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UNIVERSITY OF SASKATCHEWAN

39th Plant Science Graduate Student Symposium

Saskatoon
March 15-16, 2024

HARVESTING THE FUTURE

Contents

LAND ACKNOWLEDGEMENT

As we gather here today, we acknowledge we are on Treaty 6 Territory and the Homeland of the Métis. We pay our respect to the First Nation and Métis ancestors of this place and reaffirm our relationship with one another.

The 39th PSGSS is proud to be part of

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A Message from the USask PSGSA

The organizing committee and members of the Plant Sciences Graduate Students' Association (PSGSA) warmly welcome you to the 39th Plant Science Graduate Student Symposium (PSGSS). PSGSS gives graduate students like you an amazing opportunity to gather, share your research, learn, and expand your network. This year our theme, “Harvesting the Future”, highlights our role as students in the evolving field of plant science, where we shape a future of innovation, sustainability, and global impact, securing a bountiful harvest for generations to come.

Together, we are sowing the seeds of progress, working towards a future that ensures global food security and environmental sustainability.

Your participation makes this symposium better, and we thank you all for coming and making this event such an enriching experience. We hope you have an amazing time at the symposium and a great time in the city of Saskatoon!

Sincerely,

The PSGSA

PSGSA
USASK

TIME	ACTIVITY	LOCATION

Friday, March 15, 2024

TIME	ACTIVITY	LOCATION
8:00	**Registration**	Agriculture Atrium
9:00	**PSGSA Welcome**	Peter MacKinnon 120
9:05	**Corteva Welcome**	
9:15	**Keynote: Bryce Eger**	
10:00	**Coffee & Refreshments**	Agriculture Atrium
10:30	**Concurrent Session 1**	Geology 255 & 261
12:00	**Lunch**	Agriculture Atrium
1:00	**Keynote: Dr. Willenborg**	Peter MacKinnon 120
2:00	**Coffee & Refreshments**	Agriculture Atrium
2:30	**Concurrent Session 2**	Agriculture 2E17 & 2E25
6:00	**Social Night**	Hudsons

Saturday, March 16, 2024

TIME	ACTIVITY	LOCATION
8:30	**Concurrent Session 3**	Agriculture 2E17 & 2E25
10:00	**Coffee & Refreshments**	Agriculture Atrium
10:30	**Concurrent Session 4**	Agriculture 2E17 & 2E25
12:15	**Lunch**	Agriculture Atrium
1:00	**Campus Tour**	Agriculture Atrium
5:00	**Cocktail Hour**	Marquis Hall Exeter Room
6:00	**Banquet**	Marquis Hall Exeter Room

KEYNOTE SPEAKERS

Bryce Eger

Bryce Eger is the Vice President for Seeds R&D at Corteva Agriscience and leads innovation management and research and development strategy for seeds. In this role, Bryce has functional leadership for a team whose purpose is to develop and lead the investment decisions for the seeds pipeline from discovery through commercialization while maintaining balance for the purpose of enriching lives of those who produce and those who consume.

Prior to this role, Bryce led the Canadian business where he was responsible for the commercial strategy and business execution as well as the company governance. He joined company governance. He joined Pioneer Hi-Bred Limited in 2009 as National Sales Manager, Canada. Over his Corteva career he has taken on additional roles as Business Director, Seed Production Director, and President for Pioneer Hi-Bred Canada. He came to Corteva after 13.5 years with Cargill Limited where he had diverse experiences in grain and crop input retail operations, grain merchandising, sales, marketing, sales leadership, and general management. Bryce was also on the Board of Directors for CropLife Canada for the last 8 years where he was a member of the executive committee as well as chair of the board.

Christian J. Willenborg, Ph.D.

Dr. Willenborg is a Professor and Head of the Plant Sciences Department at the University of Saskatchewan. He is also an Adjunct Professor at the University of Alberta. Dr. Willenborg is a weed ecologist whose research focuses on better understanding the ecology and management of weeds in the agroecosystem. His main interest is weed seed management and in particular, seed predators and their contribution to weed control. Over his year career, he has authored or coauthored of over 70 peer-reviewed research publications in various international journals and has supervised over 20 graduate students in various areas of weed science and ecology. Dr. Willenborg teaches multiple undergraduate and graduate courses in the discipline of weed science. He has served as an Associate Editor and as Editor-in-Chief for the Canadian Journal of Plant Science. He currently serves as Director of Publications for the Weed Science Society of America, managing their publishing portfolio which includes overseeing the activities of the three journals published by the society. He also currently sits on the WSSA Board of Directors and Executive of the society, as well as serving on multiple university committees.

SOCIAL NIGHT & BANQUET

Please join us for the Social Night on Friday, March 15th!

Who?	39th PSGSS attendees
What?	Burger Bar, Appies, and Games!
Where?	Hudsons - 401 21 Street E Saskatoon, Saskatchewan
When?	Friday, March 15, 2024, from 6:00 pm - 9:00 pm

A private room at Hudsons is reserved from 6:00 pm to 9:00 pm. Food will be served and games are available at no cost during that time! A photo booth is also available for a cost. Please note that Hudsons is located in downtown Saskatoon and not on the University of Saskatchewan campus.

Please join us for the Banquet on Saturday, March 16th!

Who?	39th PSGSS attendees
What?	Supper and Awards Presentation
Where?	Marquis Hall Exeter Room- 97 Campus Dr, Saskatoon, SK
When?	Saturday, March 16, 2024, from 5:00 pm - 9:00 pm

The banquet will be held in the Exeter Room at Marquis Hall located on the University of Saskatchewan campus. To get to the Exeter Room, go up the stairs beside the Shop USask Bookstore. Doors open at 5:00 pm for cocktail hour and a short program along with the awards presentation will begin at 6:00 pm. Supper will be served at 6:15 pm.

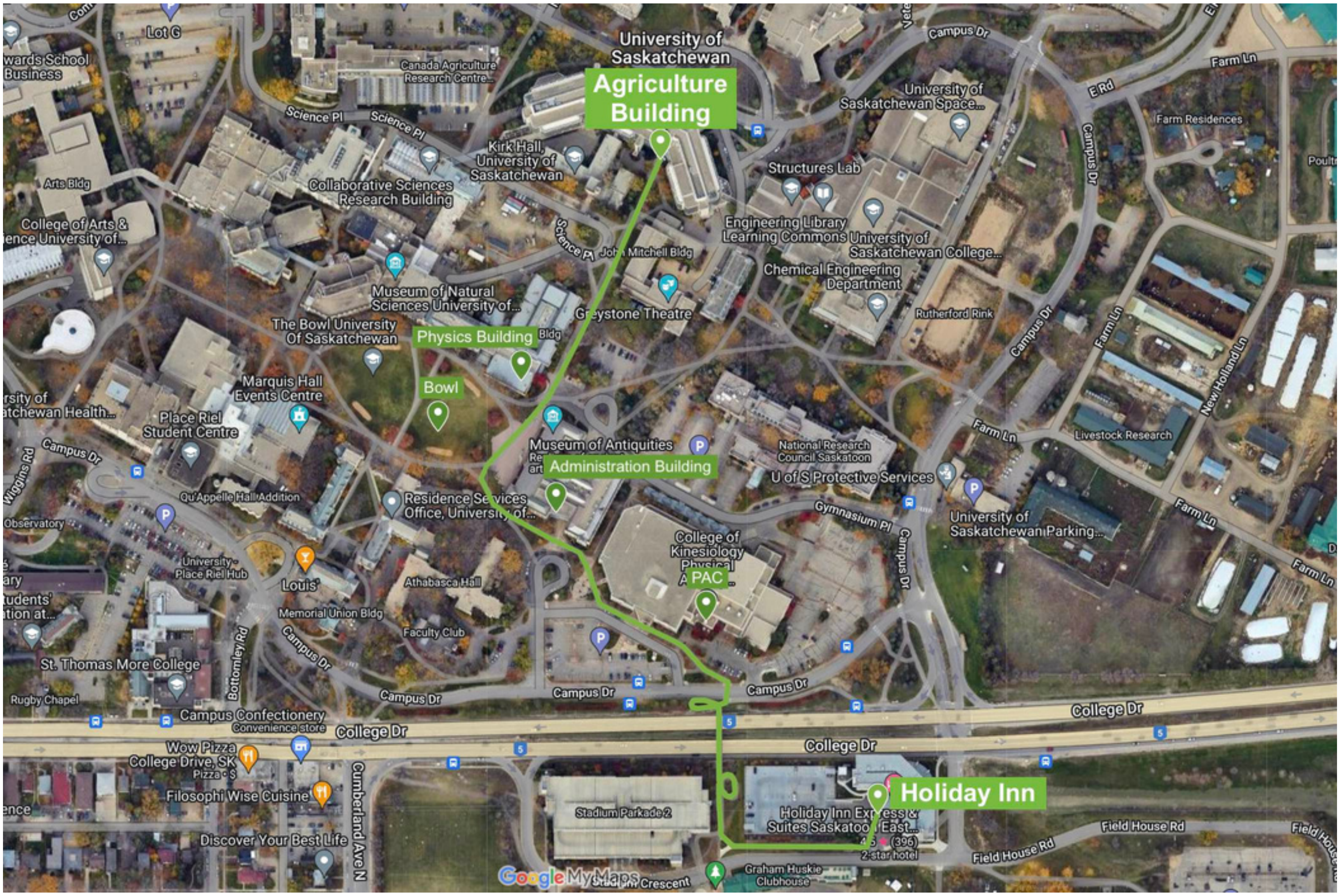
CAMPUS TOUR

The campus tour will take place in the afternoon on Saturday, March 16, and will include classroom buildings across campus, popular student hang-outs and study areas, athletic facilities, and student services. Your tour will be conducted by a current university student who can tell you what life as a USask student is like and answer some of the questions you might have about our campus.

Tours take place rain or shine, and involve both indoor and outdoor travel. We recommend you dress both for comfort and for the weather to ensure you have the best campus tour experience. Remember to check the forecast, especially if you are not familiar with western Canadian winters!

There will be two tour groups, one will leave at 1:00 pm and the other at 1:15 pm. Tours will leave from the Administration Building, but we will meet in the Agriculture Atrium and walk there together before the first group leaves at 1:00 pm.

CAMPUS MAP



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ORGANIZING COMMITTEE

USask Plant Sciences Graduate Students' Association 2023-2024

Back Row: Céline Ferré, Quinn Sturby, Daphnée Ferland, Hansanee Fernando
Front Row: Jeremy Irvine, Sainey Ceesay, Jocelyn Leidl, Anya Illingworth, Suma Ghosh, Grace Onu-Odey
Missing: Laura Carruthers

PSGSS Chair- Céline Ferré

President- Quinn Sturby

Vice President- Jocelyn Leidl

Secretary- Daphnée Ferland

Industry Liaison- Jeremy Irvine

Treasurer- Hansanee Fernando

Social Coordinator- Laura Carruthers

Social Coordinator- Grace Onu-Odey

GSA Representative- Sainey Ceesay

Faculty Liaison- Suma Ghosh

Social Media Coordinator- Anya Illingworth

PRESENTATION GUIDELINES

Please arrive a few minutes early to the session you are presenting in and have your USB drive ready. Before the session begins, the moderator will help all presenters upload their presentations to the computer. This will greatly help the symposium run on time and allow the moderator to have adequate time to get the presentations set up.

Presentation guidelines are as follows:

- The presentation type will be oral presentations.
- Presentations will be in person only. There will be no virtual presentations.
- Each presentation is allotted 15 minutes, which includes a question period. Presentations should be between 10-12 minutes, allowing for 3-5 minutes for questions.
- Presentations should be made in PowerPoint, preferably formatted to a widescreen 16:9, which can be edited under the “Design” tab on the far right where it says “Slide Size”.
- Presentations must be brought to the symposium on a USB Drive.

Awards for 1st, 2nd, and 3rd place presentations will be awarded for each category:

- Agronomy and Cropping Systems
- Crop Protection
- Physiology and Ecology
- Plant Breeding, Genetics, and Biotechnology
- Proposals

Awards will be presented at the banquet on Saturday, March 16.

Friday, March 15, 2024

Concurrent Session 1: 10:30-12:00

Agronomy and Cropping Systems - Geology 261

Daphnée Ferland	10:30 am	Nitrous oxide emission measurements from a canola-wheat cropping system in Saskatchewan
~~**Tianyi Zhao**~~	~~10:45 am~~	~~Evaluating the effects of humic-based substances on alleviating drought stress in canola~~
Jocelyn Leidl	11:00 am	A Comparative Analysis of Systematic and Randomized Designs in Nitrogen Response Studies
Janelle Gawiak	11:15 am	Are Intercropped Cover Crops Compatible with Canola Weed Management on the Canadian Prairies?
Hansanee Fernando	11:30 am	From Seed to Harvest: Mapping Canola via Radar and Optical Satellites
Sarah van Steenbergen	11:45 am	Macaroni Metrics: Forecasting Durum Wheat Yields in Saskatchewan using Remote Sensing techniques and a Machine Learning approach

Plant Breeding, Genetics, and Biotechnology - Geology 255

Ritesh Yadav	10:30 am	Understanding The Genetic Basis Of Winter Hardiness And Fusarium Head Blight Resistance In Winter Durum Wheat
Jared Bento	10:45 am	Genome-Wide Association and Genomic Selection for Oil and Fatty Acid Profile in Rapeseed (Brassica napus L.)
Quinn Sturby	11:00 am	Phenotypic and genetic analysis of common bean growth and development using UAV-derived data
Micheal Benko	11:15 am	Utilizing Micropropagation to Improve Commercial Production of "Cannabis sativa L."
Anirup Sengupta	11:30 am	Genome-Wide Association Study (GWAS) for Leaf Rust Resistance in Canada Western Red Winter (CWRW) Wheat
Ashley Barstow	11:45 am	Identifying a Core Set of Markers and Haplotype Structures to Track Segregation in Domesticated Sunflower (Helianthus annuus L.)

Friday, March 15, 2024

Concurrent Session 2: 2:30-4:00

Physiology and Ecology - Agriculture 2E25

Nathaniel Ort	2:30 pm	Accumulation of Nitrogen and Dry Matter in Early Maturing Soybean Seed
Amin Khan	2:45 pm	Unveiling the Role of Acclimation Time and Exogenous Spermine in Enhancing Strawberry Cold Hardiness
Jacob Coward	3:00 pm	Investigating the plant leaf epicuticular wax of Brassica carinata
Subarna Sharma	3:15 pm	NDVI before heading and abaxial stomatal features are early predictors of grain yield stability under drought stress in a Canadian heritage bread wheat panel
Suma Ghosh	3:30 pm	Assessing mycorrhizal traits to facilitate the selective breeding of forage legumes

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Crop Protection - Agriculture 2E17

Daniella Canon-Rubio	2:30 pm	Impact of seed imbibition on seed preferences by carabid beetles
~~**Japjyot Sandhu**~~	~~2:45 pm~~	~~Detecting Bassia scoparia (Kochia) at field scale using multi-temporal UAV imagery~~
Brianna Senetza	3:00 pm	Evaluating the Competitive Ability of Modern Oat Varieties
Uthpala Ekanayake	3:15 pm	Effect of Integrated Crop Management Strategies on Crop Yield and Weed Growth in Wheat Agroecosystems
Anya Illingworth	3:30 pm	Fungicide Timing to Mitigate Fusarium Head Blight in Cereals
Md Zahangir Alam	3:45 pm	A Comprehensive Approach for Rapid Development of Sclerotinia Stem Rot (SSR) Resistant and Elite Cultivars of Canola

Saturday, March 16, 2024

Concurrent Session 3: 8:30-10:00

Agronomy and Cropping Systems - Agriculture 2E17

Ajay Dhukuchhu	8:30 am	New Brassica Cultivars and Their Response to Changing Climatic Conditions in North Dakota
~~**Sukhveer Singh Bhullar**~~	~~8:45 am~~	~~Integrating precision Ag. techniques to access their impact on nitrogen fate, water quality and corn yield in sandy soils of Suwannee Valley, Florida.~~
Kaylie Krys	9:00 am	An Eye in the Sky: UAV Imagery Surveying of Canola Emergence at the Field-scale
~~**Franklin Omeye**~~	~~9:15 am~~	~~Establishing alfalfa or sainfoin with sorghum in an intercropping system while sampling biodiversity and its feasibility~~
Emily DeValk	9:30 am	Precision measurement of sunflower head inclination: a trigonometry-based approach

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Plant Breeding, Genetics, and Biotechnology - Agriculture 2E25

~~**Alexa Peterson**~~	~~8:30 am~~	~~Mapping of quantitative trait loci (QTLs) in Thinopyrum intermedium for Fusarium graminearum tolerance and agronomic traits.~~
Kaitlyn Pidherny	8:45 am	Genome wide association study of stem rust resistance in winter wheat
Stephen Awodele	9:00 am	Phenotypic Insights into Fusarium avenaceum Root Rot Resistance in Diverse Pea Accessions
Rajbir Kaur	9:15 am	Speed editing: High throughput gene editing using Clustered regularly interspaced short palindromic repeats- CRISPR-associated protein 9 system in Brassica napus.
Kripa Rijal	9:30 am	Use of test cross analysis to detect the presence of, and complementation among diverse FHB resistance QTL in wheat
Shahab Ahmad	9:45 am	Genetic studies on seed yield, seed oil, seed color, flower color, and other agronomic traits in flax (linum usitatissimum l.): unlocking the potential for improved cultivars

Saturday, March 16, 2024

Concurrent Session 4: 10:30-12:15

Plant Breeding, Genetics, and Biotechnology - Agriculture 2E25

Serena Page	10:30 am	Using ABA Antagonists to Break Seed Dormancy in Wild Rice (Zizania palustris)
Bhanu Dangi	10:45 am	The FHB Avengers: Uniting Genes to Save Winter Wheat
Stephen Mensah	11:00 am	Evaluating the effect of cultivar on garlic growth and yield
~~**Muhammad Usman**~~	~~11:15 am~~	~~Physic-biological treatments to upcycling pulse protein byproducts into 3D food printing gel~~
Noah Jendrasheske	11:30 am	Investigating Interspecific Lentil ‘Lens culinaris’ and ‘Lens orientalis’ Germplasm: Near-Infrared Spectroscopy for Protein and Amino Acid Profile and Quantitative Trait Locus Analysis

Proposals - Agriculture 2E25

Shaily Tandekar	11:45 am	A compatibility study of cicer milkvetch in mixtures with alfalfa
~~**Pratik Bankar**~~	~~12:00 pm~~	~~Sterility a Secret Weapon New Era in Agriculture Innovation~~

Crop Protection - Agriculture 2E17

Logan Orenchuk	10:30 am	Identification and assessment of Fusarium damaged kernels based on the infection time of Fusarium graminearum on wheat
Jeremy Irvine	10:45 am	Optimizing thresholds and sampling strategies for the control of lesser clover leaf weevils in Saskatchewan's red clover.
Teresa Aguiar-Cordero	11:00 am	Determining the duration of Lygus feeding associated with scarring damage in faba bean seeds.
Rodensky Teramene	11:15 am	Evaluation of Pea Aphid Feeding Behavior on Resistant Lentil Varieties and Breeding Lines in Saskatchewan
~~**Georgiana Antochi-Crihan**~~	~~11:30 am~~	~~Effects of Prairie Pothole Wetland Margins on Ground Dwelling Arthropod Distribution in the Prairies~~

ACKNOWLEDGEMENTS

Attendees

Thank you to all of the graduate students who attended the 39th PSGSS and thank you to all students who took the time and effort to prepare abstracts and presentations! You truly made this event a success and such a fun and exciting experience. We keep on the tradition to gather once a year and share our research with others, both the three host Universities and those that join us at this event. We hope this unique opportunity will lead us to great collaborations in the future.

Speakers

We are very grateful to our two keynote speakers for their participation and enthusiastic effort on presenting at our symposium. We are very privileged to have learned from great mentors. Thank you!

Bryce Eger, Vice President for Seeds R&D, Corteva Agriscience

Christian J. Willenborg, Ph.D, Professor and Department Head, Department of Plant Sciences, University of Saskatchewan

Judges

Thank you to our judges- professors, postdoctoral researchers, and research assistants from the Department of Plant Sciences. We greatly appreciate your time and knowledge. We hope you had as much fun as we did!

Dr. Sabine Banniza
Cheryl Cho
Dr. Thuan Ha
Dr. Kwabena Nketia
Dr. Steve Shirtliffe
Dr. Kirstin Bett
Dr. Kishore Gali
Dr. Megan House
Alejandra Oviedo-Ludena
Dr. Tom Warkentin
Dr. Ana Vargas
Dr. Adam Carter
Dr. Greg Gingera
Dr. Tamanna Jahan
Dr. Rajib Podder
Dr. Chris Willenborg

Moderators

Thank you the graduate students who volunteered their time to moderate the concurrent sessions. We appreciate your help in ensuring that the sessions and symposium ran smoothly!

Daphnée Ferland
Jeremiah Odiketa
Hansanee Fernando
Nathaniel Ort
Quinn Sturby
Kara Glor
Subarna Sharma

ABSTRACTS

AGRONOMY AND CROPPING SYSTEMS

CROP PROTECTION

PHYSIOLOGY AND ECOLOGY

PLANT BREEDING, GENETICS, AND BIOTECHNOLOGY

PROPOSALS

Session 1: Friday, March 15, 10:30-12:00

Agronomy and Cropping Systems

Nitrous oxide emission measurements from a canola-wheat cropping system in Saskatchewan

Daphnée Ferland[1], Shannon E. Brown[3], Claudia Wagner-Riddle[3], Richard E. Farrell[2], and Kate A. Congreves[1]
[1]Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK
[2]Department of Soil Science, University of Saskatchewan, Saskatoon, SK
[3]School of Environmental Science, University of Guelph, Guelph, ON

Better understanding the greenhouse gas (GHG) emissions of agricultural systems offers a pathway towards more sustainable agriculture, but accurate measurements are needed. The flux-gradient micrometeorological research station in Saskatoon provides high-frequency, year-round field-scale GHG emission measurements for a prairie canola-wheat cropping system. With nitrogen (N) fertilizer contributing to almost half (46%) of GHG emissions from prairie cropping systems, better N management practices are needed to reduce GHG emissions. Starting in 2021 and continuing to 2024, we are comparing conventional N management to an improved N management scenario that uses two 4R N strategies ("right source" and "right rate"). In 2021 and 2023, canola was fertilized with 100 kg N ha-1 urea vs 50 kg N ha-1 less than recommended N rate + enhanced-efficiency fertilizer source (i.e., AnvolTM or SuperUTM products). The fertilizer rates were lowered by 50 kg ha-1 for both scenarios in 2022 to account for the large amounts of residual soil N that were left in 2021 when drought conditions (133 mm from May-August) severely limited crop production. Here we will report the effect of N management on the N2O measurements for the 2021-2023 period under canola-wheat production. Preliminary results show that the improved N management scenario has lower N2O emissions than the conventional scenario, with no effect on crop yield.

A Comparative Analysis of Systematic and Randomized Designs in Nitrogen Response Studies

Jocelyn Leidl[1], A. Attanyake[1], E. Johnson[1], and S. Shirtliffe[1]
[1]Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK

The utilization of on-farm experimentation has emerged as an excellent method for conducting research on specific field conditions. This approach enables producers to enhance efficiency in their production processes and maximize profits. There are concerns with the results from conventional crop research using small plot Randomized Complete Block Design (RCBD) and strip trials. This study was conducted across ten site years to assess the accuracy and precision of the use of a systematic randomized row column design termed Modulated On-Farm Surface Response Experiment (MORSE) and its use in place of traditional methods (RCBD). Randomized (RCBD) and systematic (MORSE) designs were integrated into one trial by alternating the replicates of each design. Nitrogen response in canola and wheat was used to compare the accuracy and precision of each design with 11 total rates of 0-310 kg/ha applied. The precision of each design was compared using the standard error values of each design that was generated from a general additive model. Unoccupied aerial vehicles (UAV)-based vegetation indices such as Normalized Difference Vegetation Index (NDVI) and Normalized Difference Red Edge (NDRE) were used to estimate high yielding plots to support the understanding of optimal nitrogen rates, prior to the start of harvest. The MORSE design provided comparable results to the RCBD design, with a similar mean yield trend in response to nitrogen rate. Standard error values in 2022 and 2023 were 34.94 and 48.2 in the systematic design compared to 30.71 and 59.59 in the randomized design. The highest correlations between UAV derived NDVI and yield was 0.92 (2022) and 0.86 (2023) for the wheat, and 0.84 (2022) for the canola. Correlation results between NDRE and yield was 0.98 (2022) and 0.81 (2022) for canola. Based on the placement and application of treatments, the systematic design (MORSE) would be a viable option for future on-farm use.

Are Intercropped Cover Crops Compatible with Canola Weed Management on the Canadian Prairies?

Janelle Gawiak[1], Y. Lawley[1], M. Bourgault[2], and L. Gorim[3]
[1]Department of Plant Science, University of Manitoba, Winnipeg, MB
[2]Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK
[3]Department of Agricultural, Food, and Nutritional Science, University of Alberta, Edmonton, AB

The short growing season and limited fall precipitation in the semi-arid climate of western Canada hinders widespread adoption of fall cover crops. Intercropping is a potential solution by increasing the window for cover crop establishment and growth. However, intercropping also creates challenges when using herbicides to control weeds in cash crops like canola (Brassica napus L.). Field experiments at three sites in Manitoba, Saskatchewan, and Alberta were established to compare three herbicide application timing treatments (pre-emergence only, pre-emergence and in season, and a pre-emergence, in season, and desiccant) for the three herbicide tolerance systems utilized with canola hybrids (Liberty Link, Clearfield, and Roundup Ready). A cover crop mixture of red clover (Trifolium pratense), white Dutch clover (Trifolium repens), subterranean clover (Trifolium subterraneum), Persian clover (Trifolium resupinatum), alfalfa (Medicago sativa), and Italian ryegrass (Lolium multiflorum) was seeded at the same time as canola. Experiment measurements include cover crop stand, aboveground biomass, and herbicide damage ratings. Cover crops were able to establish at all sites, however persistence varied across locations, application timing, and herbicide tolerance systems. The greatest fall biomass was observed in the pre-emergence only treatments and decreased with subsequent herbicide applications. Additionally, when substantial biomass accumulated, yield penalties were observed. This project determined there is the possibility for success when intercropping cover

crops and highlights the need for future research to understand how cover crops can fit into a canola cropping system.

From Seed to Harvest: Mapping Canola via Radar and Optical Satellites

Hansanee Fernando[1], Nketia, K. Ha, T[1]. van Steenbergen, and S. Shirtliffe, S[1]
[1]Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK

Canola (Brassica napus), a leading oilseed crop is highly susceptible to heat stress, especially during the flowering stage, and has empirically been linked to substantial yield losses, underscoring the importance of timely and accurate phenological monitoring. Monitoring the dynamics of crop phenology is further compounded by the inherent drawbacks of optical imaging such as clouds and smoke. However, synthetic aperture radar (SAR) systems provide complementary insights to optical satellites, where the former has the capability to operate under all weather conditions. Radarsat Constellation Mission (RCM), Sentinel-1 (S1) and Sentinel-2 (S2) data provide diverse information with less computational requirements. This study investigates the synergistic potential of the above imagery to monitor canola phenology across three geographically diverse provinces. Phenology data are meticulously collected from 36 fields across two years. Image acquisition leverages the Earth Observation Data Management System (EODMS) for RCM data and Google Earth Engine for S1 and S2 imagery. The extracted indices were used to construct field-based time series curves. Our observations have highlighted that the majority of indices exhibit notable responses during the canola flowering stage. We noted that S1-VH, S1-VH/VV, and S2-NDYI indices exhibit peaks during the peak flowering stage. Concurrently, S1-VH, S1-Radar vegetation index, and S1-co-pol purity parameters display prominent valleys during this same peak flowering period. Notably, S1-VV follows a similar, albeit more pronounced, pattern to NDVI. It demonstrates a gradual increase in index values during growth, followed by a reduction at the onset of flowering, reaching its lowest point at peak flowering, and subsequently, as flowering diminishes, experiences a rise in values. In contrast, RCM data appears to lack a discernible pattern that correlates with specific phenological stages. Synergistic use of optical and SAR data could be used for precise and accurate phenology detection, especially for the flowering stage of canola.

Macaroni Metrics: Forecasting Durum Wheat Yields in Saskatchewan using Remote Sensing Techniques and a Machine Learning approach

Sarah van Steenbergen[1], K. Nketia[1], T. Ha[1], H. Fernando[1], and S. Shirtliffe[1]
[1]Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK

Wheat is the most widely grown crop in Canada, with over 27 million acres being seeded in 2023, of which, 6 million were durum. Like all crops, the growth, development, and final yields of spring wheat are influenced by environmental and climatic factors. The objective of this research is to generate a methodology for in-season yield forecasting of spring wheat in

Saskatchewan at specified time points within the growing season. The methodology includes a comprehensive approach, leveraging satellite datasets in Google Earth Engine and applying advanced Machine Learning (ML) techniques. Variables included yield data, precipitation, temperature, soil moisture levels, drought indices and vegetation indices. This procedure emphasized an understanding the phenological development of durum wheat and identifying when the crop is more susceptible to yield-damaging effects of environmental factors such as extreme heat during the flowering and reproductive stage of development. Three ML models, Random Forest, XGBoost and Stepwise regression were investigated using a leave-one-year-out cross validation approach. The models were compared for their coefficient of determination (R2), Concordance Correlation Coefficient (CCC) and temporal and environmental stability. Data exploration found medium to high correlations with July data including temperature ($r = 0.83$), vegetation indices (up to $r = 0.83$), soil moisture and various drought indices ($r=0.68$). Stepwise regression using backwards selection was the most accurate (average R2=0.63, CCC=0.74) forecasting model and most environmentally stable and efficient at extrapolating in environments of extremes, such as a severe drought observed in 2021. This research lays the groundwork for adaptation planning on both the regional and national scale in Canada. By understanding the changing climate and future trends, breeders can tailor genotypic development for various climatic resistance factors. Finally, this research will contribute to enhancing food security by gaining an earlier understanding of final yields and durum wheat production in Canada.

Plant Breeding, Genetics, and Biotechnology

Understanding The Genetic Basis Of Winter Hardiness And Fusarium Head Blight Resistance In Winter Durum Wheat

Ritesh K. Yadav[1,2], H.S. Randhawa, G. Humphreys[3], H.S. Chawla[1], D.S. Desta[1], M. Cordeiro[4], A. Vasudevan[3], R. Ragupathy[2], and C.A. McCartney[2]
[1]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB [2]Department of Plant Science, University of Manitoba, Winnipeg, MB
[3]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa, ON
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Canadian winter wheat breeding programs prioritize Fusarium head blight (FHB) disease resistance and winter hardiness in their efforts to mitigate yield and quality losses due to FHB epidemics and winterkill. The joint Genome-Wide Association Study-Genomic Selection (GWAS-GS) approach has shown great potential for deciphering the genetic basis of complex traits, facilitating more accurate prediction of breeding values and enhancing genetic gains for difficult-to-phenotype traits and complex traits such as FHB resistance and winter hardiness. There was only a single winter durum cultivar ‘OAC Amber’ (2010) registered in Eastern Canada which was not commercialized. At present, no winter durum wheat candidates are available for testing in Canadian prairies. The broad objective of our study is to foster the development of durum wheat germplasm with enhanced winter hardiness and FHB resistance utilizing cutting-edge genomic tools and approaches and ultimately facilitate the development of field-ready winter durum cultivars for Canada in future. In order to identify valuable genetic variants for FHB resistance and winter hardiness, several GWAS models such as mixed linear model (MLM), compressed MLM, enriched compressed MLM, and fixed and random model circulating probability unification (FarmCPU) will be employed. Our project uses an assembled panel of ~250 winter durum germplasm including pure lines from Canada, Europe, and USA and winter hexaploid wheat x durum cross derivatives. The assembled winter durum panel was phenotyped in 2021-22 and 2022-23 and is being phenotyped at multi-location in 2023-24 (Winnipeg, Carman, and Ottawa) for FHB resistance and winter hardiness. Further, the accessions were genotyped for genome-wide markers using Genotyping-by-sequencing (GBS). We will provide an update about the progress of this ongoing study, to identify quantitative trait loci (QTL) for F HB resistance and winter hardiness.

Genome-Wide Association and Genomic Selection for Oil and Fatty Acid Profile in Rapeseed (Brassica napus L.)

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The improvement of yield- and seed-quality-related traits is the overarching goal of rapeseed (Brassica napus L.) breeding efforts. Genome-wide association studies (GWAS) and genomic selection (GS) are important biotechnological methods facilitating the accomplishment of breeding objectives and significant improvements in breeding cycle efficiency. There are three main objectives in this study: 1) GWAS to identify quantitative trait loci (QTL) for five seed quality traits (overall oil content, erucic, oleic, linoleic, and linolenic acids), 2) evaluating GS accuracy in predicting rapeseed hybrid fatty acid profile components, and 3) evaluating the "GS + de novo GWAS" method proposed to improve GS prediction accuracy. This project analyzes 454 Brassica napus genotypes (92 parents, 362 hybrids) grown over 48 site-years. All genotypes were genotyped via Brassica 60K Illumina SNP array. Across 24 unique GWAS analyses, consensus QTL were compiled, revealing 161 unique QTL, including 22 QTL for erucic acid. Several QTL coincide with candidate genes identified in literature. Novel QTL have also been identified for all five traits, warranting further investigation. The accuracies of nine GS models were compared in their response to adjusting population size and composition (five model training/validation populations) and marker set density (high, intermediate, and low densities), producing 135 unique analyses. Prediction accuracies range from 25.8% (oil content) to as high as 89.1% (linoleic acid content), exhibiting positive correlation to the degree of training population/test population relatedness, negative correlation to trait complexity, and no significant correlation to marker set density or model choice. Results indicate that GS is highly accurate in certain populations and traits, especially for erucic, linoleic, and linolenic acids. Accuracy of the "GS + de novo GWAS" method will be compared to conventional GS models. The accuracy of

GS in these experiments is promising for the implementation of GS technology in future rapeseed breeding programs.

Phenotypic and genetic analysis of common bean growth and development using UAV-derived data

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Canopy height, area, and volume are informative phenotypic traits used as measurements of crop growth and development. It is advantageous to measure these traits multi-temporally over the growing season to capture plant changes over time. Measuring these traits manually is a laborious, time-consuming, subjective, and impractical method prone to human error when studying large numbers of plots requiring repetitive measurements. High-throughput digital phenotyping using unoccupied aerial vehicles (UAVs) has the potential to overcome the challenges of traditional phenotyping methods and can increase the accuracy and efficiency of phenotyping and selection which ultimately better enables crop improvement and genetic gain. The objective of this work is to investigate differences in common bean (Phaseolus vulgaris) growth and development using UAV-derived canopy height, area, and volume data to perform phenotypic and genetic analyses. Canopy height was measured manually every two weeks from 6 weeks after planting until maturity. UAV flights were performed weekly beginning in the middle of June and ending at maturity. Canopy height and area data were extracted from the UAV images and volume was calculated from those measurements. A quantitative trait loci analysis was performed to identify genomic regions related to common bean growth and development traits. It is important to establish the utilization of digital phenotyping methods and improve upon them to facilitate crop improvement.

Utilizing Micropropagation to Improve Commercial Production of "Cannabis sativa L."

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The commercial production of cannabis, 'Cannabis sativa L.', has faced an increasing array of challenges in recent years, resulting in significant financial losses and numerous major players shutting their doors entirely. What seemed like a burgeoning industry has actually been (quite literally in the case of pests and pathogens) a fight to stay alive. Cannabis cannot be treated with most pesticides we apply to other crops, thus, one of the best (if not the best) tools we have is clean starting material. Conventional propagation of cannabis involves taking many stem cuttings from 'œmother' plants and rooting them to allow for enough genetically identical material (clones) to fill out commercial production rooms, commonly hundreds or thousands of plants per room. This method relies on keeping 'œmother'stock completely free of pests/pathogens as well as avoiding introduction or spread of contaminants throughout the large-scale propagation process. Micropropagation, on the other hand, provides an opportunity to produce clean plants in an exponential manner while also significantly reducing the nursery space requirement. Explants from two distinct genetic backgrounds ('KB' & 'BT') were taken from 'œmother' plants, initiated into tissue culture containers, and subcultured for several generations before being rooted in peat moss plugs within sealed trays; these constituted 'œgeneration 0' tissue culture clones (KB0 & BT0). To manage KB0 clone height in the trays, plants were cut back to roughly half and these cuttings were again rooted in sealed trays to produce 'œgeneration 1' clones (KB1). Controls were conventionally propagated from the same 'œmother' plants, and all 960 clones were flowered out together under identical conditions. Notably, BT0 clones significantly outperformed controls with a 22.14% increase in yield and 33.28% higher Delta-9-tetrahydrocannabinol concentration. Overall, this study provides evidence that micropropagation can be successfully implemented into commercial cannabis production to help address existing industry issues.

Genome-Wide Association Study (GWAS) for Leaf Rust Resistance in Canada Western Red Winter (CWRW) Wheat

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Leaf rust, caused by Puccinia triticina, is a prevalent disease of wheat that affects both yield and quality. Leaf rust resistance is an important trait that is evaluated in the registration of wheat varieties in western Canada and is an effective strategy for sustainable disease management. Lr genes that confer resistance to wheat leaf rust can be classified into seedling resistance genes that are effective at all developmental stages and are typically race-specific, adult plant resistance (APR) genes that are effective only at the adult plant stage and are race-specific, and APR genes that are non-race-specific. However, the genetic basis of this resistance remains unclear, particularly in Canada Western Red Winter (CWRW) wheat. The objectives of this research are to identify the quantitative trait loci (QTL) controlling leaf rust resistance using genome-wide association study (GWAS) and develop genomic selection (GS) models for improving leaf rust resistance in winter wheat. The study involves a wheat population (GWAS panel) of approximately 300 western Canadian winter wheat lines and 100 winter wheat lines from the USA, eastern Canada, and Europe. The GWAS panel was evaluated for leaf rust resistance in seedling tests with multiple P. triticina races. The GWAS panel was also tested for resistance in inoculated field trials in Winnipeg and Morden, Manitoba. Genotyping was done using the 40K

wheat barley Infinium array and the 25K wheat Infinium array. Both Infinium arrays are suitable for the imputation of additional SNPs. From the preliminary GWAS, some significant QTLs associated with leaf rust resistance have been identified. Furthermore, the leaf rust and SNP marker data will be used to develop GS models for estimating leaf rust resistance in CWRW wheat breeding germplasm. Improved understanding of the resistance genes and DNA markers for selecting these genes will improve the efficiency of wheat breeding programs.

Identifying a Core Set of Markers and Haplotype Structures to Track Segregation in Domesticated Sunflower (Helianthus annuus L.)

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Sunflower, Helianthus annuus L., is a member of one of the most diverse and largest families of flowering plants, the Asteraceae family. The cultivated sunflower is a diploid species ($2n = 34$) with a relatively large genome, approximately 3.6 Gb. The complexity of assembling the sunflower genome was heightened by the prevalence of long, highly similar repeats and numerous insertions and deletions. Additionally, the Helianthus genus is characterized by a labile genome prone to various rearrangements, such as inversions and translocations. These genomic features present significant obstacles in the development of a core set of markers and haplotypes for the USDA breeding program. This study employs 15 different biparental populations, comprising 1382 individuals in total, to track segregation. Each population's mapping results will contribute to a comprehensive consensus linkage map. The presence of chromosomal rearrangements and transposons, which are abundant in the sunflower genome, leads to markers that significantly deviate from the expected Mendelian segregation ratios. Only SNPs that meet the criteria of the X2 goodness-of-fit test are used for genetic linkage mapping in this study. Furthermore, this research includes LD analysis to identify sunflower haplotypes. Creating a core set of SNPs and haplotypes will significantly enhance the understanding of the genetic architecture underlying sunflower breeding. This foundational knowledge will not only facilitate the tracking of genetic segregation within domesticated sunflower populations but also pave the way for future genomic selection strategies.

Session 2: Friday, March 15, 2:30-4:00

Physiology and Ecology

Accumulation of Nitrogen and Dry Matter in Early Maturing Soybean Seed

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Protein is required in human and animal diets and the demand for plant-based protein is increasing. Soybean [Glycine max (L.) Merr.] is a legume with high seed protein and an environmentally and economically sustainable field crop. Soybean production is new to Saskatchewan and there are challenges that must be addressed for this crop to be more favourable for farmers to produce. One major challenge is to increase the seed protein concentration which is consistently lower for Saskatchewan grown soybean compared to soybean produced in Manitoba and in eastern Canada. Environment and latitude influence protein concentration and these factors likely drive lower protein in Saskatchewan; however, the specific environmental factors resulting in lower seed protein remain unclear. Furthermore, the source and sink relationships between the developing seed, elements in vegetative organs, and photosynthesis warrant investigation for soybean in Saskatchewan's growing environment. The objective of this experiment is to gain knowledge on seed growth rate, seed nitrogen growth rate, and ultimately seed protein synthesis for soybean grown in Saskatchewan. In 2022 eight soybean cultivars differing in leaf shape, node number, and maturity group rating were grown in two locations and were either unfertilized, fertilized, or had photosynthesis limited by shade cloth during the seed filling stage. At the start of the seed filling stage pods were collected every four days until physiological maturity. From these collections the seed growth rate, seed nitrogen growth rate, and effective filling period were measured and compared with in field measurements like SPAD meter readings, vegetative organ dry weight, and vegetative nitrogen content. The results from this study have provided a model for soybean seed growth rate and seed nitrogen growth rate. The important plant traits related to these seed growth patterns were determined which soybean breeders can use to address low soybean seed protein in Saskatchewan.

Unveiling the Role of Acclimation Time and Exogenous Spermine in Enhancing Strawberry Cold Hardiness

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Strawberry cultivation in the U.S. ranks third in fruit production and significantly contributes to the economy. However, widespread distribution of strawberries has been hindered by susceptibility to cold stress, resulting in increased reliance on imports. To enhance strawberry cold hardiness and extend the growing season in colder climates such as the upper Midwest, a study was conducted to explore physiological factors associated with strawberry susceptibility to cold stress employing a hybrid mode of conventional acclimation and biotechnological approaches. Initially, 10 strawberry cultivars were acclimated at 4°C for varying periods (0, 2, 4, and 6 weeks) and subsequently exposed to -16°C for 4 hours before being returned to greenhouse conditions. After the freeze treatment, significant variations were observed among the acclimated and non-acclimated plants regarding survival rate and photosynthetic parameters, while differences among genotypes were non-significant. Plants acclimated for two weeks exhibited the best average Fv/Fm and Fv/Fo responses of 0.47 and 1.49 respectively. To assess potential effects between acclimation duration and chemical treatment with spermine in mitigating cold stress, 'Honeoye' strawberries were subjected to factorial experiment involving acclimation time (1, 2, & 3-weeks) and spermine applications (0, 20 & 100 mM) applied 8 hours before freezing. One-week of acclimation resulted in the best Fv/Fm, Fv/Fo, and survival rate with 0.73, 3.83, and 64%, respectively, after exposure to cold stress (-12°C for 4 hours). However, treatment with 20 mM spermine alone resulted in notably greater Fv/Fo (2.98) compared to un-acclimated controls. Thus, strawberry plants have the potential to activate cold-responses and adopt a defensive mode upon exposure to temperatures as low as 4°C for only one week. Nevertheless, before applying biotechnological interventions to enhance the resilience of strawberries to environmental fluctuation, further investigations are needed to understand the physiological mechanisms underlying cold acclimation and chemical treatment-induced cold tolerance in strawberries.

Investigating the plant leaf epicuticular wax of Brassica carinata

J. Coward[1]
[1]Agriculture and Agri-Food Canada

NDVI before heading and abaxial stomatal features are early predictors of grain yield stability under drought stress in a Canadian heritage bread wheat panel

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This study characterized diverse genotypes in the Canadian heritage bread wheat panel for physiological and yield traits that were best linked to drought/heat stress resistance for the purpose of screening in the early developmental stages. The Stress Tolerance Index (STI) for grain yield (GY) across all 30 genotypes was used to narrow down the key, consistent morpho-phenological and yield-attributing traits based on performance in contrasting years: 2021 (drought/heat stress) and 2022 (normal year). These responses were then validated across three field seasons: 2021, 2022, and 2023. Broad sense heritability (h2bs) was found moderate to high (>0.5), signifying the importance of these traits as a selection criterion. Principle component analysis (PCA) distribution and clustering approaches were applied to identify distinct groups based on the STI-based selected variables. Five groupings were produced that efficiently clustered the genotypes, with PC1 and PC2 explaining 39.4% and 10.8% of the total trait variation, respectively. Group 1 was associated with the most drought-resistant genotypes (STI average: 0.56), whereas Group 5 was the most sensitive to drought stress (STI average: 0.393). GYT (grain yield*trait) biplot-based approach was then applied to rank genotypes based on superiority index (SI) ranking, which also effectively distinguished modern and old varieties. Next, selected traits were modeled for grain yield prediction using a stepwise forward regression approach. The regression was done in three combinations for cross-year validation, wherein the two-year dataset was tested for the ability to predict the grain yield of the remaining year, successively using an optimized model. Incorporating these multivariate models resulted in higher prediction accuracies, up to 0.694, and consistent best predictors were identified. NDVI (2 weeks prior to the week of heading) and abaxial stomatal features (stomata aperture length, file distance) were identified as potential screening tools from measurements at the early growth stage.

Assessing mycorrhizal traits to facilitate the selective breeding of forage legumes

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Arbuscular mycorrhizal fungi (AMF) and important plant symbionts provide many benefits to plants, including increased access to soil nutrients, drought tolerance, and salinity tolerance. Optimizing plant interactions with AMF has the potential to enhance agricultural sustainability. Plant-mycorrhizal interactions are not typically considered while selecting traits for plant breeding, therefore, the traits selection most often goes against mycorrhizal dependency of plants. Our experiment addressed this issue by exploring if mycorrhizal traits are correlated to forage plants' regrowth and stress tolerance and if those traits are selectable for plant breeding purposes. We checked how AMF colonization, and other mycorrhizal traits such as, specific root length, average root diameter, root tissue density are correlated to plant regrowth and drought tolerance under fertilized and unfertilized conditions. We found substantial differences between Alfalfa and Sainfoin's AMF colonization pattern. For Alfalfa, AMF colonization rate was significantly associated with greater plant growth and drought stress tolerance ($p<0.001$), For sainfoin, the relationship between AMF colonization and plant growth was not clear, however, root tissue density and average root diameter was a significant predictor for plant growth and drought tolerance ($p<0.015$). Our results report that mycorrhizal traits might be selectable for plant breeding depending on plant species' dependency on AMF.

Crop Protection

Impact of seed imbibition on seed preferences by carabid beetles

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Carabid beetles serve as significant controllers of weed seed species, distinguished for their important role in suppressing seed bank mortality and influencing population dynamics across various weed species. Recently, seed predation has gained recognition as a natural method of weed control in agricultural ecosystems. Extensive studies on ground beetle seed predation have emphasized their preferences for specific seed species. Nevertheless, the mechanistic side of choice, discrimination, and selection is a complex phenomenon that is influenced by various factors and thus, it is necessary to continue exploring the feeding ecology of granivorous beetles to better understand the possible variables that can impact their selection decisions. Seed chemical cues and physical properties can mean a criterion for seed choice influencing whether ground beetles are likely to feed on them. Imbibition on seeds has not been fully understood, it is a characteristic that can trigger chemical compound releasement and the increase in its size and it is the biological phenomenon on which this investigation is focused, showing the evaluation of seed consumption among two carabid species, Pterostichus melanarius and Amara littoralis, by exposing them to four different duration imbibition (0, 6, 12, and 24 hours) of seeds of Bassia scoparia (Kochia) and Thlapsi arvense (Stinkweed) under laboratory choice tests. Both carabid species revealed that neither P. melanarius nor A. littoralis showed a preference for consuming the seeds of B. scoparia or T. arvense. However, A. littoralis demonstrated a higher consumption rate of Kochia seeds compared to P. melanarius. Meanwhile, Stinkweed seeds appear to be the less preferred species among both weed seeds. The absence of a clear correlation between imbibition levels and seed consumption in our study emphasizes the complex nature of carabid feeding behaviors and calls for more comprehensive investigations to unravel the diverse reasons regulating their seed choices.

Evaluating the Competitive Ability of Modern Oat Varieties

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The integration of competitive crop cultivars into a crop rotation is a valuable integrated weed management (IWM) tool. Competitive crop cultivars can be used to manage weed competition when selective control by herbicides is not possible. This is especially true when it comes to the management of wild oat in cultivated oat. The objective of this research was to evaluate and compare the competitive ability of multiple modern oat cultivars. Field studies were conducted at three locations in Saskatchewan in 2021 and 2022 using 16 different oat cultivars. Oats were planted with and without weeds in a randomized complete block design over 4 replicates at each location. All cultivars were high yielding and did not differ in grain yield under weedy or weed-free conditions. Weed competition did impact oat yield, but the various cultivars responded to competition similarly. Competition had the most significant impact on CDC Morrison and ORE3542M reducing oat yields by 706.1 kg/ha and 681.0 kg/ha, respectively. Contrary to yield data, weed seed production differed significantly among oat cultivars. The greatest weed seed production was observed in ORE3542M (76.6 kg/ha), whereas the remaining cultivars had significantly lower weed seed production with CDC Baler (14.4 kg/ha) having the lowest weed seed production of the oat varieties. Overall, results suggested that the cultivars tested were variable in their competitive ability against wild oat.

Effect of Integrated Crop Management Strategies on Crop Yield and Weed Growth in Wheat Agroecosystems

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Integrated crop management (ICM) strategies, entailing the harmonization of fertilizer and weed management, remain underappreciated as a potential approach to sustainable weed control. A field experiment was carried out in 2023 at the Carman research field, Manitoba, to assess the influence of integrating weed and nutrient management techniques on crop-weed growth and yield in spring wheat (Triticum aestivum L.). A four-way factorial experiment was carried out, consisting two levels in each; fertilizer application timing (spring, fall), placement (broadcast, banding), rate (50%, 100%), weed management (Integrated Weed Management (IWM), standard) as a split-split plot design with four repetitions. IWM involved narrow row spacing (6"), high crop density (400 plants m-2), and early seeding, whereas standard weed management entailed wider row spacing (12"), lower density (200 plants m-2), and delayed seeding. Crop biomass was significantly influenced by the interaction of fertilizer rate and weed management. The combination of half rate with standard weed management had 23% greater crop biomass than half rate and IWM. Weed density and biomass significantly affected by the interaction of fertilizer timing and weed management where the combination of fall application and IWM had 75% lower density compared to spring application with standard weed management. The lowest weed biomass was observed from the combination of fall application with IWM, which was 89% lower than spring application with standard. Wheat grain yield was significantly affected by the interaction of fertilizing time, rate, placement, and weed management. The combination of spring application, side banding, and full rate with IWM had 55.2% greater grain yield than fall application, broadcasting, half rate and standard. The study's preliminary findings suggest a dynamic interplay between fertilizer and weed management, exerting a collective influence on wheat grain yield and weed growth. ICM emerges as a prospective approach for sustainable weed management, warranting further exploration.

Fungicide Timing to Mitigate Fusarium Head Blight in Cereals

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A Comprehensive Approach for Rapid Development of Sclerotinia Stem Rot (SSR) Resistant and Elite Cultivars of Canola

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Canola (Brassica napus L.) is considered one of the healthiest oil crops, which can promote infant brain development and prevent adult heart disease. However, this important crop is severely infected by the soil-borne fungus Sclerotinia sclerotiorum, which could cause up to 80% yield loss and thus cost billions of US dollars worldwide. The lack of complete and durable resistant canola cultivars and the ineffectiveness of crop rotation and chemical fungicides necessitates the development of resistant cultivars, which is laborious, time-consuming, and costly. Our objectives are to introgress and pyramid the SSR-resistant gene(s) into elite breeding lines, to develop diversified breeding lines with enhanced SSR disease resistance, and to develop molecular markers for rapid screening in the breeding program. We have generated five very strong resistant lines with very high yield potential by screening 700 BC3S2 l ines with Petiole Inoculation Technique (PIT) and Stem Inoculation Technique (SIT), followed by backcrossing with NDOLA-2, an elite breeding cultivar developed in our lab. In addition, we have genotyped and phenotyped 350 diversified breeding lines (a total of 9450 plants) in three locations in North Dakota and identified six very strong resistant canola lines. To facilitate speed breeding, we also developed 47 KASP (Kompetitive Allele Specific PCR) markers based on the SNP (Single Nucleotide Polymorphism) markers associated with SSR resistance obtained from our lab's genome-wide association mapping experiment. We got eight promising KASP markers with the potential to identify and distinguish resistant lines from the susceptible lines of canola. Our results indicate the rapid progress toward developing resistant canola cultivars with high yield potential.

Session 3: Saturday, March 16, 8:30-10:00

Agronomy and Cropping Systems

New Brassica Cultivars and Their Response to Changing Climatic Conditions in North Dakota

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Small-scale growers in North Dakota encounter difficulties in optimizing the quantity and quality of new cauliflower and broccoli cultivars because of shifting weather patterns and the prevalence of heat-sensitive cultivars. This study aims to identify high-performing cultivars and optimal planting dates for late spring planting time to boost the competitiveness of cool-season specialty crop growers in the region. The study was conducted at the NDSU Horticulture Research Farm, located near Absaraka, ND to examine the effect of planting time on cultivar performance through field experiments spread over four planting dates: May 1st, May 15th, June 1st, and June 15th. Results showed that planting early, especially in May, resulted in higher yields and better quality, and that some cultivars performed better than others. For broccoli, 'Jacaranda' yielded significantly more than any other cultivar, which was a notable attribute. On the other hand, 'Gypsy' and 'Monty' yields were about the same as the standard 'Green Magic', whereas 'Purple Peacock' and 'Romanesco' had lower yields. Similarly, for cauliflower, 'Cheddar' and 'Snow Crown' emerged as promising performers. However, all selected cultivars performed similarly to the standard 'Amazing'. Despite this, all broccoli and cauliflower cultivars showed improved performance during early planting dates, with higher temperatures during later dates adversely affecting head formation and curd size across all cultivars. These results highlight the importance of choosing the right cultivars and planting within the best time windows in North Dakota's growing conditions to reduce heat stress and maximize production.

Eye in the Sky: UAV Imagery Surveying of Canola Emergence at the Field-scale

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Measures of crop emergence are important as it affects crop yield, especially so in canola (Brassica napus), as emergence is often variable and low. Current practices to estimate canola emergence consist of time-consuming manual plant population counts that are prone to human-based inconsistencies and most likely inadequate because of the small number of subsamples collected. Unoccupied Aerial Vehicles (UAVs) have the potential to automatically sample emergence, but the subsampling intensity and pattern required to capture spatial

variability across a field in canola emergence efficiently has not yet been determined. The objectives of this research are to determine the ability of UAV imagery to collect automated emergent plant population estimates and to identify challenges when applying UAV surveying at the field scale. These objectives were tested by partnering with canola producers across central Saskatchewan to survey over 50 canola fields, approximately 65 ha in size, in the cotyledon to second-leaf stage, in June 2021-2023. Each field was point-sample-surveyed with a Mavic 2 Pro UAV with a RGB camera, taking 50 images at random locations with an average area per sample of 1.5 m2. The Convolutional Neural Network (CNN) model used to predict canola seedlings has shown an accuracy of 90.6% and an F1 Score of 0.951 in a preliminary accuracy assessment. The Excess Green Index was applied to determine ground cover in the field. Weed cover was calculated using the area of the ground cover and object detection layers. The results of this research will provide guidance on how UAV imagery will complement standard agronomic evaluations and provide quantitative canola emergence data derived from field imagery.

Precision measurement of sunflower head inclination: a trigonometry-based approach

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Sunflower (Helianthus annuus) is a widely cultivated crop which exhibits a trait known as head inclination at maturity. This trait is influenced by various structural factors, including head weight, size, and plant height. A sunflower head should be at an angle at which the head faces the ground to avoid damage from the sun and birds. While this desired angle for agricultural benefits is known, current methods, including visual estimation and an Iranian method of measuring inclined length of the stem, fail to provide precise measurements of angle. This study introduces a novel approach to mathematically measure the head inclination angle. The research, which was conducted over the 2022 and 2023 growing seasons, involved an aluminum rod equipped with measuring tape and a digital protractor to measure various height and angle components. Using the data collected, three methods were applied for measuring inclination: a reanalysis of the Iranian method, a trigonometry-based approach using angle and height measurements, and finally a linear model developed using the trigonometry approach and the difference between the height of the plant at bloom and at maturity. The linear model resulted in a formula to calculate the head angle of any plant based solely on two height measurements, the highest point of the plant at both bloom and maturity, creating a precise alternative to existing estimation methods. The resulting formula has the potential to be applied to high-throughput phenotyping methods, such as drones and ground robots, to fully automate the process of collecting head inclination data.

Plant Breeding, Genetics, and Biotechnology

Genome wide association study of stem rust resistance in winter wheat

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The fungal pathogen Puccinia graminis f. sp. tritici (Pgt) is the causative agent of stem rust on wheat (Triticum aestivum). Pgt has the potential to cause significant losses to wheat production in Canada, making it an economically important disease. No stem rust epidemics have occurred since the 1950s in western Canada due to the cultivation of resistant varieties. Stem rust is a Priority 1 disease in the western Canadian variety registration system. The genetic basis for stem rust resistance in most wheat cultivars is not fully understood. The objective of this study is to identify resistance genes present in a winter wheat association mapping population, consisting of approximately 300 hard red winter wheats from western Canada, and 100 hard red winter wheats from other regions (United States, eastern Canada, and Europe). The population will undergo Pgt inoculations and phenotypic assessment in field and indoor trials and have been tested with single nucleotide (SNP) markers spanning the wheat genome. The 25K Infinium SNP array and the Wheat Barley 40K Infinium SNP array, will be utilized within this study. Statistical analyses will identify quantitative trait loci (QTL). Field stem rust nurseries were grown at two locations, Winnipeg and Carman, Manitoba in 2023. Field trials were randomized as alpha lattice designs with two replicates per trial. Plots were 1m long and inoculated with a mixture of Pgt races. Nurseries were mist irrigated to promote disease development. Data were collected on plant height, stand, heading date, and stem rust field severity and infection response. Field trials will be repeated in 2024. Infection type data will be recorded from indoor seedling inoculations with individual races. Preliminary results from genome wide association study (GWAS) analysis suggest there are QTL of interest for resistance to stem rust located on chromosomes 2A, 2D, 5A, and 6D.

Phenotypic Insights into Fusarium avenaceum Root Rot Resistance in Diverse Pea Accessions

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Pea (Pisum sativum L.) production in Canada is negatively affected by root rot. This disease is caused by a complex of many soil-borne pathogens, notably; Aphanomyces euteiches and Fusarium sp. Across the Canadian prairies, Fusarium avenaceum is the most prevalent and devastating pathogen of the Fusarium root rot complex of pea. Although genetic resistance to root rot is tightly linked with flower and seed coat pigmentation, breeding of disease-resistant cultivars remains the single most efficient and sustainable control method for the disease. Evaluation of F. avenaceum root rot resistance in diverse pea accessions has not been reported to date. This study evaluated 20 global pea accessions and Canadian varieties with pigmented and non-pigmented flowers and seed coats for F. avenaceum root rot resistance. Of the pea accessions evaluated, 7 accessions, which have pigmented flowers and seed coats, were identified as resistant or partially resistant to F. avenaceum. This was based on their root rot severity scores and ability to tolerate F. avenaceum infection without significant ($P > 0.05$) reductions in plant height, shoot dry weight, and root dry weight. Of the 7 white-flowered cultivars evaluated, only one variety showed partial resistance to F. avenaceum when challenged with reduced conidial concentration. Root dry weight ($R = -0.86$), plant height ($R = -0.82$), and shoot dry weight ($R = -0.78$) had a strong negative correlation ($P < 0.001$) with disease severity, confirming that F. avenaceum root rot can negatively impact the growth and development of pea seedlings. This study also emphasizes our current approach to integrating phenotypic information with genomic and transcriptomic tools for marker-assisted breeding of disease-resistant varieties.

Speed editing: High throughput gene editing using Clustered regularly interspaced short palindromic repeats- CRISPR-associated protein 9 system in Brassica napus

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Clustered regularly interspaced short palindromic repeats- CRISPR-associated protein 9(CRISPR-Cas9), is a genome editing tool that uses single-guide RNA to target specific genes, enabling the development of novel plant traits and revolutionizing crop improvement. We propose to establish CRISPR-Cas9 as a high-throughput system for improving shattering tolerance in Brassica napus by targeting the INDEHISCENT, ALCATRAZ, and SHATTERPROOF genes, which are crucial in determining shattering in this species. Pod shattering occurs when pods open at maturity and disperse seeds, leading to a significant decrease in seed yields. B. napus is an allotetraploid crop with redundant multiple-copy genes, due to which altering traits through conventional methods is challenging. Further, given the goal of targeting three shattering genes, the use of multiple sgRNAs presents a challenge, as each requires its promoter, potentially complicating vector delivery due to increased construct length. We also aim to address the issue of transformation methods currently employed for transformation of CRISPR vectors into the plant genome as the conventional Agrobacterium-mediated tissue culture technique is time-consuming and leads to the development of soma clonal variations. Our main objective is to develop a high throughput CRISPR-Cas9 system in rapeseed by simultaneously editing multiple genes (IND, SHP, and ALC). We increased the efficiency of this system by grouping multiple sgRNAs into a single transcript which can then be expressed by using a single promoter. Up to this stage, the successful transformation of two genotypes of B. napus with a CRISPR vector via a novel Agrobacterium-mediated transformation has been achieved, and the screening of T0 generation derived from these plants has gained Cas9-positive putative plants using Polymerase Chain Reaction. In conclusion, sanger sequencing and phenotypic characterization of the putative plants will provide evidence that CRISPR-Cas9 has been successfully employed to improve shattering tolerance in rapeseed.

Use of test cross analysis to detect the presence of and complementation among diverse FHB resistance QTL in wheat

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FHB occurs globally and causes regular and severe wheat yield losses. In addition, trichothecenes and other toxic fungal metabolites . Resistance breeding is a highly efficient and sustainable FHB management strategy that relies strongly on the availability of resistant germplasm and is complicated by the polygenic inheritance of the trait and strong genotype X environment interactions. This study used a line (20) X tester (3) analysis to evaluate Type II FHB resistance (greenhouse) in the 60 F1 combinations and 23 parents. The three testers were heterogeneous for the presence of uncharacterized background resistance QTL, whereas one tester also has the PI277012-derived FHB resistance QTL, Qfhb.rwg-5A.1 and Qfhb.rwg-5A.2. Among the 20 pure lines and varieties, one is known to have Fhb1, another is known to have background resistance, while the remaining are either susceptible or have not been tested for FHB resistance. The primary study aim is to determine which of the 60 F1 encompass the most promising combinations of native background and/or introduced, larger effect FHB resistance QTL. The data will also be used for estimating general and specific combining abilities whereas superior parents and F1 will be used in breeding program crosses and pure line development.

Genetic studies on seed yield, seed oil, seed color, flower color, and other agronomic traits in flax (linum usitatissimum l.): unlocking the potential for improved cultivars

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Flax (Linum usitatissimum L.) is primarily grown as an oilseed crop, with most varieties having brown seed coat, while a small proportion possesses yellow seed coat. The proposed study will address the limitations and challenges in flax production, specifically related to low concentration of omega-3 fatty acid, low seed oil content, low seed yield, and low genetic diversity. To overcome these challenges and enhance the desired traits, a Multi-parent Advanced

Generation Inter-cross (MAGIC) population is created by crossing eight carefully selected diverged parents. The objective of this study is to develop breeding populations and evaluate the level of variation in seed yield, seed oil content, and fatty acid composition, with a focus on achieving a high concentration of omega-3 in the oil. The chosen parent lines, including ND Hammond, TAMF-201, K1192, N.P. (RR) 204, DILLMAN, WIERA 5 L, CIli 2056, and Telva, have specific characteristics that contribute to the overall goal of the research. These characteristics range from high yield, flower color, seed coat color, boll number, boll type, plant stature, and flowering time. The MAGIC population is generated and advanced to F7 using the single-seed descent method involving six generations of selfing in the greenhouse. Phenotyping was conducted under field conditions at Fargo and Casselton in 2023 using hill plot design due to limited seeds availability, and this year in the summer 2024 another set of field trials will be carried out at three locations Fargo, Casselton and Carrington. The data from the first-year trail is under analysis and will be available soon. Genotyping of approximately 384 selected recombinant inbred lines (RILs) will be carried out, and genomic prediction models will be developed to predict the traits of interest. This will enable the identification of lines with superior performance in terms of seed yield, seed oil content, a high percentage of omega-3 fatty acid, and yellow seed coat colors. The selected superior lines will undergo multi-location field trials to evaluate their performance across diverse environments. The best-performing lines across locations will be identified and released as commercial cultivars, contributing to the advancement and improvement of the flax industry. Overall, this study aims to overcome the limitations in flax production by creating a MAGIC population, conducting comprehensive phenotyping, and genotyping, and developing genomic prediction models. The ultimate goal is to identify and release superior flax lines with improved seed yield, seed oil content, high concentration of omega-3 fatty acid, and desirable agronomic traits, thereby benefiting the flax industry and addressing the existing challenges.

Session 4: Saturday, March 16, 10:30-12:15

Agronomy and Cropping Systems

Using ABA Antagonists to Break Seed Dormancy in Wild Rice (Zizania palustris)

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Wild rice (Zizania palustris) is a nutritionally rich grain that has been a staple crop for Indigenous Peoples for centuries. Since it is a good source of B vitamins and protein, it has gained commercial interest as a health food with studies demonstrating its potential to remediate malnutrition. Unfortunately, the high-labour costs and insufficient yields have inflated the grain's price, making wild rice inaccessible to those affected by malnutrition. Grain price can be reduced by breeding high-yield varieties; however, breeding is time-consuming due to its annual limit of selection cycles. This limit is caused by the seed's dormancy period, which requires seeds to be stratified in cold water (1-3°C) for 3-6 months. Previous studies have used both physical and chemical methods to break seed dormancy, but most methods produce non viable or weak seedlings. In lentil, soybean, and canola, ABA (abscisic acid) antagonists have been used to break ABA- and low temperature-induced seed dormancy. In this study, ABA antagonists 1019, 1092, and 1093 were evaluated, with 100 M 1019 being the most effective for breaking dormancy. For seeds stratified for one- and two-months post-harvest, the 1019 treatment had an average germination rate of 20.9% and 75.6%, respectively. The control's average was 0% and 31.4%, respectively. For seeds stratified for four months post-harvest, the average germination rates were 95.5% and 94.4% for the 1019 treatment and the control, respectively; indicating that sufficient stratification time was reached. Throughout these three trials, 1019 treated seeds produced weak seedlings with a curled phenotype caused by improper unsheathing of the leaves. Since most control seeds germinated with minimal or no curling, the ABA antagonist must be contributing to this phenotype. Further studies are required to determine a solution for this phenotype, such as limiting 1019 exposure time or supplementing additional hormones during germination.

The FHB Avengers: Uniting Genes to Save Winter Wheat

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Fusarium head blight is a floral disease of cereal crops that decreases grain yield and quantity. Effective management of this disease requires the proper utilization of host resistance. However, wheat resistance to FHB is quantitative and complex, and no genotypes are absolutely resistant against FHB. Therefore, finding FHB resistance genotypes and pyramiding them has been the focus of many wheat breeding programs worldwide. Recently, Fhb7, a stable and robust FHB resistance gene, has become available in the bread wheat background. This study utilizes a

Thinopyrum elongatum driven Fhb7 gene from a 7BS.7BL-7E translocation accession. Crosses were made between Fhb7-harboring accession XWC14-255-3-1 and ND Allision, a winter wheat cultivar, before the start of this project. Their F1 progeny (21M3) was used for the first backcrossing with four different winter wheat cultivars. Using a 90K SNP chip array, 81 geno types, including the parents and the BC1F1 were genotyped. These genotypes were also evaluated for the presence of the dominant STS marker (xwgc-2315) using gel electrophoresis. Xwgc2315 marker was present in 36 plants out of the 81 genotypes and co-segregated with the 3 SNPs at the distal end of the 7B chromosome, validating the reliability of STS marker. A single BC1F1 genotype harboring Fhb7 with superior agronomic qualities was selected for the second backcrossing with three winter wheat cultivars. The STS marker was used for selecting individuals with the Fhb7 and the final backcrossing was made with five diverse winter wheat parents to produce B3F1 combinations. Two parents were resistant cultivars with no known FHB resistance QTL, while three had both Qfhb.rwg-5A.1 and Qfhb.rwg-5A.2, other strong FHB resistance QTL. The final backcross progenies were evaluated for the presence of the dominant STS marker, the individuals with Fhb7 were selected, and the BC3F2 were planted in October 2023. The codominant STS marker xwgc-2320 marker was used to evaluate these BC3F2 individuals and all the backcross parents for identifying Fhb7 homozygotes. A different marker analysis for 16 major disease resistance QTLs was also evaluated for these individuals. Individuals with different gene pyramids have been identified which are currently under Type II resistance evaluation in the greenhouse. The marker and disease phenotyping results will be integrated to select approximately 80 of the most promising B3F2 Plants. The selected families will serve as the diverse FHB resistance germplasms for NDSU winter wheat and will be utilized for ongoing early-generation yield testing and single-seed descent inbreeding by the breeding program.

Evaluating the effect of cultivar on garlic growth and yield

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Assessing the impact of cultivar on garlic growth and yield ensures satisfactory productivity and better management of genetic resources for growers in North Dakota. A field experiment was conducted at the NDSU Horticulture Research Farm, located near Absaraka, ND to evaluate the effect of cultivar on the growth and yield of garlic. Twenty-nine garlic cultivars were arranged in a randomized complete block design (RCBD) with 4 replications. The leaf number, bulb diameter, bulb weight, scape weight and length were recorded throughout the growing season. The results showed significant differences between cultivars for all the variables evaluated. The highest bulb diameter(60.5 cm) was recorded in 'German White', while the lowest diameter (38.9 cm) was recorded in 'German Red'. The highest bulb weight(73.4 g) was with 'German White' while 'Italian Loiacono' resulted in the lowest bulb weight(21.2 g).The number of leaves was recorded at 30, 45, 60, and 80 days after sprouting (DAS). The average number of leaves was similar for all cultivars until 60 DAS when 'Ukrainian Red' had the highest number of leaves (11) and 'German Red' had the fewest leaves (7). 'Dakota White' produced the longest scapes while 'Italian Loiacono' and 'White Spring' did not produce any scapes.'German White' recorded the heaviest scapes (13.8 g). In conclusion garlic cultivar affected the growth and yield when grown under North Dakota environmental conditions. 'German White' appeared to be the most adapted to North Dakota environmental conditions while 'Italian Loiacono' and 'German Red' were the least adapted.

Investigating Interspecific Lentil ‘Lens culinaris’ and ‘Lens orientalis’ Germplasm: Near-Infrared Spectroscopy for Protein and Amino Acid Profile and Quantitative Trait Locus Analysis

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Cultivated lentil (Lens culinaris Medik.) has a relatively narrow genetic base which poses many challenges to the improvement of the crop. Introgressing traits like biotic and abiotic stress resistance from wild relatives is often hindered by linkage drag of undesirable traits including shattering and low palatability. The objective of this study was to investigate the effects of crossing with wild lentils on protein content and amino acid profile. An interspecific recombinant inbred line population, LR-68 (L. culinaris ‘CDC Greenstar’ and L. orientalis ‘IG 72643’) was grown in four site-years and seed collected. Protein and amino acid concentrations of LR-68 samples for all site-years were estimated using a previously developed NIR model (Hang et al., 2022). CDC Greenstar is a large-seeded lentil with green seed coat and yellow cotyledons and relatively low mean protein content (24.8%). IG 72643 is small seeded with a marbled brown seed coat and red cotyledons with a relatively high mean protein content (30.0%). The RILs exhibited significant variation for predicted protein content and amino acid profile, with protein content ranging from 24.0-32.8%. Quantitative trait locus (QTL) analysis was conducted to identify regions of the genome associated with protein content and amino acid profile. QTL analyses were performed on best linear unbiased predictors (BLUP) for protein and amino acid profiles. There were multiple significant QTL for protein and all amino acids. Breeders can use this to make informed decisions about maintaining or perhaps enhancing lentil quality when using L. orientalis as a source of diverse traits.

Hang, J., Shi, D., Neufeld, J., Bett, K. E., & House, J. D. (2022). Prediction of protein and amino acid contents in whole and ground lentils using near-infrared reflectance spectroscopy. LWT, 165, 113669.

Proposals

A compatibility study of cicer milkvetch in mixtures with alfalfa

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Cicer milkvetch (Astragalus cicer L.) (CMV), is a non-bloating, perennial forage legume which provides high quality pasture throughout the grazing season. It has branched roots and long rhizomes which provide resilience to grazing and promote productivity in mixtures with grasses. Cicer milkvetch often retains its leaf after frost late in the season which makes it a desirable species for late season grazing. However, CMV has a high rate of physical dormancy, in addition to slow rate of seeding growth during stand establishment. Despite its nutritional and palatable qualities, CMV produces less yields than alfalfa and regrows later in spring. Intercropping alfalfa with other forage crops has been used to mitigate frothy bloat in grazing cattle, but recent studies suggest that CMV may not be compatible with alfalfa in the same row seeding due to its sensitiveness to allelopathic effects. Thus, alternative seeding methods need to be explored to improve CMV establishment in alfalfa mixtures. The project aims to 1) identify genetic diversity of CMV cultivars in response to allelopathic effects of alfalfa, 2) evaluate optimal seeding methods for binary mixtures with alfalfa to enhance its establishment success in alfalfa mixtures.

Crop Protection

Identification and assessment of Fusarium damaged kernels based on the infection time of Fusarium graminearum on wheat

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Fusarium head blight (FHB), caused by Fusarium graminearum, is a fungal disease that affects cereal crops, including wheat. FHB results in the development of white to pink, chalky, shrunken kernels that are identified as Fusarium damaged kernels (FDKs). FHB leads to reduced yields and low crop quality, mainly by the formation of FDKs and the production of mycotoxins, specifically deoxynivalenol (DON). The current visual assessment of FDK is time-consuming, labour-intensive, costly, and error-prone. The purpose of this study is to quantify FDKs of wheat inoculated with F. graminearum at different developmental stages and to validate red-green-blue (RGB) images as an effective approach for FDK identification. This was done by using an RGB portable imaging system (BELT). The BELT system is made for non-destructive, high-resolution

top and side images of wheat kernels. Wheat kernels are loaded into a feeder and then moved down a conveyor belt into an image chamber where a camera captures top and side images of the kernels. A convolutional neural network (CNN) model was developed and trained to process and count the infected kernels to improve the conventional methods of FDK identification. This research is important because knowledge of the most vulnerable time of F. graminearum infection will assist in management strategies to mitigate the disease and the BELT will create a new consistent and accurate measurement of FDK.

Optimizing thresholds and sampling strategies for the control of lesser clover leaf weevils in Saskatchewan's red clover

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Red Clover (Trifolium pratense) is a perennial legume grown for seed production in NE Saskatchewan and is a highly important commodity in the Canadian Prairies. However, red clover seed production can be significantly decreased by up to 50% by the lesser clover leaf weevil (LCLW; Hypera nigrirostris Fab.) (Coleoptera: Curculionidae). Primary damage occurs when LCLW larvae feed on the developing shoots, flower heads, and seeds of red clover plants. Further, secondary damage occurs by the feeding of adult LCLW. The pest is traditionally controlled using insecticides, damaging to non-target insect species, notably bees, which are essential pollinators for red clover. Further, there are no established economic thresholds for control of LCLW in red clover, leading to redundant insecticide applications, which create a multi-faceted problem. Principally, the producer will have a reduced income due to additional costs associated with applying an insecticide. Additionally, pollinator populations present during insecticide applications will be significantly decreased. Lastly, there is a substantial risk of developing insecticide resistance as only one registered insecticide material exists. This study aims to generate economic thresholds and sequential sampling plans through on-farm plot trials designed to identify the yield reduction from different LCLW densities, giving producers access to LCLW management tools that will reduce input costs and environmental harm.

Determining the duration of Lygus feeding associated with scarring damage in faba bean seeds

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In western Canada, Lygus are pests of numerous cultivated plants, including canola, seed alfalfa, and buckwheat. They also significantly impact pulse crops, particularly faba beans. Their feeding behavior leads to hull perforations, seed coat discoloration, seed pitting, localized tissue wilting, and necrosis, causing a decline in quality. Depending on the region, four Lygus species: Lygus lineolaris, Lygus borealis, Lygus elisus, and Lygus keltoni, can inflict damage on faba beans. To investigate the correlation between feeding time and seed damage for Lygus, we conducted no-choice bioassays and used the EPG technique to monitor and quantify insect feeding behavior on plants. In these experiments, one Lygus was confined to a faba bean plant at the R4-R5 stage and allowed to feed for 3 hours. Subsequently, the insects were removed, and the pods were examined for signs of feeding damage.

Evaluation of Pea Aphid Feeding Behavior on Resistant Lentil Varieties and Breeding Lines in Saskatchewan

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This study uses Electropenetrography (EPG) to investigate the feeding dynamics of pea aphids (Acyrthosiphon pisum) on distinct lentil lines displaying varying degrees of resistance in Saskatchewan. Pea aphids are notorious for their detrimental impact on lentil production as they cause yield losses and compromise crop quality by extracting plant sap and transmitting viral diseases. Recent studies underscore the increasing prevalence of pea aphid infestations in Saskatchewan, and this emphasizes the urgent need for targeted research to alleviate their impact. In this research, we aim to expose the feeding patterns of pea aphids on certain selected lentil lines with unique resistance traits. By employing EPG, a sophisticated technique that monitors insect feeding activities in real-time, we analyze the electrical waveforms generated during aphid probing and feeding activities. This approach allows us to gain insights into the interactions between pea aphids and resistant lentil lines at a finer temporal scale. By correlating EPG data with the resistance levels of the lentil lines, we aim to discern specific mechanisms of resistance that deter or impede aphid feeding. This research could enhance our understanding of lentil-aphid interactions and inform the development of lentil cultivars with improved resistance against pea aphids.