41TH ANNUAL MEETING OF THE PLANT PATHOLOGY SOCIETY OF ALBERTA

November 4-5, 2020

PPSA 2020 meeting program

First day: Wednesday, November 4th 2020

Time	Event	
09:30-09:15		Welcome and opening remarks
09:15-09:40	Invited Speaker, **Denis Guadet**	A history of the LTB snow mold fungus in Alberta: When will we identify this species?

09:40-10:25	**Paper Session I** **Technicians oral presentations** **Chair: Nora Foroud**		
Time	**ID#**	**Presenter**	**Title**
09:40-09:55	T1	**Michelle Cradduck**	Building Ug99 resistance in Canadian winter wheat germplasm by stacking up stem rust resistance genes Sr22 and Sr24
09:55-10:10	T2	**Michele Frick**	The circadian clock and plant immunity in wheat
10:10-10-25	T3	**Daria Ryabova**	Developing a Brachypodium distachyon cell suspension culture pathosystem to study cellular defence responses.

10:25-10:40 **Coffee break**

10:40-11:55	**Paper session II** **Students oral presentations** **Chair: Rodoulph Fredua-Agyeman**		
Time	**ID#**	**Presenter**	**Title**
10:40-10:55	S4	**Keisha Hollman**	Pathotypes of Plasmodiophora brassicae in western Canada (2017-2018)
10:55-11:10	S5	**Heather Tso**	Challenges in clubroot pathotype-specific molecular diagnostics
11:10-11:25	S6	**Brittany Hennig**	Evaluation of strategies for the integrated management of clubroot of canola
11:25-11:40	S7	**Sijan Pandit**	Screening of pea germplasm for partial resistance to Aphanomyces root rot
11:40-11:55	S8	**Kyle Biscaglia-Horvath**	Pathogen dynamics of the root rot complex of field pea

11:55-13:00 **Lunch break**

13:00-13:30	**Paper Session III** **Students oral presentations** **Chair: Ravinder Goyal**		
Time	**ID#**	**Presenter**	**Title**
13:00-13:15	S9	**Dianevys Gonzales**	Characterization of Fusarium graminearum transformants over-expressing the mitogen-activated protein kinase kinase, Mkk2, and a phosphomimic thereof
13:15-13:30	S10	**Anas Eranthodi**	Role of a secreted cerato-platanin protein in growth, infection and DON accumulation by Fusarium graminearum

13:30-14:30	**Poster Session** **Chair: Reem Aboukhaddour**	
ID#	**Presenter**	**Title**
11	**Febina Mathew**	Analyzing yield response to application of pyraclostrobin in sunflower (Helianthus annuus L.)
12	**Ahmed Hafiz**	An update on an indexed microbial culture collection and preservation of plant pathogens derived from Alberta crops

S13	**Swarnalatha Moparthi**	Identification of diverse chickpea pathogens in Montana State
S14	**Zhiyu Yu**	Effect of fall and spring lime applications on clubroot of canola
S15	**Longfei Wu**	Identification of quantitative trait loci (QTL) associated with root rot caused by the root rot complex in field pea
S16	**Eleanor McBain**	Detection and monitoring of Sclerotinia sclerotiorum ascospore levels in commercial canola fields during flowering
S17	**Alejandra Oviedo Ludena**	Consequences of crop diversity and climate change on Fusarium head blight across the Canadian prairies
T18	**Lipi Parikh**	Efficacy of essential oils in managing Didymella rabiei, and evaluating their putative phytotoxicity
T19	**Albert Hannig**	Effect of synthetic antimicrobial peptides on common fungal pathogens and application to field pea (Pisum sativum)
T20	**Marshall Smith**	Cloning a mitogen-activated protein kinase kinase kinase YODA from Triticum aestivum for transgenic expression in wheat
T21	**Clinton Dovell**	Development mutant wheat populations under selection pressure for Fusarium head blight resistance

Time	Event
14:30-16:30	Judges meet to select winning oral presentations and posters
18:00-19:00	Award Ceremony via zoom and group zoom pic

Second day: Thursday, November 5th 2020

09:40-10:25	Speakers Sessions Chair: Syama Chatterton	
Time	**Presenter**	**Title**
09:00-09:25	**Michelle Hubbard**	Impact of location and environmental factors on pulse, cereal and oilseed diseases in the Canadian prairies
09:25-09:55	**Andre Laroche**	Redesigning the effectiveness of the stripe rust resistance gene Yr10 against current virulent fungal isolates
09:55-10:10	**Brent Puchalski**	COVID Staycation: A Southern Alberta Gravel Road Expedition to Explore Farmer Responses to Wheat Diseases.
09:50-10:30		**Coffee break**
10:30-12:00		**Business meeting**
12:00		**Adjourn**

(S): Student (T): Technician

Oral paper abstracts

ID#

T1 **Building Ug99 resistance in Canadian winter wheat germplasm by stacking up stem rust resistance genes *Sr22* and *Sr24*.** M.H.J. Cradduck, M. Frick, R.J. Graf and A. Laroche**.** *Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB, Canada T1J 4B1.*

Wheat (*Triticum aestivum* L.) stem rust is caused by the pathogen *Puccinia graminis*. The deployment of effective resistance genes in cultivars since the 1950's has mostly controlled this pathogen. However, a new race of stem rust known as Ug99, discovered in Uganda in 1998, defeats many common resistance genes including *Sr31* and *Sr38*. Ug99 has since spread to thirteen countries in Africa and the Middle East and has evolved into a family of thirteen different races with virulence to resistance genes that were previously effective against the original race. With the majority of the world's wheat cultivars susceptible and the potential threat of further spread of Ug99, effective resistance must be developed. Pyramiding resistance genes using marker assisted selection (MAS) is an effective strategy to produce cultivars with durable resistance to Ug99 and other stem rust races. For this study, MAS was used to identify experimental winter wheat germplasm lines with two genes of interest, *Sr22* and *Sr24.* A multiplex PCR was performed using primers specific for *Sr22* and *Sr24* to identify the presence of these resistance genes. Preliminary results from a stem rust nursery in Kenya have shown the effectiveness of our approach. Lines rated as more resistant were found to match the lines that carry resistance gene *Sr22* and to a lesser extent *Sr24*. The ability to pyramid these genes in our germplasm could provide enhanced resistance to Ug99 variants in the future.

T2 **The circadian clock and plant immunity in wheat.** Michele Frick, Tiana Masic, Michelle Cradduck, Chelsi Harvey, Fengying Jiang, Nora Foroud, Robert J. Graf, John D. Laurie and André Laroche. *Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre, Lethbridge, AB T1J 4B1.*

The plant circadian clock functions to optimize cellular processes and physiological reactions with respect to light/dark cycle and seasonal changes within a 24 h cycle. Diverse physiological pathways are connected to the circadian clock (CC) and increasing evidence indicates that the plant immune responses are also connected to the circadian clock. Maximal jasmonic acid (JA) and salicylic acid (SA) accumulations occur at midday and midnight respectively. Cross talk between JA and SA signalling is an important part of plant defence against different pathogens. The plant must be ready to respond with peak expression of defence genes concordant with the time of pathogen attack. Generally, higher SA levels are needed for resistance to biotrophic pathogens and higher JA levels promote resistance to necrotrophic pathogens and insect herbivores. We are studying gene expression over 12 times points from ZT1 to ZT23 within a 24 h cycle in the susceptible wheat cultivar Fielder to determine the expression of core clock genes and other transcripts that may be regulated by the circadian clock with the overall goal of modulating the CC to improve wheat resilience to changing climatic conditions. As part of this gene expression study, we will present the response of genes in the JA and SA pathways to see the potential role of the circadian clock in the plant immune response in wheat.

T3 **Developing a Brachypodium distachyon cell suspension culture pathosystem to study cellular defence responses**. D. D. Ryabova[1], . González Peña-Fundora[1,2], N. A. Foroud[1]
[1] *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403-1st Avenue South, Lethbridge, AB T1J 4B1, Canada* [2]*University of Lethbridge, 4401 University Dr W, Lethbridge, AB T1K 6T5, Canada.*

A *Brachypodium distachyon*-21 (*Bd21*) cell suspension culture was established to study the processes of plant cellular responses to pathogens. *Fusarium graminearum* (*Fg*) is a wheat pathogen and it is known to infect different tissues of *Brachypodium* species, a model plant for cereals. The long-term objectives is establish high-throughput methods to study the *Bd21* cell cultures *Fg* infection, *Fusarium* toxins and pathogen-associated molecular patterns (PAMPs), by monitoring reactive oxygen species (ROS) production and programmed cell death using multi-well formats. As a starting point, *Bd21* cell suspensions were inoculated with *Fg* macroconidia, to observe their interactions. Spore germination and mycelium formation was observed at 22ºC, 12-36 h after inoculation. Both wild-type strain Gz3639, and a GFP-labelled strain, were used to trace fungal structures. Germinated spores formed germ tubes, developed branching hyphae and some of the hyphae coincided in with *Bd21* cells, but penetration of the host cells was not evident in most cases. The GFP strain developed fluorescent hyphae but did not form any structures inside *Bd21* cells. Different techniques were employed to monitor the

viability of plant cell culture, including MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) assay and staining with vitality dyes (e.g. trypan blue, propidium iodide and fluorescein diacetate). Incubating *Fg* spores with *Bd21* cells without shaking increased the chances to observe interaction events, but drastically dropped the viability of plant cells and also decreased fungal development.

S4 **Pathotypes of *Plasmodiophora brassicae* in western Canada (2017-2018).** K.B. HOLLMAN, S.F. HWANG, V.P. MANOLII AND S.E. STRELKOV**.** *Department of Agricultural, Food, and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada.*

Clubroot, caused by *Plasmodiophora brassicae* Woronin, is an important soilborne disease of canola (oilseed rape; *Brassica napus* L.). In Canada, clubroot management relies heavily on the planting of resistant cultivars, but since 2013, resistance has been broken in an increasing number of fields. Prior to the introduction of resistance, *P. brassicae* pathotype 3H, as defined on the Canadian Clubroot Differential (CCD) set, was predominant in Alberta. In testing of pathogen collections from 2014-2016, however, pathotype 3A was most common, indicating rapid shifts in the pathogen population. Up-to-date knowledge of pathotype composition is important for effective resistance breeding and stewardship. Therefore, clubbed roots were collected from clubroot resistant canola crops representing 166 fields in Alberta, Saskatchewan, and Manitoba in 2017 and 2018, with one isolate per field evaluated for pathotype designation on the CCD set and the differentials of Somé et al. Seventeen pathotypes were detected on the CCD set, including the previously reported pathotypes 3A, 3D, 3H, 5L, 5X, 8E, 8N and 8P, plus the novel pathotypes 2C, 6D, 8D, 9A, 9B, 9C, 11A, 13A and 13B. Five pathotypes were identified on the hosts of Somé et al. including P_1, P_2, P_3, P_4 and P_5, with P_4 and P_5 reported here from Canada for the first time. The majority of the isolates, representing 38 fields in 2017 and 93 fields in 2018, could overcome genetic resistance. The results suggest significant diversity in the virulence of *P. brassicae* populations and an increasing prevalence of resistance-breaking *P. brassicae* strains.

S5 **Challenges in clubroot pathotype-specific molecular diagnostics.** H. H. TSO, L. GALINDO-GONZÁLEZ, H. ASKARIAN, M. D. HOLTZ AND S. E. STRELKOV. *Department of Agricultural, Food and Nutritional Science, 410 Agriculture/Forestry Centre, University of Alberta, Edmonton, AB T6G 2P5, Canada; and (M.D.H.) Field Crop Development Centre, Alberta Agriculture and Forestry, 5030-50 Street, Lacombe, AB T4L 1W8, Canada.*

Clubroot, caused by *Plasmodiophora brassicae* Wor., is an important soilborne disease of canola (*Brassica napus* L.). New pathotypes have recently emerged that can overcome host resistance, and the ability to distinguish pathotypes rapidly and reliably would be valuable for clubroot management efforts. To identify diagnostic polymorphic regions, we obtained variant genome information from 45 full genome *P. brassicae* isolates and aligned them with the original e3 *P. brassicae* reference genome published in 2015. Our preliminary computational analysis indicated numerous heterozygous positions when pathotype reads were mapped to the 2015 e3 genome assembly. When the reads were mapped to the most recent e3 genome published in 2019, the apparent heterozygosity was found to have resulted from the collapsing of reads corresponding to different genomic regions. To distinguish pathotypes, we developed an RNase H2-dependent PCR (rhPCR) assay with primers bearing a polymorphic ribonucleotide at the 3' end. Although sensitive, this method produced residual unspecific amplification at times. The specificity of the rhPCR assay was improved with the incorporation of multiple SNPs expanding the primer region beyond the ribonucleotide. We also used SNaPshot, a single-base extension technology that fluorescently labels the discriminatory SNP, to compare its discriminatory power with rhPCR. Preliminary results showed a clear differentiation among pathotypes. While both technologies are useful for clubroot diagnostics, rhPCR is the most cost-effective and widely used molecular technique, and may be optimized into a quantitative assay. The main advantage of SNaPshot is the ability to distinguish all four alleles at the discriminatory SNP.

S6 **Evaluation of strategies for the integrated management of clubroot of canola.** B.C. HENNIG[1], S.F. HWANG[1], S.E. STRELKOV[1], V. MANOLII[1], AND G.D. TURNBULL[2]
[1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada
[2]Alberta Agriculture and Forestry, Crop Diversification Centre North, 17507 Fort Road, Edmonton, AB, T5Y 6H3, Canada.

Plasmodiophora brassicae Wor. is a soil-borne parasite causing clubroot of canola (*Brassica napus* L.), a serious disease managed mostly by planting clubroot resistant (CR) cultivars. Recently, new strains of the parasite have emerged that overcome resistance, highlighting the need for an integrated approach to clubroot management. Since clubroot development is favoured in acidic soils, the application of lime to increase soil pH has been suggested as a management strategy. Control of cruciferous weeds, which may serve as inoculum reservoirs, has also been proposed to reduce spore loads. In this study, a field trial was conducted at two sites in central Alberta. The effect of soil liming and weed control on clubroot severity

were compared at different inoculum levels on resistant ('45CM39') and susceptible ('45H31') canola cultivars. Preliminary data indicated that the application of hydrated lime to increase soil pH to 7.2 resulted in a decrease in clubroot severity of 44-47% in the susceptible cultivar. Disease severity was lowest in treatments consisting of CR canola grown in limed plots and highest in susceptible canola grown in non-limed plots. Greenhouse trials are underway to evaluate clubroot development on susceptible and resistant canola grown at different inoculum levels in a canola-wheat-barley-canola rotation. Preliminary results suggest limited clubroot development on the susceptible or resistant cultivars at low resting spore concentrations but significant disease reductions on CR canola at high infestation levels. The impact of the various treatments on resting spore levels will be measured by quantitative PCR analysis of the soil.

S7 **Screening of pea germplasm for partial resistance to Aphanomyces root rot.** S. PANDIT, S. CHATTERTON, AND R. GOYAL. *University of Lethbridge, 4401 University Drive, Lethbridge, AB, T1K 3M4, Canada; (S.C.) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403–1 Avenue South Lethbridge, AB, T1J 4B1, Canada; (R.G) Lacombe Research and development center, Agriculture and Agri-Food Canada, 6000 C and E trail, Lacombe, AB, T4L 1W1*

Aphanomyces root rot (ARR) caused by the oomycete *Aphanomyces euteiches* (*Ae*) is one of the most destructive diseases of field pea (*Pisum sativum*). ARR can cause yield losses of up to 100% and fully effective management options including fully resistant cultivars to ARR are not available. To identify partially resistant lines, 31 pea lines were screened in the greenhouse and 26 lines from the same collection were screened under field conditions. Inoculation of *Ae* in the form of oospores and zoospores to vermiculite was used in greenhouse experiments. The field plots were inoculated using a mixture of soil naturally infested with *Ae* and vermiculite inoculated with zoospores. ARR ratings were performed visually on a scale of 0-5. Ratings of the plants in the greenhouse were recorded after the known susceptible cultivar 'CDC Meadow' showed a disease rating of 3 or higher. The disease ratings in the field were recorded 4 weeks after seeding. Fourteen pea lines showed lower disease severity compared to 'CDC Meadow' in the greenhouse conditions. Among these 14 lines, PI 557500, PI 660729, PI 606700, 5001 and K-2 also performed well under field conditions. Pea line PI 557500 showed the highest partial resistance to ARR in the field experiment. These lines are also being tested against *Fusarium* species to determine if there is cross-resistance to multiple root rot pathogens. The best performing lines will be used for crossing, and for experiments in the greenhouse and field to explore the nature of the partial resistance of these lines.

S8 **Pathogen Dynamics of the Root Rot Complex of Field Pea.** K. Biscaglia-Horvath, S. Chatterton**.** (K.B & S.C.) *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1 Ave S, Lethbridge, AB, Canada.* (K.B.) *Department of Biology, University of Lethbridge, 4401 University Dr W, Lethbridge, AB, Canada*

Pea root rot is a disease complex comprised of multiple biotic and abiotic stressors resulting in decay of the root system. Pathogens contributing to root rot in field peas include *Aphanomyces euteiches* and various *Fusarium* spp. However, little is understood of the nature of the interactions between pathogens and environmental influences on these interactions. The objective of our study is to simulate multiple infection scenarios in greenhouse studies to (i) characterize the nature of microbial interactions within the disease complex and its effect on disease severity; (ii) relate pathogen load to host colonization; and (iii) determine how soil moisture levels influence this interaction. CDC Meadow, a susceptible cultivar, was grown for one month in soil inoculated with varying concentrations of *Fusarium avenaceum*, *Fusarium redolens* and *Aphanomyces euteiches* in difference combinations. Plants were then measured for biomass and roots were rated for disease severity against a visual rating scale. Three replicates were randomly selected per treatment, and DNA was isolated from the epicotyl, hypocotyl, tap root and lateral root to quantify host colonization and pathogen localization. Results to date have shown a positive correlation between pathogen load and disease severity in the case of all three pathogens. However, the presence of *F. redolens* as a tertiary pathogen in combination with *F.avenaceum* and *A. euteiches* resulted in a lower disease at the time of sampling. Quantitative PCR results are pending, but will reveal the nature of pathogen dynamics within the root system. Results will be applied to decision support systems to accurately advise producers lowering losses from root rot.

S9 **Characterization of *Fusarium graminearum* transformants over-expressing the mitogen-activated protein kinase kinase, Mkk2, and a phosphomimic thereof.** D. Gonzalez-Pena Fundora, A. Eranthodi, R.G. Subramaniam, C. Rampitsch, N. Thakor and N.A. Foroud. (*D.G.F., A.E., N.A.F.*) *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403, 1st Ave S, Lethbridge, AB, T1J 4B1; (R.G.S.) Ottawa Research and Development Centre, 960 Carling Ave, Ottawa, ON K1A 0C6;* (C.R.) *Morden Research and Development Centre, 101 Route 100 Unit 100, MB, R6M 1Y5; (N. T.) University of Lethbridge, Department of Chemistry and Biochemistry, Lethbridge, 4401 University Drive West, Lethbridge, AB, T1K 3M4.*

Fusarium graminearum is one of the causal agents of fusarium head blight (FHB), a fungal disease affecting cereal crops. *F. graminearum* secretes mycotoxins, such as deoxynivalenol (DON), that can cause severe illness when ingested. DON production may be regulated by the mitogen-activated protein kinase (MAPK) Mgv1, and its presumed upstream MAPK kinase (MAPKK) Mkk2. According to orthologous pathways in yeast, these MAPK proteins are predicted to be at the core of the cell-wall integrity cascade. MAPKs have a multitude of targets, and to date single transcription factor Rlm1 has been identified as Mgv1 target in *F. graminearum*. With the long term objective of identifying other downstream components of Mgv1, a constitutively active (CA) form of *MKK2* was over-expressed *in locus* in *F. graminearum* through *Agrobacterium* mediated transformation. Two strains over-expressing *MKK2* (*MKK2_OX*) and two strains over-expressing CA-*MKK2* (*CA-MKK2_OX*) were generated. The transformants showed a reduced mycelial growth in solid media, compared to the wild-type (WT), which corresponded with reduced disease in wheat spikes. Interestingly, the transcript levels of the gene encoding trichodiene synthase, the enzyme that catalyzes the first committed step in DON synthesis, was down-regulated in mycelium collected from potato-dextrose broth; however, under DON-inducing conditions *MKK2*_OX showed increased accumulation of the toxin. In addition, the *CA-MKK2_OX* strains were more susceptible than *MKK2_OX* to the cell wall stress agent Congo red. When exposed to NaCl, the opposite effect was observed suggesting that the mutation in *CA-MKK2* negatively affects cell wall integrity, mycelial growth and virulence but increases osmotic stress resistance.

S10 **Role of a secreted cerato-platanin protein in growth, infection and DON accumulation by *Fusarium graminearum*.**
A. Eranthodi, D. González-Peña Fundora, R.G. Subramaniam, T. Ouellet, C. Rampitsch, M. Smith, S. Elizabeth and N.A. Foroud. *(A.E., D.G.F., M.S., N.A.F.) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403-1st Avenue South, Lethbridge, AB T1J 4B1; (R.G.S., T.O.) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6; (C.R.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Unit 100 Morden, MB R6M 1Y5; (S.E.) University of Lethbridge, Department of Biological Sciences, 4401 University Dr W, Lethbridge, AB T1K 6T5.*

Fusarium head blight (FHB) is a devastating disease of cereals worldwide primarily caused by the ascomycete fungal pathogen *Fusarium graminearum* Schwabe. FHB leads to substantial reduction in yield and quality of grains. Most proteins in the *F. graminearum* secretome are uncharacterized and their involvement in FHB disease remain unexplored. In this study, a cerato-platanin protein (FGSG_10212, FgCPP1) with a reduced abundance in the secretome of a non-pathogenic mutant of *F. graminearum* GZ3639 strain was characterized by producing and screening *FgCPP1* disruption (*Δcpp1)* and overexpression (*CPP1-OX*) strains for growth and infection related phenotypes. Neither disruption nor overexpression of *FgCPP1* gene influenced macroconidia germination or mycelial growth in *F. graminearum*. Experiments with cell wall targeting chemicals suggested a lack of involvement of *FgCPP1* in cell wall integrity. *CPP1-OX* accumulated higher levels of deoxynivalenol (DON) in axenic culture and in spray inoculated wheat spikes. *CPP1-OX* also had a higher level of initial infection in wheat spikes, whereas disease spread caused by this strain did not differ from the wild-type. Absence of *FgCPP1* neither affected initial infection nor disease spread in wheat spike infection assays. This study provides some basic insights into the role of *FgCPP1* in *F. graminearum* infection.

COVID Staycation: A Southern Alberta Gravel Road Expedition to Explore Farmer Responses to Wheat Diseases.
B. L. PUCHALSKI, B. J. PUCHALSKI. *Paramoria Agri-Science, 216 23rd Street South, Lethbridge, AB, T1J 3M6, Canada.*

COVID19 presented unique and difficult challenges to farmers during the 2020 growing season. The disease forced rural communities to isolate, yet farming activities continued. With limited external advice and assistance, how did farmers respond to emerging wheat diseases for the season? To identify farmer responses and disease patterns, we surveyed 166 cereal fields for foliar disease incidence and severity, using a modified Cobbs scale. The survey focused on spring, winter and durum wheat. The presence or absence of signs of fungicide application was recorded. A multivariant expert system which mapped disease risk in conjunction with the ability to apply fungicide using ground-based equipment was also created. Half of all fields did not have fungicides applied at the time of the survey. 61% of those unsprayed fields exhibited disease incidence and severity below economic thresholds for applying fungicides. Surveyed fields demonstrated a spectrum of responses, with 20% of winter wheat fields at intermediate resistance and 33% of spring wheat fields being intermediate and susceptible to stripe rust. Considering the resistance of readily available varieties, this suggests that stripe rust resistance might be leaking. This same trend was not observed for tan spot of wheat. Despite a lack of resistance, tan spot struggled to capitalize to the same degree. Reliance on chemical control also presented difficulties. Multivariant analysis indicated that, for effective application of fungicides, the entire spray season might be decided in a window of only three days.

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11 **Analyzing yield response to application of pyraclostrobin in sunflower (*Helianthus annuus* L.).** F. M. Mathew, S. G. Markell, and R. M. Harveson. *(F.M.M.) Department of Agronomy, Horticulture, and Plant Science, South Dakota State University, Brookings, South Dakota 57007, USA; 605-688-5660; febina.mathew@sdstate.edu; (S.G.M.) Department of Plant Pathology, North Dakota State University, Fargo, North Dakota 58102, USA; (R.M.H.) Department of Plant Pathology, University of Nebraska-Lincoln, Scottsbluff, Nebraska 69361, USA.*

Use of foliar fungicides to manage diseases of sunflower (*Helianthus annuus* L.) in the United States has increased in the last several years. However, the current trend in sunflower production is towards an increased use of foliar fungicides as a means to maximize yields. Among diseases, Phomopsis stem canker is one of the most economically important in sunflower production across the world. Recent research in the U.S. suggests that application of Quinone outside Inhibitor fungicides on sunflower, when the miniature floral head is formed on the plant (R1 growth stage), may protect yield from Phomopsis stem canker. Data analysis was performed to determine the yield response to application of pyraclostrobin (Headline) in sunflower. For the analysis, uniform fungicide trials (n=52) were established in the U.S. states of Minnesota, Nebraska, North Dakota and South Dakota at sites with history of Phomopsis stem canker. In each trial, treatments were replicated at least four times and included a fungicide containing pyraclostrobin and a no-fungicide treatment. Each trial was planted to seeds of commercial hybrids that were considered susceptible or moderately susceptible to Phomopsis stem canker. Disease severity ratings and yield data were collected. Our research suggests that a single application of pyraclostrobin at R1 growth stage reduced the disease severity by 37.2% (significant at P=0.0004) and increased yield by 5.6% compared to plots where the fungicide was not sprayed. More research is needed to determine if a similar positive yield response occurs to pyraclostrobin in hybrids that are tolerant to Phomopsis stem canker.

12 **An update on an indexed microbial culture collection and preservation of plant pathogens derived from Alberta crops.** H. AHMED, Y. YANG AND J. FENG. *The Alberta Plant Health Lab, Crop Diversification Centre North, Edmonton, Alberta, T5Y 6H3, Canada.*

Preservation and maintenance of plant pathogens in pure culture with known identities in a living and stable state is vital for pathological research, and is of critical importance when diagnosing new or emerging plant pathogens, as well as for confirming specific diseases to enable the development of appropriate control strategies. A bacterial and fungal culture collection revitalization initiative has been undertaken in Alberta. Diseased samples from different crops collected during field surveys and sent to diagnostic laboratories by agricultural fieldmen or researchers during 2016-2020 were the principal sources for pathogen isolation. Standard protocols for each pathogen were used for isolation and purification. The microbial cultures were identified based on morphological characteristics and DNA barcoding. Some cultures were obtained from other Plant Pathology laboratories, including the Crop Diversification Centre South, Brooks, AB, the Canadian Collection of Fungal Cultures, Ottawa, ON, the University of Alberta, Edmonton, AB, 20/20 Seed Labs, Nisku and Edmonton, AB, and SGS Biovision Seed Research Ltd., Sherwood Park, AB. These cultures were stored for short periods on Potato Dextrose Agar plates at 4ºC, and for the long term in a Pro-Lab Diagnostics™ Microbank™ Bacterial and Fungal Preservation System, or in 16% glycerol at -80 ºC. Ninety-four percent of the fungal cultures and all of the bacterial cultures were collected locally by the APHL's Provincial Diagnostics Lab. Currently, three hundred-three cultures, including sixty-eight fungal and 21 bacterial plant pathogenic species are conserved and included in a database. These isolates are available on request free of cost to researchers in Alberta.

S13 **Identification of diverse chickpea pathogens in Montana State.** S. Moparthi, M. E Burrows, K. McPhee
Department of Plant Sciences and Plant Pathology, Montana State University, Bozeman, MT 59718. USA

Montana is the leading producer of chickpeas in the United States. Diseases caused by fungal pathogens are major limiting factors for its production. The objective of this study was to survey the most prevalent and pathogenic species of chickpea crops in the State. A total of 53 chickpea fields from 10 counties were surveyed in June and July of 2020 to identify common foliar and root rot pathogens. Diseased chickpea plants were collected and fungal pathogens were isolated on potato dextrose agar (PDA). Pure cultures of isolates were obtained and identified to species level by amplifying part of translation elongation factor (EF1-α) gene (for *Fusarium* spp.), cytochrome oxidase (*COI*) gene (for *Pythium* spp.), glyceraldyhyde-3-phosphate dehydrogenase (*G3PDH*) gene (for *Botrytis* spp.), and entire internal transcribed spacer (ITS) region was amplified for other fungal species identification. *Fusarium* (95%) was the predominant fungal species recovered from the diseased chickpea roots, followed by *Rhizoctonia* (4%), and *Pythium* (1%). Among the *Fusarium* species, *F. oxysporum*

(42%) was the predominant and widely distributed in all chickpea growing regions. *Alternaria* (76 %) and *Botrytis* (20 %) were the predominant fungal species from the foliage, followed by *Ascochyta* (4 %). These preliminary results illustrate the pathogen diversity in the different chickpea producing regions of Montana. This information is essential for the management of diseases and breeding resistant chickpea varieties against economically important pathogens.

S14 **Effects of fall and spring lime applications on clubroot of canola**. Z. YU, , S.F. HWANG, S.E. STRELKOV
Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada

Clubroot (*Plasmodiophora brassicae* Wor.) is a major threat to sustainable canola (*Brassica napus* L.) production in western Canada. The clubroot pathogen prefers acidic soils, and hence, the application of lime to increase soil pH represents a possible management strategy. The finely ground Zero Grind limestone (ZG) and hydrated lime (HL) were applied in replicated field and greenhouse tub trials to evaluate their efficacy for clubroot control. The treatments included an untreated control (UTC), ZG applied at rates of 5 and 10 t/ha in fall or spring, spring applications of HL at 5 and 10 t/ha, and fall application of ZG combined with spring application of HL at 2.5 or 5 t/ha each. Two canola hybrids, '45H31' (susceptible) and 'CS2000' (moderately resistant) were included in the tub trials and '45H31' was used in the field trials. In the tub trials, the application of 5 t/ha fall ZG and 5 t/ha spring HD reduced clubroot severity the most on both cultivars, but did not result in significantly ($p < 0.05$) higher yields than any other treatment except for the UTC. In the field trials, the 10 t/ha fall ZG application and the combination of 5 t/ha fall ZG + 5 t/ha spring HD applications resulted in the lowest clubroot severity and highest yield at both sites. Significant reductions in clubroot incidence also were observed in all of the lime-treated plots or tubs, relative to the untreated controls. The data suggest that the application of lime products at different times holds potential as part of an integrated management strategy for clubroot of canola.

S15 **Identification of quantitative trait loci (QTL) associated with root rot caused by the root rot complex in field pea**
L. WU[1], R. FREDUA-AGYEMAN[1], S.F. HWANG[1], K.F. CHANG[2], D. MCLAREN[3], S.E. STRELKOV[1]
[1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada*
[2]*Alberta Agriculture and Forestry, Crop Diversification Centre North, 17507 Fort Road, Edmonton, AB, T5Y 6H3, Canada*
[3]*Brandon Research and Development Centre, Agriculture and Agri-Food Canada, Brandon, Manitoba, R7A 5Y3, Canada.*

Root rot, caused by several soilborne pathogens including *Fusarium* spp., *Aphanomyces euteiches*, *Pythium* spp., *Phytophthora* spp. and *Rhizoctonia solani*, is a major threat to field pea production in western Canada. There are no completely effective strategies to manage the root rot complex, reflecting limitations in the effectiveness of cultural practices and fungicidal seed treatments, as well as a lack of completely resistant pea germplasm. The pea cultivar '00-2067' is partially resistant to Aphanomyces root rot, with a major QTL on chromosome IV. In this study, the pea genotypes '00-2067' and 'Reward' were screened for resistance to five isolates of *Fusarium* spp., one of *Pythium* spp., one of *Phytophthora* spp. and three isolates of *Rhizoctonia* spp. Two *Fusarium* spp. isolates (F4A and FG2) and one *Rhizoctonia* spp. isolate (CKP1) caused significant difference of root rot severity between 'Reward' and '00-2067'. One hundred thirty-five individuals, derived from the cross '00-2067'× 'Reward', were screened for resistance to F4A, FG2 and CKP1 in greenhouse experiments. Disease severity and plant height were evaluated as measures of resistance and agronomic traits, respectively. A significant genotypic effect and G × E interactions ($P < 0.05$) were detected with high heritability. The identification of quantitative trait loci associated with resistance to the three isolates using the 13.2K SNP array and 222 SSR markers is in progress.

S16 **Detection and monitoring of *Sclerotinia sclerotiorum* ascospore levels in commercial canola fields during flowering.**
E. F. MCBAIN[1], T. K. TURKINGTON[2], S. E. STRELKOV[1], AND J. FENG[3]
[1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5*
[2]*Agriculture and Agri-Food Canada Lacombe Research and Development Center, Lacombe, AB T4L 1W1*
[3]*Agriculture and Forestry, Plant and Bee Health Surveillance Section, Edmonton, AB T5Y 6H3*

Sclerotinia sclerotiorum (Lib) de Bary (stem rot) is a common fungal disease of canola (*Brassica napus* L.) in western Canada. The incidence of stem rot has increased in recent years due to short crop rotations and increased canola acreage, highlighting the need for improved forecasting and management practices. The main objectives of this study were to: (1) refine the use of quantitative PCR analysis and spore traps to evaluate inoculum load before and during flowering for stem rot risk assessment, and (2) develop a better understanding of the relationship between environmental conditions, inoculum levels and final disease incidence and severity. In 2019, environmental data collected from four fields in the Fort Saskatchewan, Alberta, area included ambient and within crop temperature, relative humidity (RH), rainfall, and wind direction and speed. *Sclerotinia sclerotiorum* ascospore levels were monitored with a simple passive spore trap ('Spornado') and a rotorod sampler. One field was monitored more intensively, with five pairs of rotorod samplers and Spornados deployed to evaluate ascospore levels in different areas of the same field. Preliminary results indicated that a cool, wet

summer, with a rain event occurring on at least two-thirds of days monitored, was favorable for disease development as reflected by increased disease incidence within monitored fields. Relative humidity within the crop canopy was higher relative to ambient RH. The Spornado and rotorod results showed moderate to high ascospore levels present at the start of flowering, followed by a second flush after 50% flower.

S17 **Previous crop sequences affect the severity of Fusarium head blight of cereals across the prairies.** M. Alejandra Oviedo-Ludena & Randy Kutcher. *Cereal and Flax Pathology Group. Department of Plan Sciences, College of Agriculture and Bioresources, University of Saskatchewan, 51 Campus Dr, Saskatoon, SK S7N 5A8*

Fusarium head blight (FHB) is a disease of concern across the Canadian prairies; low crop diversity within rotations increases disease risk. Approximately 60% of the area seeded to annual crops in Alberta, Manitoba and Saskatchewan consists of wheat and canola. The present study focusses on the effect of previous crop sequences on the severity of FHB of cereals across the prairies. From 2018 to 2020, six locations were seeded with a core set of five crops including wheat, barley, canola, pea, and maize; at some sites, a sixth crop was included such as lentil. Each year, yield, crop quality and FHB severity were recorded; also, *Fusarium* spp. were isolated and identified from cereal kernels. Several *Fusarium* spp. caused FHB among cereal crops and were associated with host crops. The experiment consisted of a factorial arrangement in a split block design. The diversity criteria were established by using groups A, B, and C. Where A is the crop sequences that included cereals, pulses and oilseeds in the rotation. Treatment B, consisted of cereals and pulses, or cereals and oilseeds; while C, consisted only of cereals. This year data from Saskatoon shows that the diversity criteria played an important role in the proportion of the various *Fusarium* spp. *Fusarium* spp. shows a significant difference between treatments and the frequency of *F. graminearum* isolated was similar in sequences with only cereals and cereal with pulses/ oilseeds, but both differed from a crop sequence that include three-different crops. The lack of crop diversity across western Canada is a risk factor for future disease outbreaks.

T18 **Efficacy of essential oils in managing *Didymella rabiei,* and evaluating their putative phytotoxicity.** L. P. PARIKH AND M. E. BURROWS. *Department of Plant Sciences and Plant Pathology, Montana State University, P.O. Box 173150 Bozeman, MT 59717-3150.*

Plant-derived essential oils (EOs) have potential antimicrobial benefits and can be incorporated in disease management practices as safer alternatives to synthetic fungicides. Previous studies identified *in vitro* inhibition of pathogens with palmarosa, oregano, clove, cinnamon, and thyme essential oils (EOs). In the current study, five EOs were tested *in vivo* to control *D. rabiei,* and EO-seed treatments were evaluated for putative phytotoxicity on seed germination rate and root nodulation. Efficacy of EOs (diluted 1:1000) and fungicide Headline SC (0.29lb ai/A) was evaluated *in vivo* on three chickpea varieties. Oregano (30-60%; SE 3.2-3.8) and thyme (30-45%; SE 3.1-3.8) oils significantly reduced disease severity compared to control (54-81%; SE 3.1-3.7) and were comparable to the fungicide (23-35%; SE 3.2-3.8) at $P \leq 0.05$. EO-seed treatments (1:250 dilution in 0.01% water agar (WA)) and control (0.01%WA) were prepared for three varieties each of chickpea, pea, and lentil. Treatments were applied at 100ul/g seeds. Seed germination rate was determined using a rolled paper towel assay (n=200 seeds) and the experiment was conducted twice. Results indicated no phytotoxic effects of EO-seed treatments on seed germination rate (p>0.05, n=400 seeds). In a greenhouse assay, EO-treated seeds were inoculated with Rhizobium inoculant at 2.5oz/100lb chickpea seeds and 3.2oz/100lb pea/lentil seeds, and planted. Active root nodules were counted 28 days later, and the experiment was conducted thrice. No phytotoxic effect was observed on root nodulation (p>0.05, n=24 seedlings) in chickpea, pea, and lentil. EOs can be used in disease management of pulses and can minimize synthetic chemical use.

T19 **Effect of synthetic antimicrobial peptides on common fungal pathogens and application to field pea (*Pisum sativum*)**
A. J. Hannig[1], S. Chatterton[2] , D. J. Bing[1], R. K. Goyal[1]
[1]*AAFC, Lacombe Research and Development Centre, Lacombe, AB, T4L 1W1, Canada*
[2]*AAFC, Lethbridge Research and Development Centre, Lethbridge, AB, T1J 4B1, Canada*

Plant antimicrobial peptides (AMP's) are short amino acid chains (< 100 amino acids) which form a part of innate immunity in living organisms and display antimicrobial activity against a wide range of bacterial and fungal pathogens. AMP's can be identified from transcriptomic and genomic data and be designed using computer softwares. Synthetic AMP's can be produced which have similar or improved activity compared to natural AMP's. In this study, the effect of 8 AMP's (PBL-1 to PBL-8) were tested on 20 fungal pathogens including pathogenic ascomycetes (*Fusarium spp*.), basidiomycetes (*Rhizoctonia sp*.) and oomycetes (Aphanomyces sp.). AMP's were tested at concentrations of 1, 10 and 50 uM against pathogens under *in vitro* conditions. A rating scale of 0 (no growth inhibition) to 5 (complete growth inhibition) was used to rate the effect of AMP on germination of fungal spores and mycelial growth relative to controls. In summary, PBL-1 and

PBL-5 ranked the highest in inhibition rating towards pathogens tested. The AMP's having potent activity can be developed as bio-fungicides for foliar applications.

T20 **Cloning a mitogen-activated protein kinase kinase kinase YODA from *Triticum aestivum* for transgenic expression in wheat.** M.B. Smith, D. Ryabova, S. Roy, P. Tricker, T. Lawson, J. Laurie, A. Laroche, N.A. Foroud**.** *(M.S., D.R., J.L., A.L., N.A.F) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403, 1st Ave S, Lethbridge, AB, T1J 4B1; (S.R.) School of Agriculture, Food and Wine, University of Adelaide, Hartley Grove, Waite Campus, Urrbrae S. Australia, 5064; (P.T.); (T.L.) School of Life Sciences, University of Essex, Colchester Campus, United Kingdom*

YODA is mitogen-activated protein kinase kinase kinase (MAPKKK), initially identified for its role in plant development involved in cell fate determination in embryos and on the leaf epidermis, but now also known to have a role in pathogen defence and immune response. Mutant plants expressing constitutively active forms of the YODA have increased broad spectrum resistance to a variety of bacteria and fungi. Mutants with defective YODA show compromised resistance to pathogens. However, canonical defense responses are not inhibited in these plants, indicating that the defence pathways regulated by YODA operate in parallel to the defence pathways regulated by pathogen recognition receptors (PRRs) and phytohormones. The diverse roles of YODA in plant defence and other biological processes, make this enzyme and other members of the YODA cascade attractive targets for genetic studies in wheat. With the objective of studying the role of YODA in both plant defence and plant development, and to proteins within the YODA network involved in regulating these traits, we plan to develop transgenic wheat lines overexpressing the YODA MAPKKK. As a first step, the YODA gene was cloned from the wheat cultivar Fielder, and the results along with future directions will be presented.

T21 **Development of mutant wheat populations under selection pressure for Fusarium head blight resistance**
C. Dovell, D. Ryabova, A. Badea, R. Graf, H. Randhawa, D. Spaner, P. Hucl, M.A. Henriquez, N.A. Foroud
(*C.D., D.R., R.G., H.R., N.A.F.*) *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403, 1st Ave S, Lethbridge, AB, T1J 4B1; (A.B.) Brandon Research and Development Centre, 2701 Grand Valley Road, P.O. Box 1000A, Rural Route #3, MB, R7A 5Y3; (D.S.) University of Alberta, Department of Agricultural, Food & Nutritional Sciences, Lethbridge, 9011 – 116 St NW, Edmonton AB, T6G 2P5; (P.H. Crop Development Centre, University of Saskatchewan, 51 Campus Dr., SK, Canada; (M.A.H.) Morden Research and Development Centre, 101 Route 100 Unit 100, MB, R6M 1Y5.*

Fusarium head blight (FHB) is a disease that affects wheat and barley, among other cereals, in Canada. We have been working with Canadian breeders to develop FHB resistant doubled haploid (DH) populations using an *in vitro* selection approach. In this method, Microspores are isolated from F1 hybrids provided by wheat and barley breeders, and doubled haploid plants produced in the presence or absence of *Fusarium* mycotoxins. This approach will be modified to develop an ethyl methanesulfonate (EMS) mutant population while developing DH plants from spring wheat cultivars with poor or moderate FHB resistance, in the presence or absence of the *in vitro* selection (IVS) pressure. Plants will the be screened for changes in disease response, and by comparing the control group with the IVS group, we will clearer picture on the efficacy of the in vitro selection approach. Furthermore, a TILLING approach can be employed to identify the mutations that have incurred, enabling the identification of candidate resistance and susceptibility genes. Finally, the EMS population can also be used directly in wheat breeding programs for cultivar development.

Guest speaker abstracts

A history of the LTB snow mold fungus in Alberta: When will we identify this species? D. A. Gaudet[1], S.-T. Hutter[2], S. Redhead[2] and A. Laroche[1]
Agriculture and Agri-Food Canada, [1]Lethbridge Research and Development Centre, Lethbridge, AB T1J 4B1 and [2]Ottawa Research and Development Centre, Ottawa, ON K1A 0C6

Snow mold fungi can cause serious damage to overwintering cereals and perennial forages in Central and Northern Alberta where a persistent snow cover is established early in the autumn and remains until spring. Pink snow mold caused by *Microdochium nivale* and *Myrioscherotinia borealis* cause overwintering damage to crops but the most important snow mold is the Low Termperature Basidiomycete (LTB). This sterile white basidiomycete was first reported by Broadfoot and Cormack in 1941 on alfalfa. The fungus remained unidentified until 1980 when Traquair identified LTB as *Coprinus pyschromorbidus*. An LTB causing fruit rot in Oregon (FRLTB) was reported by Spotts et al. in 1981 and sclerotial (SLTB) form reported by Traquair and Smith on winter wheat in 1982 were also reported conspecific with *C. psychromorbidus.*

Molecular techniques and conventional mating studies by Laroche et al. in 1993 refuted the species designation of LTB as *C. psychromorbidus*. Currently a collaboration between an AAFC Research Centers at Lethbridge and Ottawa using ITS and other common sequences from a large range of basidiomycetes raises hope that the LTB identity controversy will soon come to a conclusion.

Impact of location and environmental factors on pulse, cereal and oilseed diseases in the Canadian prairies. M. Hubbard, G. Peng, M. Entz, G. Semach, H. Kubota, B. Tidemann, F. Larney and K. Liu. *(MH, KL) Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, 1 Airport Road, Box 1030, Swift Current, Saskatchewan, S9H 3X2; (PG) Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, Saskatchewan, S7N 0X2; (ME) University of Manitoba, Department of Plant Science, University of Manitoba, 222 Agriculture Building, 66 Dafoe Road, Winnipeg, Manitoba, R3T 2N2; (GS) Beaverlodge Research Farm, Agriculture and Agri-Food Canada, Box 29, Beaverlodge, Alberta, T0H 0C0; (HK, BT) Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, 6000 C and E Trail, Lacombe, Alberta, T4L 1W1; (FL) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1st Avenue South, Lethbridge, Alberta, T1J 4B1*

Environmental and soil factors, including precipitation and soil pH, often affect the occurrence and severity of diseases in field crops. A multiple site-year experiment was established in the Canadian Prairies to assess the productivity, disease severity, pest incidence, soil health, resource use efficiency, environmental impact, and resilience of cropping systems. In 2018 and 2019, data on several important diseases of major field crops were collected at the seven sites in Alberta, Saskatchewan and Manitoba. Root rot of pulses, ascochyta blight of chickpea and pea, anthracnose of lentil, blackleg of canola and leaf spot diseases of cereals were assessed. Disease severity was generally low in both years, likely due to dry conditions. Overall disease did not differ between years. Disease severity varied significantly among sites, likely due to multiple site-specific characteristics. Precipitation and soil pH each explained a very small, but significant portion of overall disease severity. Root rot severity in pea or lentil, when considered separately, explained a small amount of yield variation. In contrast, pulse foliar diseases had a small, but significant impact on yield only when pea, lentil and chickpea were considered together. Blackleg was not significantly associated with canola yield. Surprisingly, higher severity of cereal leaf spot diseases or overall disease were significantly correlated with slightly increased yield, while explaining only a small portion of this parameter. Further exploration of site characteristics related to diseases, and relationships between disease and other agricultural and environmental parameters, especially in higher disease pressure years, is merited.

Redesigning the effectiveness of the stripe rust resistance gene *Yr10* against current virulent fungal isolates. M. Frick, G.T. Araujo, K. Fujita, D. Van Essen, C. Harvey, J.D. Laurie, R.J. Graf and A. Laroche**.** *Lethbridge Research & Development Centre, AAFC, 5403 1st Avenue South, Lethbridge, AB, T1J 4B1*

Stripe rust caused by *Puccinia striiformis* Westend. f. sp. *tritici* Erikss., (*Pst*), is an issue in every region of the world where wheat is grown. Ever evolving rust isolates are challenging the pool of resistance (R) genes in currently grown wheat cultivars. Although some R genes are still effective in specific regions, only two genes (*Yr5, Yr15*) are effective worldwide. Consequently, there is an urgent need to identify novel and effective resistance genes against different pathogens. The majority of known R genes in cereals and monocots belong to the CC-NBS-LRR group. Recently, roles for the coiled-coil (CC) and leucine-rich repeats (LRR) domains in the functioning of R genes for effective protection against pathogens have been shown. The *Yr10* R gene, previously characterized and cloned in our lab, has been defeated in 2010 in southern Alberta but remains functional in central and northern Alberta. Modifications of R genes functional domains in Arabidopsis, rice and barley yielded alterations in the avirulence/virulence patterns of different pathogen isolates. We will report on modification to sequences of the CC and LRR domains of *Yr10*, and the rationale for such modifications. Additionally, we will describe our approach to insert modified *Yr10* genes into the stripe rust susceptible wheat line Fielder. This work will demonstrate that target mutations toward improving the avirulence spectrum of a stripe rust R gene works within Canadian germplasm. This will also contribute to demonstrating that re-utilization of different 'versions' of defeated genes is an effective and efficient way for protecting wheat.

2020 Plant Pathology Society of Alberta Business Meeting – November 4-5 via zoom

1. Call to order @ 10:30 am
2. Adoption of the agenda, moved by Mike Harding, 2ed by Kelly Turkington
3. Review and approval of 2019 minutes moved by Mike Harding, 2ed by Kelly Turkington
4. In Memorium
5. Treasurer's report
6. CPS Updates for 2020, CPS meeting virtual, CJPP, open and non-open access option
7. Reports from standing committees
    a. Disease Survey Committee Report (Kelly Turkington)

    Kelly asked if he can step down, MH suggested this committee is redundant since now the survey is being discussed by various meetings dedicated for that.

    b. Historical Committee (Denis Gaudet)
    Denis asked to submit all meeting material to M. Holtz so it can be added to the website we have archive for PPSA
    c. Awards Committee Report (Michael Harding)
    Attached two award reports associated with this meeting
8. Conference Reports
    Ryan: bioinformatics workshop in AAFC is very helpful
    Reem: European fungal genetic meeting in Rome, 2020 Plant health on line APS and BGRI for rust online
9. Unusual/Exceptional Disease Report
    Mike and Kelly, discussed the bacterial streak disease in south AB and in the prairie as new threat, and
    Syama: Presumptive Aphanomyces euteiches was isolated from one dry bean field in southern Alberta in 2019. Sequencing of isolates to confirm identification and complete Koch's postulates is pending. More extensive sampling of dry bean fields in 2020 was performed to validate this finding and results are also pending.
10. Nomination of Honorary Life Members, Dr. Kan Fa
11. Resolutions, thanks for local organizing committee, and award committee, judges, and previous years funders and presenters and attendee.
12. Locations and Dates of Future Meetings
    2020 – Lethbridge in first or second week of November
    2021 – Edmonton
    2022 – Brooks
    2023 – Lacombe/Lloydminster
13. Election of Officers for 2020-2021
    President – Rudolph Fredua-Agyeman
    Vice President – Michael Harding
    Secretary –Ileana Strelkov
    Directors – Current: Robyne Bowness, Krista Zuzak, Ryan Gourlie, Jackie Busaan
    Motion that election of officers cease and be accepted
14. Other business
    Mike Harding and Denis Gaudet with Ryan Gourlie help will try to get list of our honorary life members in the PPSA over the years, and the award and scholarship recipient list
15. Adjournment @11:30 am

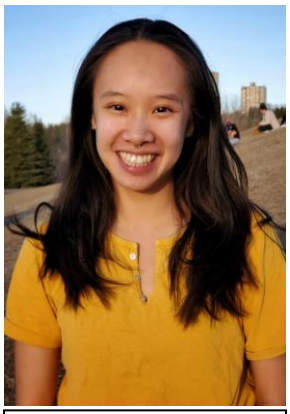
PPSA "Group Photo" – 2021 Annual Meeting.


RauhalaN
Ryan Gourlie
AboukhaddourR
Alejandra
Mike Harding
denis gaudet
Sijan Pandit Poudel
Syama Chatterton
Jackie Busaan
Anas Eranthodi
Kyle Horvath
Dianevys
Michele Frick
Daria Ryabova
Gabriela
Bohan Wei
Albert
Heather Tso
Keisha Hollman
Brittany Hennig
Mohamed's iPhone
Rudolph
LarocheA
Longfei Wu
Eleanor McBain

PPSA AWARDS COMMITTEE ANNUAL REPORT – 05-Nov-2020

The 2020 Annual Meeting of the Plant Pathology Society of Alberta was unique in that it was the first time we met virtually, rather than in person. Our annual meeting again provided the opportunity to acknowledge outstanding achievement of graduate students and technicians in plant pathology in Alberta. This year we had 14 oral and 11 poster presentations. All of the student and technician presentations were given during the day on November 4, 2020. The awards ceremony took place at 6:00pm on November 4, 2020. At the ceremony, the Awards Committee announced four winners for "best presentation", and recipients of the PPSA's two scholarships. The winners of a "best presentation" award will receive a cheque for $100, a certificate acknowledging the achievement, and copy of the book *Plant Pathology in Canada 1970-2008*. The scholarship recipients will receive a cheque for $1000, a certificate acknowledging the achievement, and copy of the book *Plant Pathology in Canada 1970-2008.*

PRESENTATION AWARDS



The outstanding student oral presentation:

- Winner was **Heather Tso** for her presentation *"Challenges in clubroot pathotype-specific molecular diagnostics"*
- Runner up was Dianevys Gonzalez-Pena Fundora for "*Characterization of Fusarium graminearum transformants over-expressing the mitogen-activated protein kinase kinase, Mkk2, and a phosphomimic thereof*"

No photo available

The outstanding student poster presentation:

- Winner was: **Fisher Yu** for *"Effect of fall and spring lime applications on clubroot of canola"*
- Runner up was Longfei Wu for *"Identification of quantitative trait loci (QTL) associated with root rot caused by the root rot complex in field pea"*

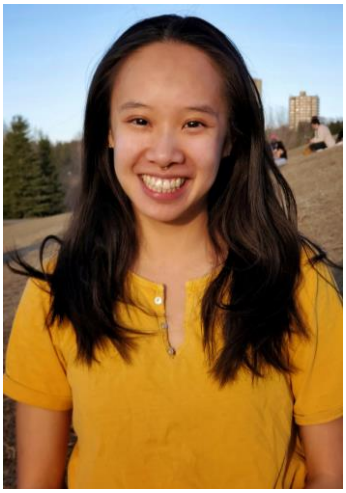
The outstanding technician oral presentation:

- Winner was **Michelle Cradduck** for "*Building Ug99 resistance in Canadian winter wheat germplasm by stacking up stem rust resistance genes Sr22 and Sr24* "
- Runner up was Michelle Frick for *"The circadian clock and plant immunity in wheat*"

The outstanding technician poster presentation:

- Winner was **Albert Hannig** for *"Effect of synthetic antimicrobial peptides on common fungal pathogens and application to field pea (Pisum sativum)"* ,
- Runner up was Marshall Smith for *"Cloning a mitogen-activated protein kinase kinase kinase YODA from Triticum aestivum for transgenic expression in wheat*"

SCHOLARSHIPS



The PPSA Graduate Student Scholarship for 2020 was awarded to a student who ranked in the top 5% of her peers at the University of Alberta. She is working on methods for molecular discrimination of *P. brassicae* pathotypes, and supervised by Dr. Stephen Strelkov (UofA). It's my pleasure to announce **Heather Tso** as the recipient of the 2020 PPSA Graduate Student Scholarship. Congratulations Heather!

The Swanson Award for Plant Pathology and Nematology for 2020 was awarded to a Ph.D. student ranked as "Superior" at the University of Alberta. She is studying the genetic structure, virulence and fungicide sensitivity of *Cochliobolus sativus* populations from the Prairies. Her research will contribute to understanding and management of spot blotch on barley. She is supervised jointly by Dr. Stephen Strelkov (UofA) and Dr. Kelly Turkington (AAFC-Lacombe). I'm pleased to announce that **Dilini Adihetty** is the 2020 recipient of the Swanson Award. Congratulations Dilini!

On behalf of the PPSA Awards committee, our sincere congratulations to our two scholarship recipients and to the outstanding presentation awardees. We wish you all the best success in your future research and careers. Due to the fact that our proceedings in 2020 were in a virtual format, rather than in person, we were not able to give the prizes directly to the award recipients. The Awards Committee will ensure that the cheques, certificates and books are mailed or delivered to the recipients' advisors/supervisors soon after the conclusion of the annual meeting.

The Awards Committee requests that the 2020 awardees be presented with their awards formally by their advisors/supervisors. Additionally, we request that photographs of the formal awards presentations be taken and submitted for inclusion in the PPSA proceedings, and for the CPS newsletter.

Finally, after more than 20 years of service on the Awards Committee, Ron Howard is ready to step away from his diligent service on the Committee. We gratefully acknowledge Ron's many years of service and many hours behind the scenes ensuring that the PPSA awards continue. The Awards Committee will be looking for a volunteer to replace Ron early in 2021, and it would be great to have a volunteer from central/northern Alberta to bring a more balanced geographical representation to the committee.

Respectfully submitted, Ron Howard, Denis Gaudet, Michael Harding

Report on the
SWANSON AWARD FOR PLANT PATHOLOGY AND NEMATOLOGY
November 4, 2020

The 2020 Swanson Award for Plant Pathology and Nematology is awarded to Ms. Dilini Adihetty at the University of Alberta. Ms. Adihetty is a 2nd year PhD student who graduated with a B.Sc. in Sri Lanka, and an M.Sc in Plant Physiology at the University of Alberta. She is currently studying the genetic structure, virulence and fungicide sensitivity of a population of *Cochlobolus sativus* (spot blotch of barley) from the Prairies.

An updated financial statement for the Scholarship Fund for 2019-20 is given below.

Dr. Terry Swanson Memorial Fund		
3 Year Springboard GIC (matures January 9, 2023)	Opening Balance	$ 13,314.86
Donations (2020 meeting – currently in chequing)		$ 78.00
Interest (2.0%) earned since last report		$ 219.17
	Balance to date	**$ 13,975.57**

Respectfully submitted by D. Gaudet, R. Howard, and M. Harding (PPSA Awards Committee)