rot pathogens and cross-pathogenicity studies in order to design effective management strategies.

[P52] Evaluating new seed-treatment chemicals to reduce early infection of blackleg on canola. X. LIU AND G. PENG. *Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, Saskatchewan S7N 0X2, Canada*
Blackleg (*Leptosphaeria maculans* (Desmaz.) Ces. & De Not.) is an important disease on canola (*Brassica napus* L.) in western Canada. Current management strategies rely primarily on resistant varieties and crop rotation, but the disease incidence and severity have increased in recent years. Foliar fungicide treatments, targeting early infection of cotyledons can mitigate the blackleg risk. However this approach is not considered cost effective due to the sporadic pattern of blackleg damage. Seed treatment (quinazoline) is used regularly in Australia to reduce early blackleg infection, but no product has been registered for this purpose in Canada. This investigation assessed several new chemistries in the development pipeline for potential seed treatment. Each candidate was applied to the seed of susceptible (S) and resistant (R) canola cultivars, at a rate deemed economical by developers. Cotyledons were inoculated by applying 10 µL of *L. maculans* conidial suspension (10^6/mL) to a light wound. The infection severity was evaluated using a 0-9 scale at 14 days after inoculation. The current seed treatment (Helix® Vibrance or Prosper® EverGol) had little effect relative to untreated controls, whereas quinazoline reduced the infection moderately, especially on the R-rate variety. The efficacy of new chemistries varied from ineffective to highly effective. The latter inhibited the infection completely, even on the S-rated cultivar. In addition to the potential fungicidal effect, this new chemistry induced the expression of PR-1 and CHI marker genes, suggesting that it may stimulate plant defense responses. Hence, this new chemistry has potential as a seed treatment against blackleg infection on canola cotyledons.

[P53] Distribution of carrot cyst nematode in the Holland Marsh, Ontario, 2016. M.R. MCDONALD, K. VANDER KOOI, D. VAN DYK, E. PONOMAREVA, F. SUN and Q. YU. *Department of Plant Agriculture, University of Guelph, Guelph ON, Canada N1G 2W; (MRM, KV) Ontario Ministry of Agriculture, Food and Rural Affairs, Guelph ON, Canada (DVD) Ottawa Research and Development Center, Agriculture and Agri-Food Canada, Ottawa, ON, Canada (EP, QY) Ottawa Plant Laboratory, Canadian Food Inspection Agency, Ottawa, ON, Canada (FS).*
Approximately 25% of all carrots in Canada are produced in the Holland/Bradford Marsh region of Ontario, Canada. *Heterodera carotae* Jones is a plant parasitic nematode commonly known as the carrot cyst nematode. The distribution of this nematode is limited to a few countries in Europe, and the state of Michigan in the USA. It is only

known to infest carrots and wild carrots, and is considered an exotic plant pest in Canada. The nematode causes stunting and deformation of the roots, and loss of marketable yield. In recent years, carrots in commercial fields were found to have patches with poor growth, stunting, smaller and forked carrots with a proliferation of secondary roots, and cysts associated with the damage. Thirty carrot fields in the Holland Marsh region were sampled in November 2016 following carrot harvest. Field size varied from 2-10 ha. Soil samples of the top 20 cm of soil were sampled in an X pattern in each field. Samples were analyzed for the presence of carrot cyst nematode. Nematodes were extracted using a Baermann funnel for vermiform nematodes and the Fenwick method for cysts. Second stage juveniles (J2), males, and cysts were recovered. The species was confirmed as *H. carotae* using morphological and molecular methods. Carrot cyst nematodes were found in 90% of the samples and were widespread throughout the sampled area. Population densities of the carrot cyst nematode ranged from 0 to 16,100 juveniles kg^{-1} of soil. Further surveys, and studies to determine damage thresholds, are needed.

[P54] Infection of canola cotyledons by *Leptosphaeria maculans* in relation to wounding and dew duration. L. MCGREGOR and G. PENG. *Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, 107 Science Place, Saskatoon, SK S7N 0X2, Canada*
Blackleg, caused *by Leptosphaeria maculans* (Desmaz.) Ces. & De Not, is a serious disease of canola in Western Canada. The disease is usually more prevalent in the field under high moisture conditions. However, there is evidence suggesting that wounding of canola by flea beetles increases the level of infection, even under low moisture conditions. The objectives of this study were to assess the effect of simulated wounding on infection of *L. maculans* under short dew or no dew conditions for susceptible canola cultivar, 'Westar' and a commercial canola cultivar, CCC1 with quantitative resistance. Cotyledons were artificially wounded at three levels of severity; zero, light and moderate wounding. A conidial suspension of an *L. maculans* isolate possessing the green fluorescent protein gene (GFP) was misted onto the cotyledons. Half of the plants received a dew period and half received no dew. Disease ratings at 14 days after inoculation (dai) and observations of *L. maculans* GFP hyphal development under a fluorescent dissecting microscope at 10 dai, showed that for 'Westar', no disease had developed on the unwounded treatment whereas high levels of infection were observed for the wounded cotyledons. There was no difference between the dew and no dew treatments. For resistant cultivar CCC1, disease symptoms were less severe than 'Westar' and the severity of infection increased as wounding increased. There was a slight reduction in symptoms when there was no dew. The results support the hypothesis that wounding increases blackleg infection and emphasizes the need for effective flea beetle control.

[P55] Meeting the challenges of carrot crown rot in Prince Edward Island. R.D. PETERS, M.M. MACDONALD, H. LU, A. RYAN, S. ADAMS, J. DRISCOLL, A. MACPHAIL, D. GREGORY, B. CRANE, G. DYKERMAN, L. HALE AND G. WANG-PRUSKI. *Agriculture and Agri-Food Canada, Charlottetown Research and Development Centre, 440 University Ave., Charlottetown, PE C1A 4N6, Canada; (M.M.M, B.C., L.H.) University of Prince Edward Island, 550 University Ave., Charlottetown, PE C1A 4P3, Canada; (H.L.,G.W-P.) Department of Plant, Food, and Environmental Sciences, Faculty of Agriculture, Dalhousie University, P.O. Box 550, Truro, NS B2N 5E3, Canada; (A.R., S.A., J.D.) Prince Edward Island Horticultural Association, P.O. Box 2232, Charlottetown, PE C1A 8B9, Canada; (G.D.) Brookfield Gardens, 1067 Millboro Rd., Brookfield, PE C0A 1Y0, Canada.*
Fusarium crown rot has caused economic losses in Prince Edward Island (PEI), Canada in recent years. Crown lesions on carrots have resulted in rejection rates as high as 60-70% in some seasons. Isolates collected from symptomatic carrot crowns from 2010-2016 have been predominantly identified as *Fusarium avenaceum* (Fr.) Sacc. or *F. oxysporum* Schlechtend:Fr. Studies to determine isolate pathogenicity revealed that isolates of *F. avenaceum* were highly aggressive on carrot tissue, whereas isolates of *F. oxysporum* were only weakly pathogenic. Based on both disease incidence and severity parameters, therefore, *F. avenaceum* is the major carrot crown rot pathogen causing crop loss in PEI. A collection of isolates obtained from 2010-2016 from diverse regions of PEI were tested for fungicide sensitivity in amended agar assays, using concentrations of technical grade difenoconazole, fludioxonil, or thiabendazole. The growth of all isolates of *F. avenaceum* was suppressed by the three fungicides *in vitro*, however, isolates were somewhat more sensitive to fludioxonil and thiabendazole (EC_{50}<1 mg/L) as compared to

difenoconazole (EC_{50}<10 mg/L). These data were used as the basis for the establishment of field trials from 2012-2016 to test various chemical programs for efficacy against Fusarium crown rot. To date, no foliar or soil-applied chemical programs have been shown to provide efficacy against this disease. In the absence of chemical control, best management practices to control Fusarium crown rot of carrot in PEI will rely on the prevention of crown injury to limit pathogen infection and the choice of less susceptible cultivars.

[P56] Assessment of strategies to enhance resistance against new Clubroot pathogens using current resources. T. SONG, K, HORNADAY, N. TONU, F. YU, AND G. PENG. *Saskatoon Research and Development Center, Agriculture and Agri Food Canada, 107 Science Place, Saskatoon, S7N 0X2, SK, Canada*
Clubroot disease is one of the most severe threats to the canola production in Canada. In Alberta, more than 2000 commercial fields have been confirmed with clubroot infestation and the disease tends to spread into Saskatchewan and Manitoba. So far, host resistance is the most effective and practical approach to control clubroot disease in canola production. However, the emergence of new clubroot pathotypes that knocked down the commercial clubroot resistance (CR) cultivars raises potential challenge to the researchers and breeders to develop new CR cultivars to prevent the potential outbreak of disease due to these virulent clubroot pathogens, thereby minimizing the economic loss for the entire industry. In this project collaborating with commercial seed company, we performed assessment of the strength and durability of CR cultivars by pyramiding multiple CR genes against the P3 and other pathotypes. Currently, we found that canola with different combinations of CR genes showed various levels of responses against the virulent pathotypes from Alberta. Interestingly, reciprocal crosses of particular CR genes possessed distinct responses. The results suggested that pyramiding current CR genes with proper configuration of crossing is promising to develop CR cultivars against the newly identified virulent clubroot pathotypes. To achieve this purpose, it is indispensable to understand the molecular mechanisms of the CR genes used in the market, which will be the target of our ongoing study. Moreover, we are also determining the risk of resistance breakdown under low levels of inoculum in order to better employ CR resources in Saskatchewan and Manitoba.

[P57] Three-dimensional coating of porous activated carbons with silver nanoparticles and its scale-up design for plant disease management in greenhouses. YANG JIAN[1], XIUJIE LI[1], OLEKSANDRA SAVCHENKO[2] and JIE CHEN[2]. *[1]InnoTech Alberta, Hwy16A&75th Street, Vegreville, AB, Canada; [2]Department of Biomedical Engineering, University of Alberta, Edmonton, Alberta, Canada*
Greenhouse vegetable production is significantly impacted by pathogens that cause diseases to the roots of plants. These diseases are increasingly problematic in hydroponic vegetable production. Standard commercial practices in modern vegetable production facilities reuse the nutrient solution to reduce costs, or use dugout water for greenhouse irrigation in rural areas. This practice of recycling water may introduce or spread pathogens. Once pathogens contaminate water systems, they can spread quickly and cause dramatic losses to yield. Water filters have been used, but do not effectively kill fungi and bacteria. Therefore, better water treatment solutions are urgently needed to manage plant disease, especially for hydroponically-grown vegetables. Numerous studies have demonstrated the efficacy of silver ion (Ag^+) and silver-based compounds for disinfection of a wide range of harmful microorganisms. In this article, we present a new filter material based on three-dimensional (3D) silver nanoparticle (AgNP)-coated substrate for water treatment. We prepared AgNP-coated active carbon materials and tested their antimicrobial efficacy against phytopathogenic bacterial and fungal spores, such as *Pseudomonas* sp., and *Fusarium* sp. We then conducted large-scale tests in a dynamic flow setting and evaluated the effect of the filter on Pythium root rot control of hydroponically grown cucumbers. Results indicated that killing efficiencies of 3D coating were greater than 95% in the laboratory and that cucumber plants had no root infection in AgNP-AC filter treatment. The developed technique is approved to be a very efficient approach and has a great potential to be used in the greenhouse to manage plant root diseases.

Agronomy

[P58] CSA Student Competition. Potential of biochar in reducing global warming potential and greenhouse gas intensities in corn silage cropping systems amended with different nitrogen sources. W. ASHIQ, W. ALI, M. NADEEM, M. ZAEEM, S. M. GILLANI, J. WU, L. GALAGEDARA, V. KAVANAGH and M. A. CHEEMA. *(W.A, W.A, M.N, M.Z, S.M.G, J.W, L.G, M.A.C) School of Science and Environment, Grenfell Campus, Memorial University of Newfoundland, Corner Brook, NL, A2H 5G4, Canada; (M.N.) COMSATS Institute of Information Technology, Vehari, 61100, Pakistan; (V.K.) Department of Fisheries, and Land Resources, Pasadena, NL, A0L 1K0, Canada*

Greenhouse gases (GHGs) emissions from agriculture sector have been accelerating global warming potential (GWP) and greenhouse gas intensities (GHGI) (GHG emission per unit of crop yield). About 8% of GHG emissions in Canada are contributed by agriculture sector largely through methane (CH_4) and nitrous oxide (N_2O). Out of these emissions 50% are contributed by manure and fertilizer application to land. Biochar (BC), a carbon-rich material has been observed to reduce the GHG emissions in different cropping systems. A field experiment was conducted to; i) determine the effect of different N sources on GWP and GHGI and ii) elucidate the effect of biochar application on the reduction of GWP and GHGIs in corn silage cropping systems. Experimental treatments were; i) dairy manure with high nitrogen (DM_1) (0.37% N), ii) dairy manure with low nitrogen (DM_2) (0.14% N), iii) inorganic nitrogen (IN), iv) DM_1 + BC, v) DM_2 + BC, vi) IN + BC vii) N_0 (Control). Results showed that nitrogen sources and BC had a significant effect on GHGs emission, GWP and GHGI. BC application significantly reduced the GHGs, GWP and GHGI. Minimum GWP was noted in IN+B (6 t CO_2eq. ha^{-1} $season^{-1}$), whereas, maximum was observed in DM_1 (8 t CO_2eq. ha^{-1} $season^{-1}$). GHGI was high in control 0.4 t CO_2eq. t^{-1} dry matter, while low in IN+B (0.28 t CO_2eq. t^{-1} dry matter). Results revealed that BC application could be considered a useful approach in reducing GWP and GHGI of corn silage cropping systems under different nitrogen sources application.

[P59] Haplotype analysis of loci associated with Fusarium head blight resistance in a collection of Brazilian spring wheat: An Update. G. HUMPHREYS, L. LANGILLE, X. WANG, C. MCCARTNEY, S. KHANIZADEH and H. VOLDENG. *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, Canada, K1A 0C6; and (C.M.)Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB, Canada, R6M 1Y5*

Fusarium head blight (FHB) is the most important disease of wheat reducing grain yield, crop grade and end-use quality. FHB can be caused by various Fusarium spp., but *F. graminearum* is the most economically important in North America due in part to the production of mycotoxins such as deoxynivalenol (DON) during infection. Food and feed safety can be compromised because mycotoxin content can make the wheat grain unsuitable for food or feed. A collection of 79 wheat lines from various Brazilian breeding institutions were genotyped using DNA markers at four FHB quantitative trait loci (QTL). These QTL were previously reported on chromosomes 3BS, 5AS and 6BS in the cultivar Sumai 3, and 3A in the cultivar, Frontana. Visual Ratings Index (VRI) for reactions to FHB were evaluated in the Ottawa inoculated FHB nursery in 2016, and deoxynivalenol (DON) content was determined from 2016 harvested nursery samples. None of the Brazilian lines possessed the Sumai 3 haplotype for FHB resistance QTL on 3BS (*Fhb1*) or 6BS (*Fhb2*). While 63% of the lines amplified the Sumai 3 allele at gwm415 on 5AS, none amplified the Sumai 3 alleles for adjacent SSR markers. Nevertheless, 2016 FHB ratings ranged from 13.3 to 95.0, and DON levels ranged from 1.8 to 30.5 ppm. Some lines in the Brazilian collection appear to possess FHB resistance that is not associated with the three major Sumai 3 FHB QTL which would make these lines useful sources of Fusarium head blight resistance for wheat breeding and research.

[P60] Buckwheat (*Fagopyrum esculentum* Moench.) cultivar and seeding date response to Newfoundland growing conditions. D.B. MCKENZIE, P.L. DIXON, C. NORONHA, AND K.N. HOBRECKER. *St. John's Research and Development Centre, Agriculture and Agri-Food Canada, 308 Brookfield Road, building 25, St. John's, NL A1E 0B2, Canada; (C.N.) Charlottetown Research and Development Centre, Agriculture and Agri-Food Canada, 440 University Avenue, Charlottetown, PE C1A 7M8, Canada*

Increasing wireworm populations in agricultural fields are of concern to farmers in Atlantic Canada. Buckwheat (*Fagopyrum esculentum* Moench.) grown as a rotation crop before potatoes has been shown to reduce damage and increase marketable yield in wireworm-infested fields in Prince Edward Island; however, summer temperatures may

be too cool for buckwheat to be as effective in Newfoundland. Buckwheat (cultivar 'Mancan") grown in field trials at the St. John's Research and Development Centre in 2014 and 2015 showed significant effects of seeding date on early bloom and full bloom dry matter yields, with a strong contrast between the two years due to differential July heat unit accumulation. The July 2015 average daily maximum temperatures were 9^{o} C cooler than in 2014 and resulted in much lower dry matter yields. In a second trial, nine Canadian buckwheat cultivars were planted at the same field location in late June in 2014 and 2015 after the risk of frost was below 10% probability. Dry matter yield differences were found between specific cultivars at early bloom and full bloom growth stage harvests; however, the most significant yield contrast was between the two years. The effects of these buckwheat treatments will be assessed by analyzing the wireworm damage in potatoes from the 2016 production year.

[P61] CSA Student Competition. Plant density effects on N fixation by soybean and dry bean in southern Alberta.T.T.N. THAI, F.J. LARNEY, J.E. THOMAS, M.S. BANDARA, D.G. PAULY, D.G. LE ROY. *Department of Biological Sciences, University of Lethbridge, 4401 University Drive,*
Lethbridge, AB T1K 3M4, Canada; (F.J.L.) Agriculture & Agri-Food Canada, Lethbridge Research & Development Centre, 5403 1st Avenue South, Lethbridge, AB T1J 4B1, Canada; (M.S.B.) Alberta Agriculture & Forestry, Crop Diversification Centre South, 301 Horticultural Station Road East Brooks, AB T1R 1E6, Canada; (D.G.P.) Alberta Agriculture & Forestry, 5401 1st Avenue South., Lethbridge, AB T1J 4V6, Canada; (D.G.L.) Department of Economics, University of Lethbridge, 4401 University Drive, Lethbridge, AB T1K 3M4, Canada
Numerous studies have reported the effects of plant density on yield of soybean [*Glycine max* (L.) Merrill] and dry bean (*Phaseolus vulgaris* L.), but effects of density on N fixation are less well documented. We conducted experiments in four environments (Bow Island and Lethbridge, AB in 2014 and 2015) using soybean, dry bean and barley (*Hordeum vulgare* L., a non-legume control) in Year 1 (2014, 2015) followed by wheat (*Triticum aestivum* L.) with no N fertilizer in Year 2 (2015, 2016). In Year 1 there were two soybean genotypes, at two row spacings (wide row, 35 cm; narrow row, 17.5 cm); and three seeding densities (30, 50, 80 seeds m^{-2}). Dry bean was planted in narrow (35 cm, 25 seeds m^{-2}) or wide rows (52.5 cm, 40 seeds m^{-2}), at 0 and 60 kg N ha^{-1}. Across all environments, genotypes, and row spacings, N fixation (using the N difference method) by soybean was greatest at highest plant density (111 kg ha^{-1}, 80 seeds m^{-2}), followed by 75 kg ha^{-1} (50 seeds m^{-2}), and 53 kg ha^{-1} at 30 seeds m^{-2}. Results indicate that despite dry bean having a lower N fixation ability compared with soybean, wheat following dry bean resulted in greater N uptake than wheat following soybean. This may be related to faster decomposition and N release from dry bean residue. Our results will provide some comparative N benefits for growers interested in growing soybean vs. dry bean in southern Alberta's irrigation districts.

[P62] Effect of long-term phosphorus fertilizer management on phosphorus and cadmium concentration and yield of soybean. R.M. MOHR, C.A. GRANT (ret'd), G.R. BARDELLA and D.N. FLATEN. *Brandon Research and Development Centre, Agriculture and Agri-Food Canada, Box 1000a, R.R. 3, Brandon, MB, R7A 5Y3, Canada; (G.R.B., D.N.F.) Department of Soil Science, University of Manitoba, 13 Freedman Crescent, Winnipeg, MB, R3T 2N2, Canada.*
Rapid expansion of soybean (*Glycine max* L.) production in Manitoba has generated a need for information regarding phosphorus (P) nutrition in this crop. Field studies were conducted at three locations in Manitoba from 2013 through 2015 to determine the effect of long-term P fertilizer management on P and cadmium (Cd) concentration in soybean. The residual effects of four rates of monoammonium phosphate fertilizer (0, 20, 40, 80 kg P ha^{-1}) and three fertilizer sources varying in Cd concentration (0.4 mg Cd kg^{-1}, 70 mg Cd kg^{-1}, and 210 mg Cd kg^{-1}), applied annually from 2002 through 2009, were evaluated. The long-term application of increasing rates of P fertilizer increased Olsen P concentration in surface soil, while DTPA-extractable Cd concentration increased as a function both of increasing P fertilizer rate together with increasing Cd concentration in the applied fertilizer. Midseason biomass P and seed P concentrations were positively related to soil P concentration, with Olsen P accounting for 40 to 78% of the variability in plant P. Increasing fertilizer rates and/or increasing Cd concentrations in applied fertilizer resulted in consistently higher plant tissue and seed Cd concentrations in soybean, and reflected differences in DTPA-extractable Cd levels in the soil. Seed yield of soybean did not increase with increasing Olsen P concentration, suggesting that soybean was generally able to effectively access sufficient soil P to optimize crop yield under the

wide range of soil test P concentrations, ranging from 5 to 93 mg kg^{-1}, arising from previous P management practices.

[P63] Indian cup plant (*Silphium perfoliatum* L.): Promising results of a possible forage for the Canadian prairies. M.P. Schellenberg. *Swift Research and Development Centre, Box 1030, 1 Airport Road, Swift Current, SK S9H 3X2 Canada*
Indian cup plant (*Silphium perfoliatum* L.) has been suggested as a plant with potential as a forage or biogas feedstock. This is a perennial species native to the Eastern United States and Canada with an ability to spread rapidly. The plant can attain a plant height of up to 2 m. Presently, no work is noted for material grown in semiarid regions of North America. A study was undertaken at Swift Current Research and Development Centre, Agriculture and Agri-Food Canada to examine the plants' potential as a forage. A randomized complete block design was utilized to examine 5 populations in a field nursery. Plants were harvested 20 July 2016 at the bud stage removing all material 15 cm above the soil surface after being planted in May 2015. Biomass was greatest for the "A" population (682 g per plant) with NDF (35% to 21%), ADF (35% to 21%) and crude protein (22% to 8%) being highly variable. These initial results do indicate the potential of the Indian cup plant as a forage in western Canada but one must also consider 2016 received well above the normal amount of precipitation. Additional research is required to determine the potential of this plant under more normal precipitation patterns. The high degree of variability in ADF, NDF and crude protein also indicates the potential for selection to improve the forage nutritional value.

[P64] Environmental correlates of creeping red fescue (*Festuca rubra* L. var. *rubra*) seed yield in Peace River region of Western Canada. N. KHANAL*, R. AZOOZ, J. OTANI AND H. W. KLEIN-GEBBINCK. *Agriculture and Agri-Food Canada, Beaverlodge Research Farm, 1 Research Road, Beaverlodge, Alberta T0H 0C0, Canada*
The Peace River region is the largest producer and exporter of creeping red fescue (*Festuca rubra* L. var. *rubra*) seed in the world. The seed crop sequence of the fescue comprises one establishment year followed by two seed crop years. To understand why there are variable responses to crop management factors, we analyzed the correlation between average temperature coupled with total precipitation of two-week periods of the preceding autumn (September) and prevailing spring (May-June) and seed yield of the fescue cultivar 'Boreal' at Beaverlodge, Alberta, from 2012 to 2016. Average temperature and total precipitation data were calculated over the first half and second half of each month. Seed yields over the four years showed a negative correlation with two-week average temperatures and precipitation totals of the preceding September. Prevailing average temperature of later-half of May and total precipitation of both early and later half of May were positively correlated with the seed yield. The total precipitation in June showed a contrasting relationship; warmer temperature coupled with lower precipitation in the early-half and cooler temperature coupled with higher precipitation in the later-half of June were associated with higher seed yield. The results implicated that dormancy-inducing cool-dry weather in the preceding autumn, and growth-promoting warm-moist weather in the prevailing spring season are favourable conditions for seed yield of creeping red fescue. Furthermore, in the later-half of June which is the flowering time for creeping red fescue, moderate temperatures and adequate moisture are critical to minimize the risk of pollen desiccation, hence enhancing pollination.

[P65] CSA Student Competition. Relationship between rhizosphere soil acid phosphatase activities and forage production in silage corn and soybean intercropping in cool climate. M. ZAEEM, M. NADEEM, W. ASHIQ, W. ALI, S.M. GILLANI, H. PHAM, V. KAVANAGH, S. ELAVARTHI, M.A. CHEEMA, L. GALAGEDARA, R. THOMAS. *(M.Z., M.N., W.A., W.A., S.M.G, H.P, M.A.C, L.G, R.T) School of Science and the Environment, Grenfell Campus, Memorial University of Newfoundland, Corner Brook, NL, A2H 5G4, Canada; (M.N.) Department of Environmental Sciences, COMSATS Institute of Information Technology, Vehari-61100, Pakistan; (V.K.) Department of Fisheries, and Land Resources, Government of NL, A0L 1K0, Canada; (S.E) Department of Agriculture and Natural Resources Delaware State University,1200 N Dupont Hwy, Dover, DE 19901, USA*
Cereal-legume intercropping system can enhance agroecosystem efficiencies through increased soil enzyme activities, mineralization and bioavailability of nutrients in root rhizosphere. These can lead to higher nutrient

uptake, improved agronomic performance and higher forage productivity. A field experiment was conducted to evaluate the production potential of silage corn (Yukon R and DKC26-28RIB) intercropped with forage soybean genotypes (Big Fellow RR, Game Keeper RR and Kester's Bob White) in cool climatic production systems. Also, the relationship between rhizosphere soil acid phosphatase activities (RS-APase) and forage production was assessed. The plants were grown in monocrop (control) and intercrop (corn and soybean) systems. Intercropping produce significantly (P<0.001) higher forage biomass than the monocropping. Significantly higher forage production i.e. 16.96 Mg ha^{-1} was recorded in the Yukon R and the Big Fellow RR under the intercropping system, whereas lowest biomass i.e. 2.15 Mg ha^{-1} was recorded in the Kester's Bob White soybean monocropping. RS-APase were also increased significantly (P<0.001) in all the intercropping systems. Maximum RS-APase was recorded in the DKC26-28 RIB-Game Keeper RR intercropping (22.485 µmole pNP g^{-1} min^{-30}), whereas minimum was recorded in the DKC26-28 RIB monocropping (16.07 µmole pNP g^{-1} min^{-30}). A significant positive correlation was recorded between RS-APase and forage production in the intercropping (r = 0.40*) while a significant negative correlation was recorded in the monocropping (r = -0.66***). Study findings suggested that intercropping might be an appropriate approach to enhance forage production due to improved soil health under cool climatic production systems.

[P66] Phenotypic and Molecular Variation in Drought Tolerance of Jordanian Durum Wheat (*Triticum durum* Desf.) Landraces. WESAM AL KHATEEB[a], ALA'A AL SHALABI[a], DANA SCHROEDER[b]. [a] *Department of Biological Sciences, Yarmouk University, Irbid, Jordan,* [b] *Department of Biological Sciences, University of Manitoba, Winnipeg, Canada*
Drought is considered one of the major constraints of plant growth and productivity worldwide. Plants respond to drought through different mechanisms including physiological, biochemical, and gene expression modulation. Studying these mechanisms will provide better understanding of drought response mechanisms and will help breeders in developing new cultivars. In this study, growth, biochemical, and molecular responses of four wheat (*Triticum durum* Desf.) landraces to drought stress (300 mM mannitol) were investigated at the seedling stage. Reverse transcription-polymerase chain reaction (RT-PCR) was used to assess gene expression level for a drought stress responsive gene (*DHN15.1*). Germination percentage, shoot length, root length, and root number for all *Triticum durum* landraces were decreased significantly under drought stress. However, drought stress caused an increase in proline content, lipid peroxidation level (LPO), and *DHN15.1* transcript level. According to the studied traits, the Karak landrace showed long shoots (48% relative to its control), the longest roots (45% relative to its control) and the highest proline content (483% relative to its control). Thus, it can be selected as the most tolerant wheat landrace and can be utilized in wheat breeding programs for adaptation to drought-prone environments.

[P67] Evaluation of western spring wheat varieties for their production potential in northwestern Ontario. T. S. SAHOTA. *Thunder Bay Agricultural Research Station, 435 James St. S, Thunder Bay, Ontario, Canada P7E 6S7 (e-mail: tarloksahota@tbaytel.net)*
Compared to southern Ontario and Quebec, climatic conditions at Thunder Bay are closer to Manitoba/and parts of western Canada. Eleven spring wheat varieties, including Sable as a check (AAC Bailey, AAC Iceberg, AAC Innova, AAC Proclaim, AAC Redwater, BW 931, BW 932, Enchant VB, HY 1312, Sable, and Whitehawk), were evaluated at Thunder Bay during 2013-'15 in completely randomized block design replicated four times. WR859CL was added in 2014 and 2015. All varieties were grown with recommended management practices. Averaged over years, Hy1312, AAC Innova, and WR859CL produced the highest grain yield (5.47 Mg ha^{-1} to 5.56 Mg ha^{-1}), which was 0.85-0.94 Mg ha^{-1} higher than Sable. AAC Proclaim was the only other variety that recorded >5.10 Mg ha^{-1} grain yield. AAC Innova registered the highest straw yield (7.54 Mg ha^{-1}; ~1.10 Mg ha^{-1} higher than Sable)! Varieties that gave 6.50 Mg ha^{-1} or more straw yield were AAC Iceberg, AAC Proclaim, Enchant VB and WR859CL. Producers in northwestern Ontario would prefer varieties that are good for both grain and straw production; for which AAC Innova was the best fit. No lodging or serious disease infestation was observed in any of the varieties.

[P68] Evaluation of Ontario and Manitoba winter wheat varieties for their production potential in northwestern Ontario. T. S. SAHOTA. *Thunder Bay Agricultural Research Station, 435 James St. S, Thunder Bay, Ontario, Canada P7E 6S7 (e-mail: tarloksahota@tbaytel.net)*

Winter wheat acts as a cover crop in fall/winter, could be a good option for grain and straw production and for spreading field operations in areas with short growing seasons. Seven Ontario and 12 Manitoba winter wheat varieties, were evaluated for their production potential in two experiments in completely randomized block design replicated four times at Thunder Bay, Ontario, during 2012-'15. CDC Falcon was the common check in the two experiments. All varieties were grown with recommended management practices. Averaged over years, it was found that none of the Ontario varieties (AC Morley, Keldin, Priesley, Princeton, Standard and Whitebear) gave higher grain or straw yield than CDC Falcon (6.00 Mg ha^{-1} grain and 11.24 Mg ha^{-1} straw yield). Whitebear (hard white) gave the lowest grain (3.63 Mg ha^{-1}) and straw (7.55 Mg ha^{-1}) yields. Only 3 out of 11 Manitoba winter wheat varieties (Swainson 7.58 7.58, Moats 6.76 Mg ha^{-1} and AAC Gateway 6.57 Mg ha^{-1}) recorded significantly higher grain yield than CDC Falcon. Aforesaid 3 varieties also produced the highest straw yields (15.5-16.4 Mg ha^{-1}); Swainson topped in the straw yield and was the best dual purpose variety. No lodging or serious disease infestation was observed in any of the varieties.

Epidemiology

[P69] CPS Student Competition. **Comprehensive survey of soybean foliar diseases in Manitoba.** G. DIAZ-CRUZ AND B.J. CASSONE. *Graduate Student, Brandon University, John R. Brodie Science Centre, 270 - 18th Street, Brandon, Manitoba, R7A 6A9; (B.J.C.) Department of Biology, Brandon University, John R. Brodie Science Centre, 270 - 18th Street, Brandon, Manitoba, R7A 6A9*

Soybean (*Glycine max*) has become a very important crop in Manitoba. The acreage dedicated to this crop has grown 10-times during the last decade and it is expected to experience further increase in the upcoming years. Due to its novelty in the province, very scarce information about foliar disease has been recorded. In order to describe the foliar pathogens affecting this legume, we conducted a comprehensive survey across Manitoba during the summer of 2016. The survey was performed twice, in June (33 fields) and August (70 fields). At least 5 leaves per field showing symptoms of disease were collected and stored in a RNA-preservation solution. RNA was extracted from each sample and pooled by field, then by region. Regional pools were analyzed using RNA-sequencing, and the sequences that mapped against the soybean genome were discarded. Un-mapped reads were then compared against the non-redundant database in NCBI using BLASTn. We identified 11 fungi, 3 bacteria, 3 viruses and 2 oomycetes as soybean pathogens. Bacterial blight, caused by *Pseudomonas syringae* pv. *glycinea*; Frogeye, caused by *Cercospora sojina*; and leaf spot, caused by *Alternaria alternata*, were present in all regions. The virus *Brome mosaic virus* was found in two different regions, and it has not been reported previously in soybean. Overall, our results provide important information on the prevalence of established and emerging pathogens in Manitoba soybean.

[P70] Optimization of a TaqMan real-time PCR for detection of Goss's bacterial wilt pathogen in corn seeds. A. SIDIBÉ, R. XU, F. DAAYF, A. SOLIMAN, L. ADAM, L. M. REID, T. BARASUBIYE AND J. T. TAMBONG. *(A.S; X.R; L.M.R; T.B; J.T.T) Ottawa Research and Development Centre, 960 Carling Avenue, Ottawa, ON Canada K1A 0C6; (F.D; A.S; L.A) Department of Plant Science, University of Manitoba, Winnipeg, Canada. Corresponding author: james.tambong@agr.gc.ca*

Clavibacter michiganensis subsp. *nebraskensis* (Cmn) is the causal agent of Goss's bacterial wilt and blight of corn. During severe epidemics, losses could be as high as 50% from systemic infections of the xylem. Even though seed transmission rates are very low, this risk leads to potential phytosanitary challenges for export countries. Recently, we published a TaqMan assay for accurate detection of Cmn in pure cultures and leaf samples. There is no publicly available assay for detection of Cmn in corn seeds. The aim of this study was to optimize our previously developed TaqMan assay for Cmn detection in corn seeds. The number of colony forming units (cfu) in cultures of strain DOAB 397 was determined. One-tenth serial dilutions were performed to obtain Cmn suspensions of 1.70 x 10^8 to17.0 cfu. The bacterial suspensions (200 µl) were added to different amounts (50, 100 and 200 mg) of autoclaved or un-autoclaved cornmeal and TaqMan assay performed after total DNA extraction. The different amounts of the cornmeal did not impact the detection limit. Significant differences, however, were observed between un-

autoclaved and autoclaved cornmeal with a very high detection limit (10^6 cfu) for the former. This suggests that one or more unknown biologically active factors in un-autoclaved cornmeal have a negative impact on either the Cmn colonies added or the DNA. Using autoclaved cornmeal, the detection limit was 170 cfu with the celB probe. The assay will be validated with greenhouse-infected seeds. This assay could be an invaluable tool in certifying corn seeds destined for export.

[P71] Collection and characterization of rust species infecting *Berberis* in Ecuador. C. W. BARNES, M. E. ORDÓÑEZ, AND T. FETCH JR. *Instituto Nacional de Investigaciones Agropecuarias, Estación Experimental Santa Catalina, Programa Cereales, Panamericana Sur Km 1, Sector Cutuglahua, Pichincha, Ecuador; (M.E.O.) Pontificia Universidad Católica del Ecuador, Escuela de Ciencias Biológicas, Av. 12 de Octubre 1076 y Roca, Quito, Ecuador; and (T.F.JR.) Agriculture and Agri-Food Canada, Brandon Research and Development Centre, 2701 Grand Valley Road, P.O. Box 1000A, R.R. #3, Brandon, MB R7A 5Y3, Canada*
The genus *Berberis* is well-known historically as the alternate host of *Puccinia graminis*, and now *P. striiformis* (Jin et al 2010). There are two centers of diversity of *Berberis,* one in Asia and one in South America, that arose from a vicariance event in the Cretaceous Period (Young-Dong et al. 2004). More than 30 species of *Berberis* have been reported in Ecuador, mostly endemic (Ordonez et al., 2015), but records are outdated and there is no mention of their role in rust epidemiology. Located between the wheat production areas of North and South America, *Berberis* species in Ecuador may serve as a potential bridge for disease movement and source of new races for both rust fungi. Because many of the *Berberis* collections found in the Ecuadorian herbariums are dated (some 20 years old or more), we have begun to re-survey the regions where *Berberis* occurs in Ecuador, collecting plant specimens and (when found) rust aecia. Using the Internal Transcribed Spacer (ITS) region for both the plant and its associated rust, we have sequenced six *Berberis* and six rust species. Generally, each *Berberis* species has a unique rust pathogen, although one *Berberis* species is host to two rust pathogens, and one rust infects two *Berberis* species. Five rust pathogens are species of *Edythea*, while the sixth is as yet unidentified. In the mountainous regions of Ecuador, geographical isolation seems to be the main factor separating the plant and their fungal pathogens.

[P72] Host range of *Phytophthora sansomeana* and the impact of inoculum density on disease severity, seedling emergence, and biomass of field pea. K. F. CHANG, S. F. HWANG, H. U. AHMED, H. FU, Q. ZHOU, R. L. CONNER, D.L. M$_C$LAREN, S. E. STRELKOV AND G. D. TURNBULL. *Alberta Agriculture and Forestry, 17507 Fort Road NW, Edmonton, AB T5Y 6H3, Canada; (R.L.C) Morden Research and Development Centre, Agriculture and Agri-Food Canada (AAFC), Unit 101 Route 100, Morden, MB R6M 1Y5, Canada; (D.L.M) Brandon Research and Development Centre, AAFC, 2701 Grand Valley Road, Brandon, MB R7A 5Y3, Canada; (S.E.S) Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada*
Root rot is a common disease of pea (*Pisum sativum* L.) in most regions where the crop is grown. In western Canada, several soil-borne pathogens including *Fusarium* and *Pythium* spp., *Rhizoctonia solani* (Kühn), and *Aphanomyces euteiches* (Drechsler) are associated with root rot of field pea. Recently, *Phytophthora sansomeana* (E.M. Hansen & Reeser) was identified for the first time as the cause of root rot of field pea in Alberta. To understand its ecology and potential impact on crop production systems, the host range of the fungus was investigated and the relationships between inoculum density and root rot severity, seedling emergence, and biomass in pea were evaluated. Eight crops including canola, faba bean, lupin, lentil, pea, soybean, barley, and wheat were inoculated with *P. sansomeana*. The fungus was pathogenic on all of the crops and reduced seedling emergence, plant height and plant biomass compared with non-inoculated control treatments. Analysis of variance showed significant effects of inoculum density on seedling emergence, root biomass and disease severity. Regression analysis showed a strong positive relationship between inoculum density and disease severity, and a strong negative relationship between inoculum density, and root weight, and seedling emergence. The ability of *P. sansomeana* to infect a wide range of crops will make it a challenging pathogen to manage via the use of cultural practices.

[P73] CPS Student Competition. **Generation and characterization of *Fusarium graminearum* mutant overexpressing MAPK (Mgv1)** D. GONZÁLEZ-PEÑA FUNDORA, A. ERANTHODI, R. GOYAL, G. SUBRAMANIAM, C. RAMPITSCH, N. THAKOR

AND N. A. FOROUD *(D.G.F., A.E, R.G., N.A.F.)Agriculture and Agri-Food Canada (AAFC)-Lethbridge. 5403 1st Ave. S., Lethbridge AB, T1J 4B1; (D.G.F., N.T.)University of Lethbridge, Department of Chemistry and Biochemistry, 4401 University Dr W, Lethbridge, AB T1K 6T5, Canada; (G.S.) Agriculture and Agri-Food Canada (AAFC)-Ottawa. 960 Carling Avenue; Ottawa, ON, K1A 0C6; and (C.R.) Cereal Research Centre, Agriculture and Agri-Food Canada (AAFC), 101 Route 100, Morden, MB R6M 1Y5, Canada*
Fusarium graminearum Schwabe is the causal agent of fusarium head blight (FHB), a devastating disease in wheat (*Triticum aestivum* L.). In this fungus, three mitogen-activated protein kinases (MAPK) pathways have been identified. MAPKs are ERK (**e**xtracellular **r**esponse **k**inase) -like proteins that relay cellular signals through phosphorylation of various proteins. The *F. graminearum* MAPK, Mgv1 (**M**APK for **g**rowth and **v**irulence **1**), plays a role in mycotoxin accumulation and disease development, though the latter may be related to a loss of fitness. Many of the components in the *F. graminearum* MAPK pathways remain unknown. With the aim of identifying downstream elements in the Mgv1 cascade, we generated *F. graminearum* mutants for *in locus* over-expression of *Mgv1* under the control of a constitutive promoter. The mutants were characterized for changes in their morphocultural pattern and virulence in the spikes of six week-old *Brachypodium distachyon* (L) P. Beauv. plants. The growth rate of the mutants measured in potato dextrose agar Petri dishes was slower than the wild type (WT), but no difference was observed in their ability to cause disease. The abundance of phosphorylated (activated) MAPK proteins was assessed by immunoblotting using anti-phosphorylated ERK1/2 antibodies, showed an increased level of a phosphorylated ERK-like protein (MAPK) in the mutants. Other analyses related to the putative role of Mgv1 in cell wall formation, are being carried out to further our understanding of Mgv1 signalling pathways. Future directions for this work include the identification of downstream targets of Mgv1 activity.

[P74] Collection and characterization of species of *Berberis* in Argentina, Brazil, Chile, Ecuador, and Uruguay. T. FETCH, S. HAMBLETON, M. S. CHAVES, J. MARTINELLI, G. B. P. DA SILVA, S. BORDIGNON, P. CAMPOS, R. MADARIANA, C. W. BARNES, M. E. ORDÓÑEZ, G. AZZIMONTI, AND S. GERMAN. *Agriculture and Agri-Food Canada, Brandon Research and Development Centre, 2701 Grand Valley Road, Brandon Research Centre, P.O. Box 1000A, R.R. #3, Brandon, MB R7A 5Y3, Canada; (S.H.) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, K.W. Neatby Building, 960 Carling Avenue, ON K1A 0C6, Canada; (M.S.C.) Centre for Temperate Climate Agricultural Research, Brazilian Agricultural Research Centre, Pelotas, RS, Brazil; (J.M., G.B.P.D.S., S.B) Universidade Federal Rio Grande du Sul, Porto Alegre, RS Brazil; (P.C) Instituto Nacional de Tecnologia Agropecuaria, Bordenave, Argentina; (R.M.) Instituto Nacional de Investigaciones Agropecuarias, National Institute of Agricultural Research, Quilamapu, Chile; (C.W.B.) Instituto Nacional de Investigaciones Agropecuarias, Estación Experimental Santa Catalina, Programa Cereales, Panamericana Sur Km 1, Sector Cutuglahua, Pichincha, Ecuador; (M.E.O.) Pontificia Universidad Católica del Ecuador, Escuela de Ciencias Biológicas, Av. 12 de Octubre 1076 y Roca, Quito, Ecuador; (G.A., S.G.) Instituto Nacional de Investigaciones Agropecuarias, La Estenzuala, Uruguay.*
South America is one of two centers of diversity for the genus *Berberis* (Kim et al. 2004). As the alternate host for both *Puccinia graminis* and *P. striiformis*, *Berberis* species are important in increasing the virulence diversity of races of these rust fungi (Jin et al 2010). However, little is known about the susceptibility of South American *Berberis* to these cereal rust species. To investigate the role of *Berberis* in cereal rust diversity, we surveyed Argentina, Brazil, Chile, Ecuador, and Uruguay in 2016 for *Berberis* species and aecial infection. While no aecial infection was found in Uruguay, rust aecia on *Berberis* were found in all other countries. Based on sequence analysis, diversity of *Berberis* forms two distinct phylogenetic groups, with *Berberis* from Argentina and Brazil differing from those in Ecuador. Analyses of *Berberis* samples from Chile and Uruguay are in progress, and we hypothesize that they will likely be related to countries from the Southern Cone. Preliminary analyses of rust aecial samples also indicate distinct grouping by region. However this may be an artifact of the small sample size. As this study continues over the next two years we may find some rust fungal species that are more widely dispersed and with wider host ranges.

[P75] Identification of strain-specific sequences in *Plasmodiophora brassicae*. M. D. HOLTZ, S. F. HWANG AND S. E. STRELKOV. *Alberta Agriculture and Forestry, Field Crop Development Centre, Lacombe, AB T4L 1W8, Canada; (S.F.H.)*

Alberta Agriculture and Forestry, Crop Development Centre North, Edmonton, AB T5Y 6H3, Canada; (S.E.S.) Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada.
Plasmodiophora brassicae Woronin is a serious pathogen of canola (*Brassica napus* L.) in western Canada. In recent years, new strains of *P. brassicae* have been identified that can overcome host resistance. To identify genomic loci that are unique to the different strains and develop strain-specific markers for identification purposes, a restriction site associated DNA sequencing data set of 10 million reads covering 21 *P. brassicae* isolates was filtered to exclude any sequences that aligned with the *P. brassicae*, *B. napus*, or *B. rapa* genomes. The remaining 910000 sequences were assembled into 2017 loci, filtered to remove any that belonged to other species, then filtered to exclude loci that were present in both isolates that can cause disease on resistant varieties and those unable to do so. After filtering 685 loci remained. Eleven PCR primers were designed for several of the remaining loci and primer specificity and sensitivity was evaluated on *P. brassicae*, host plants, non-infested soil, soil bacteria and fungi. The markers were able to distinguish isolates of the *P. brassicae* strains examined here with a sensitivity of 0.7 pg and did not produce the target amplicon in non-*P. brassicae* DNA samples. This shows that additional variation can be found in *P. brassicae* in regions that are not represented in the available genome sequence. The identification of loci in *P. brassicae* that appear to be strain-specific and markers developed from these loci will aid in the identification or monitoring of the pathogen.

[P76] Development of high resolution melting (HRM) and TaqMan assays for *Plasmodiophora brassicae* strain identification. M. D. HOLTZ, S. F. HWANG AND S. E. STRELKOV. *Alberta Agriculture and Forestry, Field Crop Development Centre, Lacombe, AB T4L 1W8, Canada; (S.F.H.) Alberta Agriculture and Forestry, Crop Development Centre North, Edmonton, AB T5Y 6H3, Canada; (S.E.S.) Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada.*
Clubroot, caused by *Plasmodiophora brassicae* Woronin, is a serious disease of canola (*Brassica napus* L.). In recent years, new pathotypes of *P. brassicae* have been identified that can overcome host resistance. Single nucleotide polymorphism (SNP) alleles specific to different strains of *P. brassicae* were identified from pathogen sequence information. These were used for the development of high resolution melting (HRM) and TaqMan assays. Forty-one primer pairs were designed to produce small amplicons including SNP sites for HRM analysis. These were then tested on multiple *P. brassicae* and *B. napus* samples. Of these, 23 amplified the product of the expected size in *P. brassicae* without non-specific amplification in *B. napus.* The resulting melt curves could be used to identify different strains of the pathogen. Two SNPs that were successfully characterized by HRM analysis were used as the basis of TaqMan assays. TaqMan allelic discrimination probes were designed for both the reference and alternate alleles at each SNP site. The sensitivity of the assays was tested on a dilution series of *P. brassicae* DNA and was determined to be 7 pg and 0.7 pg. The assays were determined to be specific to *P. brassicae* by testing on a series of host plants, non-infested soil, soil fungi and bacteria. Both the HRM and TaqMan assays described here allow for the rapid identification of *P. brassicae* samples.

[P77] CPS Student Competition. **Survey of *Pratylenchus neglectus* in Fields in Prairie Canada.** PRISCILLAR WENYIKA*, FERNANDA GOUVEA-PEREIRA, and MARIO TENUTA. *University of Manitoba, Department of Soil Science, Winnipeg, MB, R3T 2N2, Canada.*
Root lesion nematode species are among the most important plant parasitic nematodes of crops plants in Canada. Among the economically important species of this genus is *P. neglectus* (Rensch) filipjev et al. 1941 which shown in other countries to infest wheat, canola, chickpea and oat. In a survey for plant parasitic nematodes of fields sown to pulses that we conducted in 2014 and 2015, *Pratylenchus* occurred in 19% of the 93 fields sampled. The mean and maximum density of positive fields were mean of 1,170 and 3,552 for yellow pea and lentil, respectively. Maximum densities of 6,297 and 9,009 nematodes kg^{-1} soil were obtained for yellow pea and lentil fields, respectively. The mean densities are at or above that for which root lesion nematodes cause yield reductions of pulses and other field crops in other countries. Sequencing and species specific PCR analyses indicated the species of root lesion nematode to be *P. neglectus.* However, some sequencing results had low reliable matching to *P. neglectus*. The results indicate *P. neglectus* is widely distributed in fields in Prairie Canada. However, studies continue to resolve remaining

uncertainties such as the possible presence of other root lesion species, the preferred host(s) of *P. neglectus*, and yield loses caused.

[P78] Quantitative PCR analysis of *Fusarium* species dynamics in Fusarium head blight of oat and barley. M. BANIK, M. BEYENE AND X. WANG. *Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB, R6M 1Y5 Canada*
Fusarium head blight (FHB) is caused by a complex of *Fusarium* species in North America. *Fusarium graminearum* is the predominant species in wheat. *F. graminearum* produces several toxic secondary metabolites, among which deoxynivalenol (DON) and zearalenone (ZEN) are the most closely monitored due to their high detection rates and strong toxicity. The predominant *Fusarium* species in barley and oat are different than wheat. FHB in barley and oat was initially, primarily associated with *F. graminearum,* however, *F. poae* has become more frequently isolated in recent years. *F. poae* can produce a wide range of type A and B trichothecene mycotoxins as well as several non-trichothecene mycotoxins. In comparison to the abundant information that is available for *F. graminearum* and its mycotoxins, relatively little is known about *F. poae* and its impacts on the commercial production of oat and barley. We surveyed *Fusarium* species infecting oat and barley in Manitoba in 2016. Samples were collected from 90 commercial fields in Manitoba. *Fusarium* biomass in contaminated grains was assessed by real time qPCR using primer sets specific to *F. poae*, *F. graminearum* and *F. sporotrichioides.* The preliminary results indicate that *Fusarium* species infecting oat and barley are, in fact, more diverse than *Fusarium* species infecting wheat and mycotoxins other than DON need to be considered.

[P79] Isolation and Identification of *Dickeya solani* from Hyacinth Bulbs Imported from the Netherlands. X. LI, J. NIE, K. YUAN, H. XU, C. HUTTER, S. BRIÈRE, AND S.H. DE BOER. *Canadian Food Inspection Agency, Charlottetown Laboratory, 93 Mt. Edward Rd., Charlottetown, PE, C1A 5T1*
Dickeya and *Pectobacterium* have caused significant crop losses due to the emergence of new species/subspecies and the widespread of the pathogens which are highly virulent on a wide variety of hosts. In potatoes, *Dickeya* spp. and *Pectobacterium* spp. cause blackleg and soft rot diseases which have become increasingly problematic for potato production in some growing regions. While *Pectobacterium* spp. have been known as causal agents of these diseases in Canada and the US since pioneer days, potato blackleg-causing *D. dianthicola* was only discovered in the US in 2014. Blackleg outbreak caused by *D. dianthicola* have now been reported in more than 10 US states. Given the trend in the spread of *Dickeya* spp. (formerly *Erwinia chrysanthemi*) in European countries during the last 15 years, the US and Canada need to be alerted and technically prepared for possible introduction of the more aggressive variants of *Pectobacterium* and *Dickeya*, such as *D. solani*. Although it has never been detected in plants grown in Canada, *D. solani* was isolated, for the first time, from hyacinth bulbs imported from the Netherlands highlighting the potential pathway to North America. Genomic analysis using NGS technology revealed the high similarity between the hyacinth isolate and the type strain of *D. solani*, which is different from all other *Dickeya* and *Pectobacterium* species. This finding is congruent with the variations reported in pathogenicity and virulence in potato. The importation of infected hyacinth bulbs is probably an important pathway for *D. solani* to enter Canada and the US under current horticulture regulatory program.

[P80] CPS Student Competition. **Identification of *Fusarium* spp. and determination of chemotypes from bread and durum wheat samples collected during 2014 to 2016.** G. SINGH[1*], A. BROWN[2] AND H.R. KUTCHER[1]. [1]*Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada.* [2]*Saskatchewan Crop Insurance Corp, Melville, SK, Canada.*
This study determined the *Fusarium* spp., the chemotype diversity and the mycotoxins levels in wheat samples collected across Saskatchewan from 2014-2016. Quantitative real-time PCR assays were used to quantify DNA of five *Fusarium* spp.: *F. graminearum*, *F. culmorum*, *F. avenaceum*, *F. poae*, and *F. sporotrichioides* from 132 wheat samples. The primers and probes used were found to be specific and sensitive. *Fusarium graminearum* was the dominant species detected followed by *F. avenaceum* from qPCR and identification based on morphology. Multiplex PCR based on the TRI3 gene revealed the chemotypes 3-ADON and 15-ADON. The detection of the 3-ADON amplicon

among samples was more frequent than 15-ADON; no NIV amplicon was detected. Samples were tested for the presence of thirteen mycotoxins; five toxins were detected and quantified. The highest concentration was of DON, followed by 3-ADON, 15-ADON, T2 toxin and HT2 toxin. A weak correlation was detected between *F. graminearum* DNA and DON (R^2= 0.37, *P* = 0.0004), while the correlation between DNA of other *Fusarium* spp., mycotoxin levels and FDK was not significant.

[P81] Priming effects of virulent *Plasmodiophora brassicae* strains on clubroot disease development during primary infection. [1] J. JIANG, [2] R. FREDUA-AGYEMAN, [2] S.-F. HWANG AND [1] S. STRELKOV. *[1] Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada; and [2] Crop Diversification Center North, Alberta Agriculture and Forestry, Edmonton, AB, T5Y 6H3, Canada.*
Clubroot, caused by *Plasmodiophora brassicae* Woronin, causes significant economic losses to canola (*Brassica napus* L.) production worldwide. Infection by virulent strains of the pathogen is thought to compromise host defenses, which can prime the host for infection by avirulent strains. In this study, the effects of virulent *P. brassicae* populations on host defense were investigated using three pairs of virulent/avirulent strains (2x/2, 3x/3 and 5x/5) and three canola cultivars ('45H29', 'L135C' and 'L241C'). Seven-day-old seedlings were inoculated with low concentrations (10^3 spores/ml) of resting spores of the virulent strains followed by high concentrations (10^7 spores/ml) of resting spores of the avirulent strains. The positive control consisted of plants inoculated with low concentrations of the virulent strains followed by high concentrations of the virulent strains, while the negative controls consisted of plants inoculated only with low concentrations of the virulent strains or only high concentrations of the avirulent strains. Six weeks after inoculation, an index of disease (ID) was calculated. Disease severity was highest in the positive control (mean ID = 92%), followed by the virulent/avirulent inoculation treatments (mean ID = 37%), and the negative controls (inoculation with only low concentrations of the virulent strains, mean ID = 23%; or inoculation with only high concentrations of the avirulent strains, mean ID = 7%). Overall, priming effects were observed in seven of the nine (three virulent/avirulent *P. brassicae* pairs × three cultivars) treatments, suggesting that low concentrations of virulent *P. brassicae* strains compromised the host defense of the three cultivars.

[P82] Pathogenicity and plant defense response to a hypervirulent isolate of *Leptosphaeria maculans* induced by CRISPR/Cas system. Z. ZOU, F. LIU, C. SELIN, and W.G. DILANTHA FERNANDO. *Department of Plant Science, University of Manitoba, Winnipeg, MB, R3T 2N2 Canada*
Blackleg, is caused by the fungal pathogen *Leptosphaeria maculans*, which is the most important disease in canola (*Brassica napus*) fields worldwide. The clustered regularly interspaced short palindromic repeat (CRISPR)/CRISPR-associated (Cas) system has been widely used as an effective tool for genome editing. A hypervirulent isolate umavr7 was generated with a point mutation of the *L. maculans* isolate (UMAvr7) carrying only a single avirulence gene, *AvrLm7*. Pathogenicity tests indicated that the mutant isolate umavr7 can cause serious disease lesions on a set of *B. napus* differential lines which harbor different resistant (*R*) genes. Comparative pathogenicity test between UMAvr7 (wild type) and umavr7 mutant on the corresponding *B. napus* cultivar 01-23-2-1 (with *Rlm7*) showed that the umavr7 is a hypervirulent isolate. Mutant umavr7 produced large grey/green leaf lesions with which UMAvr7 isolate cannot cause such degree of disease symptoms. Gene expression pattern assay revealed that pathogenesis-related genes *PR4* and jasmonate-induced gene *PDF1.2* were significantly decreased from 7 dpi (days post inoculation) to 11 dpi in the resistant cultivar inoculated with the hypervirulent isolate. This result implies that *PR4* and *PDF1.2* may play important roles in plant defense against the hypervirulent isolate. The blackleg resistance was further evaluated on 123 *B. napus* genotypes by challenging to hypervirulent isolate, umavr7. Only six out of 123 genotypes showed resistance to the umavr7. Therefore, these six lines will be used for blackleg disease resistance breeding and novel *R* gene identification in future.

[P83] CPS Student Competition. **Telia production variability as a measure of sexual recombination in the *Puccinia striiformis* f. sp. *tritici* population of western Canada**. G.S. BRAR, K.LOU, S. ALI, AND H. R. KUTCHER. *Department of Plant Science/Crop Development Centre, University of Saskatchewan, Saskatoon, SK S7 N 5A8, Canada; and (S.A.)*

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Puccinia striiformis f.sp. *tritici* Westend./Eriks. (*Pst*) is regarded as a clonal pathogen in North America; however, it often rapidly overcomes host resistance genes, which may indicate sexual recombination. The alternate host allows the pathogen to complete sexual reproduction, which is responsible for allelic recombination and thus results in increased variation in *Pst* populations. In the evolutionary process, some sex-related structures in a sexually derived clonal population are expected to degenerate due to lack of fitness. Telia are sex-specific structures in the *Pst* lifecycle and the ability to produce telia may be an indication of sexual recombination in *Pst* populations. In the present study, we assessed telial production ability of 24 isolates from western Canada, which were randomly chosen from three genetic lineages identified using single nucleotide polymorphisms (SNPs). The isolates were inoculated on Avocet (susceptible to all known *Pst* races) at the seedling stage and telia ratings were performed weekly based on leaf area covered with telia up to seven weeks after inoculation. Area under the telia production curve (AUTPC) revealed differences among the three lineages. The AUTPC values for two lineages were not significantly different from each other, but a third lineage had higher AUTPC. These results indicate the isolates in the lineage with higher AUTPC might be recombinant and/or progeny of recombinant isolates. The Simple Sequence Repeat (SSR) marker data revealed the existence of PstS1 (MLG-99 and MLG- 99v), Old north-western European, and recombinant lineages in the population.

[P84] Interaction between spring wheat lines and deoxynivalenol (DON) chemotypes of *Fusarium graminearum*. K. HUDSON, M. SERAJAZARI, M. KAVIANI, AND A. NAVABI. *Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON N1G 2W1, Canada*.
Fusarium head blight (FHB), mainly caused by *Fusarium graminearum* in North America, not only reduces grain yield, but also produces trichothecene mycotoxins, such as deoxynivalenol (DON), in the grain. The DON-producing strains of *F. graminearum* are divided into 3-acetyl (3A) DON and 15-acetyl (15A) DON chemotypes. In this study, heads of ten different spring wheat genotypes, with different levels of resistance against FHB, were spray- or point-inoculated with ten different isolates of *F. graminearum* collected from different provinces of Canada, five of which bear the 3-ADON chemotype, and five bearing the 15-ADON chemotype. The number of infected spikelets was counted 5 days after spray-inoculation to evaluate Type I resistance (resistance to initial infection), and also 10 and 15 days after point-inoculation to evaluate Type II resistance (resistance to spread of infection within head). In both Type I and II resistance evaluations, there were significant differences among wheat genotypes and isolates. Even though the overall genotype by chemotype interaction was not significant, the susceptible cultivars responded differently to infection by different isolates of the pathogen, regardless of their chemotype. The lack of interaction mainly among resistant cultivars demonstrated the non-chemotype-specific behaviour of Type I and Type II resistance against FHB in wheat.

[P85] Study on *Verticillium longisporum* of Canola for the First Reported Farm in North America. A. AGARWAL, and M. TENUTA*. *Department of Soil Science, University of Manitoba, Winnipeg, MB, R3T2N, Canada.*
The soil-borne fungus, *Verticillium longisporum* (Stark) Karapapa et al. 1997, was first identified in North American on canola at a farm in Manitoba, Canada in 2014. *Verticillium longisporum* is a common pathogen of Brassica crops in Europe and causes Verticillium stripe in rapeseed/canola crops. Past research has established *V. longisporum* is a diploid hybrid of either two species of *V. dahliae* (parental lines D2 or D3) and also either of two other unknown species (A1 or D1). Since this is the first ever-documented case of this pathogen of canola in North America, very little is known about its ease of dispersal, spatial distribution within farms, virulence, and hybrid lineage. To help address those uncertainties, a research study was set out with objectives of: i) investigate the spatial variation of *V. longisporum* at the farm positive for the pathogen, and ii) determine the hybrid origin of *V. longisporum* isolates in Manitoba. The farm was segregated into 57 areas based on differences in management history (ex., crop sequence) from 2005 tp 2015 from field records and historical aerial images. In fall 2015, one to four composite soil samples was obtained from each area for a total of 194 samples. A real-time direct soil extraction PCR assay developed in our laboratory confirmed 132 of 194 samples were positive for the pathogen. The highest amount of the fungus

observed was 69.9 pg *V. longisporum* genomic DNA g^{-1} soil with mean across positive samples of 2.71 pg g^{-1} soil. Hybrid lineage determination of isolates from the farm indicate it to be that of V1D1; this is the most virulent line on canola. The results suggest the pathogen is easily dispersed on a farm and also the hybrid present for the first report farm in North America is the that which is most aggressive on canola.

[P86] Virulence of isolates of *Claviceps purpurea* on eight different genotypes of wheat. J.G. MENZIES, H.W. KLEIN-GEBBINCK, A. GORDON and D.M. O'SULLIVAN. *Agriculture and Agri-Food Canada, Morden Research and Development Centre, 101 Route 100, Morden, MB, R6M 1Y5, Canada, (H.W. K-G.) Agriculture and Agri-Food Canada, Beaverlodge Research and Development Centre, Beaverlodge, AB, T0H 0C0, Canada, (A.G) National Institute of Agricultural Botany, Huntingdon Road, Cambridge, CB3 0LE, United Kingdom, (D.M.O'S.) School of Agriculture, Policy and Development, University of Reading, Whiteknights, Reading, RG6 6AR, United Kingdom*
Ergot of cereals, caused by *Claviceps purpurea* (Fr.) Tul., results in yield loss and downgrading of infested grain because of toxic alkaloids in the sclerotia. Resistant wheat genotypes are known, but their effectiveness against different *C. purpurea* isolates has not been studied. The objective of this study was to examine the pathogenic variability among isolates of *C. purpurea* on wheat lines differing in resistance. Forty one single spore *C. purpurea* isolates were developed from western Canadian and United Kingdom collections and inoculated onto a set of wheat genotypes composed of durum wheat lines 'Melita', 'Kyle', and 9260B-173A, and hexaploid spring wheat lines 'Cadillac', 'Vista', 'Kenya Farmer', 'Lee' and HY630. Honeydew production and weight of sclerotia produced per spike were assessed. ANOVA indicated significant effects of the wheat lines, pathogen isolates and wheat line by pathogen isolate interactions for both honeydew and sclerotia weight production. This suggests a vertical resistance interaction (i.e. a gene for gene interaction). Correspondence analysis indicated the lowest honeydew and sclerotia weight production occurred on wheat line 9260B-173A, followed by 'Kenya Farmer'. Pathogen isolates from the United Kingdom produced more honeydew and greater sclerotia weight than isolates from Alberta, which produced more than isolates from Saskatchewan and Manitoba. Isolates obtained from rye crops produced more honeydew and greater sclerotia weight than those from other host crops, with isolates from barley producing the least. Variability in virulence exists in populations of *C. purpurea*, and knowledge of virulence phenotypes is necessary to effectively breed for resistant commercial lines.

[P87] Influence of cover crop residue management on the indigenous arbuscular mycorrhizal fungi, corn growth and yield. MASAO HIGO[A], RINA SASAKI[A], TAKAMITSU UNOKI[A], KENTO GUNJI[B], DAISUKE SUZUKI[B], KATSUNORI ISOBE[A].[A]*Department of Agricultural Bioscience, College of Bioresource Sciences, Nihon University, Kameino 1866, Fujisawa, Kanagawa 252-0880, Japan*. [B]*Graduate school of Bioresource Sciences, Nihon University, Kameino 1866, Fujisawa, Kanagawa 252-0880, Japan*. *Email for corresponding author: higo.masao@nihon-u.ac.jp*
Understanding better cover crop managements for arbuscular mycorrhizal fungi (AMF) in cropping systems can be important for rapid colonization, better crop growth, and nutrient uptake. However, there is little information regarding the impacts of incorporation and removal of cover crops in rotations on the diversity of AMF and subsequent crop performance. We investigated the impacts of incorporation and removal of cover crops on the AMF and corn growth and yield in a field trial. Four cover crop plots of hairy vetch, wheat, brown mustard and fallow in a rotation were established in the fall of 2015. A corn test crop was planted in early May 2016. The aboveground plant parts and roots of corn were sampled at V6, V10, and R1 stage. Our results showed that at any of the stage, the AMF root colonization and communities in the corn were significantly influenced by the incorporation and removal of cover crops. The introduction of hairy vetch regardless of residue management increased the corn growth at V6 compared to other plots. In the 1-year trial, the incorporation and removal of cover crops impacted the plant biomass and P uptake of corn at the V6 stage, whilst the AMF colonization and communities in the roots were not strongly related to the corn performance among cover crop species and residue management plots. A consecutive field trial will be needed to understand the benefit of AMF and the optimal residue management strategy on corn growth performance.

[P88] A potential biosensor for early detection of *Sclerotinia sclerotiorum* and *Leptosphaeria maculans* in canola

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A biosensor to detect *Sclerotinia sclerotiorum* ascospores and *Leptosphaeria maculans* pycnidiospores was designed and tested. The biosensor involves gold nanoparticles, a pathogen specific antibody, and a real-time cell electronic sensing (RT-CES) system to detect the impedance. Our results indicated that a linear relationship exists between the numbers of *S. sclerotiorum* ascospores and the impedance of their antibody-spore-gold nanoparticle complex. These signals can be easily processed electronically and converted to rapidly distributable results. Our biosensor also demonstrated an incredibly sensitive threshold of detection of 5 ascospores of *S. sclerotiorum* in the sample. A linear relationship was also obtained when *L. maculans* was used as a pathogen, indicating that the future device could be species-specific and applied to more plant disease pathogens. Based on this study, our biosensor provides a promising and useful tool for plant disease detection in the field.