34th Annual Plant Sciences Graduate Student Symposium

A Part of the DuPont Plant Sciences Symposia Series

Cultivating the Field of Big Data

Plant Science
Graduate Students Association

University of Manitoba
March 16-17, 2018

University of Manitoba

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DuPont Plant Sciences Symposia Series

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REACHING THE NEXT GENERATION OF PLANT SCIENTISTS SINCE 2008

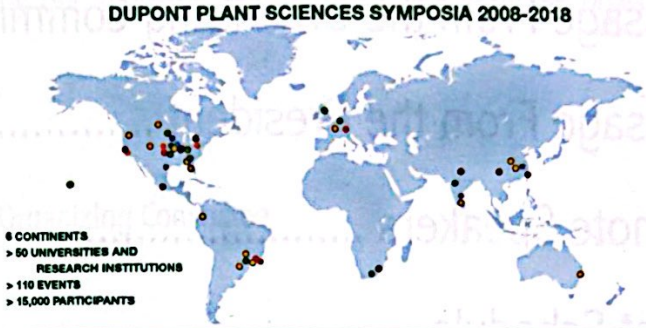
What is the DuPont Plant Sciences Symposia Series?

- The series is an opportunity for the next generation of scientists to interact with both public and private experts through student driven and organized events at different academic institutions worldwide.
- The day long events may include presentations by leading scientists, student presentations, poster sessions, round table discussions and networking opportunities.
- Symposia events are free and accessible to the general public and often offered via webinar.

How does it work?

Graduate students direct the content and organize the symposia on a fixed budget with support from the University and Departments. DuPont Pioneer provides funding.

DUPONT PLANT SCIENCES SYMPOSIA 2008-2018



YEAR JOINED THE NETWORK

- 2008: University of Minnesota
- 2011: University of Wisconsin-Madison
- 2012: Cornell University; University of California-Davis; University of Nebraska-Lincoln
- 2013: University of Hohenheim; Kansas State University; Federal University of Lavras; Federal University of Viçosa
- 2014: Iowa State University; Punjab Agricultural University; University of Pretoria; Wageningen University
- 2015: Henan Agricultural University; Professor Jayashankar Telangana State Agricultural University; Texas A&M University
- 2016: CIMMYT; Purdue University; Shandong Agricultural University; University of California-Berkeley
- University of Illinois Urbana-Champaign; University of Guelph; North-West University (South Africa); Indian Agricultural Research Institute; Sichuan Agricultural University; University of Minnesota, Production Agriculture
- 2017: Colorado State University; University of Missouri; University of Georgia; Washington State University; University of Florida; University Paris Saclay/AgroParisTech; University of Queensland; Northwest A&F University, Xianyang
- CIAT, Colombia; Huazhong Agricultural University, Wuhan; University of Saskatchewan; University of Hyderabad, India; Brazilian Congress of Plant Breeding; University of Brasilia; University of Sao Paulo, Piracicaba; Americas Society of Agronomy Meetings; University of Queensland/Yanping Meeting
- 2018: SICAN Meeting, Danforth Center; University of Hawaii; University of Manitoba; State University of Norte Fluminense, Brazil; Clemson University; University of Edinburgh; The Ohio State University

Want to get involved?

For more information on the series or to explore other opportunities of collaboration with DuPont Pioneer at your University contact Tahsin.Abadir@pioneer.com or https://www.pioneer.com/home/site/about/careers/students-events/

Vision and Goals of the Series

At DuPont Pioneer, we believe the next generation of scientists will play a pivotal role in meeting the food and energy needs of the world. Working with students to facilitate a science-based forum such as the DuPont Plant Sciences Symposia:

- enhances discussion amongst the academic community and the private sector
- builds key organizational and management skills in future plant scientists, and
- exposes students to career opportunities in agriculture

DUPONT. PIONEER.

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34th Annual
Plant Sciences Graduate Student Symposium
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Message From the Organizing Committee

On behalf of the University of Manitoba Plant Science Graduate Students Association it is our pleasure to welcome you to the 34th Annual Plant Sciences Graduate Student Symposium. Since its inception in 1984, this symposium has been an opportunity for Plant Science Graduate Students to network, collaborate, and proudly share their research.

Within the field of plant science, our ability to make advances is increasingly dependent on the use of large, highly complex data sets. This year's theme "Cultivating the Field of Big Data" aims to reflect the importance of making use of all the opportunities big data provides.

We hope that this symposium acts as a springboard for collaboration, innovation and learning for all attendees. Please take the time to recognize the support provided by our sponsors, and the effort put in by the organizing committee.

Best wishes,

34th Annual Plant Sciences Graduate Student Symposium Organizing Committee

Anjan Neupane, President, Symposium Coordinator
Ashley Ammeter, Vice President Internal, Registration and Communications
Jon Rosset, Vice President External, Speaker Coordination
Yang Lin, Treasurer, Fundraising
Daniel Chan, GSA Representative, Website Design
Deanna McLennan, Social Director, Event Management
Additional Support From: Kenny So, Harunur Rashid, M M Uzzal Ahmed Liton, Mourita Tabasum,Parneet Kaur Toora, Pawanpuneet Rehal, Rupinder Kaur, Keval Shah, Jia Sun, Bruce Pei, Leanne Koroscil, April Stainsby, Younyoung Lee

Message From the President

I am pleased to welcome each of you to the 34th annual Plant Science Graduate Student Symposium at the University of Manitoba. Research-intensive universities, such as the ones that we all represent, drive the innovation that keeps our economies competitive, and develop industry, government and community leaders.

As you explore topics in plant pathology, physiology, breeding and agronomy, I invite you to consider one of the strategic research themes of the University of Manitoba –*Safe, Healthy, Just and Sustainable Food Systems.* We believe that effective local and global food systems must yield safe, nutritious, culturally-appropriate and affordable food for all. Together, we can address the health of our agricultural and other ecosystems, minimize negative impacts on the environment and contribute to developing strong communities and economies.

Part of innovative research is collaboration, and this symposium reinforces and promotes the importance of sharing and networking. I encourage each of you to take this opportunity to connect with colleagues and friends, to learn and to grow. Best wishes on a productive and enjoyable symposium.

David T. Barnard, Ph.D.
President and Vice-Chancellor
University of Manitoba

Keynote Speakers

Dr. Brent McCallum

Research Scientist, Science and Technology Branch, Agriculture and Agri-Food Canada

Dr. Brent McCallum grew up in the St. Vital neighbourhood in Winnipeg. He received his Bachelor of Science in Agriculture from the University of Manitoba in 1998, and his M.Sc. from the Department of Plant Science in 1991. He received his Ph.D. in 1995 from the University of Minnesota. Throughout his graduate training Dr. McCallum studied various diseases of wheat. From 1996-1998 he did a post-doc on Fusarium Head Blight disease of cereals. In 1998 he was hired as a Research Scientist at the Cereal Research Centre on the U of M campus. He has researched various aspects of cereal diseases, primarily rust, Fusarium Head Blight and tan spot. He collaborated with plant breeders to develop many of the current cultivars of wheat and has been a member, secretary and chair of the Disease Evaluation Team for the Wheat, Rye and Triticale recommending committee.

Dr. Maria Trainer

Managing Director, Science and Regulatory Affairs, Chemistry, Croplife Canada

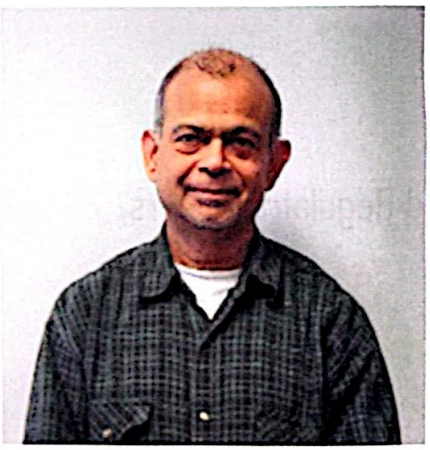
Dr. Maria Trainer holds a Ph.D. in Bacterial Molecular Genetics from the University of Waterloo; an M.Sc Biochemistry from Washington State University; and B.Sc. degrees in Microbiology and Molecular Biolog Biochemistry from the University of Idaho. Maria Trainer joined CropLife Canada in April 2012 and prov technical expertise on a broad range of science and regulatory priorities related to pesticides, which is one o main business lines at CropLife Canada. Maria is passionate about environmental issues and sustai agricultural development. She is a strong advocate for science-based regulation and enjoys explainin importance of using an evidence-based approach to navigate hot-button science issues. In her free time, Mar usually be found doing something active, preferably outside and usually involving a bike or a pair of hiking bo

Keynote Speakers

Dr. Rob Gulden

Associate Professor, Department of Plant Science,
University of Manitoba

Dr. Rob Gulden joined the Department of Plant Science as a faculty member in 2007, after working as a post-doc in corn-soybean systems at the University of Guelph. He received his Ph.D from the University of Saskatchewan studying volunteer canola and his M.Sc. from the University of Manitoba studying nitrogen fixation. His research specializes in weed and crop ecology and weed and crop management to develop crop protection systems that minimize the effect of weeds on crop production while reducing the reliance on pesticides. He has over 20 years experience working in weed research and his expertise ranges from plant ecology through agronomy to molecular biology and biostatistics.



Dr. Jay (Jayantilal) D. Patel

Plant Breeding, Quantitative Genetics, DuPont Pioneer
Canada

Dr. Jay Patel finished his Ph.D. in India in 1982 and started as a Post-Doctoral Fellow in the Crop Science Department at the University of Guelph in 1983. Dr. Patel was hired as canola breeder at the Georgetown Research Center of Pioneer Hi-Bred in 1986. He ran a very successful canola breeding program and developed and registered 70 new canola varieties and hybrids for the Western Canadian canola growing areas, most of them having either IMI or Roundup herbicide resistance. Under his leadership, 34 new canola varieties and hybrids were developed and commercialized in Australia. Dr. Patel is leading DuPont Pioneer's North American and Asia Pacific canola breeding effort supervising and mentoring eight canola breeders in Canada, Australia, and India.

Dr. Mark Belmonte

Associate Professor, Department of Biological Sciences,
University of Manitoba

For 15 years Professor Mark Belmonte has contributed to the field of plant biotechnology and food security where his work holds the promise of solving world food shortages while significantly bolstering Canada's agricultural economy. With an admirable scholarly record of over 50 peer reviewed journal articles, 6 invited review articles, 3 book chapters, and 2 patents, Dr. Belmonte has been invited to present his research over 60 times at regional, national, and international meetings and institutions and is a recognized international leader in his field. Many of the journals where he has published have high impact factors including Proceedings of the National Academy of Sciences (PNAS), The Plant Cell, and Plant Journal. Dr. Belmonte has been recognized for his innovative research contributions using cutting-edge next generation molecular and plant laser microdissection techniques by the University of Manitoba, the CBC, and the Rh Institute Foundation.

Friday, March 16th

9:00-9:30 am	**Registration and Refreshments** Atrium of Agriculture Building
9:30-9:40 am	**Opening Remarks: Dr. Martin Scanlon** Room 138 Agriculture Building
9:40 – 9:50 am	**Opening Remarks: DuPont Pioneer** Room 138 Agriculture Building
10:00-11:00 am	**Keynote Speaker: Dr. Brent McCallum** *Progress on Disease Resistance in Canadian Wheat* Room 138 Agriculture Building
11:00-11:30 am	**Keynote Speaker: Dr. Maria Trainer** *Helping Canada Grow: The Value of Plant Science Innovations to Canadians* Room 138 Agriculture Building
11:45- 1:00 pm	**Lunch** Atrium of Agriculture Building
1:00-2:00 pm	**Keynote Speaker: Dr. Robert Gulden** *TBA* Room 130 Agriculture Building
2:45 – 4:15 pm	**Tour: Manitoba Museum** 190 Rupert Avenue
6:30-9:30 pm	**Social Mixer** Barley Brothers, 2005 Pembina Hwy

Saturday, March 17th

8:00 – 9:00 am	**Breakfast** Atrium of Agriculture Building
9:00-10:00 am	**Keynote Speaker: Dr. Jay Patel** *Big Data in Plant Breeding Research – The Things You Need To Know* Room 130 Agriculture Building
10:00-10:30 am	**Refreshment Break** Atrium of Agriculture Building
10:30-11:30 am	**Keynote Speaker: Dr. Mark Belmonte** *Protecting Canada's Crops Using RNAi Technology* Room 130 Agriculture Building
11:30- 12:30 pm	**Lunch** Atrium of Agriculture Building
12:15-2:00 pm	**Session 1: Agronomy and Weed Science Student Presentations** Room 218 Plant Science Building
12:30-2:00 pm	**Session 1: Research Proposal Student Presentations** Room 138 Agriculture Building
12:30 – 2:00 pm	**Session 1: Plant Breeding and Genetics Student Presentations** Room 130 Agriculture Building
2:00-2:15 pm	**Refreshment Break** Atrium of Agriculture Building
2:15-4:30 pm	**Session 2: Plant Pathology Student Presentations** Room 218 Plant Science Building
2:15 – 3:15 pm	**Session 2: Research Proposal Student Presentations** Room 138 Agriculture Building
2:15 – 4:00 pm	**Session 2: Plant Breeding and Genetics Student Presentations** Room 130 Agriculture Building
6:00 – 10:00 pm	**Banquet** Ambassador A Room, Canad Inns Hotel, 1824 Pembina Hwy
6:00 pm	**Cocktails**
6:30 pm	**Dinner**
7:30 pm	**Banquet Address** Dr. Fouad Daayf, Department Head **Presentation of Awards**

Session 1

Agronomy and Weed Science

Room 218 • Chair: April Stainsby
Judges: Dr. Doug Cattani, Dr. Don Flaten, Ms. Kristen MacMillan

12:15 pm	**Jonathan D. Rosset**	*University of Manitoba*
	Cultural weed control in soybean: Does it matter?	
12:30 pm	**Leila N. Kamino**	*University of Manitoba*
	Response of the soil microbial community to crops and weediness levels from a long term field experiment	
12:45 pm	**Nathan Hans Haugrud**	*North Dakota State University*
	Delayed cultivation to supplement chloroacetamide herbicides in sugarbeet	
1:00 pm	**Nickolas Theisen**	*North Dakota State University*
	Hop (*Humulus lupulus*) a potential specialty crop in the Upper Midwestern United States	
1:15 pm	**Supun Fernando**	*North Dakota State University*
	Effects of pretreatments on separating the seed coat from the cotyledon of black beans	
1:30 pm	**Leanne Koroscil**	*University of Manitoba*
	Exploring the relationship between The Law of Constant Final Yield and field bean (*Phaseolus vulgaris*) production in Manitoba	
1:45 pm	**Sergio Fabian Cabello Leiva**	*North Dakota State University*
	Cover crops decreased soil nitrogen (N-NO3) previous sugarbeet production in the Northern Great Plains	

Research Proposals

Room 138 • Chair: Deanna McLennan
Judges: Dr. Martin Entz, Dr. Atta Soliman, Dr. Mohamed Elhiti

12:30 pm	**Adebimpe Oyeneye**	*University of Saskatchewan*
	Creation of Alpha-glycerylphosphorylcholine from wheat ethanol production	
12:45 pm	**Ramandeep Kaur Bamrah**	*University of Saskatchewan*
	Evaluation of X-ray fluorescence spectroscopy for quantification of minerals in pea seeds	

1:00 pm	**Edgar Escobar**	*North Dakota State University*
	Genetic improvement of dry bean (*Phaseolus Vulgaris* L.) for resistance to while mold (*Sclerotinia sclerotiorum* Lib de Bary) using a MAGIC population	
1:15 pm	**M M Uzzal Ahmed Liton**	*University of Manitoba*
	Genetic and transcriptomic analysis of pre-harvest sprouting in a mapping population of wheat	
1:30 pm	**Sarah Allen**	*University of Manitoba*
	Understanding the response of field populations of *Fusarium graminearum* to fungicide application in Manitoba	
1:45 pm	**Preeni Kaur Bawa**	*University of Saskatchewan*
	Identification of Candidate genes for resistance against race 0 of *Colletotrichum lentis* in *Lens ervoides*	

Plant Breeding and Genetics

Room 130 • Chair: Ashley Ammeter
Judges: Dr. Anita Brûlé-Babel, Dr. Rhodesia Celoy, Dr. Genyi Li

12:30 pm	**Keval Shah**	*University of Manitoba*
	Introgression of blackleg resistant gene from hexaploid lines and *B. juncea* to *B. napus*	
12:45 pm	**Kevin Falk**	*Iowa State University*
	Exploring the diversity of root system architecture in soybean using plant phenomics	
1:00 pm	**Anjan Neupane**	*University of Manitoba*
	Identification of QTL associated with Fusarium head blight disease resistance in winter wheat	
1:15 pm	**Valeria Lobos Sujo**	*University of Manitoba*
	Development of *Brassica napus* L. *Ogu*-INRA cms restorers using recurrent full-sib selection	
1:30 pm	**Jayanta Roy**	*North Dakota State University*
	Association mapping for Sclerotinia stem rot disease in *Brassica napus*	
1:45 pm	**Cunchun Yang**	*University of Manitoba*
	The regulation of intrinsic signalling in *Brassica napus* defending against *Leptosphaeria maculans*	

Session 2

Plant Pathology

Room 218 • Chair: Win Jian (Daniel) Chan
Judges: Dr. Dilantha Fernando, Dr. Carrie Selin, Dr. Mario Tenuta

2:15 pm	**James R. Tucker**	*University of Manitoba*
	RNA-sequencing analysis of resistance to deoxynivalenol accumulation in Two-row malting barley 'Norman' infected by multiple chemotypes of *Fusarium graminearum*	
2:30 pm	**Rebecca Spanner**	*North Dakota State University*
	A genome wide association study to identify mutations associated with DMI fungicide resistance in *Cercospora beticola*	
2:45 pm	**Shaun James Clare**	*North Dakota State University*
	Pyrenophora teres f. *maculata* effector gene identification using genetic mapping and whole genome sequencing	
3:00 pm	**Cecilia Monclova Santana**	*North Dakota State University*
	Population structure of the dry bean rust pathogen *Uromyces appendiculatus* in North Dakota	
3:15 pm	**Rasanie Padmathilake**	*University of Manitoba*
	Is *glutathione-S-transferase 6* involved in canola defense against *Leptosphaeria maculans*?	
3:30 pm	**Harunur Rashid**	*University of Manitoba*
	Effect of *Brassica napus-Leptosphaeria maculans* interaction in the emergence of virulent isolates of *L. Maculans*, a causal agent of blackleg disease in canola	
3:45 pm	**Keiko Nabetani**	*University of Saskatchewan*
	Mitigation of stripe rust and leaf spot diseases in winter wheat in western Canada	
4:00 pm	**Xiaohan Zhu**	*University of Manitoba*
	Investigation of *Verticillium dahliae* gene activity during potato invasion	
4:15 pm	**Nick Wytinck**	*University of Manitoba*
	RNA interference as a molecular fungicide targeting necrotrophic fungal pathogens *Sclerotinia sclerotiorum* and *Botrytis cinerea*.	

Research Proposals

Room 138 • Chair: Deanna McLennan
Judges: Dr. Martin Entz, Dr. Atta Soliman, Dr. Mohamed Elhiti

2:15 pm	**Amy Mangin**	*University of Manitoba*
	Agronomic practices to minimize lodging stress while maintaining yield potential in spring wheat	
2:30 pm	**Surendra Bhattarai**	*University of Saskatchewan*
	Study on salt tolerance of alfalfa (*Medicago sativa* L.) using synchrotron and transcriptome approaches	
2:45 pm	**Felicity Merritt**	*North Dakota State University*
	Identification of genes involved in sugar-end disorder in tetraploid potato (*Solanum tuberosum* L.)	
3:00 pm	**Manpreet Kaur**	*University of Saskatchewan*
	To determine the effect of univalent at meiosis on recombination in wheat	

Plant Breeding and Genetics

Room 130 • Chair: Ashley Ammeter
Judges: Dr. Anita Brûlé-Babel, Dr. Rhodesia Celoy, Dr. Genyi Li

2:15 pm	**Raju Chaudhary**	*University of Saskatchewan*
	Exploration of genetic diversity in *Camelina* wild relatives	
2:30 pm	**Elena Benic**	*University of Saskatchewan*
	Chloroplast ultrastructure and thylakoid architecture affects photosynthetic performance in *Amaranthus* spp.	
2:45 pm	**Bruce Pei**	*University of Manitoba*
	Genetic mapping of leaf rust resistance in the tetraploid wheat cross Strongfield/Blackbird	
3:00 pm	**Kenny So**	*University of Manitoba*
	Development of canola with unique meal protein profiles	
3:15 pm	**Dilanganie Dissanayaka**	*University of Saskatchewan*
	Genome wide association study of field pea for Fe, Zn, and Se concentration	
3:30 pm	**Yang Lin**	*University of Manitoba*
	QTL mapping of Fusarium head blight resistance in one elite winter wheat doubled haploid population	
3:45 pm	**Endale Tafesse**	*University of Saskatchewan*
	Leaf pigments and wax as heat tolerant traits, and their association with vegetation indices in pea	

Agronomy and Weed Science

Cultural Weed Control in Soybean: Does it Matter?

Jonathan D. Rosset* and Robert H. Gulden
Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada.
*Correspondence/Presenting Author: umrosse2@myumanitoba.ca

At the northern fringes of the North American soybean (*Glycine max* (L.) Merr.) growing region lies the Canadian Prairies. Short-season soybean variety development has enabled producers in the eastern prairies to eagerly adopt the crop for primary grain production. During the last decade, the prairie region has seen over a six-fold increase in soybean production area. Current production recommendations have largely been appropriated from the warmer, long-season soybean growing regions of North America. Soybean production in these long-season areas have contributed to the selection of many 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. Cultural weed management tools used to interfere with weeds and reduce selection pressure for HR weed biotypes include narrow row widths, high population densities, and competitive cultivars. This study evaluated the influence of row width (19 cm vs. 76 cm), population density (0.75, 1, and 1.5 times a 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 choosing 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.

Response of the soil microbial community to crops and weediness levels from a long term field experiment

Leila N. Kamino[1]* and Robert H. Gulden[1]
[1]Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada.
*Correspondence/Presenting Author: kaminoln@myumanitoba.ca

Plant species and community composition in addition to edaphic factors are great driving forces on microbial community structure and function. This is because plants are the primary providers of specific carbon and energy sources through exudates and litter which are readily available to soil microbes for mineralization. Modern agroecosystems are largely characterized by monoculture with weeds species being the source of aboveground plant diversity. There is a lack of information on how crops grown in rotation and with different weed densities influence soil microbial communities. The objectives of this study were to determine how different crops grown in rotation and weediness levels influence soil microbial communities over time. Research was initiated in a long term fully phased field study at the Ian N. Morrison Research Farm located in Carman, Manitoba. The study consists of an annual crop rotation, with three levels of selective in-crop herbicide applications and two controls (fallow and prairie) arranged as a RCBD with three replicates. A total of 27 phyla groups were detected in all the bulk soils by illumina sequencing with *Proteobacteria* and *Acidobacteria* being the most dominant groups. Crop species and weediness levels influenced the bacterial community of the bulk soil over time. Both fallow and prairie clustered differently from each other and also from all other crop treatments on the PCA ordination plots at most sampling dates. Weediness level was important at shaping the bacterial community in most treatments which shifted with sampling date, but its effect was more profound in wheat treatments. The results indicate that aboveground plant species greatly influence the composition of soil microbial communities. Knowledge of relationship between plant diversity and soil microbial communities is essential to understanding the links between aboveground and belowground communities and modulation of ecosystem functioning.

Delayed Cultivation to Supplement Chloroacetamide Herbicides in Sugarbeet

Nathan H. Haugrud[1]* and Thomas J. Peters[1]
[1]North Dakota State University, Fargo, ND
*Correspondence/Presenting Author: nathan.haugrud@ndsu.edu

The increased prevalence of glyphosate-resistant weeds in the upper Midwest has made weed management increasingly difficult for sugarbeet producers. Glyphosate-resistant weeds, particularly waterhemp (*Amaranthus tuberculatus*), has become an important challenge affecting sugarbeet production in eastern North Dakota and Minnesota, leaving producers with limited weed control options. The use of soil residual chloroacetamide herbicides has dramatically increased in response to this issue. Chloroacetamides are soil-applied and provide residual control of emerging weeds. Producers have also used inter-row cultivation in

efforts to manage weeds that escape herbicide application. There is a lack of published research on the use of cultivation in a sugar beet system using chloroacetamide herbicides and producers have concerns about effects of cultivation on chloroacetamide efficacy after the herbicide is activated in soil solution. Field experiments were conducted in two locations, Wheaton, MN and Renville, MN in 2017 to evaluate the effect of cultivation on chloroacetamide activity and weed escapes. Herbicides were applied to sugarbeet at the four-leaf stage followed by cultivation approximately 2 weeks later. Percent visual control (VC) and percent visual new emergence control (VNEC) were evaluated 14, 28, and 42 days after cultivation. The number of waterhemp plants per plot were also counted. Cultivated treatments had better overall control compared to non-cultivated treatments and cultivation did not have a negative effect on herbicidal activity. Average number of waterhemp plants per plot 42 days after cultivation was 10 and 22 in the cultivated and non-cultivated plots, respectively. The effects of cultivation and herbicide were non-significant for VNEC. However, for VC, the effect of cultivation and herbicide were both significant. VC 42 days after cultivation was 86% and 65% for the cultivated and non-cultivated plots, respectively. Cultivation appears to be a valid rescue treatment with no apparent negative effects in sugarbeet fields infested with herbicide-resistant weeds.

Hop (*Humulus lupulus* L.) a Potential Specialty Crop in the Upper Midwestern United States

N. Theisen[1]* and H. Hatterman-Valenti[1]
[1]Department of Plant Sciences, North Dakota State University, Fargo, ND United States
*Correspondence/Presenting Author: Nickolas.theisen@ndus.edu

Hop (*Humulus lupulus* L.) a herbaceous perennial, is a high value crop critical in beer production. Interest to grow hop as niche local market crop has become increasingly popular in areas not known for the crop's culture, such as North Dakota. Little research on hop growth and production techniques in the United States have been conducted outside the Pacific Northwest. Therefore, it is critical to evaluate cultivar performance to establish a foundation for research and production in these non-traditional areas. A field experiment was conducted in 2017 at the NDSU Horticulture Research site near Absaraka, ND to evaluate the growth and yield characteristics of twelve commercial hop cultivars in response to varied trained densities. Plants were trained under 2, 4, or 8 bines per plant on a standard hop trellis system. Plant height, cone moisture, and yield were taken prior and after mechanical harvest. Cultivars 'Nugget' and 'Cascade' were the highest performing cultivars whereas, 'New Brundswick' and 'Spalt Select' performed lowest in the trail. Initial results show promising potential for Hop as a specialty crop in North Dakota, but further data needs to be collected as the crop matures in subsequent years.

Effects of pretreatments on separating the seed coat from the cotyledon of black bean

Supun Fernando[1] *, Frank Manthey[1], Clifford Hall[1]
[1]North Dakota State University, Fargo, ND, U.S.A
*Correspondence/Presenting Author: supun.fernando@ndsu.edu

Globally, dry beans (*Phaseolus vulgaris* L.) are important staple food in human nutrition. Removing seed coat without negative effects on chemical and functional properties of black bean flour is important for the food applications since it can reduce the antinutrients and increase the protein availability. The objective of this study was to evaluate the effect of pretreatments on seed coat removal from black bean with minimal changes of physical, chemical and functional properties. Black beans were cooked in boiling water for 5, 10, and 20 min or were tempered to 10, 20, 30, 40 and 50% moisture. Then all samples were dried to the original moisture content at ambient air conditions or in a forced air oven at 90°C. Seed coat was removed from treated black beans by milled on a burr mill. Seed coat was separated from cotyledon by aspiration. Physical seed properties, color, ash, moisture, protein, total starch, starch damage, lipid and pasting properties were determined. Seed coat yield was significantly greater from seeds that were tempered (30, 40, or 50% moisture) and dried at 90°C than from boiled seeds that were dried at 90°C. Cooking followed by drying of the seeds significantly affected the physical seed properties, starch damage, ash content and pasting properties of the flours. Tempered-dried pretreatments had little or no effect on physical seed properties, starch damage, ash content and pasting properties of the flours. These results indicate that tempering black bean seeds to 30, 40, or 50% moisture and drying at 90°C can generate the cleanest and greatest seed coat yield with little or no effect on chemical and functional properties of flour.

Exploring the Relationship Between The Law of Constant Final Yield and Field Bean (*Phaseolus vulgaris*) Production in Manitoba

L. Koroscil[1]* and R. Gulden[1]
[1]Department of Plant Science, University of Manitoba, Winnipeg, Canada
*Correspondence/Presenting Author: korosci3@myumanitoba.ca

Research has shown that row spacing and plant density have positive influences on weed control and management, yet local and current research is scarce a outdated. As one of the provinces with the most field bean (*Phaseolus vulgaris*) acreage across the country, Manitoba would benefit from recent and releva local research to optimize yields and control weed populations using plant spatial arrangement and weed management techniques. The Law of Constant Fir Yield states that plant biomass increases in proportion to plant density, then plateaus and remains constant after a certain density. Recent research in fie beans by Laura Schmidt (unpublished) has shown that as planting row width decreases, the field bean yield-density relationship increasingly does not conform the Law of Constant Final Yield. The objectives of this research are to explore the underlying reasons behind these observations.

Cover crops decreased soil nitrogen (N-NO3) previous sugarbeet production in the Northern Great Plains

S. Cabello-Leiva[1*], M. Berti[2]
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Sugarbeet (*Beta vulgaris* L.) is valuable crop in North Dakota, but it leaves the soil uncovered after harvest decreasing soil health. The lack soil coverage during the winter increases soil losses due to wind erosion. In addition to that, high levels of residual deep nitrogen after cereal production can decrease sugar yield in sugarbeet. Cover crops provide soil coverage, preventing soil erosion, and reducing NO_3-N leaching. The experiment was conducted at two locations, Prosper and Hickson at ND, from April to November of 2017. The experimental design used was a RCBD with four replicates. The cover crops were radish (*Raphanus sativus* L.), winter camelina [(*Camelina sativa* (L.) Crantz.], winter wheat (*Triticum aestivum* L.), oat (*Avena sativa* L.), winter rye (*Secale cereale* L.) and a check plot (without cover crop), established into spring wheat residue in August. Biomass production across locations was 2.2 Mg ha^{-1} in both radish and oat. Soil cover in oat and radish was 70% while in rye was only 57%, providing an important soil protection form wind. Nitrogen, P, and total ash content were significantly higher in oat and radish than in rye biomass. Soil NO_3-N, after growing season, was significantly higher in the check plots (25.9 kg ha^{-1}) than in plots with a cover crop; oat (12.3 kg ha^{-1}), winter rye (13.2 kg ha^{-1}) and radish (16 kg ha^{-1}).This indicates cover crops are scavenging residual NO_3-N and keeping it in their biomass, preventing it from potential leaching and run-off. In conclusion, radish, winter rye, and oat provided soil cover protecting the soil from erosion and reduced soil residual NO_3-N prone to leaching.

Research Proposal

Creation of Alpha-Glycerylphosphorylcholine from Wheat Ethanol Production

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A dynamic system that favours the utilization of all grades of wheat produced would not only ensure sustainability of the industry but would also increase revenue generation. Bioethanol industry can utilize all market grades of wheat to produce renewable energy while simultaneously feeding animals with ethanol by products; thin stillage and wet grains. Similarly, valuable chemical coproducts can be recovered from this process, some of which includes acetic acid, 1, 3 propanediol, and α-glycerylphosphorylcholine (Alpha-GPC). Alpha-GPC rarely occurs naturally, but this compound is highly beneficial because of its potential application in medicine. It has been used for psychiatric and neurological disorders of the human brain such as; Alzheimer's disease, bipolar affective disorder, and schizophrenia. Alpha-GPC production from wheat ethanol production could be a product of wheat choline catabolism by yeast's phospholipase. Production and recovery of Alpha-GPC from ethanol production was carried out with three commonly cultivated wheat market classes. Cultivars from Canadian Western Red Spring (CWRS), Canadian Prairie Spring Red (CPSR), and Canadian Western Soft White Spring (CWSWS) were analysed to determine if their varied composition affected Alpha-GPC production. Quantitative NMR analysis was performed at 24, 48, and 72 hours of fermentation, and α-GPC concentrations increased over time. Efficient production and recovery of this compound would not only increase revenue generated from the ethanol industry, as the value of α-GPC as a nutraceutical is currently weighted at about a dollar per milligram, but it would sustain Canadian wheat production.

Evaluation of X-ray fluorescence spectroscopy for Quantification of Minerals in Pea Seeds.

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Breeding pulse crops with enhanced nutritional profile is important for marketing premium quality grain, processed foods. Current methods for quantifying mineral concentration in seeds are time consuming, expensive, involve hazardous chemicals and are relatively low throughput, therefore, there is need for the development of new and effective methods for mineral analysis. We are developing a standard protocol for rapid analysis of minerals including Fe, Zn, K, and Se in pea seed flour using synchrotron-based X-ray fluorescence spectroscopy (XRF). A wide diversity of pea genotypes has been analyzed with X-ray fluorescence spectroscopy and results were compared with data arising from the standard Atomic Absorption Spectroscopy method (AAS). 13 mm diameter pellets from 120 pea seed samples were scanned to collect 13 different spectra from each pellet and the XRF concentration values were correlated to AAS values. The technique will further be validated on another set of 120 pea seed samples.

Genetic Improvement of Dry Bean (*Phaseolus vulgaris* L.) for Resistance to White Mold (*Sclerotinia sclerotiorum* Lib de Bary) Using a MAGIC Population

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Dry Bean is one of the most important and ancient crops cultivated around the world. Its importance lies on the amount of protein, vitamins and minerals it provides to human diets. White mold, a fungal disease caused by *Sclerotinia sclerotiorum* Lib de Bary, is considered as one of the most important diseases for dry bean in U.S.A. and can cause seed yield losses up to 100%. Chemical control is a recommended practice to control white mold. However, disadvantages of chemical control includes high costs, environmental pollution, and variable fungicide efficacy. Therefore, the existence of genetic resistance within dry bean varieties is the most adequate option to overcome the disease. The objectives of this research are to identify white mold resistant lines with good agronomic performance and second to identify new or previously reported genomic regions associated with white mold resistance and developing markers for Marker-Assisted Breeding. To pursue it, 500 lines from a Multi-parent Advanced Generation Inter-Crosses (MAGIC) Population using eight founder parents was developed due to its advantages such as higher genetic diversity, smaller haplotype blocks, higher recombination and a better mapping resolution. The seedling straw test method will be used in the greenhouse to screen lines under white mold pressure. WM-MAGIC population will be sequenced using genotyping –by-sequencing (GBS) Genome-Wide-Association Mapping (GWAS) will be used to identify genomic regions related with resistance.

Genetic and transcriptomic analysis of pre-harvest sprouting in a mapping population of wheat

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Wheat is the most important cultivated cereal in Canada and second most-produced cereal worldwide. More than 40% of the world's population use wheat as their staple food and it provides more than 20% of calories and proteins for human consumption. The production of wheat is affected by different biotic and abiotic factors that influence the quality of the end product. Pre-harvest sprouting (PHS), is one of the factors causes significant variation in grain yield and quality during harvest. This is indicating a need of developing varieties resistance to PHS. PHS is a complex trait which is governed by the different genotypic and physiological factors. Among them, seed dormancy is considered as a major factor for resistance to PHS. Sprouting of seed at the harvest time can be reduced by adequate seed dormancy. The genetic mechanism underlying seed dormancy is still not well known in wheat, which is an important study area for the breeding of wheat varieties highly resistant to PHS. My project is aimed at identifying the genomic regions (QTL) and genes for seed dormancy in wheat using double haploid lines derived from a cross PHS resistant and susceptible lines. The outcome of this project will be extremely beneficial for the farmers in Canadian Prairies, research community and the end users/consumers.

Understanding the response of spring wheat field populations of *Fusarium graminearum* to fungicide application in Manitoba

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Fusarium Head Blight (FHB) is an important disease of wheat in Canada. The disease causes direct yield loss and downgrading of grain due to the presence of infected kernels and mycotoxins. Due to limitations in applying individual disease control measures, an integrated pest management strategy is required to reduce losses to this disease. Application of synthetic fungicides is part of the management strategy, but field efficacies have been variable. The main causal agent of FHB in Canada is *Fusarium graminearum senso stricto.* This species has multiple characteristics that can drive rapid adaption to its environment. These include a homothallic mating system with a potential for sexual recombination and long distance dispersal of air-borne sexual spores. Recent genome wide single nucleotide polymorphism analysis has identified highly polymorphic areas of the genome, predominantly in protein-encoding regions. High genetic diversity has been demonstrated at the field level, supporting the species' ability to rapidly adapt. The high genetic diversity of *F. graminearum* over small geographical scales may be a contributing factor in the observed variation in fungicide efficacy. This study aims to assess the response of field populations of *F. graminearum* on spring wheat to fungicide application in Manitoba. Spring wheat field trials with untreated and fungicide treatment at two timings were sampled for infected wheat spikes in 2017. An Amplified Fragment Length Polymorphism approach will be used to test the hypothesis that fungicide application acts as a selecting force on *F. graminearum* field populations. This will be followed up with a controlled environment study designed to determine the competitiveness of isolates obtained

from different field trial treatments in the absence and presence of fungicide application. This research will provide an increased understanding of the within field variability of *F. graminearum* and the field population response to fungicide application.

Identification of candidate genes for resistance against race 0 of *Colletotrichum lentis* in *Lens ervoides*

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Anthracnose, one of the major damaging diseases of lentil in western Canada remain an impediment for maintaining high seed quality and yields of lentil. Accessions of *Lens ervoides*, a species in tertiary gene pool of Lens have been identified with high levels of resistance to both races of *Colletotrichum lentis*, the causal pathogen of anthracnose. Interspecific hybrids have been created with the help of embryo rescue, but segregation distortion in resulting populations has prevented genetic studies and development of markers. An intraspecific *L. ervoides* population (LR-66) was developed from L01-827A X IG 72815 to study genetic control of resistance to pathogen. This RIL population was phenotyped for resistance to anthracnose and genotyped on Illumina HiSeq 2500 platform which led to the identification of five QTLs conferring resistance to *C. lentis* race 0. Evidence is already available of extensive shared synteny between cultivated lentis (*L. culinaris*), *L. ervoides* and model legume *M. truncatula*. Synteny-based comparisons of identified QTL locations will help to identify resistance gene candidates which upon validation can be used to generate perfect markers to trace the introgression of these genes into hybrid populations from which lentil varieties can be developed.

Agronomic practices to minimize lodging stress while maintaining yield potential in spring wheat

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Lodging in spring wheat, resulting in reduced yield and grain quality, is a common occurrence across western Canada. The high yield potential of current varieties indicates high fertility requirements and when paired with favorable growing conditions high lodging potential can occur. There're two different forms of lodging; stem and root that can be present within a field and they do not necessarily use the same plant morphological characteristics to resist lodging. Agronomic management practices such as varietal selection, nitrogen management, seeding rate and plant growth regulator (PGR) applications have potential to beneficially influence these characteristics to reduce lodging potential. Therefore, determining the most effective strategies to manipulate plant morphology to decrease lodging risk without taking resources away from the developing grain must be determined. The objectives of this study include, evaluating the influence of cultivar, N fertilizer management, PGR applications, plant density and their interactions on spring wheat yield and lodging potential. This project will be conducted through two field experiments at two field locations during the 2018 and 2019 growing seasons. Experiment one explores the influence of spring wheat varieties (AAC Brandon, AAC Cameron, Prosper), N management strategies (reduced rate, split application, controlled release), PGR application (+/-) and their interactions, while the second experiment will investigate nitrogen application timing (split application), plant density (high, medium, low), PGR application (+/-) and their interactions influence on canopy structure, yield and lodging potential. Key measurements for both experiments include yield, protein, lodging ratings, plant morphological characteristics, straw strength, and dry matter and nitrogen partitioning. Upon completion of this project knowledge of agronomic management practices influence on lodging potential will be increased and allow growers to fine-tune their agronomy management practices to reduce the risk of lodging without sacrificing grain yield and quality.

Study on salt tolerance of alfalfa (*Medicago sativa* L.) using synchrotron and transcriptome approaches

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Soil salinity is one of the most problematic abiotic stress factors limiting agricultural productivity and quality. Selecting plants that are tolerant to salinity and bringing marginal lands under cultivation is imperative for sustainable crop production. Alfalfa (*Medicago sativa* L.), the queen of forages, is the most important forage crop for the $8-12 Billion Canadian beef and dairy industries. It is characterized by numerous superior traits such as wide adaptability, high forage yield, good forage quality, and resistance to frequent cuttings as well as moderate saline tolerance. In Canadian Prairies, alfalfa is cultivated to about 76% of the total national production area of pure alfalfa or alfalfa mixture (Statistics Canada, 2012) where about 1.4 million hectares has been salinity effected to the extent of moderate or severe (Eilers et al., 1997).

In this study many phenotypic and physiological responses of alfalfa cultivars will be characterized in sand based hydroponics system in the greenhouse. The novelty of this work lies in application of synchrotron beam lines to uncover the sodium and chlorine ions along with other elements and organic molecules in leaf, stem and root tissues of two alfalfa cultivars with contrasting tolerances. Finally, alfalfa leaf transcriptome study in response to different salinity treatments will be studied using high throughput mRNA sequencing. By the end of this study we sought to understand sodium and chlorine ions composition and distribution

in different tissues of alfalfa and identify specific candidate genes that increase salinity resistance in alfalfa. Taken together, the outcome of this study will facilitate comprehensive understanding of the mechanism underlying tolerance to salt stress in alfalfa.

Identification of genes involved in sugar-end disorder in tetraploid potato (*Solanum tuberosum* L.)

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As fried potato products become more prevalent, it is important that the quality of these products be maintained. The sugar end disorder is a common affliction in production of processing potatoes affecting fried products, particularly french fries. Sugar ends occur when reducing sugars accumulate in the stem end of the tuber, rather than starch. When fried, the stem end of the french fries display a dark color impacting appearance, flavor, and smell, making them unfit for marketing and consumption. Due to the widespread production of processing potatoes for fried potato products in the United States, this disorder often has damaging effects on the potato industry. Tetraploid potato (Solanum tuberosum L.) is genetically complex, thus most approaches to handling sugar ends have been practical management solutions. However, these management strategies are only a temporary fix as the industry attempts to avoid sugar end and translucent tissue defects. By using a genetic approach, more resistant cultivars could be developed. Although genetic studies on sugar ends have been somewhat limited up to this point, sugar end resistance has been shown to be highly heritable. The aim of this work is to identify and understand the genes involved in resistance to sugar end disorder. By combining a genetic approach with good crop management, sugar end production could be diminished.

To determine the effect of univalents at meiosis on recombination in wheat

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Polyploidy is very common among plants, meaning they have more than two paired (homologous) sets of chromosomes. Durum wheat is an allotetraploid species, having 4 sets of chromosomes for a total of 28, originated through intergeneric hybridization and polyploidation involving two diploid grass species: *T. urartu* (2n=2x=14, AA genome) and a B-genome diploid related to *Aegilops speltoides* (2n=2x=14, SS genome). On the other hand, triticale (a hybrid of wheat (Triticum) and rye (Secale)) is a distant parent and used as a source of variation. A cross is made that will result in unpaired chromosomes being present at meiosis in the F1 generation as well as pairs of parental wheat chromosomes. We are using W9262-260D3 (durum wheat) and Langdon triticale (cross between Langdon wheat and Rye-13). The crosses involve crossing between the wheat and triticale (mapping of rye univalent) and wheat parents (as normal cross between wheat parents). The rye chromosomes will have nothing to pair with in meiosis of that cross and it is expected that their presence will disrupt recombination among the wheat chromosomes. Progeny from these crosses will then be screened with the wheat SNP chip and a map developed. If as expected recombination frequency and location are disturbed this will show up as differences between the original map (normal cross between the parents) and the new one. Hence, this unequal crossing over will give rise to univalent and serve to introduce novel variation allowing for species diversification and adaptation. We have developed a new method for detecting effect of univalent on recombination using a single nucleotide polymorphism (SNP) array. By this methodology, we are going to measure the recombination between A, B and R genomes and will determine whether the recombination is increased or not.

Plant Breeding and Genetics

Introgression of blackleg resistant gene from hexaploid lines and *B. juncea* to *B. napus*

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Blackleg disease in canola is caused by hemi-biotrophic fungal plant pathogen *Leptosphaeria maculans* that causes up to 100% yield losses. Canada is the leading producer and exporter of canola that comprises Alberta, Saskatchewan, and Manitoba. Brassica species with B genome (*B. nigra, B. juncea, and B carinata*) and C genome (*B. oleracea*) shows higher level of disease resistance against blackleg. Study shows that testing of different *B. juncea* and hexapl *rapa* x *B. carinata*) lines against highly aggressive *L. maculans* isolate PG4-1-M has high level of resistance. Introgression of blackleg resistance gene fron lines into *B. napus* cv. Westar displayed high level of resistance at cotyledon stage. Individual plants exhibiting higher level of resistance were self-pollinate backcrossed with Westar to develop BC_4, BC_4F_2 and BC_5 generations. To identify the marker that is linked with resistance, more than 90 Simple Sequence Repeats (SSR) primers were designed and screened. Out of these, one primer gave specific amplification in *B. juncea* parent and resistant plants, while a Westar and susceptible plants. This primer may help to discriminate resistant plants from susceptible. Advanced plant population will be screened under f

condition during summer for disease resistance against blackleg pathogen. Plants with high level of resistance with good seed setting, good segregation ratio and higher level of field resistance will be advanced.

Exploring the Diversity of Root System Architecture in Soybean using Plant Phenomics

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Root system architecture (RSA) studies are tedious, susceptible to introduced variation and the extracted features may not translate to a meaningful outcome. With the advent of high-throughput phenotyping, computer vision and machine learning there is a renewed interest in uncovering "the hidden half". Our study included 300 diverse soybean accessions from a wide geographical distribution (17 countries) of which genotypic information is available. We deployed a 2-D (in controlled conditions) and stereo imaging platforms (field tests), image processing algorithms and data analytic tools to deep phenotype for RSA traits using in-house software. The 2-D platform developed is non-destructive, adding observations throughout seedling growth and development. The stereo imaging platform of multiple cameras at multiple angles allows creation of a 3-D point cloud of a mature root.

Tens of thousands of images were collected from thousands of plants using the imaging platforms developed in this study. Moving forward, we are adapting machine learning techniques via convolutional neural networks will allow for the extraction and prediction of novel root architectural information. Utilizing phenotyping techniques has allowed us to capture tremendous RSA variability of these 300 diverse genotypes throughout various stages of development that will drive gene discovery and breeding methods forward.

Identification of quantitative trait loci (QTL) associated with Fusarium head blight resistance in winter wheat

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Fusarium head blight (FHB) caused by *Fusarium graminearum* is a major disease of wheat in North America. FHB infection reduces grain yield, affects end-use quality, and accumulates mycotoxins such as deoxynivalenol (DON) in the grain. The objective of this research was to identify QTL associated with FHB resistance. A doubled haploid soft white winter wheat population consisting of 107 lines from the cross D8006W/Superior was used. Evaluation for FHB reaction was performed using spray inoculation of a macroconidia mixture of four *F. graminearum* isolates representing two chemotypes in replicated field disease nurseries in three locations in Canada in 2016 and 2017. Disease incidence and severity were recorded 21 days post inoculation and FHB index was calculated. Percentage Fusarium damaged kernels and DON content were measured from collected grain samples. Both parental lines showed moderate reaction across all environments for FHB traits. However, the population showed transgressive segregation for FHB reaction with a wide continuous distribution. Genotyping of the population was performed using the 90K Illumina Infinium iSelect single nucleotide polymorphism array and 5194 high quality SNP were selected for analysis. Linkage mapping and QTL analysis is under processing. This experiment will be repeated in field nurseries in 2018. Significant FHB resistance QTL identified from this project will be used in winter wheat breeding programs using marker assisted selection.

Development of *Brassica napus* L. *Ogu*-INRA cms restorers using recurrent full-sib selection

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The *Ogu*-INRA cms system in canola and rapeseed (*Brassica napus* L.) uses a cytological variant of the radish- (*Raphanus sativus* L.) derived *Ogu* cms pollination control system introduced through interspecific introgression. The restorers (R-lines) contain an introgression that is associated with poor agronomic performance due to a large undesired segment of the radish chromosome that was introgressed along with the *Rfo* gene. The introgression contains pentatricopeptide (PPR) motif repeats that confer fertility restoration to the R-lines. The objective of this research was to test the hypothesis that multiple cycles of intermating will result in R-lines with improved agronomic performance. A base population was developed by designing five R-line by R-line crosses. Twelve plants from each initial cross were grown and chain-crossed at random, without selection, other than the presence of the *Rfo* SCAR marker. Twelve flowers from each plant were crossed and the remainder of the plant was selfed. Three intermating crossing cycles (C_0, C_1 and C_2) were completed and each was selfed twice in order to compare all populations at the C_0S_2, C_1S_2 and C_2S_2. This generation was then selfed again in order to compare the cycles at C_0S_3, C_1S_3 and C_2S_3. Total pod number, seeds per pod, a visual pod rating, thousand seed weight and yield were evaluated. The visual pod rating showed a positive correlation with seeds

per pod (r= -0.44) and yield (r= -0.43) (scale goes from 1 – 9 where 1 is best hence the negative score). Improvements for all traits were found at C_0 and C_1 when compared to the best parent. Individual families from two of the crosses showed a yield increase of over 78 % from the best parent. This suggests that improvements in yield components can be obtained from restorer by restorer crosses.

Association Mapping for Sclerotinia Stem Rot Disease in *Brassica napus*

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Sclerotinia stem rot is one of the most destructive fungal diseases of canola caused by *Sclerotinia sclerotiorum* (Lib) de Bary, that significantly reduce seed yield as well as oil content and quality. In North Dakota, average yield losses have been estimated 13 percent, and the loss can reach to 50 percent in some locations and economic losses estimated upto 20.8 million dollars due to this disease. Since, there is no completely resistant varieties available, identification of resistant genotypes and genes in diverged germplasm accessions is one of the best options to develop durable disease resistant cultivar for the growers. In the present study, a panel of 250 germplasm accessions originated from 27 countries will be screened in a controlled environment in randomized complete block design (RCBD) with 3 replications, to identify potential resistant germplasm. The germplasm will be evaluated using agar plug mycelial stem inoculation at flowering stage. For each accession, lesion length, along with a visual estimation of the percentage of the main stem that is girdled by the lesion and the number of dead plants will be recorded 3, 5, 7, 9, 11, 13 and 15 days after inoculation. Mean stem lesion length, width and mortality percentage will be calculated to evaluate each accessions. We have already screened 90 spring type rapeseed/canola germplasm accessions. A total of five promising lines have been identified as tolerant based on lower stem lesion length, percentage of stem girdling and mortality. The germplasm accessions have been genotyped using Ilumina genotyping-by-sequencing (GBS) platform at the Institute for Genomic Diversity at Cornell University, and 42,575 single nucleotide polymorphisms have been identified. Finally, a genome-wide association study will be conducted to identify the genomic region containing sclerotinia stem rot resistant genes in *B. napus*.
Support: The study was supported by the National Sclerotinia Initiative.

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

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Gene-for-gene interaction is triggered by the recognition between R proteins from host and Avr effectors from pathogen. The interaction between host R protein and pathogenic effectors initiates set of localized and rapid signaling cascades called hypersensitive response (HR). This response subsequently induces several signaling pathways including ROS accumulation, hormonal biosynthesis/signaling and programmed cell death (PCD). In this study, the general objective is to explore the crucial factors modulating the defense of *Brassica napus* against fungal pathogen *Leptosphaeria maculans*. The cultivars Surpass400 and 01-23-2 exhibited the HR phenotype while the cultivar Westar showed susceptibility. RT-qPCR results suggest that the early activation (3 days post-inoculation, dpi) of salicylic acid (SA) signaling was related to the initiation of the processes resulting to HR. Similar early induction also happened to the genes related to ROS generation and signaling. Histological staining revealed that the cultivars with HR induced the localized ROS accumulation at 3 to 5 dpi, this event was able to block hyphal development. This was supported by hydrogen peroxide (H_2O_2) accumulation, lignification and localized cell death. Moreover, the co-inoculation between *L. maculans*/*L. biglobosa* mixed inoculum and the chemical treatment with a catalase inhibitor aminotriazole (AT) (which induces higher H_2O_2) exhibi smaller leaf lesions in the susceptible cultivar Westar. These observations agreed with the findings that the early induction of cellular signaling in basal defens the key to induce HR.

Exploration of Genetic Diversity in *Camelina* Wild Relatives

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Camelina sativa an important industrial oilseed crop, is an allohexaploid species. Low levels of genetic diversity in *C. sativa* have been identified as an im issue for the *C. sativa* breeding program. An attempt to explore genetic diversity among wild relatives of *C. sativa* has been carried out using genotyping sequencing (GBS) approaches. Altogether, 104 *Camelina* genotypes consisting of three crop wild relatives and domesticated *C. sativa* were studied. The reference genome for the hexaploid enabled the ploidy level from different *Camelina* wild relatives to be determined. All the *C. sativa* and one *C. microca* found to have the three subgenomes from the hexaploid; whereas, the majority of *C. microcarpa* possessed two subgenomes, and one had a single sub

It was difficult to predict the genome organization of *C. rumellica* from GBS data. GBS data indicated that there is a need for slight rearrangements to the subgenome assignment of the reference *C. sativa* genome. Lower numbers of single nucleotide polymorphism were found in domesticated *C. sativa* (16272) in comparison to wild relatives (24093). However, the gene diversity was higher in domesticated *C. sativa* (0.37) in comparison to wild relatives (0.25). Population structure analysis clearly differentiated these genotypes into two populations; where among populations variation was found to be very high (37%). Gene diversity at the sub-genomic level showed similar levels of variation in genes in all three subgenomes among domesticated *C. sativa*; however, subgenome two was dominant in case of wild relatives where the majority of genotypes were tetraploid. RNA-Seq analysis suggested there is clear differentiation in levels of gene expression among the ploidy series of *Camelina*. This study reveals that there is higher potential of generating variability in domesticated *C. sativa* utilizing wild relatives.

Chloroplast ultrastructure and thylakoid architecture affects photosynthetic performance in *Amaranthus* spp.

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The process of photosynthesis occurs in the chloroplast which is a double membrane bound organelle containing thylakoid membranes. The thylakoids are organized into stacked (granal lamellae) and unstacked (stromal lamellae) membranes and contain components involved in the electron transport chain. However, these components are not distributed evenly within the thylakoid membranes resulting in what is referred to as lateral heterogeneity which is thought to provide flexibility of the photosynthetic apparatus to respond to changes in the light environment. The objective of this research was to evaluate chloroplast ultrastructure and determine the effect on thylakoid stacking in an attempt to explain differential rates of photosynthesis observed between red and green vegetable varieties of *Amaranthus*, a C4 NAD-malic enzyme containing plant. Photosynthetic performance was examined using O_2 evolution whereby the red variety demonstrated a 35% greater value of maximal photosynthetic rate (P_{max}) in comparison to the green variety. Chloroplast ultrastructural analyses revealed the presence of peripheral reticulum and cytoplasmic protrusions in various cell types of the green variety. These structures are thought to enhance photosynthesis by increasing overall plastid area and inner envelope membrane surface area, although we see no evidence of this reflected in P_{max} values. The granal index, which expresses appressed thylakoids as percentage of total thylakoids, as well as the ratio of appressed to non-appressed thylakoids were 26 and 68% greater in the bundle sheath cells (BSC) of the red variety, respectively. In addition, the ratio of thylakoids per granum was 55 and 36% greater in the BSC and mesophyll cells (MC) respectively, in the red variety in comparison to the green variety. No differences in any of these parameters were observed between the BSC and MC in either variety. These results suggest thylakoid architecture may play a role in varietal differences in P_{max}.

Genetic mapping of leaf rust resistance in the tetraploid wheat cross Strongfield/Blackbird

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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 a doubled haploid (DH) population of the cross Strongfield/Blackbird. Strongfield is a widely grown durum wheat variety (*Triticum turgidum* var. *durum* L.; genome AABB) in Canada, which was developed at Agriculture and Agri-Food Canada, Swift Current. Strongfield is highly resistant to *Pt* in Canada. Blackbird (*Triticum carthlicum*; genome AABB) is susceptible to *Pt* at the seedling stage but possesses partial adult plant resistance. The genetic basis of leaf rust resistance was studied in a doubled haploid (DH) population of the cross Strongfield/Blackbird which was previously genotyped with SSR markers and the 90K wheat Infinium SNP array. Four QTLs were found on chromosomes 1B, 2B, 3A, and 3B based analysis of leaf rust reaction from inoculated field nurseries in 2016 and 2017. This population was then screened for leaf rust resistance with multiple races at the seedling stage indoors. One Lr gene was identified on chromosome 3A, mapping to the same location as the 3A QTL detected with the field leaf rust data.

Development of canola with unique meal protein profiles

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Canola meal contains approximately 40% protein, the majority of which is composed of the seed storage proteins cruciferin and napin. Cruciferin functions to form emulsions while napin foams stable foams, two essential processes for food processing. However, cruciferin and napin are antagonistic in their functions and must be separated prior to industrial use. The development of canola cultivars with high napin or high cruciferin content can circumvent the costly chemical separation of the two storage proteins. High cruciferin genotypes will be developed through a classical breeding approach. To facilitate this effort, we assessed cruciferin content across *Brassica napus* accessions within the University of Manitoba Brassica germplasm collection to identify genotypes divergent in cruciferin content. Mapping populations will be developed to identify quantitative trait loci and associated genetic markers for marker-assisted selection. Concurrently, high napin lines are being developed using a biotechnological approach. The Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)/CRISPR-associated protein (Cas9) system is used to target select cruciferin genes for editing to down-regulate cruciferin production. Relying upon the compensatory mechanism within the seed protein pool, we aim to shift the seed storage protein composition towards napin without increasing total protein content. In this way, we negate the possibility of reducing oil content given the negative correlation between seed oil and protein. The subsequent removal of the CRISPR/Cas9 cassette either through segregation or doubled-haploid generation should enable the high-napin lines to bypass labeling as a transgenic event.

Genome wide association study of field pea for Fe, Zn, and Se concentration

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Iron (Fe), zinc (Zn) and selenium (Se) are essential micronutrients for human health. Our previous studies indicated substantial variation in micronutrient concentration in field pea (*Pisum sativum L.*). In this research, 177 diverse pea accessions were evaluated for Fe, Zn, and Se concentration from five location-years (2013 Saskatoon, 2014 Fargo, 2015 Saskatoon, 2016 Saskatoon and 2016 Rosthern) using atomic absorption spectroscopy. Accessions differed significantly ($P < 0.001$) for Fe and Zn in all location-years, but not for Se. Year and location effects were significant for all three micronutrients. Mean concentration for the combined analysis were 50.46, 29.49, and 0.95 and the concentration (ppm) ranged from 29.22 to 90.53, 12.83 to 51.47 and 0.06 to 8.75 in the ground whole pea seeds for Fe, Zn, and Se, respectively. Significant positive correlations ($P < 0.01$) were observed between Fe, Zn, and Se concentration. Concentration of Fe, Zn, and Se were significantly correlated ($P < 0.01$) between each location with the exception of Se concentration between Fargo and Rosthern. These phenotypic data were associated with genotypic data generated from genotyping-by-sequencing using genome wide association study (GWAS) to identify significant SNP markers associated with Fe, Zn, and Se concentration. After Bonfferoni correction, 3 markers were detected for Fe concentration and 7 markers for Zn concentration; these will be validated on two pea recombinant inbred line populations. Soil samples and respective seed samples were analyzed for ten randomly selected accessions in Rosthern and Saskatoon, 2017 for Fe, Zn, and Se concentration. Se concentration in Rosthe soil was significantly correlated ($P < 0.05$) with Se concentration in seeds. Significant correlation ($P < 0.05$) was detected between the soil and seed concentration of Zn and Fe in Saskatoon.

QTL mapping of Fusarium head blight resistance in a winter wheat doubled haploid population

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Resistance to Fusarium head blight (FHB) in wheat is complex and often involves multiple genes with relatively small effects. As a result, the breeding s to combine different types of FHB resistance into a single genotype. The breeding line 32C*17 showed strong FHB resistance under severe disease p both Canada and Germany. Two hundred doubled haploid lines (named as the DH population 8I3C) were made from a cross between 32C*17 and a r resistant line 18I*45. The 90K wheat Illumina Infinium iSelect single nucleotide polymorphism array was used to genotype this population. Field trials with a *F. graminearum* macroconidial suspension were conducted at Carman, Winnipeg and Ottawa. Dual floret inoculations were performed in the gre The inoculum was a mixture of two isolates of 3ADON producers and two isolates of 15ADON producers. Plant height, disease incidence, and disease were measured in the field nurseries. Fusarium damaged kernels and deoxynivalenol (DON) contents were determined from the field harvested samp

Greenhouse disease severity data was also estimated. Transgressive segregation was observed for all FHB measured traits. Multiple quantitative trait loci (QTLs) were detected. Further characterization of FHB resistance in this population is ongoing.

Leaf pigments and wax as heat tolerant traits, and their association with vegetation indices in pea

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Pea (*Pisum sativum* L.), is the most widely grown pulse crop in western Canada where heat stress during late vegetative and reproductive stage leads to yield loss. The yield loss can be minimized if we identify traits associated with heat tolerance of pea. Twenty-four pea cultivars were tested in field trials to investigate the role of pigments and leaf surface wax on pea heat tolerance. Heat tolerant cultivars with a high heat tolerance index, had greater concentrations of chlorophyll and wax in their flat leaf surfaces and petioles (tendrils and stalks). The increased levels of both pigments and wax were associated with cooler canopy temperature in hot years in the field. Vegetative indices including water band index, photochemical reflectance index, and normalized pigments and chlorophyll index had a significant association with the heat tolerance traits. This study highlighted roles of pigments and wax as heat tolerant traits; and emphasized the potential use of spectral indices in selecting heat tolerant pea cultivars.

Plant Pathology

RNA-Sequencing Analysis of Resistance to Deoxynivalenol Accumulation in Two-row Malting Barley 'Norman' Infected by Multiple Chemotypes of *Fusarium graminearum*.

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Fusarium head blight (FHB), incited by *Fusarium graminearum*, has been a devastating disease of cereal production in Canada for the past two decades. The trichothecene mycotoxin, deoxynivalenol (DON) is associated with grain infection. DON is associated with decreased grain quality and very low limits have been set by malting and brewing industries. While deployment of genetically resistant varieties remains the most economically viable strategy for disease mediation, development of resistance in malting barley has been difficult as sources of resistance generally demonstrate poor malting quality. One method utilized at Agriculture and Agri-Food Canada, Brandon Research and Development Centre, was *in vitro* selection through tissue culture using laden growth media containing mycotoxin. 'Norman' is a moderately resistant, doubled-haploid variety that was developed from 'CDC Kendall' via anther-culture on growth media containing DON (1.71 mg kg^{-1}). 'Norman' and 'CDC Kendall' were grown in a growth chamber, and inoculated with mixtures of *F. graminearum* chemotypes (15ADON, 3ADON, NIV) and Mock. Spikes were sampled at 72 and 96 hours post infection and placed in liquid nitrogen. RNA was extracted using Qiagen RNeasy Plant kits and tested for quality on an Agilent 2100 Bioanalyzer (RIN > 6.5). Sequencing was conducted on an Illumina HiSeq 4000 PE 100 bp (mRNA libraries). On average, 64 x 10^6 reads (X2 PE) were observed for each sample. Data quality was evaluated using FastQC, followed by data trimming using Trimmomatic. Reads were aligned to the barley reference genome (Hv_IBSC_PGSB_v2) using HISAT2. Cufflinks suite was used for transcriptome assembly. Differentially expressed genes will be presented at the conference.

A genome wide association study to identify mutations associated with DMI (triazole) fungicide resistance in *Cercospora beticola*

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Cercospora leaf spot (CLS) is caused by the fungus *Cercospora beticola* and is the most serious and destructive foliar disease of sugar beet worldwide. Current management strategies are comprised of cultural practices such as rotation and tillage in combination with the use of CLS-tolerant cultivars and fungicide applications. The sterol demethylation-inhibiting (DMI) fungicides are the most important class for managing CLS (Dahmen and Staub 1992). DMI fungicides inhibit the cytochrome P450 14α-demethylase CYP51, an enzyme that catalyses a key step in the biosynthesis of fungal ergosterol required for cell membrane integrity and survival. Quantitative resistance to DMIs has emerged in *C. beticola* populations due to their widespread use. By determining mutations responsible

for fungicide resistance, facile PCR screens can be performed to monitor sensitivity that will enable fungicide recommendations and guide resistance management. Although no mutation associated with *CbCYP51* has been identified, isolates with higher EC_{50} values overexpress *CbCYP51* compared to DMI-sensitive strains (Bolton *et al.* 2012). In order to identify mutations responsible for DMI resistance, a genome-wide association study was carried out. Over 4C *C. beticola* isolates were obtained from 100 leaf samples taken from each of two adjacent fields both pre- and post-DMI application in Fargo, North Dakota in 2016. DNA was extracted and eight SSR markers (Vaghefi *et al.* 2017) were used to identify unique genotypes. Unique strains were phenotyped for sensitivit the DMI tetraconazole via growth on amended potato dextrose agar plates to calculate EC_{50} values. Thirty "sensitive" (EC_{50} value <1) and thirty "resistant" (value >1) isolates underwent paired-read Illumina whole genome resequencing. Haplotype analysis at the *CbCYP51* locus identified mutations upstream of t gene that could contribute to phenotypic variation. Genome wide association identified a locus on chromosome 1 contributing significantly to tetraconazole resistance, but linkage disequilibrium in the region is too high to pinpoint this causal SNP(s) with the current population size.

Pyrenophora teres f. *maculata* effector gene identification using genetic mapping and whole genome sequenci

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Net blotch is caused by *Pyrenophora teres*, a devastating necrotrophic foliar pathogen of barley that causes reduced grain quality and typical yield loss 40% under conducive conditions. There are two forms of net blotch: net form and spot form caused by *P. teres* f. *teres* and *P. teres* f. *maculata* (*Ptm*), respectively. Both forms are present worldwide; however, *Ptm* has become prevalent in major barley producing regions including North Dakota (ND), U investigate the genetics of the *Ptm*-barley interaction, a 105-progeny bi-parental mapping population was developed from the ND isolate 'FGO' and the Australian isolate 'SG1'. Progeny isolates were phenotyped on a differential set of barley lines and genotyped using restriction-site associated DNA – g by sequencing (RAD-GBS). A genetic map was developed for quantitative trait loci (QTL) analysis identifying a total of six QTL across five linkage grou locus designated *PtmWel1* mapped to a 10.7 cM genetic interval on chromosome 2 and accounted for 30-37% of the phenotypic variation. Comparis *PtmWel1* locus using single molecule real-time (SMRT) whole genome sequencing of the two parental isolates delimited a 113.5 Kb region containing Only five of the 34 genes were predicted to contain a secretion signal, of which only two were under 250 amino acids. However, only one gene is exp using RNAseq data and is therefore our top candidate gene for *PtmWel1*. Validation of this candidate gene will utilize loss-of-function split marker ge and gain-of-function gene transformation.

Population structure of the dry bean rust pathogen *Uromyces appendiculatus* in North Dakota

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Dry bean rust has caused up to 16% yield loss in North Dakota in past epidemics, resulting in approximately $12 million in losses to growers in season. Dry bean rust, caused by *Uromyces appendiculatus*, is primarily controlled using genetic resistance; however, the pathogen has overcc employed *Ur-3* resistant gene. Urediniospores of *U. appendiculatus* have been reported to overwinter in North Dakota and pycnia and aecia ha documented, suggesting the survival and viability of teliospores. Pathogen surveys were conducted in major dry-bean growing counties in Nor and 2016. Sixty-five percent of the 90 *U. appendiculatus* single-pustule derived isolates evaluated were race 20-3; virulent on resistant genes *Ur-7*. The 20-3 virulence phenotype expressed on PC-50 (*Ur-9, Ur-12*), Early Gallatin (*Ur-4*) and Mexico 235 (*Ur-3+*) ranged from hypersen intermediate pustule sizes (0.2-0.4 mm), indicating greater diversity in the pathogen population than is currently reported in race nomenclat additional races were identified, all at less than 10% frequency. Collectively, these races overcome all known host resistance genes with the Preliminary results from RAD-GBS conducted to study the genomic diversity of the pathogen population substantiates previous evidence tha *appendiculatus* is sexually reproducing in North Dakota. Results from this research will bring an increased understanding of population dyna assist dry-bean breeding for rust resistance.

Is *glutathione-S-transferase 6* involved in canola defense against *Leptosphaeria maculans*?

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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 RNA-seq 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 and act as antioxidants involved in cellular detoxification. To determine the involvement of *GST6* in defense against *L. maculans*, an inoculation assay was performed using a *L. maculans* isolate with avirulence gene, *AvrLm1*. A *B. napus* resistant variety with *Rlm1*, Quinta, and susceptible variety, Westar, were used to represent incompatible and compatible interactions, respectively. Cotyledon samples were collected at zero, three, seven, and eleven days after inoculation (dai). The induction of *GST6*, the production of H_2O_2 and programmed cell death were analysed at each time point. In both susceptible and resistant cultivars, *GST6* expression was upregulated at three dai and then decreased. The expression was elevated again starting from seven dai. Lesion expansion at inoculated sites started from seven dai. Lesion development, H_2O_2 production and cell death were significantly higher in Westar in which, the expression of *GST6* increment was significantly lesser than in Quinta.
The results support *GST6* involvement in defense 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 is involved in defense mechanisms.

Effect of *Brassica napus-Leptosphaeria maculans* interaction in the emergence of virulent isolates of *L. Maculans*, a causal agent of blackleg disease in canola

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Canola (oilseed rape, *Brassica napus* L.) is one of the most stable oilseed crops grown today in Canada and other temperate parts of the world. The crop is prone to a few major diseases including blackleg, caused by the fungus *Leptosphaeria maculans*. In Canada, growers have recently begun to grow canola more intensively because of the market demand and the development of cultivars harbouring single *R* genes. A 4-year study from 2014 to 2017 at the Ian N. Morrison Research Station Carman Manitoba was conducted to investigate the effect of *B. napus-L. maculans* interaction in the emergence of virulent isolates toward specific *R* genes under field conditions over a 2-year rotation. Blackleg incidence was reduced by a maximum of 40% in 2017 compared to 2014 for all *R* genes tested, except for *Rlm4*. Disease severity was reduced by 52–21% in the 4th year compared to the 1st year, regardless of the *R* genes tested, except for *Rlm2*. Severity rating based on the susceptible cultivar Westar showed that the *R* genes tested here all were resistant to blackleg in 2017. There were no *AvrLm2*- and *AvrLm4*-carrying isolates in 2017, which led to the generation of virulence towards *Rlm2* and *Rlm4* within a year. Sequencing of the *AvrLm2* gene from 2014- and 2015-isolates revealed a shift in the *AvrLm2* to the *avrLm2* allele due to the accumulation of point mutations. In addition to that, masking of the *AvrLm3* phenotype by the presence of the *AvrLm4-7* allele was also confirmed by analysing the phenotypes and genotypes of the isolates collected from 2014 to 2017. Based on previous and current studies, we predict that alternating *Rlm3*, *Rlm4*, and *Rlm7* could provide an opportunity to increase the durability of those *R* genes in a 2-year crop rotation in Canada. Additionally, this study propose the development of a generic epidemiological model that takes into account complex molecular mechanisms, allowing plant breeders to select appropriate *R* genes in the proposed cultivar rotation strategies on the Prairies.

Mitigation of stripe rust and leaf spot diseases in winter wheat in western Canada.

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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 and 2016/2017 crop seasons.

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.

Investigation of *Verticillium dahliae* gene activity during potato invasion

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Previous comparative study of proteomic files between the highly and weakly aggressive isolates of *Verticillium dahliae*, as well as differential genes' subtractive hybridization /cDNA-AFLP study with potato root extract elicitation, indicate potential roles of some genes in spore germination or pathogenicity. However, their function during potato invasion is still not clear, and the quantitative expression data of these genes in response to different potato extracts were not available. In this project, we employ quantitative real time PCR (QRT-PCR) to analyze the fold change of target genes between a highly aggressive isolate and a weak isolate while invading detached potato leaves in a time series manner, as well as response to different type of potato extracts. In response to above different treatments, genes such as serine/threonine-protein kinase, Ras-GAP like protein, Thioredoxin, NADH-ubiquinone oxidoreductase, Ubiquitin-conjugating enzyme variant MMS2, myo-inositol 2-dehydrogenase, xanthine dehydrogenase, Pyruvate dehydrogenase E1 component subunit b, and HAD-superfamily hydrolase, wer shown to be upregulated more in highly aggressive isolates than weak ones. These results indicated higher activities of enzymes involved in cellular process like DNA repair, cellular metabolism, ROS regulation, detoxification, cell differential and proliferation, during *V. dahliae* invading host and spore germination. These results provide new important incorporation views in controlling this disease on host.

RNA interference as a molecular fungicide targeting necrotrophic fungal pathogens *Sclerotinia Sclerotiorum* and *Botrytis cinerea*

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Necrotrophic fungal phytopathogens, such as *Sclerotinia sclerotiorum and Botrytis cinerea,* devastate a wide range of important crop species. These fungi capable of infecting more than 500 different plant species worldwide, including economically significant crops such as canola, pulses and fruits. In particu canola, which contributes 27 billion dollars to the Canadian economy annually, is especially susceptible to infection from necrotrophic fungi. Control pract currently used by producers predominantly include the use of broad spectrum fungicides. Unfortunately, these chemicals are becoming increasingly ineff 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 r bioinformatics pipeline, our lab has already identified dsRNAs in *Sclerotinia* that have proven effective in limited fungal growth *in planta* in canola. Speci were able to reduce *Sclerotinia* infection significantly by using RNAi technology both as a foliar spray as well as through transgenic canola. Additionally used this technology to target a related phytopathogen, *Botrytis cinerea*, and also shown a reduction in fungal infection through *in planta* assays. The by which dsRNA is taken up in fungi is also being investigated and has been shown to occur through endocytotic processes. Ultimately, using leading- technologies in molecular biology, we developed molecular, species specific fungicides that will be of utility to both producers and researchers in Can abroad.

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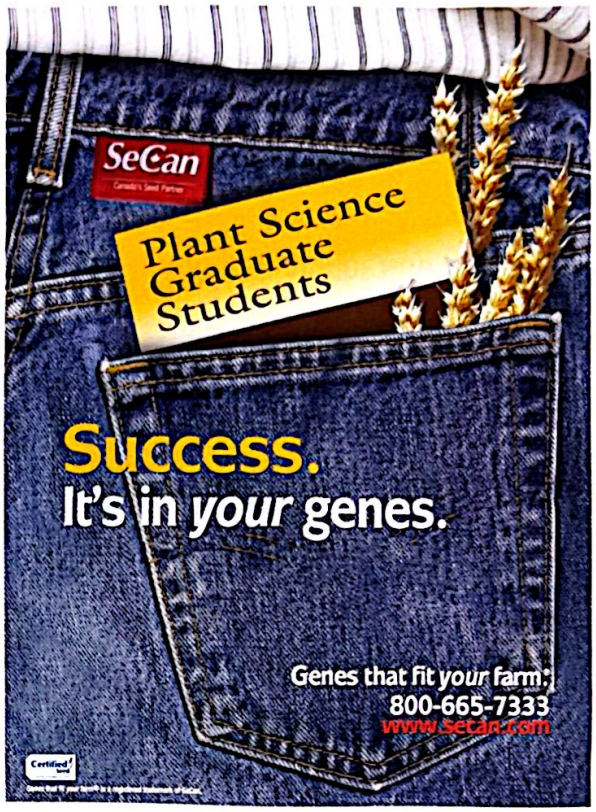
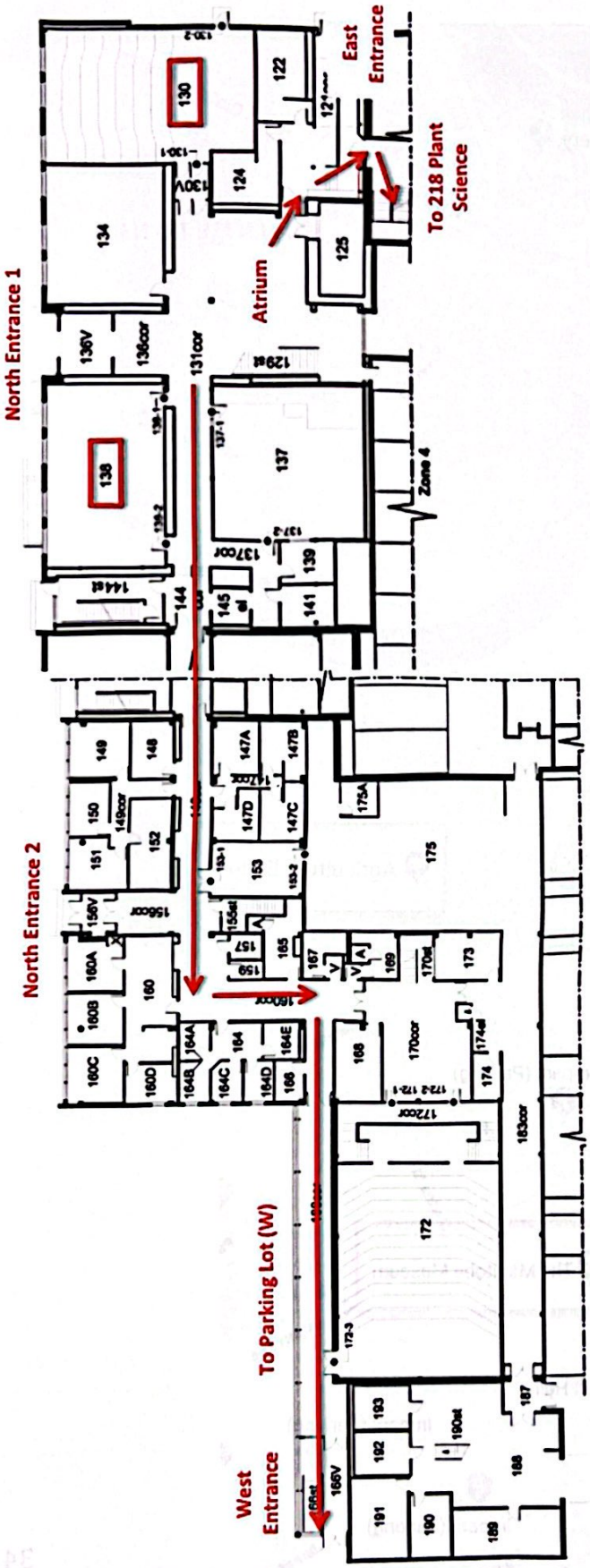
  - Plant biotechnology

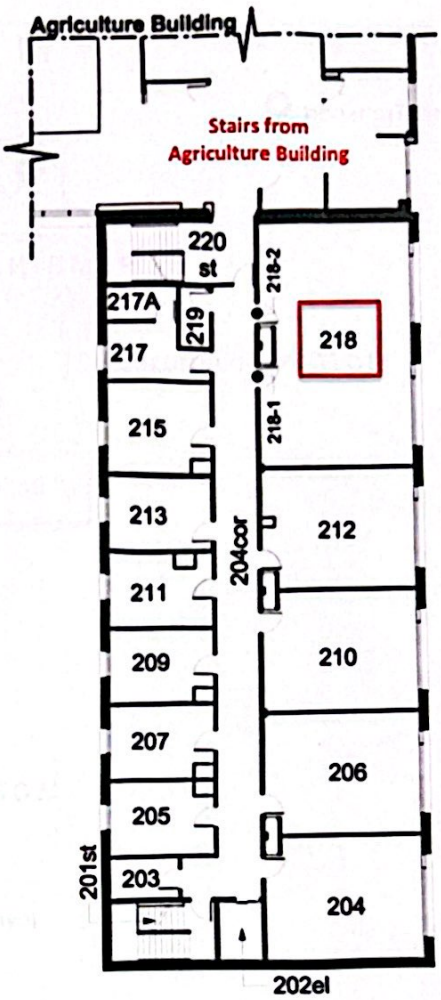
SPONSORS



Agriculture Building – First Floor



Plant Science Building – Second Floor



Maps

Social Events