NOVEMBER 6-8

2019 NAPIA BIENNIAL MEETING

The Radisson Hotel, Fargo, ND

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WEDNESDAY, NOVEMBER 6, 2019

2:00 PM	**BIC & NAPIA TOUR** NDSU Agricultural Experiment Station Research Greenhouse Complex NDSU Northern Crop Institute Brewhalla – Drekker Brewing Co.	**Bus Departs** **Last Shuttle at 6:00**
4:00 to 6:00 PM	**NAPIA Registration**	**Atrium**
5:30 PM	**NAPIA Board Meeting**	**Cityscapes Ballroom**
6:00 to 8:00 PM	**NAPIA Reception**	**Atrium**

THURSDAY, NOVEMBER 7, 2019

7:00 AM	**Breakfast**	**Cityscapes Ballroom**
8:15 AM	President's Welcome	Bunyamin Tar'an
8:30 AM	**Keynote** Five Thoughts About Pulses	Gerald Combs, Jr

Session 1: Quality and Nutrition

Bunyamin Tar'an, moderator

9:00 AM	Water Supply Affecting Pea Seed Yield and Protein Formation	Chengci Chen
9:15 AM	Strategies to Improve Pea Protein Yields in Eastern Montana: Evaluation of Rhizobium Inoculants and Foliar Nutrient Applications	Fatemeh Etemadi
9:30 AM	Towards Identification of Candidate Genes for Agronomic and Seed Quality Traits of Field Pea	Krishna Gali
9:45 AM	Iron (Fe) Absorption and Accumulation at Different Growth Stages in Chickpea (*Cicer arietinum* L.)	**Tamanna Jahan***
10:00 AM	**Coffee Break**	**Atrium**
10:30 AM	Prebiotic Carbohydrate Enriched Lentil Cultivars to Combat Obesity, Malnutrition, and Climate Change	**Nathan Johnson***

Student Presenter*

THURSDAY, NOVEMBER 7, 2019

Session 2: Genomics and Tools

Mike Grusak, moderator

10:45 AM	Long-Read Sequencing Reveals Fragile Lentil Genomes	Kirstin Bett
11:00 AM	Tools for Visualizing and Analyzing Genotype, Genetic, and Genomic Information for Pulse Crops	Steven Cannon
11:15 AM	The Pulse Crop Database: Expanding the Cool Season Food Legume Database into a Resource for Pulse Crop Research and Improvement	Jodi Humann
11:30 AM	Genome-Wide Association Study for Seed Quality Traits in Chickpea	**Alanna Orsak***
11:45 PM	Fingerprinting Pea Varieties Using Genes of Interest to Breeders and Extending the Variation Within the Green/Yellow Cotyledon Color Gene (*I*) to Wild Germplasm	Norman Weeden
12:00 PM	Expanding the Genetic Resources of *Lens* to Improve the Biological Nitrogen Fixation Ability in the Lentil Crop	**Ana Vargas Palacios***

12:15 PM	**Meritorious Service Lunch**	**Cityscapes Ballroom**
1:15 PM	**Keynote** Utilizing Field Acquired Imagery for Pulse Phenotyping	Steve Shirtliffe

Session 3: Imaging

Julie Pasche, moderator

1:45 PM	A Study of Optical Properties and Genotypic Variability in Lentils Seed Coat using Fiber Optics Spectroscopy	**Nsuhoridem Jackson***
2:00 PM	High-Throughput Phenotyping Techniques for Evaluating Aphanomyces Root Rot Resistance in Lentil	**Afef Marzougui***
2:15 PM	Estimation of Crop Volume and Growth Rates in Lentil using UAV Imagery	Sandesh Neupane
2:30 PM	High-Throughput Phenotyping Technologies in Monitoring Agronomic and Performance Traits in Pulses	**Chongyuan Zhang***

Student Presenter*

THURSDAY, NOVEMBER 7, 2019

2:45 PM	QTL Analysis for Flowering Time Across Four RIL Populations of Chickpea (*Cicer arietinum* L.)	Shweta Kalve

3:00 PM	**Break**	**Atrium**

Session 4: Genetics and Agronomics

Nonoy Bandillo, moderator

3:15 PM	Pushing Peas South: Production and Management of Spring Field Pea in Western Kansas	Lucas Haag
3:30 PM	Screening Field Pea (*Pisum sativum* L.) for Tolerance to High Salinity Conditions	**Jake Tracy***
3:45 PM	Functional Analysis of Chickpea Polygalacturonase-Inhibiting Protein and its Response to Pathogenic Fungi	**Vishnutej Ellur***
4:00 PM	Horizontal Transmission of the Mycovirus Sshadv-1 from Strain DT-8 to US Isolates of *Sclerotinia sclerotiorum*	Min Fu
4:15 PM	QTL Mapping of Lentil Anthracnose (*Colletotrichum lentis*) Resistance in Lens Ervoides Accession IG 72815 Using an Interspecific RIL Population	**Tadesse Gela***
4:30 PM	High Density Mapping of Phenological Traits in Lentil	Teketel Haile
4:45 PM	Root Rot Alters the Structure of Pea Root and Rhizosphere Microbiome and Defense-Related Gene Expression	Zakir Hossain
5:00 PM	Integration of Traditional and Image-Based Phenotyping Tools to Identify QTL for Aphanomyces Root Rot Resistance in Lentil	Yu Ma
5:15 PM	Phenological Characterization and Modeling of Diverse Lentil (*Lens culinaris* Medik.*)* Germplasm Grown in Multiple Environments	Derek Wright

6:00 PM	**Evening Reception & Poster Session**	**Atrium**

Student Presenter*

FRIDAY, NOVEMBER 8, 2019

7:00 AM	Breakfast	Atrium

8:00 AM	**Keynote** Ascochyta Does Not Sleep! Monitoring Aggressiveness in Populations of *Ascochyta* spp.	Jenny Davidson

Session 5: Pathology, Epidemiology and Disease Management

Mary Burrows, moderator

8:30 AM	Changes in Pea Yield and Root Rot Levels in Field Trials Naturally Infested with *Aphanomyces euteiches* in Alberta from 2015 – 2019	Syama Chatterton
8:45 AM	*Fusarium oxysporum* Contributes to Fusarium Root Rot Complex of Field Pea in North Dakota	**Taheni Gargouri-Jbir***
9:00 AM	Disease Management Potential of Chickpea-Flax Intercropping in the North American Prairies	Michelle Hubbard
9:15 AM	Chocolate Spot Risk Periods in Faba Bean in Alberta and Saskatchewan	Surinder Kaur
9:30 AM	Identification and Prevalence of Seedborne *Botrytis* spp. in Pulses of Montana	Swarnalatha Moparthi
9:45 AM	In-Field Distribution of *Aphanomyces euteiches* in Montana	**Carmen Murphy***
10:00 AM	Importance of *Fusarium* Species in the Field Pea: Cereals Rotation	Kimberly Zitnick-Anderson

10:15 AM	Coffee Break	Atrium

Session 6: Disease Control

Syama Chatterton, moderator

10:45 AM	Insects and Insect Vectored Pathogens in Western Canada: Status and Research	Sean Prager
11:00 AM	Vermiform Plant-Parasitic Nematodes in North Dakota Pea Fields and Effects of Pin Nematode on Plant Growth of Selected Pea Cultivars	Guiping Yan

Student Presenter*

FRIDAY, NOVEMBER 8, 2019

11:15 AM	Insensitivity to Pyraclostrobin in *Peyronellaea pinodes* Affecting Field Pea	**Dimitri Fonseka***
11:30 AM	Efficacy of Five Herbal Essential Oils for Management of *Didymella rabiei*	Lipi Parikh
11:45 AM	Effect of Leaf Surface Hairs (Trichomes) in Natural Herbicide and Aphid Tolerance in Lentil	**Ishita Patel***
12:00 PM	Pea Aphid Resistance in the *Lens* Core Collection as a Potential Means to Reduce Spread of Virus in Lentil Production Areas	Lyndon Porter

12:15 PM	**Student Presentations Award Lunch**	**Cityscapes Ballroom**

1:30 PM	NAPIA Business Meeting
2:00 PM	*Pisum* and Cool Season Legume CGC Meetings

Student Presenter*

KEYNOTE SPEAKER

Gerald F. Combs Jr., Ph.D.

Senior Scientist, Jean Mayer USDA Human Nutrition Research Center on Aging, Tufts University
Professor of Nutrition Emeritus, Cornell University

Gerald F. Combs, Jr., is internationally recognized as a leader in Nutrition; having published widely and conducted research ranging from fundamental studies with cultured cells and animal models to human metabolic and clinical investigations. His specialties include the metabolism and health roles of minerals and vitamins and the linkages of agriculture and human health in national development. He has published more than 340 scientific papers and 14 books and lectured in some 30 countries. For 28 years he was on the faculty of Cornell University, Ithaca, NY, after which he served 14 years as Director of the USDA Human Nutrition Research Center in Grand Forks, ND. He is presently a Senior Scientist at the Jean Mayer USDA Human Nutrition Research Center on Aging at Tufts University in Boston and is a Professor of Nutrition Emeritus at Cornell University. He lives in midcoast Maine.

Five Thoughts About Pulses

Imbalances in access to and consumption of nutritious foods occur the world over. Many people in low-income countries lack access to balanced diets containing varieties of foods, and many in wealthy countries have excessive intakes of food energy from diets that are often insufficient in several vitamins and minerals. Pulses (grain legumes, i.e., beans, peas, lentils) offer significant potential for improving the nutritional status in both situations. They are of medium energy density, contain twice the protein of cereal grains, are good sources of folate and dietary fiber, have slowly utilized carbohydrates that offer low glycemic loads, and are already parts of most food cultures and cropping systems. Global population growth, which is projected to double food needs by the middle of this century, will increase demands for pulses to meet protein needs. Global climate changes will shift opportunities for producing pulse crops, favoring cultivars that are drought tolerant and early maturing (to fit into triple crop rotations). Climate change is also likely to increase consumer's interest in foods with small carbon- and water footprints. This will favor pulses, particularly as they compete for meats in sustainable diets. This opportunity space, presently occupied mostly by soy, is expanding and will offer new possibilities for pulse flours and pulse-based 'further processed' foods.

Student Presenter*

KEYNOTE SPEAKER

Steve Shirtliffe, Ph.D.

Professor, Department of Plant Sciences, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon

Steve Shirtliffe grew up on a grain farm in Manitoba where received his MSc and Ph.D. in the '90s. For over 20 years, he has been a professor in the Department of Plant Sciences at the University of Saskatchewan. His position involves teaching, research, and extension in the areas of crop imaging, weed control, and agronomy. Past and research current projects have focused on the pulse agronomy, non-herbicidal weed control as well as phenotypic and agronomic applications of crop imaging using UAV, ground and satellite imagery.

Utilizing Field Acquired Imagery for Pulse Phenotyping

Utilizing remotely gathered imagery from Unpiloted Aerial Vehicles (UAVs) and ground platforms of field-grown pulse breeding trials has the potential to improve response to selection by quantifying previously unmeasurable plant phenotypes. Digital phenotypes can precisely quantify phenotypic variations that were previously only classified by breeder qualitative ratings. Within breeding programs, these phenotypes can be utilized directly as a selection criterion or to associate these with regions of the genome using structured mapping populations or unstructured diversity panels. We will present several examples of recent research (past three years) utilizing remotely gathered imagery to estimate crop volume, herbicide damage, yield, and biomass, to detect foliar disease incidence, green leaf area duration, and plant spatial arrangement. We have utilized this imagery with a variety of techniques ranging from vegetation index analysis, conventional image analysis, and deep learning with convolutional neural networks. We will discuss the applicability of these techniques and how this information is being utilized in a large breeding program.

Student Presenter*

KEYNOTE SPEAKER

Jenny Davidson, Ph.D.

Science Leader, Plant Health & Biosecurity, PIRSA-SARDI, Sustainable Systems

Dr. Jenny Davidson is the Science Leader of the Plant Health & Biosecurity Program and leader of the Pulse & Oilseed Pathology Laboratory at PIRSA-SARDI in Adelaide South Australia. She has over 25 years' experience in this discipline, including research projects on diseases of field peas, lentils, faba beans, and chickpeas. Dr. Davidson is very experienced in research of epidemiology and disease management, and resistance screening to the main fungal diseases of pulse crops, in particular, ascochyta blights of pulse crops, as well as downy and powdery mildew of field peas. She also provides an extension program for disease management consisting of timely electronic reports (CropWatch) which includes rapid response to significant outbreaks of new and emerging diseases, in coordination with cereal pathology at SARDI. Her laboratory also provides a diagnostic service to the cropping industry.

Ascochyta Does Not Sleep! Monitoring Aggressiveness in Populations of *Ascochyta* spp.

The causal pathogens of ascochyta blight on faba bean and lentil have teleomorphs (*Didymella fabae*, *D. lentis*) and anamorphs (*Ascochyta fabae*, *A. lentis*, respectively) present in Australia, increasing genetic variability in pathogen populations. Conversely, for chickpea, the anamorph *A. rabiei* is the dominant form of the pathogen causing ascochyta blight in Australia. Extensive testing by other researchers has identified only one mating type across the nation, concluding that epidemics are driven by the asexual stage of this pathogen. Despite these lifecycle dynamics, the consequent evolution and selection of aggressiveness has compromised host resistance in all host crop types. National pathogen population studies to investigate variation in aggressiveness in these Ascochyta pathogens have been conducted for more than 5 years. A wide variability in aggressiveness was found among isolates of *A. lentis*. This natural diversity, coupled with selection pressure in intensive farming systems, resulted in the loss of effective resistance in popular cultivars within 4-5 years of commercialization. The rapid loss of resistance indicates one or more major genes for resistance to *A. lentis* in these cultivars. However, there is also an apparent continuum of aggressiveness among the *A. lentis* isolates on the differential host set. This fits with the theory that resistance against necrotrophs is polygenic, and can be quantitative as well as qualitative, rather than only discreet responses as seen against biotrophs. Conversely, responses of Australian *A. fabae* isolates on a faba bean differential host set are more discriminatory, identifying 2, or possibly 3, discrete pathotypes, suggesting that major genes are more important in this system. The aggressive isolates of the three pathogens identified in these studies are used to screen germplasm in national breeding programs, and in collaborative inheritance and transcriptome studies in hosts and pathogens.

Student Presenter*

POSTERS

P01 Identification of Heat Tolerant Lentil Genotypes (*Lens culinaris*) in Field Condition through Morphological and Physiological Traits

P02 Growth, Yield and Grain Zinc Concentration Response of Chickpea (*Cicer arietinum* L.) Varieties in Zinc Deficient Soils of Southern Ethiopia

P03 Current Status and Future Oprtunities with the Pulse Crop Health Initiative

P04 QTL Mapping for Protein Concentration in Pea

P05 Iron Biofortification of Chickpea (*Cicer arietinum* L.): A Tale of Addressing Fe Deficiency Problem in Less Fe Fed Population

P06 Genomic Analyses Reveal Important Regions Controlling Carotenoid Concentration in Lentil Seeds

P07 Development of 60K Axiom SNP Chip in Chickpea and its Uses in the Next-Generation Breeding

P08 BELT: Accelerating Lentil Phenotyping with a High-throughput Imaging Platform

P09 Integration of Molecular Markers in an Applied Pulse Breeding Program

P10 Going Organic: Breeding Biofortified Pulse and Cereal Crops for U.S. Organic Cropping Systems

P11 Breeding Organic Pulse and Cereal Crops Towards Protein Biofortification for Complete Plant-based Meat

P12 Brassicaceae Cover Cropping as a Method to Control Root Rot in Field Pea caused by *Aphanomyces euteiches*

P13 Evaluating the USDA Pea Single Plant Plus Collection for Phosphorus Use Efficiency Variability

P14 Pathogen Dynamics of the Root Rot Complex in Field Pea

P15 *Fusarium* Species Affecting Field Pea, Dry Bean and Soybean in Manitoba

P16 Genetic Characterization of *Aphanomyces euteiches*

P17 Building a Better Lentil from the Ground Up

P18 Weeds as Alternative Hosts of Fusarium Pathogens Causing Root Rot in Lentils

P19 Evaluation of Field Pea Cultivars for Resistance to Root Lesion Nematode *Pratylenchus neglectus*

P20 High-selenium Lentil Combats Arsenic Poisoning in Bangladesh – More Evidence

P21 Enhancement of Cowpea Development through Molecular Breeding

Student Presenter*

Session 1: Quality and Nutrition

Water Supply Affecting Pea Seed Yield and Protein Formation

Chen C [1], Stevens B [2], Iversen W [2] and Sutradhar A [2]

[1] Eastern Agricultural Research Center, Montana State University, Sidney, MT, USA;
[2] Northern Plaines Agricultural Research Laboratory, USDA-ARS, Sidney, MT, USA

Previous studies showed significant environmental effects on pea (*Pisum sativum*) seed yield and protein concentrations. The two major environmental factors that affecting plant growth are temperature and precipitation. The objective of this study was to investigate irrigation strategies affecting pea seed yield and protein concentration. A yellow pea (cv. CDC Treasure) was planted in the spring of 2017 and 2018 in a field on Montana State University Eastern Agricultural Research Center Irrigated Farm after sugar beet crop. Three irrigation treatments were applied, i.e., 1) irrigated water was applied throughout the growing season and ended at flowering stage (EarlyIrr), 2) irrigation water was applied throughout the growing season and ended at pod filling stage (LateIrr), and 3) no irrigation was applied throughout the growing season. Results showed that no irrigation resulted in the lowest seed yield and protein concentration. EarlyIrr treatment had higher protein concentration but lower seed yield than the LateIrr treatment. The LateIrr treatment produced the greatest seed and protein yield (seed yield multiplied by protein concentration). Both seed yield and protein concentration were greater in 2017 than in 2018 due to the higher growing season air temperature and irrigation water supply.

Strategies to Improve Pea Protein Yields in Eastern Montana: Evaluation of Rhizobium Inoculants and Foliar Nutrient Applications

Etemadi F [1], Franck W [1], Rich W [2], Franck S [1] and Chen C [1]

[1] Eastern Agricultural Research Center, Montana State University, Sidney, MT, USA;
[2] Ingredion, Indianapolis, IN, USA

Plant-based proteins have received more and more attention by consumers as a healthier alternative to whey protein. Pea (*Pisum sativum*) protein has rapidly become one of the fastest-growing products targeting health-focused consumers. The purpose of this study was to evaluate the impact of different inoculant products, foliar applications of nutrients or signaling molecules, and the environment on pea seed and protein yield. Two field experiments were conducted in 2019 at the Montana State University Eastern Agricultural Research Center in Sidney, MT on both dryland and irrigated land. Pea variety Salamanca was used, and nine treatments were analyzed that included combinations of 4 rhizobia inoculant products, foliar applications of 5 plant nutrient products at 3 growth stages, and seed or foliar application of plant signaling molecules. The experimental design was a randomized complete block design with four replications. The results obtained revealed that seed yield was higher in irrigated land than in dryland. Conversely, seed protein levels were higher in dryland. Foliar application of nutrients during flowering and pod fill improved seed yields under dryland conditions. Seed protein levels in irrigated land were not significantly different amongst treatments. However, seed protein levels in dryland showed more variation and one inoculant product produced protein levels lower than the others. The protein yield varied dramatically among the treatments. Under irrigated conditions, inoculant selection was a critical factor driving protein yield. In dryland, foliar nutrient applications improved protein yields. In both instances improvements in protein yields were driven more by seed yield, rather than protein concentration. We conclude that to have higher production in yield and protein, selection of the appropriate rhizobium inoculant is important and foliar application of nutrients during reproductive growth may be beneficial in dryland settings.

Towards Identification of Candidate Genes for Agronomic and Seed Quality Traits of Field Pea

Gali K [1], Huang S [1], Jha A [1], Tar'an B [1] and Warkentin T [1]

[1] Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada

This study was designed to understand the genetic architecture of agronomic (days to flowering, days to maturity, plant height, lodging resistance, seed weight and yield) and seed quality (seed dimpling, shape, fiber concentration, starch concentration and protein concentration) traits of field pea. A genome-wide association study (GWAS) was performed with 175 global pea accessions, using field data from at least three years and two stations. The accessions were genotyped using genotyping-by-sequencing (GBS) and 16,877 high quality SNPs were used for association mapping. SNP markers associated with the test traits have been identified. These SNP sequences were used to identify the candidate genes using the recently available pea genome sequence. One hundred and seventy five candidate genes were identified within close proximity (100Kb) of 52 SNP markers identified for association with the target traits. The identified genes encode a range of proteins and their association with metabolic pathways is under study. For example, transmembrane proteins, zinc finer like proteins, heat shock proteins and protein kinases were associated with plant height. Additionally, we are also using RNA-seq methodology to identify markers associated with response to heat stress. To further refine the association mapping we have assembled a separate GWAS panel of 212 pea accessions which includes the landraces and recent Canadian cultivars. The new GWAS panel will be phenotyped from 2020-22 in multiple locations for fine mapping / identification of new trait-associated markers, particularly with reference to seed protein concentration.

Iron (Fe) Absorption and Accumulation at Different Growth Stages in Chickpea (*Cicer arietinum* L.)

Jahan TA [1], Kalve S [1], Deokar A [1] and Tar'an B [1]

[1] Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada

Chickpea (*Cicer arietinum* L.) is a staple food in many developing countries where iron deficiency often occurs in their population. The crop is a good source of protein, vitamins and micronutrients. Biofortification of Fe in chickpea seeds can be part of long-term strategy to enhance iron intake in human diet to help to alleviate iron deficiency. To develop cultivars with high Fe concentration in seeds, understanding the mechanisms of absorption and translocation of Fe into the seeds is critical. An experiment was conducted using a hydroponic system to evaluate the dynamic of iron accumulation in seeds and other organs of selected genotypes from the cultivated and the wild relative of chickpea. Plants were grown in Fe deficient and Fe sufficient condition. Six chickpea genotypes were grown and harvested at six different growth stages: V3, V10, R2, R5, R6, and RH for analysis of iron concentration in roots, stems, leaves, flowers and seeds. The relative expression of Fe-metabolism related genes including *FRO2*, *IRT1*, *NRAMP3*, *V1T1*, *YSL1*, *FER3*, *GCN2*, and *WEE1* was analyzed. The results showed that the highest and lowest accumulation of iron throughout the plant growth was found in the roots and stems, respectively. Results of gene expression analysis confirmed that the *FRO2* and *IRT1* were involved in Fe uptake and expressed more in roots under Fe sufficient condition. All transporter genes: *NRAMP3, V1T1*, *YSL1* along with storage gene *FER3* showed higher expression in shoots. Novel candidate gene *WEE1* for Fe metabolism expressed more in roots under Fe affluent condition; however, *GCN2* showed over-expression in roots of Fe deficient condition. Current finding will contribute to better understanding of Fe translocation and metabolism in chickpea seeds. This knowledge can further be used to develop chickpea varieties with high Fe in seeds.

Prebiotic Carbohydrate Enriched Lentil Cultivars to Combat Obesity, Malnutrition, and Climate Change

Johnson N [1], Thavarajah P [1], McGee R [2], Kumar S [3], Kresovich S [1,4] and Thavarajah D [1]

[1] Department of Plant and Environmental Sciences, Clemson University, Clemson, SC, USA;

[2] Grain Legume Genetics and Physiology Unit, USDA-ARS, Washington State University, Pullman, WA, USA;

[3] Biodiversity and Integrated Gene Management Program, ICARDA, Rabat-Institute, Rabat, Morocco;

[4] Advanced Plant Technology Program and Dept. of Genetics and Biochemistry, Clemson University, Clemson, SC, USA

Lentil, “poor man’s meat,” is an important staple crop in many parts of the world, particularly south Asia and Africa. In addition to protein and minerals, lentil is rich in prebiotic carbohydrates, which support a healthy digestive system and have been linked to the prevention of chronic illness, including obesity/overweight, micronutrient deficiency, type II diabetes, and cancer. In addition, certain prebiotic carbohydrates play a role in abiotic stress tolerance (heat, cold, and salinity) in plants. Consequently, biofortification of prebiotic carbohydrates in lentil is an essential target for nutrigenomic breeding efforts, both to promote human health and develop cultivars resistant to climate change. This breeding effort can be accelerated through genomic-assisted breeding. However, genetic markers have yet to be identified for prebiotic carbohydrates in lentil. To meet this need, this seed grant characterized the type and concentration of prebiotic carbohydrates in two lentil association mapping populations. Ongoing study results reveal the following prebiotic carbohydrate ranges per 100g of lentil: sorbitol (38-3631mg), mannitol (0.3-300mg), raffinose+stachyose (2.8-10.1g), and verbascose+kestose (1.6-9.7g). A genome-wide association study will be conducted on these populations using genotyping-by-sequencing data and the phenotypic data to identify quantitative trait loci for prebiotic carbohydrates in lentil.

Session 2: Genomics and Tools

Long-Read Sequencing Reveals Fragile Lentil Genomes

Ramsay L [1], Koh K [2], Caron C [1], Konkin D [3] and Bett KE [1]

[1] Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada;
[2] Global Institute for Food Security, University of Saskatchewan, Saskatoon, SK, Canada;
[3] National Research Council of Canada, Saskatoon, SK, Canada

Long read sequencing has been a game-changer for the assembly of large, repeat-laden genomes, such as lentil. Long reads allow us to span large regions of repeats that were collapsed in the previous, short-read assembly. They also allow us to see chromosomal rearrangements in other lines relative to the reference assembly. This is seen in wild lentil, as expected, but we are now seeing rearrangements within cultivated germplasm as well. We will present CDC Redberry v2.0, the newest *L. culinaris* assembly as well as some of the interesting features that are starting to be revealed through sequencing of additional lines.

Tools for Visualizing and Analyzing Genotype, Genetic, and Genomic Information for Pulse Crops

Cannon SB [1], Kalberer SR [1], Brown AV [1] Campbell JD [2], Huang W [3], Wilkey A [3], Cleary A [4], Cameron CT [4], Redsun SG [4], Berendzen J [4], Hokin S [4], Dash S [4] and Farmer AD [4]

[1] USDA-ARS, Corn Insects and Crop Genetics Research Unit, Ames, IA, USA;
[2] Department of Computer Science, Iowa State University, Ames, IA, USA;
[3] ORISE Fellow, USDA-ARS, Corn Insects and Crop Genetics Research Unit, Ames, IA, USA;
[4] National Center for Genome Resources, Santa Fe, NM, USA

As sequencing costs continue to fall, genome assemblies for multiple pulse crops are or will soon be available. In the coming years, more genomic and genetic data will soon be available for many crop species. Similarly, dense genotyping (e.g. SNP chips) have also become routine. Methods for utilizing genomic and genetic data have generally lagged data creation. We will describe new on-line tools for investigating genotype data, mapped traits, genome assemblies, and homologies across genome assemblies within and between legume species. For genotype data, a new visualization and query tool called GCViT (Genome Chromosome Visualization Tool) allows a user to pick a set of accessions and see visually where there are similarities or differences (genomic variants) between accessions. This enables a user to visualize pedigree relationships or to track introgressions or other regions of interest. We will also show on-line tools for comparing and visualizing multiple genome assemblies for a species or group of closely related species, for visualizing relationships among orthologous genes, and for quickly doing complex analyses of collections of genomic features. Lastly, we will raise some questions for researchers working in this field regarding how to manage and make accessible the rapidly-growing collection of genetic and genomic data for this important group of crops.

The Pulse Crop Database: Expanding the Cool Season Food Legume Database into a Resource for Pulse Crop Research and Improvement

Humann J [1], Crabb J [1], Cheng C-H [1], Lee T [1], Zheng P [1], Buble K [1], Jung S [1], Yu J [1], Frank M [1], McGaughey D [1], Scott K [1], Sanad M [1], Hough H [1], Coyne C [2], McGee R [3] and Main D [1]

[1] Department of Horticulture, Washington State University, Pullman, WA, USA;
[2] Plant Germplasm Introduction and Testing Research, USDA-ARS, Pullman, WA, USA;
[3] Grain Legume Genetics Physiology Research, USDA-ARS, Pullman, WA, USA

The Cool Season Food Legume Database (CSFL) is being expanded under National Research Support Project 10 (NRSP10, www.nrsp10.org) to include common bean, cowpea, pigeon pea, groundnut, lupin, and vetches. Renamed the Pulse Crop Database (PCD, www.pulsedb.org), the new online resource focuses on providing access to curated and integrated data and tools to enable pulse crop research, translation and improvement. PCD includes publicly available genomics, genetics and breeding data including genomes, genes, transcripts, genetic maps, markers, QTL, germplasm, phenotype and publications, with integrated tools to easily access, view, filter and download the data. PCD users can: view and compare genetic maps using the MapViewer tool; search markers by type, organism, and/or location; search genome sequences with BLAST; view genomes with JBrowse and the Synteny Viewer; and explore genome metabolic pathways using PathwayCyc. The Breeding Information Management System (BIMS) in PCD allows for management of breeding programs via private user accounts while also enabling access to publicly available pulse phenotype data downloaded from the GRIN database. BIMS works with the Android app Field Book for streamlined phenotype data collection and upload, or with spreadsheet templates provided for data upload. Once the breeding program data is in BIMS, the secure data can be viewed, filtered, analyzed, and archived and used to create templates for data entry. BIMS is being furthered developed to include genotype data upload and querying with more advanced analysis capability using high performance computing.

Genome-Wide Association Study for Seed Quality Traits in Chickpea

Orsak A [1], Deokar A [1], Arganosa G [2] and Tar'an B [1]

[1] Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada;
[2] Grain Innovation Lab, University of Saskatchewan, Saskatoon, SK, Canada

Chickpeas are an important source of nutrition. Global demand for improved nutritional quality is growing. Breeding efforts for Canadian varieties are increasingly targeting seed quality. Seed protein and oil content are among the important traits and are quantitatively inherited. To improve nutrition and quality of chickpeas an understanding of the genetic basis and underlying the traits is crucial. Genome-wide association studies (GWAS) have been employed to study the genetic basis and to aid in marker assisted selection (MAS) and genomic selection (GS).

A panel of 184 diverse chickpea accessions including materials developed at the Canadian breeding program were grown during the summers of 2017-18. The population was grown at two locations each year, with three replications per location. 134 kabuli and 50 desi types were included in the panel. The panel was phenotyped for total crude protein, oil content and flour colour. A 60K Axiom single nucleotide polymorphisms (SNP) chip based on the diversity in the Canadian germplasm were used to analyze the genetic diversity and population structure of the 184 chickpea accessions. Population structure analysis revealed several distinct groups, mainly composed of either desi or kabuli type accessions.

Preliminary results identified 21 SNPs associated with seed protein over six chromosomes. A candidate gene on chromosome 2 for an aspartic proteinase-like protein with a marker r2 value of 0.10 was identified. 15 SNPs were associated with seed oil across five chromosomes. A candidate gene for a bidirectional sugar transporter (N3-like) was identified on chromosome 1 with a marker r2 of 0.14.

Fingerprinting Pea Varieties Using Genes of Interest to Breeders and Extending the Variation Within the Green/Yellow Cotyledon Color Gene (*I*) to Wild Germplasm

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For variety protection applications and quality control purposes DNA fingerprints need to be discriminating, convenient, and reproducible. In pea there exists so much variability and we know so much about the genetics of traits, it seems appropriate to focus on genes (e.g. seed quality, disease resistance, plant habit) that are of particular interest to breeders. We selected 26 such genes or markers for these genes for initial sequencing, with a minimum of 3 genes on each linkage group. Eventually, conveniently amplified sections of 21 of these genes were sequenced on 96 pea varieties. In general, two to five differences (usually Single Nucleotide Polymorphisms) were identified for each gene, and each variety could be easily distinguished by various combinations of genes. We suggest that the use of these sequences will be the most practical method for describing new varieties in variety protection applications. The *I* gene (green/yellow cotyledon color) gave a relatively normal level of polymorphism within the yellow dry pea germplasm (5 alleles), but exhibited an amazingly high level in wild pea accessions (41 alleles among 50 accessions). We believe this sequence can be used as an internal 'bar code' to identify and compare wild Pisum accessions in germplasm facilities throughout the world.

Expanding the Genetic Resources of Lens to Improve the Biological Nitrogen Fixation Ability in the Lentil Crop

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Increasing the efficiency of symbiotic nitrogen fixation (SNF) could improve the productivity of lentil and reduce the use of nitrogen fertilizer. Wild lentil species are a source of biotic and abiotic stress tolerance and are used in lentil breeding programs. In this study, 15 *Lens culinaris* and 21 wild genotypes (*L. orientalis, L. tomentosus, L. odemensis, L. lamottei, L. ervoides, L. nigricans*) were evaluated for SNF ability to assess their potential for increasing SNF in cultivated lentil. Experiments were stablished under greenhouse conditions using a commercial R. leguminosarum (R) strain and nitrogen fertilizer (N). A split plot design was used with N+R-, N-R+, N-R- treatments. At flowering, nodulation traits (number of nodules-NN, nodule dry weight-NDW), shoot dry weight (SDW), root dry weight (RDW) and SDW/nodule) were estimated. Total N accumulation (mg/plant) and N2-fixed were determined using the N-difference method. Two subsequent experiments were conducted to determine seed number-SN, 1000 seed weight-1000SW and seed weight - SW. Differences were found between and within species for all parameters related to N-accumulation. *L. culinaris* genotypes exhibited higher NN and NDW compared to the other species, however a few wild genotypes accumulated 80-30 mgN/nodule, higher than the values observed for all *L. culinaris* (≤10 mgN/nodule). Grain production with R was lower compared to those plants with N only in some cultivated genotypes but not in any of the wilds. The inheritance of these traits in currently under study using interspecific populations.

Session 3: Imaging

A Study of Optical Properties and Genotypic Variability in Lentils Seed Coat using Fiber Optics Spectroscopy

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Cotyledon quality, especially color, is one of the most important market criteria in the lentils market. Thus, cotyledon color is an important quality criteria in some lentils breeding programs. Consequently, non-destructive determination of cotyledon quality using imaging techniques is an area of interest in lentils research. In this work, fiber-optic spectrometers were used to study light reflectivity and transmission properties of seed coats from 20 lentil genotypes. The aim was to investigate their transmission properties and ultimately test for protective effects against cotyledon color loss. The measurement system comprised two compact diode-array spectrometers with fiber-optic probes viewing the outside (reflectivity) and inside (transmission) surfaces of lentil seed coats, a light source, desktop computers and sample holder. The reflectivity (0°\0°) and nadir-aligned transmission spectra of seed coats of each genotype were measured (N = 20) in wavelength ranges of 250 nm to 850 nm; signal pre-treatment involved smoothing by moving average filtering using the R statistical package (R Core Team, Texas, United States). The spectra obtained showed that seed coats of all studied genotypes have significant light transmission in wavelength ranges of 350 nm to 700 nm. Genotypic variation in light transmission was tested using non-parametric multivariate analysis of variance (MANOVA assumptions not met), which revealed significant ($p < 0.01$) differences in both reflectivity and transmission properties. Relative effects tables were also produced and cluster analysis carried out to enable selection of varieties based on lower transmission and higher reflectivity at wavelengths of interest.

High-Throughput Phenotyping Techniques for Evaluating Aphanomyces Root Rot Resistance in Lentil

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Current advances in high-throughput plant phenotyping have enabled the evaluation of a large number of genotypes more rapidly, accurately, and objectively. Plant sensing technologies have generated big data in terms of the number of samples that can be screened or the number of traits that can be extracted. In this study, we evaluated Aphanomyces root rot resistance in two different panels of lentil using Red-Green-Blue (RGB) and hyperspectral imaging at greenhouse level and unmanned aerial system-based multispectral imaging at field level. We developed supervised machine learning approaches for data analysis and trait extraction. The greenhouse experiments revealed that root traits extracted from digital images were significantly correlated with disease visual scores. In the first machine learning approach, we were able to accurately predict disease visual scores using elastic net regression models (R^2 = 0.45–0.73 and RMSE = 0.66–1.00 for RGB-root traits, R^2 = 0.25–0.54 and RMSE = 1.64–0.86 for hyperspectral-root traits). In the second machine learning approach, we were able to classify root images into three classes of disease levels with an overall accuracy ranging between 63 and 78% using deep convolutional neural networks. Furthermore, the field experiment indicated that vegetation indices at plot level (single rows) were significantly correlated with disease visual scores across multiple time points ($0.36 \leq |r| \leq 0.70$, $P < 0.0001$). These findings will provide insights on how the use of high-throughput phenotyping techniques and machine learning approaches could help plant breeders to reduce subjectivity in the selection of candidate genotypes.

Estimation of Crop Volume and Growth Rates in Lentil using UAV Imagery

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Plant phenotyping is a costly and time-consuming procedure in any plant breeding program. This job is particularly tedious for the collection of time-series data that demand repetitive collection procedures and difficult for traits that require destructive sampling. Recent technological developments in digital imaging is making this work more efficient, precise and robust. This study was conducted to investigate the potential use of UAV-derived images to elucidate crop volume (representing biomass) and canopy height, as well as the derived crop growth rate of diverse lentil genotypes. UAV images were collected from a field experiment of 324 diverse lentil genotypes conducted at Saskatchewan, Canada, in the summers of 2017 and 2018. Images were pre-processed, orthomosaics were generated, plots were segmented, and height and volume data were generated for each time point. Crop growth rates were derived from sequential images. We will share the results and show how this new approach can enhance phenotyping in lentil.

High-Throughput Phenotyping Technologies in Monitoring Agronomic and Performance Traits in Pulses

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Pulse crops, such as dry pea and chickpea, are important rotational crops that provide nutrition to human diet and enrich nitrogen in soils. Pulse breeding programs focus on the development of stress tolerant, high yielding varieties. In this research, high-throughput phenotyping techniques were evaluated to assess key agronomic and performance traits in dry pea and chickpea to complement breeding programs. Visible (Red-Green-Blue/RGB) and multispectral imaging cameras were integrated with both proximal and remote sensing platforms to monitor flowering; while, thermal and multispectral cameras were used to evaluate Ascochyta blight severity in chickpea remotely. In addition, plant height was assessed using proximal and remote sensing techniques utilizing light detection and ranging (LiDAR) system and RGB imaging camera, respectively. The results indicate that flowers can be monitored with high accuracy (r up to 0.95), depending on image resolution, sensor type, flower size, background, and image processing method. Ascochyta disease severity can be monitored using features from thermal and multispectral cameras, such as canopy area, normalized difference vegetation index (NDVI), normalized difference red edge index (NDRE), and mean canopy temperature. Plant height estimated by LiDAR- and digital surface model (derived from RGB data) was highly correlated with manually measured plant height with r up to 0.91 and 0.73 for pea and chickpea, respectively. It is expected that high-throughput phenotyping technologies can improve the throughput, objectivity, and accuracy of evaluating traits and accelerate the pulse breeding efforts.

QTL Analysis for Flowering Time Across Four RIL Populations of Chickpea (*Cicer arietinum* L.)

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Flowering time is considered as one of the crucial agronomic traits for adaptation of chickpea (*Cicer arietinum* L.) in areas with short growing seasons. Changing the seasonal timing of reproduction has always been a major interest for chickpea breeders to improve varieties which can adapt to fluctuating environments. This study was conducted to map quantitative trait loci (QTLs) controlling flowering time in chickpea using four recombinant inbred populations derived from four crosses CPR-02 (ICCV 96029 × Amit), CPR-03 (ICCV 96029 × CDC Luna), CPR-04 (ICCV 96029 × CDC Corinne) and CPR-05 (CDC Luna × CDC Corinne). The RILs were genotyped using the genotyping-by-sequencing approach and Illumina® GoldenGate array. The RILs were examined for its flowering response under field conditions at two locations in Saskatchewan, Canada over two year period. Flowering data from field was used for QTL analysis. 8 QTLs in CPR-02, 11 QTLs in CPR-03, 8 QTLs in CPR-04 and 8 QTLs in CPR-05 were mapped on all chromosomes except Ca6. Major QTLs on Ca8 in CPR-02, CPR-03 and CPR-04 were identified which accounted for approximately 37%, 34% and 28% of phenotypic variations for days to flowering, respectively. QTL on Ca2 in CPR-05 was accounted for around 51% phenotypic variations for days to flowering. In addition, second major QTLs were found on Ca5 in CPR-02, CPR-03 and CPR-04 which contributed 24%, 28% and 27% PVE, respectively, whereas Ca3 in CPR-05 explained 40% phenotypic variation. QTL on Ca5 was identified in CPR-02 overlapped with the QTL on Ca5 in CPR-03. Similarly, a QTL on Ca2 in CPR-04 overlapped with QTL in CPR-05 indicating conserved regions for flowering time across different chickpea populations. We are currently examining potential candidate genes (such as CaTFL1, CaSLY1, CaELF3, CaFT, CaLFY, CaFD etc) in these QTL regions that are involved in controlling flowering time in chickpea under SK conditions.

Session 4: Genetics and Agronomics

Pushing Peas South: Production and Management of Spring Field Pea in Western Kansas

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Research into spring field pea production in western Kansas was initiated in 2009. Since then a variety testing program has been established as well as various studies into best management practices including seeding rates and in-furrow fertility. Recently, collaborate efforts have begun in early generation selection and evaluation of breeding lines under central High Plains conditions. An overview of current research and potential future opportunities will be discussed.

Screening Field Pea (*Pisum sativum* L.) for Tolerance to High Salinity Conditions

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Field pea (*Pisum sativum* L.) is an important salt-sensitive crop utilized in rotation with cereals in semi-arid cropping systems in the Northern Great Plains (NGP). Saline soils (EC > 4 dS/m) negatively impact over 10.8 million acres in Montana, the second largest producer of field pea in the US. Despite its global importance, few studies have explored field pea response to high salinity conditions outside of germination testing and even fewer have looked at tolerance to sodium sulphate (Na_2SO_4), the dominant salt affecting plant growth in the NGP. In this study, accessions within the genetically diverse USDA Pisum single plant (PSP) core collection were screened under high Na_2SO_4 conditions in germination and seedling experiments. Germination screening was conducted in petri dishes within a dark growth chamber. Accessions received H_2O (control) or 16 dS/m Na2SO4 (highly saline) solution for 8 days. The mean percent germination compared to the control was used as the indicator for tolerance. A preliminary greenhouse concentration series experiment using 7 levels of Na_2SO_4 (0, 3, 6, 9, 12, 15, and 18 dS/m), supported screening seedlings at 9 dS/m Na_2SO_4. Greenhouse screening was conducted in plastic pots of course sand media. Accessions received a nutrient solution (control) or 9 dS/m Na_2SO_4 and nutrient solution. Salinity symptom scores were assessed on days 21, 28, 35, and 38 post-sowing using a visual growth response scale of 1-9 (healthy-dead). Phenotypic measurements and the Area Under the Injury Curve (AUIC) were used as indicators for tolerance. A Genome Wide Association Study (GWAS) was conducted using the phenotypic data collected and a large (> 66,000) Single Nucleotide Polymorphism (SNP) dataset developed from the PSP core. Significant marker-trait associations, potential Marker-Assisted Selection (MAS) opportunities, and candidate breeding germplasm conferring high salinity tolerance will be discussed.

Functional Analysis of Chickpea Polygalacturonase-Inhibiting Protein and its Response to Pathogenic Fungi

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Polygalacturonase inhibiting proteins (PGIPs) are leucine-rich repeat (LRR) cell wall proteins that inhibit fungal polygalacturonases (PGs), which are key virulence factors in pathogenesis. PGs are produced during early stages of infection to degrade pectin in the plant cell wall and facilitate infection. Interaction of plant PGIPs with fungal PGs produce oligogalacturonides that can activate plant innate immunity by functioning as damage associated molecular patterns (DAMPs). PGIPs have been used to improve fungal resistance in several legumes including common bean and soybean. However, little is known about PGIPs in chickpea, the third most important pulse crop in terms of global production. The objective of this study was to characterize chickpea PGIPs. Chickpea PGIP1 (CaPGIP1) was cloned and sequenced, which matched that with the NCBI sequence except for a synonymous substitution at 720th amino acid position. A phylogenetic tree was constructed and CaPGIP1 was grouped within the cluster of legume PGIPs. Results from immunofluorescence localization carried out using a 35sCaMV:CaPGIP1-GFP reporter fusion indicated that CaPGIP1 was located on cytoplasm and predominantly on cell wall or in the plasma-membrane, which was consistent with the prediction that CaPGIP1 would be located in the extracellular space. CaPGIP1 will be over-expressed in Arabidopsis to investigate its role in disease resistance. In addition, CaPGIP1 will be expressed and extracted from yeast Pichia pastoris, and the extracted protein will be used in inhibition assays. Changes in CaPGIP1 gene expression due to fungal infection, abiotic stress and wounding will be evaluated using RT-qPCR.

Horizontal Transmission of the Mycovirus Sshadv-1 from Strain DT-8 to US Isolates of *Sclerotinia sclerotiorum*

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The mycovirus *Sclerotinia sclerotiorum* hypovirulence-associated DNA virus 1 (SsHADV-1) was discovered in the strain DT-8 of *Sclerotinia sclerotiourm* in China. The strain DT-8 is hypovirulent and can be used as an agent in biological control of Sclerotinia white mold. In order to explore the potential of using the mycovirus SsHADV-1 in the United States, attempts were made to transfer the mycovirus from DT-8 to US strains. Strain DT-8 was used as the donor and co-cultured on a 150-mm PDA plate for two weeks with the US strain WMA1 (ATCC MYA-4521) originally isolated from a pea plant in the Columbia Basin of US Pacific Northwest. The dramatic differences in sclerotial size served as a convenient morphological marker for separating the two isolates. Agar plugs were taken from near the inoculation plug of the WMA1 colony and transferred to new PDA plates and were further purified through hyphal transfers in order to generate WMA1-derived strains carrying the mycovirus SsHADV-1. Initially the WMA1-derived strains were examined for colony morphology and scleorial formation in comparison with the progenitor and donor strains on PDA. Slower growth rates and serrated colony edges suggested presence of the mycovirus, but the obviously large sclerotial size suggested the strains were derived from WMA1. Presence of the mycovirus was detected in the WMA1-derived strains using PCR with the mycovirus-specific PCR primers (CP-FP/CP-RP and REP-FP/REP-RP). Nuclear DNA markers are being developed for further confirmation of the origin of the derived strains. In pathogenicity tests, the derived strains became hypovirulent, and functioned as a biocontrol agent in reducing white mold disease on dry bean plant, features of strains carrying the SsHADV-1 mycovirus. The derived strain WMA1-V3-1 is being used as a donor in transmitting the mycovirus to other US isolates of *S. sclerotiorum*.

QTL Mapping of Lentil Anthracnose (*Colletotrichum lentis*) Resistance in *Lens ervoides* Accession IG 72815 Using an Interspecific RIL Population

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Anthracnose caused by *Colletotrichum lentis* is one of the most damaging diseases of lentil in western Canada. Two physiological races, race 0 and race 1, of the pathogen have been identified. Lens culinaris and its related species in the primary gene pool have little or no effective resistance to race 0. *Lens ervoides* (tertiary gene pool) accession IG 72815 exhibits high levels of resistance to both races. A recombinant inbred line population (N=168) from a wide cross between IG 72815 and the susceptible cultivar 'Eston' was genotyped by sequencing and evaluated for anthracnose race 0 and race 1 resistance in a growth chamber and polyhouse. Four QTL for race 0 resistance were identified on chromosomes 3, 5 and 7, accounting for more than 58.0% total phenotypic variance. Two QTLs were identified for race 1 resistance on chromosomes 2 and 3. A QTL for race 1 resistance on chromosome 3, explaining 36% of phenotypic variance, was co-localized with a major-effect QTL for race 0 resistance and was consistent with the phenotypic correlation ($r > 0.77$, $P<0.0001$) of race 0 and race 1 for the RIL population. The SNP markers linked with these QTLs will be useful in breeding for resistance through marker-assisted selection.

High Density Mapping of Phenological Traits in Lentil

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Incorporation of new alleles from exotic germplasm is crucial to broaden the genetic base and overcome challenges from new biotic and abiotic stresses in lentil. However, incorporation of valuable alleles from unadapted germplasm into elite crop gene pools is often accompanied by unwanted alleles, particularly for phenological traits that are important for adaptation to the long day environment of western Canada. Use of molecular markers would greatly enhance the precision and speed of breeding when exotic crosses are used. The objective of this study was to identify genomic regions controlling important phenological traits in lentil. We used two RIL populations: a Mediterranean (ILL 1704) × temperate (CDC Robin) set and a temperate (CDC Milestone) × south Asian (ILL 8006-BM4) set. These lines were phenotyped at Rosthern and Saskatoon, Saskatchewan from 2017 to 2019 and genotyped using a lentil exome capture assay. A major QTL for maturity was detected on chromosome five that explained 37 to 41% of the phenotypic variance at each location and combined across both locations. Two flowering time QTL were detected on chromosome six that explained 16 to 28.5% and 13 to 26.7% of the phenotypic variance at each location and across both locations. The identified QTL will be anchored to the lentil reference sequence to identify candidate genes and to develop markers for marker-assisted breeding

Root Rot Alters the Structure of Pea Root and Rhizosphere Microbiome and Defense-Related Gene Expression

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Understanding how root and rhizosphere microbiomes are affected by plant health is vital for developing sustainable crop production systems. Here we studied the impact of root rot on pea (*Pisum sativum* L.) root and rhizosphere microbiomes using amplicon metagenomic sequencing, and validated the results by expression analysis of selected genes. At early flowering, diseased and healthy samples were collected from nine fields in Saskatchewan, Canada. Bacterial and oomycete alpha-diversity (i.e., richness, Shannon index) was higher in diseased root and rhizosphere samples than their healthy counterparts, while fungal diversity was unaffected. The community structure of the root and rhizosphere microbiomes were also significantly affected by the health status of the plants, with bacterial communities exhibiting the strongest differences between healthy and diseased samples. Overall, the microbiome structures of diseased samples were more predictable than healthy samples (i.e., higher number of indicator species: 42 diseased vs. 11 healthy). We then compared the expression of pathogenesis (R genes)- and hormone-related genes in healthy and diseased roots from plants grown in a growth chamber. The expressions of most of the genes (10 out of 13) were significantly greater in diseased than healthy roots. Pathogen attack activates plant immune responses, which generally upregulate defense-related gene expression. The gene expression pattern was largely consistent with the relative abundance of indicator species. Overall, our results show key differences between the microbiomes of healthy and diseased pea. Further research into determining whether differences in the microbiome influence pea susceptibility to root rot, as opposed to root rot inducing changes in the microbiome, are merited. Combined with the current results, such information could help assess root rot risks and/or develop management strategies to improve the potential of agricultural soils to suppress disease.

Integration of Traditional and Image-Based Phenotyping Tools to Identify QTL for Aphanomyces Root Rot Resistance in Lentil

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Lentil (*Lens culinaris* Medikus) plays an important role as a nutritional source in developing countries. Aphanomyces root rot (ARR), a soil-borne disease, has emerged as one of most devastating diseases affecting lentil production in North America. The most effective and sustainable management of ARR is through the development and utilization of cultivars with high levels of partial resistance, however, no lentil cultivars resistant to ARR are currently available. In this study, we combined traditional phenotyping with features extracted from digital Red-Green-Blue (RGB) and unmanned, aerial system-based multispectral images to evaluate ARR in an F6-derived recombinant inbred line (RIL) population and an association mapping population. Genotyping by sequencing (GBS) was used to discover novel SNPs. QTL mapping across two environments identified 19 QTLs associated with ARR resistance explaining from 5.2% to 12.1 % of the phenotypic variance. GWAS detected a total of 38 QTLs within 33 linkage disequilibrium (LD) blocks, explaining 1.4% to 21.4% of the phenotypic variance, and highlighted accumulation of favorable haplotypes in the most resistant accessions. Seven QTL clusters were discovered on six chromosomes and five putative genes involved in plant disease response were detected. Expression analysis revealed four of them, encoding ABC transporter A family protein, cytochrome P450 family 71 protein, chalcone-flavanone isomerase family protein, and pectin esterase, were differentially expressed between resistant and susceptible accessions. This indicates that genes involved in secondary metabolism and cell wall modification are potentially related to ARR resistance. Our findings provide valuable insight into the genetic control of ARR and can be used to accelerate the development of lentil cultivars with high levels of partial resistance to this disease.

Phenological Characterization and Modeling of Diverse Lentil (*Lens culinaris* Medik.) Germplasm Grown in Multiple Environments

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A lentil diversity panel of 324 genotypes was grown in nine locations over three years to assess the response of phenological traits to the environmental conditions of the major lentil production regions and to evaluate a previously described photo-thermal model for predicting days from sowing to flowering (DTF). Across all site-years, the photo-thermal model had a high goodness-of-fit of R^2 = 0.888, however, in certain site-years it was unable to accurately predict DTF, warranting caution and is suggestive of temperature and photoperiod interactions and/or additional environmental factors that can influence DTF. Hierarchical clustering of principal components revealed the presence of eight cluster groups based on the responses of DTF to contrasting environments. Results from this study can be exploited by breeders looking to predict flowering time in a given environment and identify adapted genotypes with appropriate phenology under variable temperature and photoperiod sensitivity.

Session 5: Pathology, Epidemiology and Disease Management

Changes in Pea Yield and Root Rot Levels in Field Trials Naturally Infested with *Aphanomyces euteiches* in Alberta from 2015 - 2019

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Aphanomyces root rot, caused by *Aphanomyces euteiches* Drechs., was first detected in pea (*Pisum sativum* L.) fields in Saskatchewan and Alberta in 2012 and 2013, respectively, and has caused significant crop loss in both provinces. Currently, extending the cropping interval between susceptible crops and avoiding infested fields are the only root rot management recommendations for this pathogen. Field trials were conducted at four locations in Alberta from 2015 – 2019 to determine the effects of various seed treatments. Trial sites were located in producers' fields that last had peas in 2014 and had high levels of natural inoculum of *A. euteiches* and *Fusarium spp*., based on root rot ratings during the 2014 growing season. Trials were conducted in the same fields but research plots were placed at unique sites within the fields every year, with some exceptions due to producer practices. Some seed treatment products provided early season suppression of root rots at some locations, but did not result in significant yield differences. Average yields across all treatments varied from 0 to >4,000 kg/ha at different locations, regardless of disease pressure, emphasizing the seasonal and regional variability of root rot severity, and difficulties assessing impacts of root rots on pea yields. At some locations yields improved slightly as the length of time out of peas increased, but root rot severity did not, except at one location. In 2018 and 2019, *A. euteiches* and *Fusarium spp.* biomass in the roots were quantified using droplet digital PCR at 2-3 time points. At all locations, *A. euteiches* levels peaked in roots in early June, but was replaced by *Fusarium* spp. by flowering (July). Results highlight the long-term impact of *A. euteiches* on yield loss, and the lack of effective management options for this destructive pathogen.

Fusarium oxysporum Contributes to Fusarium Root Rot Complex of Field Pea in North Dakota

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Fusarium root rot is among the most important diseases of field pea. This disease complex comprises numerous *Fusarium* species. *Fusarium solani* is the primary causal agent in many areas worldwide, while *Fusarium avenaceum* is the primary root rot pathogen in the North American Great Plains. *Fusarium oxysporum* was isolated from 60% and 55% of North Dakota pea fields in 2014 and 2015, respectively, predominantly associated with root rot symptoms. Historically, *F. oxysporum* has been associated with wilt of pea and its contribution to root rot remains poorly understood. Greenhouse essays were conducted to evaluate root rot pathogenicity and virulence of 25 *F. oxysporum* isolates obtained from recent North Dakota surveys when compared to virulent isolates of *F. solani* and *F. avenaceum*. All *F. oxysporum* isolates produced brown to black lesions on tap roots, similar to those produced by *F. solani* and *F. avenaceum*, and the root disease index (RDI) ranged from 17 to 89%. The RDI of *F. solani* and *F. avenaceum* were 80% and 43%, respectively. Four *F. oxysporum* isolates were highly virulent (81-100% RDI), 20 were moderately virulent (31- 80% RDI), and one was weakly virulent (0-30% RDI). Reductions in emergence, root length and dry weight were also observed when *F. oxysporum* isolates were inoculated onto field peas under greenhouse conditions. Results from these experiments indicate that *F. oxysporum* is an important contributor to the root rot disease complex of field pea in North Dakota. Further research is needed to determine how *F. oxysporum* interacts with other soil-borne pathogens of field pea.

Disease Management Potential of Chickpea-Flax Intercropping in the North American Prairies

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Chickpea (*Cicer arietinum* L.) is nutritionally dense and potentially high-value pulse crop grown in the Canadian and US prairies. However, the disease Ascochyta blight and delayed maturity are both significant constraints to chickpea production. Intercropping is defined as growing two or more crops in the same field with at least some overlap in time. This practice has recently become insurable under Saskatchewan crop insurance. Intercropping chickpea with flax has the potential to alleviate both of these issues. Ascochyta blight, caused by the fungus *Ascochyta rabiei*, is often managed by multiple fungicide applications. However, fungicides are a significant cost to chickpea growers. Resistance to strobilurin fungicides has also been documented in the *A. rabiei* population. If chickpea-flax intercropping can reduce the number of fungicide applications needed, it could increase the profitability of chickpea production. Research conducted in Saskatchewan, Canada between 2012 and 2018, and in North Dakota, USA in 2018, as well as partial 2019 Saskatchewan data, indicate that intercropping with flax can reduce Ascochyta blight in chickpea, in some, but not all, circumstances. One North Dakota study also found Sclerotinia in monocropped chickpea, but not in chickpea intercropped with flax. These findings, combined with increasing producer adoption of intercropping in Saskatchewan, point to the need for additional research on the potential of chickpea-flax in the management of chickpea disease, to be used in conjunction with other tools. Research in Saskatchewan is currently exploring the roles of flax seeding rate, crop row arrangement and canopy microclimate in disease development. In the US, the impacts of irrigation or fungicides are being investigated. The results will help Canadian and US producers decide if, when and how to adopt chickpea-flax intercropping.

Chocolate Spot Risk Periods in Faba Bean in Alberta and Saskatchewan

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Chocolate spot, caused by *Botrytis fabae* Sard., is one of the most important diseases of faba bean (*Vicia faba* L.) in Alberta and Saskatchewan. Favorable weather conditions can initiate sporulation and secondary infection. However, information on Chocolate spot risk periods and weather factors leading to inoculum release under prairie conditions is lacking. Therefore, this study was conducted to determine the duration of inoculum discharge and infectious periods under field conditions using 3-week-old faba bean plants (cv. 'Malik' (tannin) and 'Snowdrop' (zero tannin)) as trap plants. A total of sixteen trap periods from mid-June to mid-August were assessed in 2017 and 2018. Five plants of each cultivar were placed in pots within the faba bean crop canopy for a period of four days during each trap period at locations in Lethbridge and Lacombe, AB and Saskatoon, Melfort and Scott, SK. After the exposure period, plants were incubated in the greenhouse and Chocolate spot severity was rated after 14 days. Data analysis showed significant interaction of year × location, year × trapping period and year × cultivar on Chocolate spot severity (%). Average temperature (°C) and average dew point temperature (°C) were negatively correlated with the disease severity in both cultivars while average rainfall (mm) and average relative humidity (%) were not significantly correlated with disease severity. Modelling infectious periods to weather parameters and disease risk periods is underway following the last year of the experiment, and models will be used to develop risk forecasting models for this disease.

Identification and Prevalence of Seedborne *Botrytis* spp. in Pulses of Montana

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The genus *Botrytis* includes approximately 30 species that infect over 1400 plant hosts and can be responsible for severe economic losses. Botrytis grey mold is an important disease of pulse crops. Previous research has shown that seedborne infections could lead to soft rot of seedlings and establishment problems. The objectives of the study were to identify *Botrytis* spp. associated with pulse seeds and their pathogenicity on pulse crops. *Botrytis* spp. isolates (n=103) were obtained from the pea, chickpea and lentil seed samples submitted to Regional Pulse Crop Diagnostic Laboratory at Montana State University. The isolates were characterized based on colony morphology, pathogenicity, and sequence data. Morphological features, including conidial characteristics and sclerotial production were evaluated. Sixty isolates were identified as *Botrytis cinerea*, using polymerase chain reaction (PCR) with species specific (C729+/729-) primers and restriction fragment length polymorphism for the Bc-hch locus. The identity of the isolates was further determined by amplification of glyceraldehyde-3-phosphate dehydrogenase, heat shock protein 60, and DNA-dependent RNA polymerase subunit II genes. Based on the genetic information, the other *Botrytis spp*. associated with pulse seeds include *B. euroamericana* (n=20), *B. prunorum* (n=15), *Botrytis spp.* (n=7). Pathogenicity trial for *B. cinerea, B. prunorum,* and *B. euroamericana* was conducted on leaves collected from dry pea variety-Lifter, chickpea variety-Sierra and lentil variety-Riveland. In all crops, large lesions were produced by *B. cinerea* (9.9-16.0 mm) and *B. euroamericana* (9.2-16.0 mm) compared to the control (no lesions). Lesions from *B. prunorum* were only produced in pea (4.6 mm) and lentil (11.6 mm). This study reveals the presence of diverse *Botrytis* spp. from pulse crops and could be useful for breeding programs and monitoring efforts in quarantine and exports.

In-Field Distribution of *Aphanomyces euteiches* in Montana

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Aphanomyces euteiches is a soilborne pathogen capable of causing severe losses in peas and lentils. This oomycete pathogen was detected in two northeastern Montana fields in 2016 and its incidence has been recorded in five Montana counties since its initial discovery. Between 2017 and 2019, seven fields with root rot issues on pulses were surveyed for pathogen distribution with the intention of providing guidance on sampling strategies. Soil samples were taken from transects starting at the field point of entry and moving inward to assess changes in *A. euteiches* distribution and disease severity with increasing distance from the entrance. A greenhouse bioassay used a susceptible pea variety (DS Admiral) to check for *A. euteiches* presence in soil samples and disease severity index on pea. In 2018, there was evidence of a difference ($p<0.05$) in disease severity index as measured in the greenhouse bioassay along field entrance transects from two heavily infested fields in Roosevelt County MT. Hot spots for *A. euteiches* were located at the field entrance and disease severity fluctuated with distance from the entry. This research is ongoing, with additional locations to be sampled in fall 2019.

Importance of *Fusarium* Species in the Field Pea: Cereals Rotation

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Field pea production in northwestern North Dakota has provided small grain producers a valuable rotation crop in zero- to minimum-till production. This rotation has been successful due to the nitrogen fixation credit. Diseases caused by *Fusarium* species have resulted in significant losses in field peas and small grains. The rise in Fusarium-associated damage has prompted growers to question the relationship of *Fusarium* pathogens in rotations of field pea and small grains. Root rot of field pea is caused by a complex of pathogens primarily within the genus *Fusarium*. The most common causal agent of FHB, *F. graminearum*, is not commonly associated with pea root rot; however, wheat residue may become infested with other Fusarium species. The objectives of this research were to determine the importance of *Fusarium* species isolated from wheat residue on the development of root rot in a subsequent field pea crop. During 2017 and 2018, nine and 12 fields, respectively, were selected with criteria of field peas being seeded into wheat residue from the previous season. Prior to seeding field peas, wheat residue was collected from five areas in each field. Prior to bloom, pea plants were collected from the same georeferenced areas of each field and assessed for root rot. Laboratory isolations were conducted on wheat residue and pea roots. A sub-set of recovered *Fusarium* species were used to inoculate wheat and field peas under greenhouse conditions and disease severity was evaluated. Preliminary results suggest *F. graminearum* and *F. avenaceum* were most frequently isolated from wheat residue and pea roots, respectively. Regardless of isolate source, greenhouse studies indicated *F. graminearum* caused the highest amount of disease severity on wheat, and the highest disease severity in field peas was caused by *F. avenaceum* and *F. solani.* The results from this study will improve our understanding of *Fusarium*-associated diseases in rotations of field peas and wheat

Session 6: Disease Control

Insects and Insect Vectored Pathogens in Western Canada: Status and Research

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Saskatchewan is the foremost producer of pulse crops in Canada, while the neighboring western Provinces also have areas with substantial amounts of pulse production. Despite this, many insect pests and vectored pathogens are unstudied in the region. In some instances, this is because the pests are new to the region. In other instances, this is because they have not historically represented a consistent or significant economic threat. We will present a brief history on these pests in the Canadian Prairies and an update on current status of some of these pests. Finally, we will present some ongoing research into the biology and management of these pests.

Vermiform Plant-Parasitic Nematodes in North Dakota Pea Fields and Effects of Pin Nematode on Plant Growth of Selected Pea Cultivars

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Plant-parasitic nematodes restrict crop growth and cause yield loss in field pea. A four-year survey of commercial pea fields was conducted in North Dakota to investigate nematode occurrence. A total of 243 soil samples were collected from 16 counties during 2014 and 2017. Seven genera of vermiform plant-parasitic nematodes were detected. The nematode genera, *Paratylenchus* (absolute frequency = 58 to 100%; mean density = 470 to 1,558/200 g of soil; greatest density = 7,114/200 g of soil) and *Tylenchorhynchus* (30 to 80%; 61 to 261; 1,980), were the most frequent and widely distributed. *Pratylenchus* and *Helicotylenchus* were identified in one-third of the counties surveyed with mean densities at 43-224 and 36-206/200 g of soil, respectively. *Xiphinema* was found relatively frequently but at low densities. *Hoplolaimus* and *Paratrichodorus* were rarely detected at lower densities. Greenhouse experiments were conducted to determine the reproductive ability and effects of the most prevalent nematode, pin nematode (*Paratylenchus nanus*) on field pea cultivars. Reproduction of *P. nanus* was determined on seven field pea cultivars using naturally infested field soils at low (1,500/kg of soil) and high (4,500/kg soil) initial densities. Nematode effects on plant growth and seed yield were evaluated at 4,500 *P. nanus*/kg of soil by artificially inoculating *P. nanus* on six field pea cultivars. Reproductive factor of *P. nanus* was observed to be greater at the low density than the high density of the nematode. In experiments evaluating *P. nanus* effects on cultivar growth, the nematode (4,500 P. nanus/kg) caused reduction ($P < 0.05$) of plant height in most cultivars tested, and also significantly impacted dry shoot weight and seed weight in some tests. This research demonstrated for the first time the negative impact of *P. nanus* on field pea in controlled greenhouse conditions, which is an important step towards developing management strategies to improve the productivity of this crop.

Insensitivity to Pyraclostrobin in *Peyronellaea pinodes* Affecting Field Pea

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Ascochyta blight, one of the most destructive foliar diseases of field pea, is favored by cool, wet weather from bloom until mid-pod development. The disease is caused by a complex of host-specific fungal pathogens, including *Peyronellaea pinodes, P. pinodella,* and *Ascochyta pisi*. The three Ascochyta blight pathogens infect all above-ground parts of the pea plant including stems, leaves, pods, and seeds. Seed quality and quantity are reduced through seed discoloration and deceleration of seed development, respectively. The application of foliar fungicides is necessary under environmental conditions conducive for disease development. Three modes of action are registered for Ascochyta blight in North Dakota: quinone outside inhibitors (QoI), demethylation inhibitors and succinate dehydrogenase inhibitors available as single modes of action and in premix combinations containing two modes of action. Reduced efficacy of QoI fungicides on Ascochyta blight was observed under field conditions in North Dakota in 2016. Subsequent in vitro and greenhouse evaluations indicated reduced sensitivity of pyraclostrobin in *P. pinodes*. Isolates collected from two locations in 2017 and 2018 exhibited resistance to pyraclostrobin in mycelial growth assays. In vitro resistance factors ranged from approximately 5 to >1,400 when compared to sensitive isolates. Disease control of some resistant isolates was less than half that of sensitive isolates at 100 µg/ml pyraclostrobin (Headline®) in greenhouse efficacy tests. Samples were collected in 2019 from across pea producing regions of North Dakota to evaluate the frequency and distribution of QoI resistant *P. pinodes* isolates. High frequencies and vast distribution of resistant isolates will result in the fungicide to be of no value to growers. Implementing resistance management tactics may delay, or prevent the development of a fully resistant *P. pinodes* population.

Efficacy of Five Herbal Essential Oils for Management of *Didymella rabiei*

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Ascochyta blight, a major disease problem of pulses, reduces yield and seed quality. Control relies primarily on fungicides. Demand for organic pulse crops has necessitated the search for effective and safe disease management. Previous studies identified in vitro inhibition of pathogen with herbal essential oils (EO)-palmarosa, oregano, clove, cinnamon, and thyme. The objectives of this study were to test inhibitory effects of EOs on *D. rabiei* isolates, determine their effect on seed health and germination, and evaluate their *in-vivo* efficacy to control *D. rabiei.* Inhibitory effects on 11 isolates were tested with EOs and fungicide (Headline SC) infused food poisoning method. Oregano, clove, cinnamon, and thyme oils at 1/1000 dilution completely inhibited all isolates. EOs (1/250, 1/500, & 1/1000 dilutions; 0.1ml/g seed) and fungicide (MERTECT 340-F; 0.237mg ai/seed) effect on seed health and seed germination was tested on Ascochyta-infected seeds from Regional Pulse Crop Diagnostic Lab. Seed health was tested by plating 20 seeds of each treatment on potato dextrose agar and scored for disease incidence. Higher incidence was noted with higher EO dilution; e.g. incidence with palmarosa at 1/1000 was high (100%) followed by 58% at 1/500 and 20% at 1/250 (SE 3.2, $P \leq 0.05$). Seed germination was determined with a rolled towel assay. Only clove oil (1/250) reduced germination compared to untreated seeds (81% vs 94%; SE 1.6, $P \leq 0.05$). Efficacy of EOs (1/1000) and Headline SC (0.29lb ai/A) was evaluated *in vivo* on chickpea varieties-Sierra, Leader and Orion. Foliar treatments and spore inoculation (106-108) was incorporated 2 weeks after planting. Across all varieties, oregano (30-60%; SE 3.2-3.8) and thyme (30-45%; SE 3.1-3.8) oils effectively reduced disease severity compared to control (54-81%; SE 3.1-3.7) and were comparable to fungicide (23-35%; SE 3.2-3.8) at $P \leq 0.05$. Effective use of EOs in integrated pest management of pulses can minimize chemical use over time.

Effect of Leaf Surface Hairs (Trichomes) in Natural Herbicide and Aphid Tolerance in Lentil

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Lentil (*Lens culinaris* Medik.) is an important pulse crop of the Canadian agriculture industry. While cultivated lentil varieties are grown commercially worldwide and have been bred for agronomic traits such as high yield, tall stature, and large biomass; their wild relatives are native to extreme conditions in the Mediterranean basin and have lower yield, shorter stature, and lower biomass. However, research has shown that wild lentils have the potential to be used as sources of genetic diversity in making cultivated lentil drought proof and disease resistant. In our experiments, we looked at trichomes, or surface hairs on lentil leaves, which we have found to vary greatly in density and length among wild and cultivated lentil genotypes. Wild lentil species, specifically *Lens tomentosus*, have greater density of trichomes on its leaf surface as compared to cultivated lentil, *L. culinaris*. We evaluated differences in aphid fecundity on wild vs. cultivated lentil. Pea aphids are a significant pest in lentil that can cause both direct damage by feeding, as well as indirect damage by spreading viruses. Preliminary results from our research suggest that trichomes might not have a significant role to play in influencing pea-aphid maturity and development in lentil. Additionally, we assessed the response of wild and cultivated lentil to herbicide and evaluated how trichomes influence retention of herbicide droplets on lentil leaves. Being very susceptible to herbicides as well as poor competitor with weeds, lentil has few herbicides registered for use in Canada. We found that trichomes reduce herbicide retention on lentil even when mixed with nonionic surfactant, which is often added to herbicides in the field for increased retention. Our preliminary results suggest that breeding for more trichome coverage might impart natural herbicide tolerance in lentil and might be a useful trait for sustained lentil production.

Pea Aphid Resistance in the *Lens* Core Collection as a Potential Means to Reduce Spread of Virus in Lentil Production Areas

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Pea aphid (*Acyrthosiphon pisum*) is the primary aphid vector of viruses in lentil production areas of the U.S. Pacific Northwest. Aphid reproduction rates on different lentil genotypes impact population levels, which can affect the movement of aphids and spread of the viruses they vector. Lentil (*Lens culinaris*) accessions (188) from the USDA-NPGS *Lens* Core Collection were screened for their ability to inhibit reproduction rates when a single aphid was placed on a leaf at the third node under greenhouse conditions and the number of nymphs and adults present on each plant were determined after 10 days in replicated, repeated trials. Six accessions (PI 163589, PI 193547, PI 212100, PI 297284, PI 432033, and PI 432085) held mean aphid reproduction rates below 1 aphid after 10 days of feeding and are considered highly resistant accessions. Mean reproduction rates of aphids on accessions ranged from 0.17 to 57.0. A genome-wide association study was used to identify quantitative trait loci (QTL) associated with the resistance and four highly significant QTL associated with the number of nymphs reproducing on the plants were located on Chromosomes 1, 2, 4 and 7 explaining 5.3, 10, 10.7 and 16.2% of the total phenotypic variation observed, respectively. In addition, two QTL on chromosomes 1 and 4 associated with the number of adults reproducing explained 3.1 and 6.6% of the variation, respectively. This information combined with screening of lentil accessions for resistance to the major viruses impacting lentil production will be utilized in an integrated pest management approach to limit the impact of virus and aphids on lentil production.

Poster Presentations

P01 Identification of Heat Tolerant Lentil Genotypes (*Lens culinaris*) in Field Condition through Morphological and Physiological Traits

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The elevated temperatures, particularly in tropical and subtropical regions, are markedly affect the growth and yield of various pulses including lentil (*Lens culunaris* Medik.). Heat stress is detrimental to all growth stages from germination to maturity, reproductive stage is the most sensitive. So, it is utmost necessity to find out heat tolerant genotypes and their inherent mechanism. In our two-year (November 2016 - March 2018) field study, ten promising lentil genotypes (selected from previous study) were screened against high temperature. Heat stress was imposed by altering sowing dates i.e. 15th November (Normal Sowing, NS), 5th December (Late Sowing, LS1) and 20th December (LS2) at three geographical locations i.e.Gazipur, Ishurdi and Jessore. Experiments were conducted in randomized complete block fashion with three replications. Field evaluations were studied on different morphological and physiological traits. Among different genotypes, the highest number of viable pollen/plant (70.72), pods/plant (44.67), 100 seed weight (3.10 g), yield/plant (2.37g) and yield/ha (1441) were recorded from G2 for both years at LS2. Leaf level antioxidants were also examined. Late-sown (LS2) plants produced more superoxide dismutase (SOD), catalase (CAT) and ascorbate peroxidase (APX) than NS plants. Genotypes G3 produced most APX under LS2 conditions. Genotypes G3, G6 and G7 had the most enzyme activity in respect of heat tolerance. Apart from this, analysis of variance exhibited significant effects on genotype (G), environment (E), and genotype × environment (G×E) interaction on grain yield over three locations. Based on grain yield and stability performance, G3 ranked first while the worst performing genotypes were G9 and G10. Ishurdi location identified as an ideal environment for growing lentil in high temperature. Based on stable response across the environments revealed that genotypes G3, G6, and G7 may considered as good sources for heat tolerance breeding program.

P02 Growth, Yield and Grain Zinc Concentration Response of Chickpea (*Cicer arietinum* L.) Varieties in Zinc Deficient Soils of Southern Ethiopia

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Field experiment was conducted on zinc deficient soil at three locations in the Southern Nations Nationalities and Peoples Region of Ethiopia during the 2012 and 2013 cropping seasons to evaluate growth, yield and grain zinc concentration response of chickpea genotypes. Fifteen chickpea genotypes were evaluated in a randomized complete block design with three replications. Combined analysis across six environments (location-year) revealed that the introduced chickpea genotypes provided the highest plant height and above ground biomass than either local or the improved varieties. Significantly highest number of pod bearing branches, number of pods plant-1 and number of seed pod-1 were obtained from landraces. The mean grain yield of 2895kg ha-1 of Naatoli was the highest whereas the yield obtained from the introduced materials were the least except FLIP07_81C, which gave relatively better yield (2300kg ha-1) among the introduced materials. The variety Arerti and the introduced FLIP07_27C gave the highest grain zinc concentration of 47.5ppm and 47.4ppm, respectively. Moreover, varieties differed in their zinc and agronomic efficiency. Zinc efficiency of land race (Wolayita local) found to be highest (88.1%), while 33.4% of the introduced material (FLIP07-81C) was the least. 68.4 kg yield increase due to a kg zinc application to genotype Naatoli was the highest while 11.5 kg yield increase kg-1 zinc application of wolayita local was the least. This result therefore, could be concluded that the varieties with high yield and highest agronomic efficiency (Natoli), the variety with better seed zinc concentration (Arerti), and landrace (Wolayita local) with highest zinc efficiency could be an attractive option for resource poor farmers who cannot afford fortified foods for their zinc nutrition deficiency.

P03 Current Status and Future Oprtunities with the Pulse Crop Health Initiative

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The Pulse Crop Health Initiative (PCHI), administered through the USDA, Agricultural Research Service, Edward T. Schafer Agricultural Research Center in Fargo, ND was inaugurated in fiscal year 2018. The goal of the Initiative is to use cooperative research on pulse crops (dry beans, dry peas, lentils, and chickpeas) to provide solutions to the critical health and sustainability challenges facing the citizens of the United States and the global community. Expected outcomes of this Initiative are to discover and promote the health and nutritional benefits of regular pulse consumption, to enhance the sustainability of the global food supply through optimized production of pulses, and to increase the consumption of pulses through enhanced functionality of whole pulses and pulse ingredients in foods. The Initiative is guided by a Steering Committee that includes commodity group, food industry, health community, and ARS representatives. A comprehensive research plan has been drawn from a previously developed Pulse Health Initiative Strategic Plan, which arose from planning sessions that included industry, academic, and government representatives. Each year, proposed plans-of-work are solicited for cooperative projects that fall within the scope and priorities of the Initiative. These proposals are reviewed by independent scientific review panels and by stakeholder research committees. In fiscal year 2019, 46 proposals were received and 24 projects were approved for funding as part of the Initiative. In this presentation, we will provide an update on the breadth of the current projects, plans for future research priorities and opportunities, and information on how to contribute to this new Initiative.

P04 QTL Mapping for Protein Concentration in Pea

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Seed protein concentration is an important quality character in legumes that is influenced by both genotypic and environmental factors. The present study used QTL mapping to discover genetic factors associated with protein concentration in pea (*Pisum sativum* L) seed. A field study was conducted at two different locations (Spillman and Whitlow) using 154 recombinant inbred lines (RILs) derived from a cross between cv. 'Aragorn' a round, green, dry pea and cv. 'Kiflica', a wrinkled green pea. 1609 single nucleotide polymorphisms (SNPs) previously identified using GBS were used to identify putative QTLs for protein concentration. Six QTL, identified on four linkage groups (LG II, LG IV, LG V and LG VII), explained 3.1-25.4% of the variance (LOD 2.6-14.8). QTL on LG V, Prot-Ps5.1, explained up to 25.4% of the phenotypic variation for seed protein concentration and could be used in marker-assisted selection. The identified QTL have potential for use in MAS through trait predictions in breeding programs after further validation in other populations and environments.

P05 Iron Biofortification of Chickpea (*Cicer arietinum* L.): A Tale of Addressing Fe Deficiency Problem in Less Fe Fed Population

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Micronutrient deficiencies in human populations are one of the major global health issues. Among all micronutrient deficiency iron deficiency (ID) is the most common nutritional disorder due to insufficient absorbable iron, especially in less iron fed population. Chickpea (*Cicer arietinum* L.) is the second most important pulse after dry bean with good source of protein; but low bioavailability of Fe like other pulse crops. Biofortification, a process of enriching the nutrient content of staple crops by providing a sustainable and cost effective strategy such as: mineral fertilization, is one of the ways to address Fe deficiency problem in less developed countries. Chickpea (*Cicer arietinum* L.) biofortification is a possible solution for the ID problem. A chickpea biofortification experiment was conducted at the University of Saskatchewan to evaluate the effect of different doses iron fertilizer (0,10 kg/h and 30 kg/h of Fe-EDDHA) on 18 chickpea cultivars. The experimental design was arranged as with 4 replications at Elrose and Moose Jaw, Saskatchewan in 2015 and 2016. Total iron concentration across 18 different chickpea genotypes differed significantly between unfertilized and fertilized cultivars, ranging from 50 ppm to 53ppm. Cultivars X05TH20-2 and Frontier were increased iron concentration level from 57 ppm to 59 ppm and 56 ppm to 58ppm, respectively after adding Fe fertilizer in both location in the year 2015 and 2016.

P06 Genomic Analyses Reveal Important Regions Controlling Carotenoid Concentration in Lentil Seeds

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Genotypic date from 100 lines of a lentil diversity panel (LDP; 50 yellow and 50 red cotyledon) and 120 lines of LR-68, a recombinant inbred line population derived from a cross between a red cotyledon wild (IG 72643) and yellow cotyledon cultivated (3339-3) lentil, were obtained from an exome capture array. Both populations were analyzed for carotenoids, including violaxanthin, lutein, zeaxanthin, and β-carotene, using high-performance liquid chromatography (HPLC). In general, the concentration of the carotenoid components was higher in red cotyledon lentils compared to the yellow ones. β-carotene was present in less than 5% of the individuals in both populations. A genome-wide association study for cotyledon color in the LDP lines identified a major peak on chromosome 1 where we have previously mapped Yc. In LR-68, the cotyledon color also mapped on chromosome 1. QTLs were also identified for each carotenoid component, including violaxanthin, lutein, zeaxanthin, and total carotenoids. The combination of a diverse genetic panel, accurate phenotyping for carotenoids and high throughput genotyping resulted in the identification of important genomic regions associated with carotenoid concentration in lentil seeds.

P07 Development of 60K Axiom SNP Chip in Chickpea and its Uses in the Next-Generation Breeding

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Chickpea (*Cicer arietinum* L.) cultivars with improved ascochyta blight resistance, early flowering, superior visual seed quality and high nutritional value have been the major goal of the Canadian chickpea breeding program. Next generation genotyping tools such as DNA chip will greatly enhance genetic study and molecular breeding in chickpea. We resequenced 251 diverse accessions from the Canadian chickpea collection. Resequencing was completed with a range of 8 to 32X sequencing depth, and reads were aligned to the CDC Frontier reference genome. On an average 625,063 SNPs per genotype were identified. Based on the array design criteria of the manufacturer's protocol and minor allele frequency of 10%, we selected 61,669 SNPs and used for designing chickpea Axiom® SNP chip. A total of 56,816 SNPs were located on 8 chickpea chromosomes, whereas 4,853 SNPs were located on unplaced scaffolds. Around 59% of these SNPs are located within the annotated genes, while the remaining SNPs are located in inter genic regions. The chip was used to develop dense genetic maps of five RIL populations and a consensus map that allow high precision mapping of important traits in chickpea. The chip was also tested for association analysis using a panel of 185 chickpea accessions that had been evaluated for multiple agronomic traits across multiple locations and years in Saskatchewan. Markers associated with important traits will be further used for selection of important traits in breeding program. The chip was also examined for its prospect in genome selection in chickpea breeding.

P08 BELT: Accelerating Lentil Phenotyping with a High-throughput Imaging Platform

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Seed quality traits including seed size, shape, color and pattern are determining factors for the market price of lentil. These traits are traditionally evaluated visually, which not only is a very laborious and time-consuming task, but is also lacking in precision and error-prone. We have developed BELT (Better Evaluator of Lentil Traits) – an imaging and computational device that takes images of single seeds from two different views (top and side) and then delivers metrics related to size, shape and colour. Data will be shared to demonstrate the utility of BELT for a range of seed phenotyping activities.

P09 Integration of Molecular Markers in an Applied Pulse Breeding Program

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Pulse crops including pea, lentil, and chickpea are important crops across the northern tier states and the upper Midwest region including North Dakota and eastern Montana (Mon-Dak) lead the nation in production, accounting for about 80 percent of total US pulse production. The Pulse Breeding Program at North Dakota State University continues to develop new high-yielding varieties of pea, lentil and chickpea with increased resistance to pest and diseases and superior quality traits, best suited for landscapes and climate of the Mon-Dak region. The breeding program uses the conventional breeding method and a network of controlled environment and field experiments to develop elite breeding lines. While breeders have successfully used the conventional procedure to develop better varieties, making this process faster and more efficient is a perennial challenge for plant breeders. The emergence of cost-effective high-throughput genotyping and modern sequencing technology are revolutionizing plant breeding. The plummeting costs of genotyping are allowing crop breeding programs to routinely genotype breeding lines with gene-based and genome-wide DNA markers at a large scale. We aim to test and integrate marker-assisted selection to increase the accuracy of selection for large-effect genes conferring disease resistance. For traits with complex genetic architecture, we aim to systematically evaluate the efficacy of genomic selection for seed yield and quality traits. Our exploration and implementation of molecular markers for pulse breeding would spur interest to other pulse breeding programs and will provide a big step forward for integration of genomic selection in a public breeding program.

P10 Going Organic: Breeding Biofortified Pulse and Cereal Crops for U.S. Organic Cropping Systems

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Currently, there is a widespread acceptance within the agriculture community that organic agricultural systems, when properly managed, are environmentally friendly and more sustainable than high-yielding conventional farming systems. Organics have become more popular with both consumers and producers, as they are becoming more cognizant of the environmental and health benefits of organics.

As part of the USDA Organic Agriculture Research and Extension Initiative (OREI), this project aims to "solve current organic agriculture issues, priorities, or problems through the integration of research, education, and extension activities"(USDA-NIFA, 2019). To accomplish the task at hand, the project's research objectives and goals directly address the crucial demands of both producers, processors, and consumers.

Agriculture has been dominated by conventional farming systems since it’s industrialization and Green Revolution. Conventional farming’s dominance greatly influenced many aspects of agriculture, as a result, most grain and pulse cultivars that have been bred are not suited for organic production. To fill this void, the project's main objective is to develop biofortified organic field pea and sorghum varieties specifically for organic cropping systems.

P11 Breeding Organic Pulse and Cereal Crops Towards Protein Biofortification for Complete Plant-based Meat

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Consumer demand from the food and feed markets for organically grown plant-based protein is increasing. Perceived protein quality, i.e., high levels of essential amino acids, ease of digestibility, and chemical safety, are the main reasons for this increasing demand. An excellent source of organic plant-based protein to meet growing needs from the allergen- and gluten-free markets is field pea. An equally well-suited cereal for organic production is sorghum, a gluten-free ancient grain that has tremendous natural genetic diversity for nutritional traits. Contrary to customer perceptions, organically grown crops have lower protein quality and content than conventionally grown crops. Therefore, it is essential within the organic farming framework to focus on plant breeding activities that will result in cultivars that deliver all essential amino acids at sufficient concentrations and digestibility to fulfill consumer demands.

P12 Brassicaceae Cover Cropping as a Method to Control Root Rot in Field Pea caused by *Aphanomyces euteiches*

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Root rot of pea caused by *Aphanomyces euteiches* emerged as a serious problem in North America in the last decade and has since become a major problem for pulse crop producers. Due to a lack of fungicides that can effectively control this disease, the normal recommendation to producers is a long rotation cycle. Brassicas have been shown to reduce disease symptoms of root rot of pea and the propagation of *A. euteiches* in greenhouse and *in vitro* conditions through their production of glucosinolates. To test the effectiveness of brassicas as a cover crop to control root rot of pea under field conditions, a field trial is under way at four sites in Alberta and Saskatchewan, Canada. In May 2019, plots were sown to a variety of *Brassica* spp., a resistant pulse crop (farops (rye and oats) that may also have suppressive activity and will be planted to peas the following year. The effectiveness of these treatments will be tested by scoring disease symptoms on the peas planted in the following year. Cover crops were either mowed down at vegetative stage (green manure), or were grown until seed, and were then harvested. Biomass of green manure and chaff at harvest was weighed in plots, and then one-half the plot was tilled under or left as is. The inoculum potential of *A. euteiches* in the soil before seeding and 2 weeks after the tillage treatment was estimated using greenhouse soil bioassays. In addition, methods to improve accuracy of DNA quantification of *A. euteiches* in the soil are being tested, and an optimized methodology will be applied to soil samples. The field trial will be repeated in 2020-2021. Preliminary results from soil quantification of inoculum levels over the 2019 growing season, and methods tested to improve molecular quantification, will be presented.

P13 Evaluating the USDA Pea Single Plant Plus Collection for Phosphorus Use Efficiency Variability

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Investigations regarding the incorporation of better sustainable production strategies into current agricultural-food systems are necessary to grow crops that reduce negative impacts on the environment yet will meet the production and nutritional demand of 10 billion people by 2050. The introduction of organic, alternative staple food crops, such as nutrient-dense field pea (*Pisum sativum* L.), to the everyday diet may alleviate micronutrient malnutrition and incorporate more sustainable agriculture practices globally. Varieties grown in organic systems currently yield less than conventionally produced foods, with less bioavailable nutrients, due to poor soil nutrient content. One of the most limiting nutrients for field pea is phosphorus (P), because this legume crop requires significant inputs for nodule formation. Therefore, P use efficiency (PUE) should be a breeding target for sustainable agriculture and biofortification efforts. PUE is defined as the total biomass per unit of P taken up and encompasses the plant's ability to acquire P from the soil, then translocate, remobilize, and efficiently utilize it for various physiological processes. It is necessary to investigate available field pea germplasm for genetic variability in PUE to identify potential breeding targets. Field pea are underrepresented in agricultural research yet are important crops for a sustainable future, so this research has the potential to improve future agriculture and food systems.

P14 Pathogen Dynamics of the Root Rot Complex in Field Pea

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Root rot in field peas (*Pisum sativum* L.) is caused by a complex of soilborne pathogens that can result in complete root loss under optimal environmental conditions. *Aphanomyces euteiches* and various *Fusarium* spp. are the primary pathogens attributed to root rot on the Canadian prairies. However, little is understood of the nature of the interactions between pathogens and disease severity; as well as the environmental influence on these interactions. The objective of our study is to simulate a multiple infection scenario under glass house conditions in order to (i) characterize the nature of inter-species interactions within the pathogen complex and its effect on disease severity and (ii) relate pathogen load to host tissue colonization using quantitative PCR (qPCR). CDC Meadow was selected as a susceptible cultivar and grown for one month in soil inoculated with varying concentrations (low to high) of *Fusarium avenaceum, Fusarium redolens* and *Aphanomyces euteiches*. Plants were processed for biomass and roots were indexed for disease severity using a visual rating scale. Three replicates were randomly selected from each treatment for DNA isolations from the epicotyl, hypocotyl, tap root and lateral root; and used in qPCR to determine host colonization and pathogen localization. Preliminary results indicate that there is either a synergistic or additive interaction between multiple pathogens, and statistical analysis and qPCR from repeated trials are currently underway. Results from these trials will be used to further develop a decision support system for producers based on risk assessment of pathogen load of multiple pathogens in the soil.

P15 *Fusarium* Species Affecting Field Pea, Dry Bean and Soybean in Manitoba

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Fusarium root rot of field pea, dry bean and soybean is a concern in Manitoba. In recent years, there has been an increasing number of reports of severe losses in plant stand and yield caused by root rot. Annual surveys of dry bean, field pea and soybean have been conducted to determine the prevalence and severity of root rot, to identify the common root pathogens and to detect the presence of any new root diseases. These annual surveys date back over 10 years for dry bean and field pea, but as soybean is a relatively new crop to Manitoba, the annual soybean root disease surveys began in 2012. Since 2014, approximately 40 crops each of pea, bean and soybean were sampled per year where roots were rated for the incidence and severity of root rot disease and fungal species were identified. The isolation and identification of fungal species was based on morphology and analyses of the IGS and ITS regions and the *EF1-α* gene. Our research has shown that root rot of pea, bean and soybean in Manitoba is primarily caused by several species of *Fusarium*. *Fusarium* species isolated in each year included *F. oxysporum, F. graminearum, F. redolens, F. acuminatum, F. avenaceum,* and *F. solani*, with some *Fusarium spp*. common to all three crops. A *Fusarium* species of concern is *F. graminearum* which is the main causal agent of Fusarium Head Blight (FHB) in cereals. FHB is considered to be the most serious disease affecting cereals causing significant yield losses worldwide. An important finding from our research was the identification of *F. graminearum* in dry bean and soybean. With increasing acreages of these crops in Manitoba, *F. graminearum* may be problematic in current crop rotation regimes with cross-pathogenicity and source of inoculum issues. Overall, findings from our research will support the development of effective management strategies for root rot disease associated with different *Fusarium* spp. affecting field pea, dry bean and soybean in Manitoba and across Canada.

P16 Genetic Characterization of *Aphanomyces euteiches*

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Aphanomyces root rot, caused by *Aphanomyces euteiches* Drechsler, is one of the most devastating diseases of pea (*Pisum sativum* L.) worldwide. *A. euteiches* was confirmed in pea fields across 16 dry pea producing counties in western North Dakota in 2014 and 2015. Current management strategies are ineffective under high disease pressure and no cultivars with resistance are available. QTL have been associated with resistance to *A. euteiches*, but have been confirmed using only a small number of isolates. High genetic variability has been reported in *A. euteiches* isolates across growing regions, but this research has focused mainly on French pathogen populations. To date, little research evaluating the genetic diversity has been conducted on *A. euteiches* populations across North America. Pathogen characterization of the North American *A. euteiches* population is imperative to develop stable host resistance. The objective of this research was to characterize A. euteiches populations from North America and France using next generation sequencing technology. Sequence data from 102 isolates collected from Minnesota [3], North Dakota (49) and Washington [4], U.S., Saskatchewan (20) and Alberta (18) Canada and France (8) were used to develop a UPGMA tree and perform Discriminant Analysis of Principal Component (DAPC) and Principle Component Analysis (PCA). UPGMA cluster #1 included isolates from Alberta and WA and one isolate from ND, #2 included isolates from Alberta, Saskatchewan and ND, #3 included isolates from ND and MN and one isolate from Alberta, #4 consisted of only one isolate from ND, and #5 included all of the isolates from France, and one from Saskatchewan. DAPC and PCA results supported these clusters. This understanding of the genotypic variability in *A. euteiches* populations will enable accurate resistance screening for developing durable resistance to *A. euteiches*.

P17 Building a Better Lentil from the Ground Up

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Lentil is a uniquely suited and profitable rotational crop within the dry-land wheat systems of the northern Great Plains and Pacific Northwest. However, root rot is a major threat to the lentil industry in North America and worldwide and there are few effective management options. Fusaria are the most predominant and difficult to manage of the root rot fungi. This project seeks to discover the major species of *Fusarium* causing root rot in lentil in the Northern Great Plains, explore their interactions and the role of seed transmission in establishment and spread of the disease; develop resistant varieties using genetic marker-assisted selection techniques; determine the role of agronomic practices in establishment of a healthy crop; determine the role of agronomic practices and disease in nutritional content of lentil seed; engage stakeholders in using best management practices for root rot prevention; and enhance graduate student education and collaboration among international scientists in North American growing regions by supporting a student exchange program. This project was developed as a direct result of the Pest Management Strategic Plan for Pulse Crops published in 2017 and numerous discussions with growers, seed dealers, crop consultants, grower organizations, Farm Service Agency and financial institutions. The nutritional aspects of the proposal are exploratory, and have potential to benefit the industry and consumers in the long term.

P18 Weeds as Alternative Hosts of Fusarium Pathogens Causing Root Rot in Lentils

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Fusarium root rot is a major cause of yield losses in lentil production in the Northern Great Plains of the US. However, the role of weeds in the disease cycle and its establishment are not fully understood. The objective of this study was to determine the host status of major weeds found in lentil fields, and the pathogenicity of the weed-isolated Fusarium on lentil plants. A survey was conducted in 29 fields from the counties of Gallatin, Hill, Sheridan, Judith Basin and Richland in Montana to establish the common weed species. Out of the thirty-nine weed species identified in lentil fields, *Capsella bursa-pastoris, Sanchus arvensis, Salsola spp., Taraxacum* spp*, Bassia scoparia, Cirsium arvense, Thlaspi arvense, Sinapis arvensis, Amaranthus albus, Malva neglecta* and *Salvia reflexa* were the dominant species. Based on brown and black discoloration of lateral and tap roots, weeds were categorized as symptomatic (36 plants) and asymptomatic (81 plants). A root section (1.5 to 2 cm length) was cut from each weed plant. A total of 8 root pieces per sample were plated on half strength potato dextrose agar and placed under alternating 12:12 hours of light and dark conditions at room temperature for seven days. Based on colony color, spore size and shape, preliminary results showed successful isolation of *Fusarium* from *Filago arvensis, Bromus tectorum, Setaria viridis, Bassia scoparia, Hordeum jubatum, Avena fatua, Salsola spp, Convolvulus arvensis, Descurainia* spp*, Solanum nigrum, C. arvense, Amaranthus blitoides, Fallopia japonica, Portulaca oleracea, M. neglecta,* and *Triticum aestivum*. There was no successful isolation of *Fusarium* from *Echinochloa* spp*, Crepis tectorum, Medicago lupilina, Chenopodium album, C.bursa-pastoris, Tragopogon dubius, Taraxacum spp*, and *Vicia faba*. *Fusarium* isolates from weeds with a positive host status will be identified to species and tested for pathogenicity on lentils.

P19 Evaluation of Field Pea Cultivars for Resistance to Root Lesion Nematode *Pratylenchus neglectus*

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Root-lesion nematodes are important nematode pests on field pea crop. The root-lesion nematode species *Pratylenchus neglectus* and *P. thornei* together with the pin nematode *Paratylenchus hamatus* have been reported to cause yield reduction to dryland peas in Idaho. Recently, root-lesion nematodes were detected in pea fields during the nematode surveys in the major field pea production areas in North Dakota (ND). The species commonly found was identified as *P. neglectus*. We evaluated two field pea cultivars (Columbian and Cooper) for hosting ability to *P. neglectus*. In a preliminary experiment with low, initial population of *P. neglectus* (350/kg of soil), the reproductive factors (final population/initial population) were 3.4 and 2.6 in Columbian and Cooper, respectively, suggesting that the root-lesion nematode population in ND pea fields can infect and reproduce in field pea. In June 2019, soil samples were collected from a field infested with *P. neglectus* for the greenhouse bioassay. Nematodes were extraction from soil and the average initial population density of root-lesion nematodes was 1,775 /kg of soil. Thirty field pea cultivars used in the region were selected and evaluated for resistance to the root-lesion nematode. All the entries including the field pea cultivars and an unplanted control were grown in pots with the infested field soil in five replicates in a greenhouse room maintained at 22 °C. After 11 weeks of growth, plants were harvested, and nematodes are being extracted from soil and roots in each pot. Reproductive factor will be calculated and used to determine the resistance reaction of each cultivar to the root-lesion nematode. This research will help understand resistance or susceptibility of the field pea cultivars to this nematode disease.

P20 High-selenium Lentil Combats Arsenic Poisoning in Bangladesh – More Evidence

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Naturally high levels of arsenic occur in 'hotspots' worldwide, posing the major toxicological threat to human health, and affecting over 100 million people exposed daily through drinking water and food, notably rice. Malnutrition increases the toxicity of arsenic. Selenium is an essential element that antagonizes arsenic in the blood; therefore, low blood Se increases the risk of arsenic-induced skin lesions and other manifestations of arsenic poisoning. Pre-clinical trials show that in animals fed high Se diets, Se decreases body burdens of arsenic, reduces oxidative damage in tissues, and reverses arsenic-induced immunosuppression, as well as arsenic-induced atherosclerosis. This study provides evidence of the potential effectiveness of a simple, whole food solution of consuming lentils naturally high in selenium to reduce absorption of arsenic from water and food.

P21 Enhancement of Cowpea Development through Molecular Breeding

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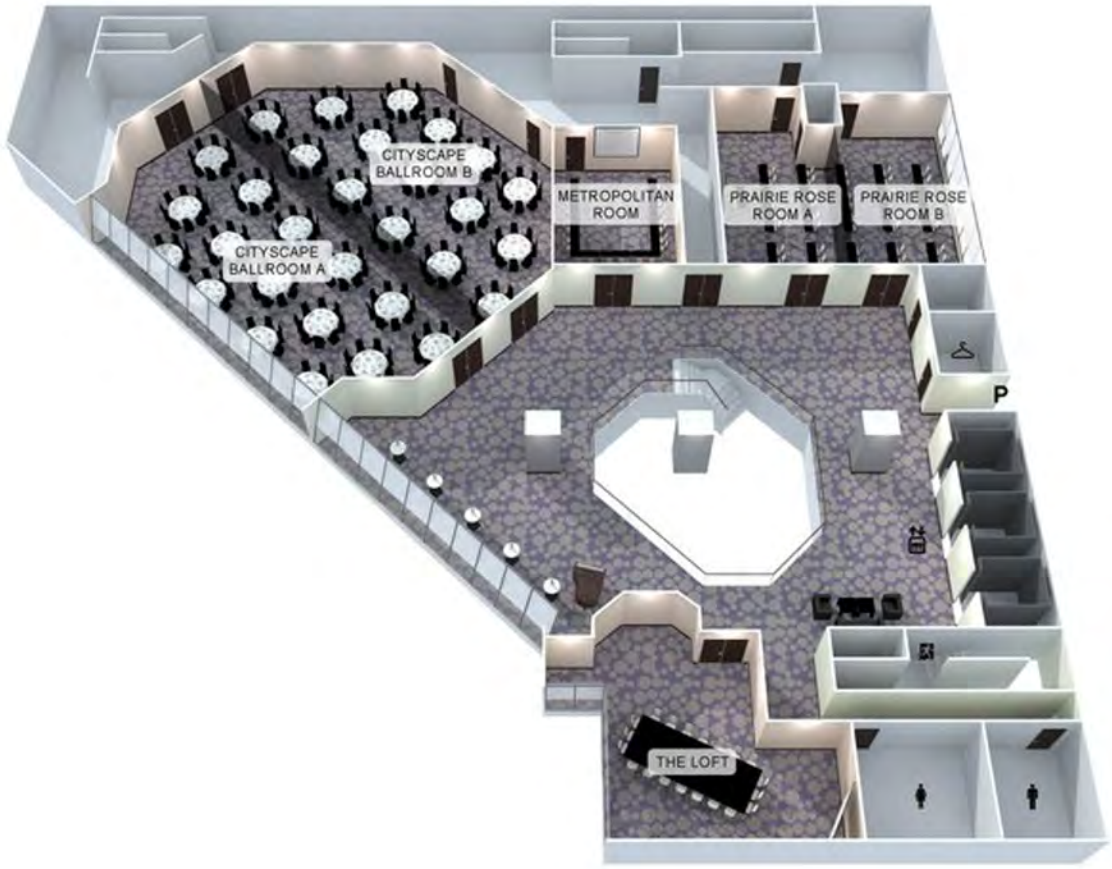
Cowpea (*Vigna unguiculata* L. Walp.) (2n=2x=22) is an important annual legume world-wide. The plant has multiple uses: producing seed as a grain crop for food, or biomass useful as animal fodder and even fresh pods as a vegetable. This purpose of the project is to build a molecular breeding platform integrated into a classical breeding approach in cowpea through DNA sequencing platform. So far, 768 accessions of USDA cowpea germplasm accessions were sequenced using genotyping by sequencing and 350 cowpea genotypes using whole genome resequencing with 10x coverage of cowpea genome size and a total of 14.85 million SNPs were identified distributed on the 11 chromosomes ranged from 894,785 SNPs on Vu02 and 2,046,094 SNPs on Vu10. Genome-wide association study have been conducting on 11 quantitative traits using the SNPs discovered from DNA sequencing in cowpea: cowpea mosaic virus resistance, bacterial blight resistance, cowpea aphid tolerance, iron deficiency chlorosis tolerance, salt and drought tolerance, seed protein and sugar content, seed antioxidant content, low phosphorus efficiency, and plant habit. Meanwhile, the SNP markers associated with these traits were identified. The research will provide a tool to use these SNP markers in cowpea molecular breeding through marker-assisted selection and genomic selection.



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