36th Annual Meeting of the Plant Pathology Society of Alberta

November 16-18, 2015
Lethbridge, Alberta

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Program

Monday, November 16th

Best Western Plus Inn

7:00-9:00 PM	Registration
7:30-9:00 PM	Reception (light snacks)

Tuesday, November 17th

Lethbridge Research Centre, Cafeteria Conference Room

8:00-8:30 AM	Registration
8:30-8:45 AM	Welcome & Opening Remarks *– Syama Chatterton, Brent McCallum*
8:45-10:05 AM	Paper Session I – Keynote & Feature Presentations *– Chairs: Raman Dhariwal, Pinderpal Brar*
10:05-10:30 AM	Refreshment Break
10:30-12:00 PM	Paper Session II *– Chairs: Ahmad Esmaeili Taheri, Gabriela Araujo*
12:00-1:30 PM	Lunch (Provided)
1:30-3:00 PM	Paper Session III *– Chairs: Fei Wang, Reyhaneh Pordel*
3:00-3:30 PM	Refreshment Break
3:30-5:00 PM	Poster Session & flash'n'dash *NOTE: presenters must be at posters* *– Chairs: Gaganpreet Dhariwal, Dianevys González-Peña Fundora*

Galt Museum & Archives

6:00-6:30 PM	Coktails
6:30-8:30 PM	Banquet

Wednesday, November 18th

Lethbridge Research Centre, Cafeteria Conference Room

8:30-10:00 AM	Paper Session IV *– Chairs: Surinder Kaur, Anas Eranthodi*
10:00-10:30 AM	Refreshment Break
10:30-12:00 PM	PPSA Business Meeting
12:00 PM	Adjourn

Scientific Program

PAPER SESSION I – Tuesday November 17, 8:45-10:05

Chairs: Raman Dhariwal, Pinderpal Brar

8:45-9:15 **Lamb Farms: Production System and Philosophy.** JOSH FAUKHAUSER. *Lamb Farms, Clareshom, AB.* Keynote Presentation

9:15-9:45 **What Do Data, Art, and Agriculture Have In Common?** TAELYNN GRAHAM, CORWIN SMITH, DENTON FREDRICKSON. *Fine Arts Data Visualization Lab, University of Lethbridge, AB.* Keynote Presentation

9:45-10:05 **Stripe rust in Southern Alberta in 2015.** DENIS A. GAUDET, E. AMUNDSEN, M. FRICK, A. LAROCHE. *AAFC-Lethbridge, AB.* Feature Presentation

PAPER SESSION II – Tuesday November 17, 10:30-12:00

Chairs: Ahmad Esmaeili Taheri, Gabriela Araujo

10:30-10:45 **An update on *Aphanomyces euteiches* research since its first detection in Alberta pea fields in 2013.** S. CHATTERTON, T. WILLSEY, K. PINTO-LARSEN, S. BANNIZA. *AAFC-Lethbridge, AB; (S.B.) University of Saskatchewan, SK*

10:45-11:00 **MAP kinases and defence signalling for disease resistance in wheat.** R. GOYAL, C. WEST, L. HUI, J. CHIU, M. FRICK, N. CHOMISTEK, B.E. ELLIS, D. TULPAN, A. LAROCHE, N.A. FOROUD. *AAFC-Lethbridge, AB; (B.E.E.) University of British Columbia, BC; (D.T.) NRC Canada-Moncton, NB*

11:00-11:15 **Evaluation of host range of *Fusarium* species from pea fields in Alberta.** S. SAFARIESKANDARI, S. CHATTERTON, L. HALL. *AAFC-Lethbridge, AB; (L.H.) University of Alberta, AB*

11:15-11:30 **Goss's Bacterial Wilt and Leaf Blight on Corn in Alberta in 2015.** M.W. HARDING, G.C. DANIELS, A. GILL, C.J. HILL, R.J. HOWARD. *AAF-Brooks, AB; (RJH) RJH Ag Research Solutions Ltd., Brooks, AB*

11:30-11:45 **Differential gene expression in incompatible/compatible reactions between Pst and wheat.** M. FRICK, P. BUCKOLL, E. AMUNDSEN, B. PUCHALSKI, H.S. RANDHAWA, R.J. GRAF, P. FOBERT, D.A. GAUDET, A. LAROCHE. *AAFC-Lethbridge, AB; (P.F.) NRC-Ottawa, ON*

11:45-12:00 **Management of cucumber green mottle mosaic virus in Alberta greenhouses through surveillance and varietal screening trials.** W. ELLOUZE, V. MISHRA, R.J. HOWARD, K-S. LING, W. ZHANG. *AAF-Brooks, AB; (R.J.H.) RJH Ag Research Solutions Ltd., Brooks, AB; (K.S.L.) USDA-ARS-Charleston, U.S.*

PAPER SESSION III – Tuesday November 17, 13:30-15:00

Chairs: Fei Wang, Reyhaneh Pordel

13:30 -13:45 **Toward the identification of Cmc1 in wheat, a resistance gene against wheat curl mite, the vector of wheat streak mosaic virus.** G. FRICK, M. FRICK, R.J. GRAF, A. LAROCHE. *AAFC-Lethbridge, AB*

13:45-14:00 **Production of double haploids with resistance to *Fusarium* mycotoxins.** D. RYABOVA, H.S. RANDHAWA, L. BIHARI, F. EUDES, D. SPANER, P. HUCL, R.J. GRAF, J. PRUS, E. AMUNDSEN, N.A. FOROUD. *AAFC-Lethbridge, AB; (D.S.) University of Alberta, AB; (P.H.) University of Saskatchewan, SK*

14:00-14:15 **Drought modulates expression of ABA and defence pathways genes in wheat.** G.K. DHARIWAL, M. FRICK, E. AMUNDSEN, M. SCHUSSLER, D.A. GAUDET, A. LAROCHE. *AAFC-Lethbridge, AB*

14:15-14:30 **Transgenerational response to pathogens in plants.** A. BILICHAK, P. KATHIRIA, Y. YAO, I. KOVALCHUK. *University of Lethbridge, AB; (A.B.) AAFC-Lethbridge, AB; (P.K.) NRC-Alberta, AB; (Y.Y.) Yangzhou University, Yangzhou, China*

14:30-14:45 **Seasonal dynamics of *Botrytis cinerea* and *Sclerotinia sclerotiorum* in seed alfalfa fields of Southern Alberta.** J. REICH, D. JOHNSON, S. CHATTERTON. *University of Lethbridge, AB; (J.R., S.C.) AAFC-Lethbridge, AB*

14:45-15:00 ***Fusarium graminearum* mutant screening towards identification of pathogen-associated molecular patterns in the Fusarium head blight-wheat interaction.** A. ERANTHODI, R. SUBRAMANIAM, T. OUELLET, C. RAMPITSCH, E.A. SCHULTZ, N.A. FOROUD. *AAFC-Lethbridge, AB; (R.S., T.O.) AAFC-Ottawa, ON; (C.R.) AAFC-Morden, MB; (A.E., E.S.) University of Lethbridge, AB*

PAPER SESSION IV – Wednesday November 18, 8:30-10:00

Chairs: Surinder Kaur, Anas Eranthodi

8:30-8:45 **Detection of stripe rust spores by real time immuno-PCR (RT-iPCR).** F. WANG, A. LAROCHE, C. SHEEDY. *AAFC-Lethbridge, AB*

8:45-9:00 **The impact of crop rotation and fungicide application on wheat leaf disease severity and crop productivity**. T.K. TURKINGTON, K. XI, G. PENG, D. PAGEAU. *AAFC-Lacombe, AB; (K.X.) AAF-Lacombe, AB; (G.P.) AAFC-Saskatoon, SK; (D.P.) AAFC-Québec, Normandin, QC*

9:00-9:15 **Understanding the mechanism *Fusarium* mycotoxin inhibition of protein synthesis through structure and dynamics.** N.A. FOROUD, N. THAKOR, R.A. SHANK, F. EUDES, P. HAZENDONK. *AAFC-Lethbridge, AB; (F.E., P.H.) University of Lethbridge, AB*

9:15-9:30 ***Pyrenophora tritici-repentis*-barley specificity.** R. ABOUKHADDOUR, S.E. STRELKOV. *University of Alberta, AB*

9-30-9:45 **Identity and host specificity of root rot pathogens colonizing standing pea from the Canadian Prairies.** A. ESMAEILI TAHERI, S. CHATTERTON, N.A. FOROUD, B.D. GOSSEN, D.L. MCLAREN. *AAFC-Lethbridge, AB; (B.D.G.) AAFC- Saskatoon, SK; (D.L.M.) AAFC-Brandon, MB*

9:45-10:00 **Towards identification of new sources of stripe rust resistance in spring wheat.** R. DHARIWAL, H.S. RANDHAWA, R.J. GRAF, A. LAROCHE, D.A. GAUDET. *AAFC-Lethbridge, AB*

POSTER SESSION – Tuesday November 17, 15:30-18:00

Chairs: Gaganpreet Dhariwal, Dianevys González-Peña Fundora

Poster 1 **Overwintering of stripe rust on winter wheat in Southern Alberta in 2015.** E. AMUNDSEN, A. LAROCHE, H.S. RANDHAWA, M. ASCIONE, D.A. GAUDET. *AAFC-Lethbridge, AB*

Poster 2 **Survey of Dry Bean Field Demonstrations for Sclerotinia White Mold.** M.W. HARDING, R.J. HOWARD, D.A. BURKE, S.L.I. LISOWSKI, G.C. DANIELS, C.A. PUGH. *AAF-Brooks, AB; (R.J.H.) RJH Ag Research Solutions, AB*

Poster 3 **Response of soybean cultivars/lines to seedling blight and root rot (*Rhizoctonia solani*) under field conditions in Southern Alberta.** K.F. CHANG, S.F. HWANG, H.U. AHMED, S.E. STRELKOV, G.D. TURNBULL, D.A.
BURKE, M.W. HARDING. *AAF- Edmonton, AB; (S.E.S.) University of Alberta, AB; (D.B; M.W.H.) AAF-Brooks, AB*

Poster 4 **Diseases of garlic and onion in Alberta in 2015.** G.C. DANIELS, R.C.J. SPENCER, J. BROATCH, J. FENG, S.L.I. LISOWSKI, R.J. HOWARD, J.M. NIELSON, M.W. HARDING. *AAF-Brooks, AB; (R.C.J.S) AAF-Stettler, AB; (J.B.) AAF-Lacombe, AB, (J.F.) AAF-Edmonton, AB; (R.J.H.) RJH Ag Research Solutions, AB*

Poster 5 ***Plasmodiophora brassicae*** **resting spore dynamics in clubroot resistant canola (*Brassica napus*) cropping systems.** T.W. ERNST, D. STANTON, D.C. RENNIE, I. FALAK, S.F. HWANG, S.E. STRELKOV. *University of Alberta, AB; (D.S., I.F.) DuPont Pioneer Canada; (S.F.H) AAF-Edmonton, AB*

Poster 6 **Survey for blackleg on canola in Southern Alberta in 2015.** T.B. HILL, C.J. HILL, G.C. DANIELS, D.A. BURKE, C.A. PUGH, M.W. HARDING. *AAF-Brooks, AB*

Poster 7 **Characterization of populations of *Plasmodiophora brassicae* by genotyping-by-sequencing.** M.D. HOLTZ, S.F. HWANG, J. ZANTINGE, S.E. STRELKOV. *AAF-Lacombe, AB; (S.F.H.) AAF-Edmonton, AB; (S.E.S.) University of Alberta, AB*

Poster 8 **Molecular phylogeny of *Rhynchosporium commune* from central Alberta**. M.D. HOLTZ, J. ZANTINGE, K. XI, T.K. TURKINGTON. *AAF-Lacombe, AB; (T.K.T.) AAFC-Lacombe, AB*

Poster 9 **Effects of post-application land treatment on the efficacy of Vapam to control clubroot (*Plasmodiophora brassicae*) of canola.** S.F. HWANG, H.U. AHMED, Q. ZHOU, S.E. STRELKOV, B.D. GOSSEN, G. PENG, G.D. TURNBULL. *AAF-Edmonton, AB; (S.E.S.) University of Alberta, AB; (B.D.G. and G.P) AAFC-Saskatoon, SK*

Poster 10 **Effect of irrigation and plant canopy architecture on white mold development in dry bean.** K.A. KADER, P.M. BALASUBRAMANIAN, S. CHATTERTON. *AAFC-Lethbridge, AB*

Poster 11 **A simple in vitro assay to measure enhanced "pathogenesis-related" enzyme expression during scald barley interaction.** K. KUMAR, J. ZANTINGE, K. XI, S. WATERMAN, P. JUSKIW. *AAF-Lacombe, AB*

Poster 12 **Molecular characterization of the Lethbridge Research and Development Centre snow mold collection.** C. SEHN, M. FRICK, J. YANKE, D.A. GAUDET, S. REDHEAD, A. LAROCHE. *AAFC-Lethbridge, AB; (S.R.) AAFC-Ottawa, ON*

Poster 13 **Effect of seed dressing fungicide and inoculum density on *Aphanomyces* root rot of field pea in Alberta.** L.F. WU, K.F. CHANG, S.F. HWANG, S.E. STRELKOV, G.D. TURNBULL, R.L. CONNER. *University of Alberta, AB; (K.F.C., S.F.H., G.D.T.) AAF-Edmonton, AB; (R.L.C.) AAFC-Morden, MB*

Poster 14 **Barley and wheat leaf disease survey in central Alberta, 2015.** K. XI, L. VANDERMAAR, K. KUMAR, M.D. HOLTZ, J. PALY. *AAF-Lacombe, AB; (J.P.) Ducks Unlimited Canada, AB*

PAPER SESSION I

Tuesday, November 17, 2015
8:45 - 10:00 AM

Keynote Presentation

Lamb Farms: Production System and Philosophy

JOSH FAUKHAUSER

Lamb Farms, Clareshom, Alberta

Josh Fankhauser is the Agronomy Manager for Lamb Farms in Claresholm, Alberta. He Farms with five other family members and is married with 3 children.

Josh attended Lethbridge College where he revived his Diploma in Plant and Soil Science. He then worked on Farms in Europe and Quebec before coming back to the farm in 2008.
He will be talking about his farm's unique grain and cattle production philosophies. They use stripper headers, disc seeders, a large variety of crops and a systems approach to limit the use of pesticides and other inputs.

Keynote Presentation

What Do Data, Art, and Agriculture Have In Common?

TAELYNN GRAHAM, CORWIN SMITH, DENTON FREDRICKSON

Fine Arts Data Visualization Lab, University of Lethbridge, Lethbridge AB

The Fine Arts Data Visualization Lab at the University of Lethbridge in Southern Alberta, Canada, explores this intersection. Each year we work with a dedicated scientist from Agriculture and Agri-Food Canada in visualizing one of their data sets. We begin by visiting their research facility to get close to the science and ask questions. We take that knowledge back to our lab and let our curiosity drive how we analyze the story the data is trying to tell, and begin to build projects from that. We strive to combine traditional art-making materials and processes with new ones, and have worked with everything from interactive bar charts to weaving, from meticulously hand-drawn graphs to 3D printed data physicalizations, from crocheted data to electro-acoustic sound compositions.

Feature Presentation

Stripe rust in Southern Alberta in 2015

DENIS A. GAUDET, E. AMUNDSEN, M. FRICK, A. LAROCHE

Agriculture & Agri-Food Canada, Lethbridge Research & Development Centre, 5403 1st Avenue South, Lethbridge, AB, T1J 4B1, Canada

Severe epidemics of stripe rust (*Puccinia striiformis* Westend.) can cause extensive yield and quality losses and fungicides are recommended to reduce losses. We surveyed winter wheat fields in Southern Alberta in the autumn of 2014 and at regular intervals throughout growing season in 2015. We observed 5% incidence in early December in two fields and trace levels in a third. It was widespread in volunteer winter wheat throughout the region and in LRC research plots. There was evidence for overwintering of stripe rust; two of the ten winter wheat fields surveyed were had low levels in late April. Stripe rust remained localized throughout May with only one field of 19 reporting low levels stripe rust early June. By the early July, stripe rust had become widespread, occurring in 70% of surveyed fields. The severity remained low with 30% of fields observed at 10%-15% and the remainder at ≤ 5%. Stripe rust remained at these constant levels throughout July and until the end of the growing season. Regionally, stripe rust levels were highest in the Lethbridge-Cardston-Warner districts with levels diminishing towards Medicine Hat. Fungicide application was widespread in both winter and spring wheat by mid-July. Results will be discussed with reference to prevailing environmental conditions.

PAPER SESSION II

Tuesday, November 17, 2015
10:30-12:00 AM

An update on *Aphanomyces euteiches* research since its first detection in Alberta pea fields in 2013

S. CHATTERTON, T. WILLSEY, K. PINTO-LARSEN, S. BANNIZA

Agriculture & Agri-Food Canada, Lethbridge Research & Development Centre, 5403 1st Avenue South, Lethbridge, AB, T1J 4B1, Canada; (S.B.) Crop Development Centre, University of Saskatchewan, 51 Campus Dr., Saskatoon, SK, S7N 5A8, Canada

Aphanomyces root rot was first reported in Saskatchewan and Alberta pea fields in 2012 and 2013, respectively. Several research projects to understand disease development and potential seed treatment options have been initiated. Standard curves describing the relationship between oospore levels of *Aphanomyces euteiches* and disease severity in soils from three soil zones (black, dark brown and brown) were developed in greenhouse trials. Peas grown in dark brown, autoclaved soils had higher disease severities compared to disease levels at the same inoculum densities in peas grown in brown and black soils. However, presence of *Fusarium* spp. in non-autoclaved soils significantly increased disease severity at all *A. euteiches* inoculum levels compared to autoclaved, inoculated soils. Seed treatments with a mixture of different active ingredients that included the newly registered product, ethaboxam, were effective in reducing Aphanomyces root rot of seedlings in greenhouse trials. The trials are being expanded to assess yield and disease response at naturally-infested field sites throughout Alberta. Host range testing indicated that peas, lentils, alfalfa and cicer milkvetch are susceptible hosts, while dry beans, faba beans, chickpeas, soybeans, fenugreek and sainfoin are moderately resistant or non-hosts. Results to date suggest that dark brown soils, susceptible host crops and *Fusarium* spp. increase the risk of developing severe Aphanomyces root rot.

MAP kinases and defence signalling for disease resistance in wheat

R. GOYAL, C. WEST, L. HUI, J. CHIU, M. FRICK, N. CHOMISTEK, B.E. ELLIS, D. TULPAN, A. LAROCHE, N.A. FOROUD

Agriculture & Agri-Food Canada, Lethbridge Research & Development Centre, 5403 1st Avenue South, Lethbridge, AB, T1J 4B1, Canada; (B.E.E) Michael Smith Laboratories, University of British Columbia, #301 - 2185 East Mall, Vancouver, BC, V6T 1Z4; (D.T.) National Research Council of Canada, Moncton, NB, E1A 7R1, Canada

Plants have a well-developed mechanism of abiotic/biotic stress perception, which is relayed through an intricate network of signalling to mount a defence response. MAP kinases form an important component of the defence signalling cascade. There exists a large repertoire of MAP kinases in plants; some of them have been implicated in disease resistance in plants. Among monocots, with exception of rice and Brachypodium, the information on MAP kinases is limited and not well organized especially in wheat and related cereals. We constructed full length sequences of wheat MAP kinases by sequencing the cDNA amplicons and analyzing the contigs in database using bioinformatics tools. The MAP kinases belonging to families of MAPKs, MAPKKs and MAPKKKs were annotated following Arabidopsis nomenclature. Using yeast two-hybrid assays the mutual MAP kinases interactions were studied at protein level. The positive interactions identified suggest a preserved architecture of MAP kinase signalling in plants. The studies are underway to identify specific MAP kinases associated with Fusarium head blight defence signalling.

Evaluation of host range of *Fusarium* species from pea fields in Alberta

S. SAFARIESKANDARI, S. CHATTERTON, L. HALL

Agriculture & Agri-Food Canada, Lethbridge Research & Development Centre, 5403 1st Avenue South, Lethbridge, AB, T1J 4B1, Canada; (L.H.) Department of Agricultural, Food & Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada

Fusarium root rot is one of the most important diseases of pea, as it can cause severe yield losses. Multiple *Fusarium* species have been found associated with pea root rot in Canada. Previous studies demonstrated that *F. avenaceaum* and *F. solani* are commonly associated with root rot symptoms on pea in Canada. The objective of this study was to determine the host range of these *Fusarium* species. Isolates used in the study were obtained from pea root samples collected during field surveys in Alberta and have different levels of virulence on pea as determined by pathogenicity tests. Pathogenicity to different crops include: pea, lentil, faba bean, chickpea, wheat, canola, dry bean, soybean and barley was assessed by a seed inoculation method, disease severity were determined approximately 4 weeks after planting. For *F. avenaceum*, dry bean, chickpea and faba bean had significantly greater disease severity compared to uninoculated plants of the same species. Other crops had disease severity ratings not statistically different from uninoculated plants. For *F. solani,* disease severity was not significantly different among tested plants except for chickpea, which had significantly greater disease severity compared to uninoculated plants. Results indicate that *F. avenaceum* isolates have a broad host range on pulse crops which can influence crop rotation decisions to manage impact and persistence of Fusarium root rot.

Goss's Bacterial Wilt and Leaf Blight on Corn in Alberta in 2015

M.W. HARDING, G.C. DANIELS, A. GILL, C.J. HILL, R.J. HOWARD.

Crop Diversification Centre South, Alberta Agriculture & Rural Development, 301 Horticultural Station Road East, Brooks, AB, T1R 1E6, Canada; (RJH) RJH Ag Research Solutions Ltd., Box 1456, Brooks, AB, T1R 1C3, Canada

Clavibacter michiganensis subsp. *nebraskensis,* the causal agent of Goss's bacterial wilt and leaf blight on corn, recently expanded its geographical range to a number of new regions in North America. For example, it was first reported in Alberta in 2013 and while it has not caused serious economic consequences, the potential for spread and increased severity is a concern for Alberta corn producers. A survey for Goss's wilt and leaf blight symptoms in Alberta in 2015 included 55 corn fields in ten counties. Symptoms were found in 20 of 55 fields surveyed (prevalence = 36%). The incidence of leaf blight ranged from trace levels to 50%. Only one field had signs and symptoms of vascular wilt. Seventeen of the 20 positive fields were reported in Southern Alberta, from Census Agricultural Regions 1 and 2. The remaining three symptomatic fields were found in central Alberta (Census Agricultural Region 5).

Differential gene expression in incompatible/compatible reactions between *Pst* and wheat

M. FRICK, P. BUCKOLL, E. AMUNDSEN, B. PUCHALSKI, H.S. RANDHAWA, R.J. GRAF, P. FOBERT, D.A. GAUDET, A. LAROCHE

Agriculture & Agri-Food Canada, Lethbridge Research & Development Centre, Lethbridge, AB, T1J 4B1, Canada; (P.F.) National Research Council of Canada, 100 Sussex Dr., Ottawa, ON, K1A 0R6, Canada

We evaluated the *Pst*-wheat interaction at the transcriptome level between *Pst* isolates LSW3_2012_SP2 and SWS484_SPF on resistant and susceptible hosts. The number of clean reads obtained from inoculated tissues between incompatible and incompatible reaction with isolates SWS484 and LSW3 ranged from 78 M and 184 M. Over 2.9 M reads were obtained from haustoria isolated from tissues infected with LSW3. Mapping of reads against the PST-78 transcripts reveals that 54% of the reads are mapped in the compatible reaction while only 0.5% did map in the incompatible reaction. The proportion of the reads mapping to cereal transcriptomes was 28% and 86% for compatible and incompatible reactions. These results show an important differential regulation of genes in both the fungal pathogen and the wheat host. Genes differentially regulated between the incompatible and compatible reactions were characterized by annotation and GO term classification. To validate *Pst* transcripts involved in the infection process, we adapted a leaf rust haustorial isolation protocol for characterization of proteins and modified it to protect the integrity of RNA in enriched *Pst* haustoria. A list of potential effectors present in LSW3_2012_SP2 in haustoria-enriched tissues will be presented.

Management of cucumber green mottle mosaic virus in Alberta greenhouses through surveillance and varietal screening trials

W. ELLOUZE, V. MISHRA, R.J. HOWARD, K-S. LING, W. ZHANG.

Alberta Agriculture & Forestry, Crop Diversification Centre South, 301 Horticultural Station Rd. E., Brooks, Alberta T1R 1E6; (R.H.) RJH Ag Research Solutions Ltd., Box 1456, Brooks, AB, T1R 1C3, Canada; (K.S.L.) USDA-ARS, U.S. Vegetable Laboratory, 2700 Savannah Highway, Charleston, SC, 29414, United States

Cucumber green mottle mosaic virus (CGMMV) is an increasing threat to greenhouse cucumber crops worldwide. Our analysis of symptomatic samples from commercial greenhouses in Alberta revealed that an Asian genotype of CGMMV was predominantly responsible for the disease. Growing resistant cucumber varieties that prevent infection, replication and symptom development is the most practical approach to controlling the virus. Currently, no high-yielding cucumber variety with CGMMV resistance is commercially available. Six Mini and nine Long English (LE) cucumber varieties were screened for resistance to CGMMV and effects of infection on productivity. Among Mini varieties, Sunniwell was the most sensitive (infection rates (IR) of 100%), but had the highest fruit yield. Katrina was the most resistant (IR: 79%), but was intermediate in yield compared to Sunniwell. Among nine varieties of LE screened for resistance to CGMMV, Bonbon was highly sensitive (IR: 83%) without compromising yield, which was highest. The most sensitive LE variety was DR4879CE (IR: 90%), while Verdon, the most widely grown cultivar in Alberta, was intermediate (IR: 55%) in its resistance. In yield comparisons, DR4879CE and Verdon were poor performers. This trial revealed the relative suitability of commercial cucumber varieties for use in greenhouses at risk from CGMMV infection and where minimizing production losses is a key consideration.

PAPER SESSION III

Tuesday, November 17, 2015
1:30-3:00 AM

Toward the identification of *Cmc*1 in wheat, a resistance gene against wheat curl mite, the vector of wheat streak mosaic virus

G. FRICK, M. FRICK, R.J. GRAF, A. LAROCHE

Agriculture & Agri-Food Canada, Lethbridge Research & Development Centre, 5403 1st Avenue South, Lethbridge, AB, T1J 4B1, Canada

The wheat curl mite (*Aceria tosichella* Keifer) transmits and spreads the wheat streak mosaic virus (WSMV) which causes severe losses in wheat. Genetic resistance to colonization by the mite is an efficient approach to limit impact of WSMV on wheat. Numerous resistance genes have been identified and transferred to wheat from various species. The dominant *Cmc*1 resistance gene has been identified on the 6DS chromosome arm and originates from *Aegilops tauschii* Coss. Availability of a molecular marker linked to *Cmc*1 would accelerate the identification of resistant wheat lines as screening large numbers of breeding lines is time and labour intensive. We are using bulk segregant analysis and RNA-Seq on Radiant (W337) resistant (R) and susceptible (S) lines. In this work-in-progress, we will describe the different steps we are using to identify a limited number of candidate genes linked to *Cmc*1 given that about 106,000 functional protein coding genes have been reported in wheat. By identifying unique transcripts to R and S lines, we have decreased the number a potential sequences to ≈1600. We have generated an annotation of these transcripts to further decrease this number of potential candidate coding genes. Studying the transcriptome represents an important complexity reduction considering that the genome of wheat includes ≈17 G nucleotides.

Production of double haploids with resistance to *Fusarium* mycotoxins

D. RYABOVA, H.S. RANDHAWA, L. BIHARI, F. EUDES, D. SPANER, P. HUCL, R.J. GRAF, J. PRUS, E. AMUNDSEN, N.A. FOROUD

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Fusarium graminearum, the causal agent of *Fusarium* head blight (FHB), is known to produce mycotoxins that contaminate of cereal grain crops. The most effective way of controlling FHB is to grow cultivars with resistance to FHB. An *in vitro* selection procedure was previously developed for common wheat *Triticum aestivum* L. to produce double haploids (DHs) with resistance to trichothecenes. The procedure involves microspore culture in the presence of *Fusarium* mycotoxins (DON, 3-ADON, 15-ADON, NIV, T-2). Microspores possessing mechanisms of resistance or tolerance to mycotoxins will develop into embryos, while susceptible genotypes are screened out. The objective of this study is to produce double haploid lines resistant to *Fusarium* mycotoxins. Fourteen crosses were used for microspore culture and 569 double haploids were generated. The addition of mycotoxins to culture media decreased viability of microspores, embryo formation, as well as regeneration of embryos into plantlets. Mycotoxin treatments resulted in a 5 to 35 % reduction in embryo germination relative to the control. Winter wheat had spontaneous doubling 84-85%, whereas spring wheat plantlets, which are expected to have low spontaneous doubling, were treated with colchicine to produce double haploids. Double haploids generated in this study are going to be used in breeding programs towards germplasm development.

Drought modulates expression of ABA and defence pathway genes in wheat

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Drought and infection by microbial pathogens are two important stresses limiting plant performance and productivity. Induction of abscisic acid (ABA) signalling pathway has been previously associated with resistance to drought but its role in regulating plant responses to pathogen attack still remains to be established in cereals. An effort was made to elucidate the role of drought stress and plant hormone signalling pathways in regulating defence responses in drought susceptible wheat (cv. Neepawa) and drought tolerant triticale (cv. AC Certa). Cultivars were subjected to severe water stress at four Zadok's developmental stages (Z12, Z21, Z45 and Z59). Leaves were sampled for RNA extraction at each stage and gene expression studies were carried out with primers designed from key genes involved in biosynthesis pathway for ABA and for the defence signalling hormones salicylic acid (SA), jasmonic acid (JA) and ethylene (ET). Drought stress caused an increase in abundance of the transcripts for ABA-responsive genes encoding dehydrin (DHN) and 9'-cis-epoxycarotenoid dioxygenase (NCED3). Expression of both DHN and NCED3 was higher in wheat as compared to triticale. Some important genes involved in SA, JA and ET pathways were also up regulated at different developmental stages in Neepawa indicating a cross-talk between these defence responsive pathways and drought stress.

Transgenerational response to pathogens in plants

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Pathogens and plants are in constant arms race. On somatic level, plants respond to pathogen infection with changes in transcription, protein turnover, metabolites accumulation and production of free radicals. Some plants are able to form immediate hypersensitive response and delayed systemic acquired resistance. Several publications in the last decade, including our work demonstrated that plants are also able to mount certain form of transgenerational response – the progeny of infected plants exhibit higher tolerance to the same pathogens and substantial degree of cross-tolerance. *Nicotiana tabacum* or *Arabidopsis thaliana* plants infected with tobacco mosaic virus generate a systemic recombination signal that precedes the spread of pathogens and results in changes in the somatic and meiotic recombination frequency. The progeny of infected plants exhibit changes in global and locus-specific DNA methylation patterns, genomic rearrangements at transgenic reporter loci and resistance gene-like-loci, tolerance to pathogen infection and abiotic stress and various molecular changes, including changes in transcriptome, DNA repair capacity and metabolite levels. To date, transgenerational changes were demonstrated in response to many different pathogens, including viruses, bacteria, fungi and insects. In this presentation, we will discuss the contribution of environmental stresses to genome evolution and will focus on the role of heritable epigenetic changes in response to pathogen infection.

Seasonal dynamics of *Botrytis cinerea* and *Sclerotinia sclerotiorum* in seed alfalfa fields of Southern Alberta

J. REICH, D. JOHNSON, S. CHATTERTON

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Blossom blight of seed alfalfa (*Medicago sativa* L.) is caused by the fungal pathogens *Botrytis cinerea* Pers.:Fr. (Bc) and *Sclerotinia sclerotiorum* (Lib.) de Bary (Ss). Nineteen commercial seed alfalfa fields in Southern Alberta were surveyed over three growing seasons (2013-2015) to determine the seasonal occurrence of Bc and Ss. Each field was surveyed four times during July and August in each year. Disease incidence and severity ratings were assigned in the field, and floret and pod samples were plated on semi-selective media in the lab. In 2014 and 2015, aerosol samples were collected by three spore samplers installed in three fields. Aerosol samples were analyzed in a real-time quantitative polymerase chain reaction (qPCR) assay to quantify the daily spore concentrations of Bc and Ss. In all three years, blossom blight symptoms were present at trace levels. Plated samples revealed greater variability in pathogen incidence among fields, although seasonal trends were similar between years despite considerable differences in macroclimatic variables. Spore discharge for both pathogens did not follow the same seasonal trends as plated samples. Overall, these results suggest that management and microclimatic factors (e.g. irrigation) may play a more important role than macroclimatic factors in the development of blossom blight of alfalfa in Southern Alberta.

Fusarium graminearum mutant screening towards identification of pathogen-associated molecular patterns in the Fusarium head blight-wheat interaction

A. ERANTHODI, R. SUBRAMANIAM, T. OUELLET, C. RAMPITSCH, E.A. SCHULTZ, N.A. FOROUD

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Fusarium head blight (FHB), caused primarily by *F. graminearum,* is a major disease affecting wheat and other cereals worldwide. This destructive disease is responsible for substantial reduction in yield and quality of grains. With the objective of screening candidate pathogen-associated molecular patterns (PAMPs), we selected seven proteins (PAMP1-PAMP7) from the *F. graminearum* secretome based on their sequence homology to proteins with pathogenicity roles in other plant-pathogen interactions. Knockout (KO) and overexpression (OX) mutants of *F. graminearum* were generated for the genes that encode these proteins. The KO and OX constructs were generated by USER cloning and the constructs were electroporated into *Agrobacterium tumefaciens*. Mutants were generated by homologous recombination between a modified T-DNA of Agrobacterium and the *F. graminearum* genome during Agrobacterium-mediated transformation. Two wheat lines, Superb and GS-1-EM0040 ('CIMMYT 11'/'Superb'*2), were point-inoculated with mutants *PAMP1*-OX, *PAMP2*-KO, or *PAMP2*-OX and screened against wild-type inoculated wheat lines. The number of infected spikelets was significantly lower for wheat lines inoculated with *PAMP1*-OX or *PAMP2*-OX than for those inoculated with wild-type strain. Likewise, *PAMP2*-OX inoculated wheat lines had significantly fewer infected spikelets than *PAMP2*-KO inoculated wheat lines. Based on these preliminary results, we postulate that PAMP1 and PAMP2 activate receptors in wheat leading to the basal immune response known as PAMP-triggered immunity. Analysis of the remaining five genes is currently underway.

PAPER SESSION IV

Wednesday November 18
8:30-10:00

Detection of stripe rust spores by real time immuno-PCR (RT-iPCR)

F. WANG, A. LAROCHE, C. SHEEDY

Agriculture & Agri-Food Canada, Lethbridge Research & Development Centre, 5403 1st Avenue South, Lethbridge, AB, T1J 4B1, Canada

An early detection of *Puccinia striiformis* West f. sp. *tritici* (*Pst*) (causal agent of stripe rust) spores would facilitate deployment of an effective strategy to mitigate impact of this pathogen on susceptible wheat in commercial fields. A sensitive real-time immuno-PCR (RT-iPCR) assay was developed and adapted from an enzyme-linked immunosorbent assay (ELISA). The utilization of an antibody eliminates the needs of spores DNA isolation required for DNA-based PCR. Two protocols were developed for detection of a 2006 *Pst* isolate, based on labelling primary or secondary antibody with DNA. Results with the labelled secondary antibody show a 14X higher sensitivity than the ELISA with a limit of detection (LOD) of 40 and 570 spores respectively, while the assay with the labelled primary antibody was 28X more sensitive (20 spores) than that of the ELISA. The RT-iPCR assay was effective with LSW3-2012, SWS-484SPF-2011 and LRC L5-9-2013 *Pst* isolates. An advantage of the assay with labelled secondary antibody is its universal nature for reacting with any antibody from rabbit, while the other assay requires labelling of every primary antibody. Comparing to traditional field screening and DNA-based PCR methods, the RT-iPCR assay is the most sensitive, rapid and simple technique to detect and quantify presence of *Pst* spores.

The impact of crop rotation and fungicide application on wheat leaf disease severity and crop productivity

T.K. TURKINGTON, K. XI, G. PENG, D. PAGEAU

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The impact of previous crop and fungicide application on leaf disease and productivity of wheat was assessed at Lacombe, AB, Melfort, SK and Normandin, QC in 2014. Moderate disease occurred at Lacombe and Melfort, where Prosario® application at anthesis significantly reduced flag leaf disease severity. At Normandin where the rotation sequence did not include flax, although disease was lower, fungicide resulted in a small, but significant reduction in disease, while rotation had no effect. Rotation and its interaction with fungicide had no effects on leaf disease severity at Lacombe and Melfort. Although the interaction was significant at Normandin, differences in disease were too small to show substantial biological significance. The fungicide treatment resulted in a significant increase in yield at Lacombe and Melfort, but not Normandin. Previous crops affected yields at Lacombe and Melfort, and were highest when planted into field pea or flax stubble and lowest when planted into barley or canola, although at Normandin yields were highest and similar for field pea and barley stubble. At Melfort there was an interaction of fungicide and rotation; yield differences among previous crops were not significant for no-fungicide treatments. However, when a fungicide was applied, yield was highest for field pea stubble, while the remaining stubble types produced lower and similar yields.

Understanding the mechanism *Fusarium* mycotoxin inhibition of protein synthesis through structure and dynamics

N.A. FOROUD, N. THAKOR, R.A. SHANK, F. EUDES, P. HAZENDONK

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Fusarium species involved in Fusarium head blight (FHB) of wheat and related cereals, produce a class mycotoxins called trichothecenes. These toxins are potent inhibitors of protein synthesis in eukaryotic cells and are known to accumulate in the kernels of *Fusarium*-infected kernels. Type A and B trichothecene classes are associated with FHB, where the B type predominates. Type B trichothecenes include nivalenol, deoxynivalenol (DON) and their acetylated derivatives. The degree of toxicity among the trichothecenes varies widely, and also depends on the class of organism infected. For instance, DON is known to be more phytotoxic than nivalenol, whereas the latter is more harmful in mammalian systems. While it is known that these toxins inhibit protein synthesis by disrupting peptidyl transferase activity, the exact mechanism of this inhibition is poorly understood. Furthermore, it is not known how differences in trichothecene structure can affect different levels of toxicity; hence a much deeper understanding of the trichothecene structures is required. The three-dimensional structures and hydrogen-bonding behavior of type B trichothecenes were evaluated using advanced nuclear magnetic resonance (NMR) spectroscopy techniques. Results provide some insights into differences in degree of toxicity among different trichothecene, and also identify structural features that confer toxicity.

Pyrenophora tritici-repentis-barley specificity

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Pyrenophora tritici-repentis (Ptr) is a destructive fungal pathogen of wheat worldwide. In addition to wheat, Ptr has been isolated from various other hosts in the family Poaceae, yet the nature of its interaction on those hosts is unknown. In this study, the Ptr-barley interaction was explored. A collection of 85 barley genotypes representing varieties grown or developed in Canada since 1886 were screened for their reaction to this pathogen. Symptoms development on those genotypes was evaluated in bioassays and toxin infiltration into barley leaves, this was followed by a cytological analysis to understand the infection process in barley. Ptr ToxB-producing isolates of the fungus were able to cause significant damage when inoculated onto certain barley genotypes, and Ptr ToxB was able to induce chlorosis in a highly selective manner when infiltrated into those same genotypes. Twelve of the genotypes were rated as susceptible (14%), while the other 73 (85%) were resistant. The fungus penetrates through the host epidermal cells and advances to colonize the mesophyll layer intercellularly. Here, evidence is provided for a specific interaction between barley and Ptr, expanding understanding of Ptr-host specificity and breaking the assumption that the highest level of specificity seen with Ptr is restricted to particular genotypes of the wheat host.

Identity and host specificity of root rot pathogens colonizing standing pea stubble from the Canadian Prairies

A. ESMAEILI TAHERI, S. CHATTERTON, N.A. FOROUD, B.D. GOSSEN, D.L. MCLAREN.

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The composition and host specificity of pathogenic fungal communities colonizing pea residues from Alberta and Manitoba was studied. Standing pea stubble was sampled from diseased and healthy patches of 16 commercial fields in 2013–2015 after harvest and in the following year prior to crop seeding. Canola, wheat and pea were grown in pots filled with ground pea stubble mixed with sterile Cornell potting mix. Root rot severity of the hosts was evaluated and sections from diseased roots were plated on agar media. Fungal communities isolated from roots were characterized using characteristics in culture and PCR-based identification. Approximately 2700 fungal isolates, belonging to some 50 species, were identified. *F. avenaceum* and *F. culmorum* were most prevalent in wheat, and *F. avenaceum, F. solani* and *F. oxysporum* were most abundant in pea, and *F. avenaceum* was most abundant on canola. *Aphanomyces euteiches* was isolated only from one Manitoba field, and only on pea. Fungal communities of healthy and diseased patches of fields were similar, but the fungi isolated from post-harvest stubble were different from that of pre-plant stage. Root rot incidence and severity were lower on canola than on pea or wheat, which indicates that canola is less susceptible to the fungal root pathogens of pea than either pea or wheat.

Towards identification of new sources of stripe rust resistance in spring wheat

R. DHARIWAL, H.S. RANDHAWA, R.J. GRAF, A. LAROCHE, D.A. GAUDET

Agriculture & Agri-Food Canada, Lethbridge Research & Development Centre, 5403 1st Avenue South, Lethbridge, AB, T1J 4B1, Canada

Wheat stripe rust, caused by *Puccinia striiformis* Westend. f.sp. *tritici*, is a devastating foliar disease of wheat. In order to identify novel sources of resistance for this disease, five recombinant inbred line (RILs; $F_{6:7}$) and five doubled haploid (DH) populations were developed utilizing different sources of resistance including Sadash and AAC Innova (both registered cultivars) and several uncharacterized germplasm lines of spring wheat. These populations were screened in stripe rust disease screening nurseries under natural infection from 2011 to 2014. F_2 and $F_{2:3}$ phenotypic data showed presence of either a single or two genes in RILs, which are being advanced to develop homozygous populations. Two DH populations segregated for two major genes while the other three for one major and one set of two minor additive genes. Three (AC Reed/N9195; Sadash/Proclaim; Sadash/P2711) of these DH populations were utilized for genotyping using either 90K SNP Infinium iSelect assay or 15K SNP Assay. High density genetic linkage maps were constructed followed by QTL analysis, which identified one major QTL from each DH population besides other minor QTLs on wheat chromosomes 2A, 3A, 4B, 7A and 7D. Majority of these QTLs were detected in multiple environments. The identification of these new sources of resistance will facilitate marker-assisted breeding for stripe rust resistance.

POSTER SESSION
&
Flash'n'dash Presentations

Tuesday November 17
3:30-5:00 PM

Overwintering of stripe rust on winter wheat in Southern Alberta in 2015

E. AMUNDSEN, A. LAROCHE, H.S. RANDHAWA, M. ASCIONE, D.A. GAUDET

Agriculture & Agri-Food Canada, Lethbridge Research & Development Centre, 5403 1st Avenue South, Lethbridge, AB, T1J 4B1, Canada

Puccinia striiformis f. sp. *tritici* (*Pst*) causal agent of stripe (yellow) rust in wheat is a obligate parasite that has the ability to survive on winter wheat through increasingly common mild winters in Southern Alberta. With the right weather, overwintered stripe rust could be a source of inoculum for spring wheat and become costly for producers. A fall survey of winter wheat fields in 2014 found stripe rust in three winter wheat fields in an area including the Counties of Lethbridge, Warner, and Cardston, and in experimental plots at the Lethbridge Research Centre. The purpose of this study was to sample plants from plots showing fall infection throughout the winter to determine if the pathogen could survive and if not, which winter conditions are inhibitory to survival of the pathogen. Winter wheat plants were transplanted from field plots to the greenhouse monthly throughout the winter and spring and evaluated for presence of rust pustules. Initially, viability was determined by the ability to infect susceptible wheat with rust from field samples. Later, plants were allowed to grow and monitored for the appearance of rust symptoms. Our study showed that rust was able to survive the winter of 2014.

Survey of Dry Bean Field Demonstrations for Sclerotinia White Mold

M.W. HARDING, R.J. HOWARD, D.A. BURKE, S.L.I. LISOWSKI, G.C. DANIELS, C.A. PUGH.

Alberta Agriculture & Forestry, Crop Diversification Centre South, 301 Horticultural Station Road East, Brooks, AB T1R 1E6, Canada; (R.J.H.) RJH Ag Research Solutions, AB.

Data from annual surveys for Sclerotinia white mold of Viterra Inc. Alberta Bean Division demonstrations in commercial fields was compared to meteorological data for accumulated precipitation in July of the corresponding years. Overall disease incidence was relatively high for all years (18-29%) with the exception of 2014 (5%), although this year did not appear to have significantly less precipitation for the month of July.

Response of soybean cultivars/lines to seedling blight and root rot (*Rhizoctonia solani*) under field conditions in Southern Alberta

K.F. CHANG, S.F. HWANG, H.U. AHMED, S.E. STRELKOV, G.D. TURNBULL, D.A. BURKE, M.W. HARDING.

Crop Diversification Centre North, Alberta Agriculture & Forestry, Edmonton, AB, T5Y 6H3, Canada; (S.E.S.) Department of Agricultural, Food & Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada;(D.A.B; M.W.H.) AAF-Brooks, AB, T1R 1E6, Canada

Soybean (*Glycine max* L.) has great potential as an alternative crop in western Canada. In Southern Alberta, the area seeded to soybeans has grown from a few hectares to about 4,050 hectares in 2014, and this area is expected to continue to increase as early maturing and cold-resistant cultivars become available. Root rot is a common constraint to crop production, and the occurrence of root rot was documented in all 29 soybean fields surveyed in Southern Alberta in 2014. *Rhizoctonia solani* Kühn caused seedling blight, including pre- and post-emergence damping-off and root rot of young and adult plants of soybean. The reactions of 22 soybean cultivars/lines to *R. solani* were assessed in inoculated field trials conducted at Brooks, Alberta, in 2014 and 2015. In all trials, *Rhizoctonia*-inoculated plots had lower emergence, nodulation and yield and higher disease severity compared with the non-inoculated plots. None of the lines were resistant to *R. solani*, however, the soybean cultivar/lines NSC Portage, TH29002RR, TH27005RR and LS 003R22 had the smallest reduction in stand establishment, and NSC MoosominRR2Y, NSC TilstonRR2Y, P001T34R and 23-60RY had the smallest reduction in seed yield. These cultivars/lines, when combined with seed treatments, may be effective in improving stand establishment and the seed yield of soybean in *R. solani*-infested soils.

Diseases of garlic and onion in Alberta in 2015

G.C. DANIELS, R.C.J. SPENCER, J. BROATCH, J. FENG, S.L.I. LISOWSKI, R.J. HOWARD, J.M. NIELSON, M.W. HARDING.

Alberta Agriculture & Forestry (AAF), Crop Diversification Centre South,301 Horticultural Station Road East, Brooks, AB, T1R 1E6, Canada; (R.C.J.S) AAF, Alberta Ag-Info Centre, Provincial Building, Bag 600, Stettler, AB T0C 2L0, Canada; (J.B.) AAF, Lacombe Research Centre, 6000 C&E Trail, Lacombe, AB, T4L 1W1, Canada, (J.F.) AAF, Alberta Plant Health Lab, Crop Diversification Centre North, 17507 Fort Road, Edmonton, AB, T5Y 6H3, Canada; (R.J.H.) Ag Research Solutions, P/O Box 1456, Brooks, AB, T1R 1C3, Canada

Plant and soil samples were collected from five garlic and ten onion fields in Alberta in 2015. In total, 5 garlic and 16 onion plants were evaluated. Symptoms of disease and signs of fungal pathogens were evaluated visually upon receipt. Samples were then incubated in humid chambers to encourage additional growth of pathogens. Fungi were identified by spore or hyphal morphology observed by phase contrast microscope at 400x. Presence of the aster yellows phytoplasma was detected by nested PCR. Nine fungal genera were observed on symptomatic plants, including *Fusarium, Embellisia*, *Penicillium*, *Botrytis*, *Alternaria*, *Rhizoctonia*, *Arthrobotrys, Stemphyllium and Sclerotium.* The aster yellows phytoplasma was detected in three of the 21 samples. Bacterial soft rot was noted, but causal agents were not identified. Additional soil and bulb samples were evaluated for the presence of plant parasitic nematode species. Results from the nematode identifications will be presented in a separate report.

Plasmodiophora brassicae resting spore dynamics in clubroot resistant canola (*Brassica napus*) cropping systems

T.W. ERNST, D. STANTON, D.C. RENNIE, I. FALAK, S.F. HWANG, S.E. STRELKOV

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Clubroot of canola (*Brassica napus* L.), caused by the obligate parasite *Plasmodiophora brassicae* Woronin, has proven difficult to manage due to the longevity of its resting spores, its ability to produce large amounts of inoculum, and the prohibitive costs of effective fungicides. Aside from a long rotation away from clubroot susceptible hosts, the cropping of resistant canola cultivars is one of the few effective strategies for clubroot management. There is evidence from greenhouse studies that resistant cultivars may induce resting spore germination, while supporting limited production of new inoculum, thereby serving to deplete spore loads in the soil. In order to evaluate the impact of resistant cultivars on inoculum loads under field conditions, *P. brassicae* resting spore concentrations were monitored. Pre-seeding and post-harvest soil sampling at geo-referenced locations was conducted over four years within commercial fields with natural clubroot infestations. Quantitative PCR was used to assess *P. brassicae* resting spore concentrations. The cultivation of resistant canola in soil where quantifiable levels of *P. brassicae* DNA (>4.0 x 10^3 spores g^{-1} soil) was present resulted in an increase in inoculum loads. There was a notable lag in the release of inoculum after harvest, and quantifiable *P. brassicae* inoculum peaked in the spring following years when resistant canola was cultivated. Inoculum loads can rapidly decline after 2-years without the cultivation of canola.

Survey for blackleg on canola in Southern Alberta in 2015

T.B. HILL, C.J. HILL, G.C. DANIELS, D.A. BURKE, C.A. PUGH, M.W. HARDING

Crop Diversification Centre South, Alberta Agriculture &Forestry, 301 Horticultural Station Road East, Brooks, AB, T1R 1E6, Canada.

Blackleg is a disease on canola caused by the phytopathogenic fungus *Leptosphaeria maculans,* which attacks all above-ground parts of the host plant. Infected plants often form dry, sunken cankers at the stem base. The results of infection can be reduced yield and quality, often due to premature senescence and lodging. A survey for blackleg was performed in Southern Alberta in 2015. A total of 50 canola fields in 19 municipalities were surveyed. Surveyors walked a W-shaped pattern, stopping at five locations that were at least 20-m apart. At each location, 20 stems were evaluated for blackleg for a total of 100 stems/field. All stems were cut in cross-section at the soil line and then visually rated for blackleg symptoms. Symptoms included vascular discoloration at the cut surface and/or the presence of basal stem cankers. Blackleg prevalence was calculated as the percentage of fields with symptoms present. Incidence was calculated as the percentage of plants with blackleg symptoms, and severity was estimated using 0-5 scale for rating vascular discoloration. The prevalence of blackleg was 57.5%, the incidence was 8.8% and the severity was 0.11. The most recent previous survey for blackleg in Alberta was done in 2012. In that year, the prevalence, incidence and severity were 99%, 21%, and 1.26, respectively. The fact that 2015 was extremely dry for much of the growing season in many parts of Alberta, while 2012 was not, may account for some of these differences.

Characterization of populations of *Plasmodiophora brassicae* by genotyping-by-sequencing

M.D. HOLTZ, S.F. HWANG, J. ZANTINGE, S.E. STRELKOV

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Plasmodiophora brassicae Woronin is a serious obligate soil-borne pathogen that causes clubroot disease in canola and other cruciferous crops. Recently, new aggressive populations of the pathogen, virulent on clubroot resistant canola (*Brassica napus* L.) cultivars, have been found in Alberta, Canada. In order to determine the relationship of members of these aggressive populations to other *P. brassicae* populations present in Alberta a next-generation genotyping-by-sequencing (GBS) method was employed. Twenty-one populations or single-spore isolates were analyzed. DNA was extracted from spores purified from infected roots and used for GBS. Over 10 million sequences were generated and thousands of variable nucleotides were identified. The new aggressive populations could be easily distinguished from other *P. brassicae* populations using the data generated. Additionally, the sequence information produced should allow for the development of markers and assays for the detection of resistance-defeating *P. brassicae* populations.

Molecular phylogeny of *Rhynchosporium commune* from central Alberta

M.D. HOLTZ, J. ZANTINGE, K. XI, T.K. TURKINGTON

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Rhynchosporium commune Zaffarano, McDonald, and Linde sp. nov. (formerly: *R. secalis* (Oudem.) J.J. Davis) is the causal agent of the foliar disease scald of barley. Recent evidence has shown that *R. commune* originated in northern Europe then proceeded to disperse into barley producing areas around the world. Phylogenetic analysis was undertaken to determine the relatedness of *R. commune* from central Alberta to populations in other regions. Multilocus sequence analysis was performed using the housekeeping gene β-tubulin, the mating-type genes *MAT1-1-3* and *MAT1-2-1*, and two non-coding RFLP loci, pRS6 and pRS52. The resulting sequence information was then compared to publically available *R. commune* sequences from five continents. The degree of relatedness to other populations varied with the locus and isolate examined. Most sequence haplotypes found were either present in *R. commune* populations on multiple continents or they have not been reported previously. However, sequences previously detected only in Scandinavia, Australia, or the Middle East were present in Albertan isolates. Results show the *R. commune* population in central Alberta is diverse and that previously undocumented gene flow has occurred between Alberta and other continents.

Effects of post-application land treatment on the efficacy of Vapam to control clubroot (*Plasmodiophora brassicae*) of canola

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Clubroot, caused by *Plasmodiophora brassicae* Woronin, has become a serious threat to canola (*Brassica napus* L.) production in western Canada. The efficacy of Vapam (metam sodium) for the control of clubroot in Brassica vegetable crops has been variable, reflecting different application methods and post-fumigation land treatment. Experiments were carried out to evaluate the effects of the amount of watering, soil incorporation and tarping on the efficacy of Vapam fumigant in reducing clubroot severity in *P. brassicae*-infested soils. Levels of watering or watering + plastic tarping did not affect the efficacy of Vapam, but, compared with the non-treated control, Vapam fumigation improved seedling emergence, plant growth, plant biomass, pod number and seed yield, and reduced gall weight and clubroot severity. Post-application incorporation of Vapam into the soil improved plant biomass and seed yield, and reduced clubroot severity compared with a non-incorporated control. Covering the treated soil with a plastic tarp after Vapam fumigation significantly improved seedling emergence, plant vigor and reduced gall weight and clubroot severity compared with non-treated plots covered with plastic. A 12-day duration of covering increased emergence and yield compared with a 7- or 16-day covering duration. In summary, soil incorporation and tarping of the land after application increased the effectiveness of Vapam in controlling clubroot.

Effect of irrigation and plant canopy architecture on white mold development in dry bean

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Dry bean (*Phaseolus vulgaris* L.) is the most profitable pulse crop grown under irrigation in Southern Alberta. White mold (WM) caused by the fungus *Sclerotinia sclerotiorum* (Lib.) de Bary is a major constraint to dry bean production. Field studies were conducted at AAFC-Lethbridge in 2015. Three levels of irrigation (high, medium and low) and five cultivars with different canopy architecture (semi-upright bush, upright bush and prostrate) were arranged in a split-plot design and plots were evaluated for WM incidence and severity, flower infection, yield and thousand seed weight (TSW). Microclimate variables were monitored using data loggers and sensors. WM incidence, severity and flower infection observed were significantly higher in high irrigation plots compared to medium and low irrigation plots. Higher water content within the top 5-cm of soil, prolonged leaf wetness and cooler canopy temperatures were maintained in high irrigation plots compared to medium and low irrigation plots. Plots grown under medium and low irrigation had similar WM levels, but yield and TSW were reduced under low irrigation. WM development in AAC Burdett and I9365-31, lines with partial resistance, were not affected by irrigation regime. Thus, irrigation schedule and choice of cultivars can be effective tools for WM management in Alberta. This trial will be conducted for 2 more years.

A simple in vitro assay to measure enhanced "pathogenesis-related" enzyme expression during scald barley interaction

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Leaf scald, caused by Rhynchosporium commune, is a major barley disease in central Alberta and around the world. Yield losses from severe leaf scald infection have been estimated as much as 20 – 36% in Alberta. The objective of the present study was to develop an in vitro assay to screen barley germplasm for scald pathogen recognition and pathogenesis-related (PR) protein expression of β 1-3 glucanase. Sterile barley seeds were inoculated by soaking in a scald spore suspension or mock inoculated with sterilized water. Inoculated seeds were placed on culture media containing a base layer of 0.5% water agar, and a second thin assay layer containing 0.2% dye linked (AZCL- β-Glucan). In the presence of β 1-3 glucanase activity, water soluble blue dye was released from the AZCL- β-Glucan substrate into the assay media. Blue colour was measured visually, by diffusion area (mm) and optical density (OD, 595nm). Blue coloration present in the media directly correlated with enzyme activity and resistant cultivar-scald interaction. However, some lines showed variation in both the lab and field and, this variation emphasized the complex nature of the pathogen-plant relationship. There is a need for more research to determine the experimental conditions for the measured parameters that potentially caused inconsistent or variable results observed in this investigation.

Molecular characterization of the Lethbridge Research and Development Centre snow mold collection

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The pathogenic psychrophilic fungal collection at the LRDC of 67 accessions of fungal isolates collected between 1945 and 1994 in North America (mostly Western Canada) includes several different species in different genera, and many isolates within each species. Although the origin of these isolates and what species some isolates may represent is known, we have very limited knowledge about the level of homology within species, taxonomic relationship among these pathogens and the genetic elements conferring the ability to grow and develop at low temperature and to infect different hosts. The goal is to use Next Generation Sequencing (NGS) to survey the genome of these isolates and subsequently identify the genes that allow these fungi to thrive at low temperatures. We were able to regrow the majority of the 67 accessions that were stored in liquid nitrogen for 25 years or more. We will present data on the growth characteristics of these isolates and describe the sequencing libraries preparation and data analysis techniques that will be used in this project. An important aspect of the project will be accurate generic identifications for the low temperature basidiomycetes (LTB) and the sclerotial (SLTB) forms. Identified genes may lead to a better understanding of specific sequences involved in the compatible/incompatible interaction with host species.

Effect of seed dressing fungicide and inoculum density on *Aphanomyces* root rot of field pea in Alberta

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Field pea (*Pisum sativum* L.) is an important commercial crop in Alberta with high protein content and the ability to improve the nitrogen content in soil. Root rot caused by soil-borne pathogens is common in field pea crops in Alberta. Recently, root rot caused by *Aphanomyces euteiches* was reported to be a concern where above-normal spring rainfall occurred. Experiments were conducted to determine effects of seed treatment and inoculum density on *Aphanomyces* root rot of field pea under greenhouse and field conditions. Five seed-treatment fungicides, including Apron Advance, Intego Solo, BAS 516F, BAS 720F and BAS 516F + BAS 720F (1:3), were evaluated in 2015. All of the treatments with the exception of Apron Advance reduced root rot severity, and BAS 516F, BAS 720F and Intego Solo improved plant vigour compared with the control treatment under greenhouse conditions. Under field conditions, the treatment effects were generally not significant. In an inoculum density study, increasing inoculum density significantly reduced seedling emergence and plant vigour, and increased root rot severity under both field and greenhouse conditions. The experiments will be repeated in 2016 to confirm the results.

Barley and wheat leaf disease survey in central Alberta, 2015

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During 2014 to 2015, 24 barley, 24 spring wheat and 33 winter wheat fields in central Alberta were surveyed for leaf diseases. The majority of barley fields showed low levels of two forms of net blotch and spot blotch with severe scald in only one field. The leaf spotting complex was the major disease in most spring wheat fields. Light and severe levels of stripe rust in spring wheat were observed in six and two fields, respectively. In 33 winter wheat fields surveyed at the seedling stage during mid-October 2014 and mid-October 2015, the majority of diseased fields displayed low levels of stripe rust. A range of stripe rust levels from 15 to 90% disease incidence was observed in six fields during mid-October 2015. Stripe rust was also observed in the majority of winter wheat research plots in the breeding nurseries of central Alberta in the fall of 2014. Plots in a few of the tests showed variable levels of stripe rust severity by early spring of 2015.

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