CANADIAN PHYTOPATHOLOGICAL SOCIETY ANNUAL MEETING

Harnessing the Phytobiome for Sustainable Plant Health

JULY 4-8, 2022

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WELCOME

Dr. José R. Úrbez-Torres

Dr. Guus Bakkeren

In 2020, Penticton, BC, was chosen to hold the annual CPS meeting. In the fall of 2019, the Local Organizing Committee spent many hours to develop an enticing program to invite Canadian plant pathologist and US colleagues to our beautiful neck of the woods. In summer, the Okanagan Valley is truly a place to visit and a marvelous venue at the South end of the lake was chosen for the convention. Alas, by the spring of 2020 it became obvious that we had to abandon our plans for an "in-person meeting" (as it is called now), because of COVID-19 restrictions.

Fast forward and Penticton, BC, was given the opportunity for a redress for the 2022 annual meeting. We dusted of our plans, re-contacted keynote and symposium speakers, and went full steam ahead finishing what we started. With the pandemic retreating, we had good hopes that the meeting could be held "in person". Then the next wave hit and in consultation with the CPS board, we again had to change gears and decided to make this meeting virtual. Not deterred, we continued and are certain we put together a great program so we can learn about each other's research and be educated. We have over 200 attendees, an outstanding number with many students. We have tried our best to give everyone the opportunity to present orally. With 43 student presentations, we have several prizes for MSc and PhD students in their respective competitions.

We would like to thank all of those who have contributed to make this meeting happening, the local organizing committee for their endless hours of work putting this together, the CPS board for their support and guidance, our meeting sponsors, judges and moderators for stepping forward and dedicate their time to the meeting, and of course, all of you presenting and attending the meeting. It is unfortunate to not be able to welcome all our friends and colleagues to the beautiful Okanagan, enjoy the sunshine and a good glass of local wine. Nevertheless, we are welcoming all participants to this years' annual CPS meeting and know we are all here in spirit. We hope to welcome you all again in person soon at this magical part of Canada.

Okanagan Valley, BC

On behalf of the local organization committee,

José Ramón Úrbez Torres and Guus Bakkeren

MEETING THEME:

"HARNESSING THE PHYTOBIOME FOR SUSTAINABLE PLANT HEALTH"

Phytobiome research has reached maturity and is making an impact on various other fields of research, often providing a more holistic approach to solve various problems, including plant/tree productivity, promoting health, mitigating environmental impacts and diseases (pathologies), and assisting general plant/tree management. Aboveground, endophytic, and underground microbial communities are being investigated for their roles, made easier lately by inventories of such communities revealed using various high-throughput analysis tools, sequencing, proteomics and metabolomics. Contributions of various constituents in natural communities, and effects of plant-associated microbial assemblages are being investigated. Our keynote speaker and three symposium speakers will address various aspects of microbiome research.

KEYNOTE SPEAKER

Dr. Julia A. Vorholt

ETH Zurich, Institute of Microbiology, Switzerland

"The leaf microbiota: disassembling and rebuilding to explore plant microbe interactions"

Plant-associated microbiomes contribute to host phenotypes such as growth, health, and resilience. Ongoing research aims to uncover the molecular basis by which host-microbe and microbe-microbe interactions shape and maintain microbial communities, and to understand the role of individual microorganisms and their collective ecosystem function. Reductionist approaches are discussed to disentangle the inherent complexity of interactions in situ. Such experimentally tractable, synthetic communities enable hypotheses to be tested through targeted manipulation in gnotobiotic systems. Altering microbial, host, and environmental parameters allows quantitative assessment of host and microbial characteristics. The use of multifaceted approaches to detect interactions and functions provides new insights into the fundamental biology of plant-microbe interactions and helps to harness the power of the microbiome.

Biography: Julia Vorholt is Full Professor at ETH Zurich (Swiss Federal Institute of Technology in Zurich). She studied biology at the Universities of Bonn and Marburg, Germany. During her PhD thesis (1994-1997) she focused on the biochemistry of methanogenesis, the biological process resulting in methane formation, under the supervision of Prof. Dr. R. K. Thauer at the Max-Planck-Institute for terrestrial Microbiology in Marburg. Thereafter, she initiated work on the one-carbon metabolism of methylotrophic bacteria as a postdoc at the University of Washington in Seattle with M. E. Lidstrom (1998) and at the MPI Marburg (1999-2001) where she built up a research group on the biochemistry of methylotrophic bacteria. From 2001 to 2006 she headed an independent research group at the Laboratory of Plant Microbe Interactions in Toulouse, France, within the frame of an exchange program of the Centre National de la Recherche Scientifique (CNRS) and the Max-Planck-Society. Julia Vorholt was appointed as Associate Professor of ETH Zurich at the Institute of Microbiology in 2006 and is Full Professor since 2012.

In her research, she investigates how the environment, in particular the phyllosphere, shapes bacterial physiology and microbial interactions, with an emphasis on metabolism, novel protein function, gene regulation, and beneficial functions to the host. Julia Vorholt is Director of Studies at the Department of Biology at ETH Zurich and Co-director of the Swiss National Center of Competence in Research (NCCR) Microbiomes. She is a member of the German National Academy of Sciences Leopoldina, the European Academy of Microbiology and the European Molecular Biology Organization (EMBO) and received two ERC Advanced Grants.

SYMPOSIUM:

"TWEAKING THE PHYTOBIOME FOR SUSTAINABLE PLANT HEALTH"

Dr. Niklaus J. Grünwald

Research Plant Pathologist, United States Department of Agriculture, Corvallis, Oregon, United States of America.

"*Novel computational and genomic approaches to understand oomycete emergence*"

Oomycetes are a group of fungus-like eukaryotes known for causing many devastating plant diseases such as potato late blight, Jarrah dieback, and sudden oak death. We have studied the emergence of several pathogens using a combination of genomic and computational approaches to characterize the role of oomycetes in plant health. Metabarcoding is revolutionizing microbial ecology by circumventing the limits of traditional culture-based techniques. We developed novel computational tools including Metacoder and propose a new metabarcode locus, rps10. Metacoder implements a novel visualization called heat trees that use the color and size of nodes and edges on a taxonomic tree to quantitatively depict up to 4 statistics distributed over a hierarchy. This allows for rapid exploration of data and information-dense, publication-ready graphics. In addition, metacoder provides tools for reading common file formats and evaluating primers and barcode loci using simulated PCR. These tools and approaches provide a new resource for understanding the role of oomcyetes in agricultural and natural ecosystems.

Biography: Niklaus J. Grünwald is a Research Plant Pathologist with the Horticultural Crops Research Laboratory, USDA Agricultural Research Service, in Corvallis, Oregon and Professor in the Department of Botany and Plant Pathology and the Center for Quantitative Life Sciences at Oregon State University. He received his Ph.D. in plant pathology from the University of California at Davis and conducted postdoctoral research at Cornell University. His principal research interests include the ecology, genetics, evolution, and management of emerging Phytophthora diseases with a special emphasis on the Sudden Oak Death pathogen Phytophthora ramorum and the Irish famine pathogen P. infestans. More recently, he has started working on projects involving oomycete biodiversity, comparative genomics of the genus Phytophthora, and development of computational and bioinformatics tools for comparative genomics, genotyping-by-sequencing, population genomics, metabarcoding, metagenomics and diagnostics based on CRISPR-Cas. Grünwald has served as associate editor, senior editor and

editor-in-chief for Phytopathology and PhytoFrontiers, editor for Plant Pathology, and currently serves as founding editor-in chief for CABI Agriculture and Bioscience. He has held numerous leadership positions including chair of the American Phytopathological Society (APS) Publications Board overseeing all APS journals that launched the new Phytobiomes open access journal. He currently is the vice president of the American Phytopathological Society (APS). He is a recipient of the 2006 USDA ARS Early Career Scientist of the Year award, the 2007 APS Syngenta award, the 2015 APS Ruth Allen Award recognizing outstanding, innovative research contribution that have changed the direction of research in any field of plant pathology and became APS fellow in 2016 and American Association for the Advancement of Science (AAAS) fellow in 2019.

Dr. Cara Haney

Faculty of Science, University of British Columbia, Vancouver, British Columbia, Canada

"*Mechanisms in plant regulation of rhizosphere microbiota*"

The composition of microbes in agricultural soils, along with the interplay of plant-microbiome-pathogen genotypes, can influence disease incidence in the field. Pseudomonas fluorescens and related species are enriched in the plant rhizosphere and have been repeatedly implicated in disease suppression. To determine the genetic mechanisms by which plants shape levels of rhizosphere P. fluorescens, we screened a collection of Arabidopsis mutants affecting root immunity and hormone crosstalk. We identified several plant mutants with altered rhizosphere P. fluorescens levels without phylum-level dysbiosis. This talk will present several genes identified from this screen and their roles in regulating rhizosphere P. fluorescens. Understanding the genetic basis of how plants shape levels of beneficial bacteria in the rhizosphere will facilitate harnessing the microbiome to enhance plant disease resistance.

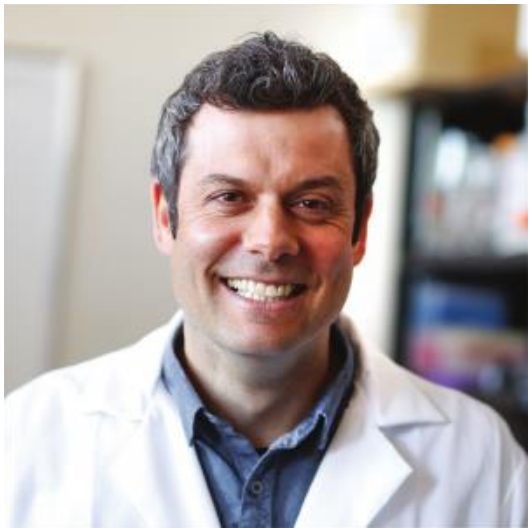
Biography: Dr. Cara Haney is an Associate Professor and Canada Research Chair in plant-microbiome interactions in the Department of Microbiology & Immunology at the University of British Columbia. She completed her PhD in 2011 from Stanford University focused on rhizobia-legume symbiosis. Prior to joining the UBC faculty in 2016, she was a postdoctoral fellow at Harvard Medical School where she began working on the Arabidopsis microbiome. Her lab uses high throughput screening combined with genetic and genomic approaches to identify the genetic basis of beneficial traits in plant-microbiome interactions. Her research focuses on elucidating basic mechanisms in host-microbiome interactions, and in finding sustainable solutions for agronomically important challenges.

Dr. Martin Filion

Research Scientist, Agriculture and Agri-Food Canada, Saint-Jean sur Richelieu, Quebec, Canada

"*A functional tailored inoculation approach for plant-beneficial* Pseudomonas *spp. promoting sustainable plant health*"

A myriad of plant-associated Pseudomonas strains has been used as biocontrol agents against different plant pathogens. Although some success stories have been reported, inconsistencies under field conditions are often observed. To favor large-scale implementation of plant-beneficial Pseudomonas spp. in agroecosystems, key factors such as sufficient plant colonization, in situ expression of biocontrol mechanisms and environmental impact/persistence must be controlled. Genomics, amongst other approaches, has been successfully used in our laboratory as a powerful tool for providing key functional information about Pseudomonas strains of interest. Such functional information is needed to bridge the gap between results obtained under laboratory conditions and the efficient deployment of these microorganisms in the field. In this presentation, we will discuss how comparative genomics and other functional approaches can support the successful identification, characterization and implementation of plant-beneficial Pseudomonas spp. in agroecosystems for controlling plant diseases.



Biography: Dr. Martin Filion earned his Ph.D. from McGill University (QC) in 2002 in the field of molecular plant-microbe interactions. He was hired in 2003 as an Assistant Professor in the Department of Biology, Université de Moncton (NB) and promoted to the rank of Associate Professor in 2008 and Full Professor in 2016. In 2019 he joined Agriculture and Agri-Food Canada (AAFC) as a research scientist at the Saint-Jean-sur-Richelieu (QC) research centre. To date, Dr. Filion has secured more than $25 million in research funding (including major grants from Genome Canada, NSERC, CFI, and AAFC). He has authored more than 85 peer-reviewed publications and published numerous book chapters, as well as a book. Dr. Filion has established valuable collaborations with other research groups as well as with the private sector, including more than 20 different commercial partners. A patent originating from his research on plant-microbe interactions was obtained in 2018. Dr. Filion is very active on various editorial boards, including senior editor of Phytopathology, editor of the Canadian Journal of Microbiology, assistant editor of Frontiers in Microbiology and the Canadian Journal of Plant Pathology, and editorial board member of Applied and Environmental Microbiology and Microorganisms. In the last 20 years, various research projects conducted in Dr. Filion's laboratory have focused on various aspects of plant-microbe interactions, with a special focus on the development of plant-beneficial Pseudomonas spp. inoculants for the agricultural sector. His research team has made significant progress in better understanding the molecular mechanisms that some of these strains use to protect plants from diseases.

CANADIAN PHYTOPATHOLOGICAL SOCIETY ANNUAL MEETING

JULY 4-8, 2022

"Harnessing the phytobiome for sustainable plant health"

PROGRAM SCHEDULE

All in Pacific Daylight Saving Time - Vancouver (GMT-7)

MONDAY JULY 4, 2022	
7:30 – 8:00	**Introduction/Welcome**
8:00 – 9:30	**Key Note Speaker Dr. Julia Vorholt**
9:30 – 10:00	**Break**
10:00 – 13:00	**CPS AMOM**
13:00 – 13:30	**Break**
13:30 – 14:30	**SESSION 1 – DISEASE ETIOLOGY**

TUESDAY JULY 5, 2022	
7:30 – 9:30	**Symposium – Dr. Filion, Dr. Grünwald, Dr. Haney**
9:30 – 9:45	**Break**
9:45 – 12:00	**SESSION 2 – HOST-PATHOGEN INTERACTIONS**
12:00 – 12:30	**Break**
12:30 – 14:00	**SESSION 3 – HOST-PATHOGEN INTERACTIONS**

WEDNESDAY JULY 6, 2022	
7:30 – 9:30	**SESSION 4 – HOST-PATHOGEN INTERACTIONS**
9:30 – 9:45	**BREAK**
9:45 – 11:00	**SESSION 5 – HOST-PATHOGEN INTERACTIONS**
11:00 – 11:15	**BREAK**
11:15 – 12:30	**SESSION 6 – DIAGNOSTICS**
12:45 – 13:15	**BREAK**
13:15 – 15:00	**SESSION 7 – DIAGNOSTICS**

THURSDAY JULY 7, 2022	
7:30 – 9:30	**SESSION 8 – DISEASE CONTROL**
9:30 – 9:45	**Break**
9:45 – 12:00	**SESSION 9 – DISEASE CONTROL**
12:00 – 12:30	**Break**
12:30 – 13:15	**SESSION 10 – DISEASE CONTROL**
13:15 – 14:30	**SESSION 11 – PATHOGEN BIOLOGY**

FRIDAY JULY 8, 2022	
8:00 – 9:00	**SESSION 12 – PATHOGEN BIOLOGY**
9:00 – 9:15	**BREAK**
9:15 – 11:00	**SESSION 13 – DISEASE/PATHOGEN EPIDEMIOLOGY**
11:00 – 11:30	**BREAK**
11:30 – 12:15	**STUDENT COMPETITION & PHOTO CONTEST AWARDS**
12:15 – 12:30	**ADJOURN**
12:30 – 14:00	**STUDENT SOCIAL**

MSc – SC: MSc Student Competition

PhD – SC: PhD Student Competition

MONDAY JULY 4, 2022

7:30 – 8:00	**Welcome Address**

Dr. José R. Úrbez-Torres
Dr. Lone Buchwaldt
Dr. Tom Forge
Dr. Gurcharn Singh Brar

8:00 – 9:30	**Key Note Speaker Presentation**

Moderator: Dr. Guus Bakkeren

Dr. Julia Vorholt - ETH Zurich, Institute of Microbiology, Switzerland
"The leaf microbiota: disassembling and rebuilding to explore plant microbe interactions."

9:30 – 10:00	**Break**

10:00 – 13:00	**CPS AMOM**

13:00 – 13:30	**Break**

13:30 – 14:30	**SESSION 1 – DISEASE ETIOLOGY**

Moderators: Dr. Tom Forge and April Mahovlic

13:30 **Z.K. PUNJA**, K. WANG, L. NI, S. LUNG AND L. BUIRS. *Symptomology and prevalence of Hop Latent Viroid on greenhouse grown cannabis (Cannabis sativa L.) plants.*

13:45 **S.F. SHAMOUN**, K. RUFF, N. FEAU, G. BRADLEY, C. HALLDORSON, AND A. COSTER. *Root and soil-borne oomycetes and fungi associated with western white pine (Pinus monticola) mortality in British Columbia's seed orchards.*

14:00 **M.N. ISLAM**, O. MOLINA, R. KUTCHER, AND X. WANG. *Crop rotation affects the structure and diversity of soil pathogenic and non-pathogenic microbial communities*

14:15 **J.L. MacDONALD**, K.D. HANNAM, AND H. XU. *Signs and symptoms of sudden apple decline in British Columbia, impacts on tree physiology, and the potential role of environmental stressors.*

TUESDAY JULY 5, 2022

7:30 – 9:30	**CPS SYMPOSIUM** ***"Tweaking the phytobiome for sustainable plant health"***

Moderators: Dr. Barry Saville and Dr. Mary Ruth McDonald

7:30 **Dr. Martin Filion** – Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu Research Centre, Québec, Canada.
"A functional tailored inoculation approach for plant-beneficial Pseudomonas spp. promoting sustainable plant health"

8:00 **Dr. Niklaus J. Grünwald** – USDA Agricultural Research Service, Corvallis, Oregon, USA.
"Novel computational and genomic approaches to understand oomycete emergence"

8:30 **Dr. Cara Haney** – Department of Microbiology and Immunology, University of British Columbia, Vancouver, Canada.
"Mechanisms in plant regulation of rhizosphere microbiota"

9:00 **Round Table Discussion**

9:30 – 9:45	**Break**

9:45 – 11:45	**SESSION 2 – HOST-PATHOGEN INTERACTIONS**

Moderators: Dr. Rishi Burlakoti and Sanjib Sapkota

9:45
MSc - SC
V. FETTERLEY, D. GILBERT, K. GAURAV, H. S. CHAWLA, G. GERARD, S. HOLDEN, H. R. KUTCHER, X. CHEN, P. HUCL, B. B. H. WULFF, C. J. POZNIAK, S. ARORA AND G. S. BRAR. *Summoning the ancestors: using an* Aegilops tauschii *diversity panel to improve stripe rust resistance in wheat.*

10:00
MSc - SC
S. LI, H. KAUR, C. JAYASINGHEGE, D. REINECKE, AND J. OZGA. *Characterization of clubroot disease development in* Arabidopsis auxin *receptor mutants, and peat-based and partially-hydroponic assay systems*

10:15
MSc - SC
H. LIU, H. KAUR, S.E. STRELKOV, S.F. HWANG, AND J.A. OZGA. *Transcriptome analysis of rutabaga (*Brassica napus*) cultivars indicates that the indole glucosinolate pathway may play a role in inducing plant defense against clubroot disease.*

10:30 MSc - SC — **E.J.R. MARCHETTA**, K. YOSHIOKA, W. MOEDER, E. DÉZIEL AND C.D.M. CASTROVERDE. *Temperature regulation of plant-rhizobacteria interactions within the soil-rhizosphere-rhizoplane interface.*

10:45 MSc - SC — **R. SALIH**, J.-D. COTÉ, AND E. P.ÉREZ-LÓPEZ. *A hydroponic based system to phenotype the clubroot pathogen.*

11:00 MSc - SC — **Y. ZHANG** AND G.S. BRAR. *Quantitative trait locus (QTL) mapping of aggressiveness in* Fusarium graminearum*, causing Fusarium head blight in durum wheat*

11:15 MSc - SC — **S.G. CHESNEY**, B.D. GOSSEN, J. ROBSON, AND M.R. MCDONALD. *Type of soilless mix influences the development of clubroot (*Plasmodiophora brassicae*).*

11:30 MSc - SC — **S. SINGH** AND G.S. BRAR. *Fusarium head blight (FHB) resistance in 'Paragon/Watkin 1190580' bi-parental mapping population.*

11:45 – 12:30	**BREAK**

12:30 – 14:00	**SESSION 3 – HOST-PATHOGEN INTERACTIONS**

Moderators : Dr. Michael Cruickshank and Jared Hrycan

12:30 PhD - SC — **G.A. DIAZ CRUZ** AND D.R.D. BIGNELL. *Regulation of nigericin and geldanamycin biosynthesis in* Streptomyces *sp. 11-1-2 by N-acetylglucosamine.*

12:45 PhD - SC — **K. HOLLMAN**, V.P. MANOLII, S.F. HWANG AND S.E. STRELKOV. *Characterizing the virulence of* Plasmodiophora brassicae *on canola with 'second-generation' clubroot resistance.*

13:00 PhD - SC — **J. HRYCAN**, T. FORGE, P. BOWEN, M. HART, AND J.R. ÚRBEZ-TORRES. *Studying the effect that ring nematode (*Mesocriconema xenoplax*) has in disease development in young grapevines infected with* Phaeomoniella chlamydospora.

13:15 PhD - SC — **S.O. OSADOLOR**, M. MAYERHOFER, C. McALLISTER, R. PEERY, L.I. ZAHARIA, S. DANG, J.E.K. COOKE. *Comparative molecular responses in lodgepole and jack pines showing differential resistance to infection by* Cronartium harknessii *reveals a non-canonical defense response to biotrophic rust fungi.*

13:30 PhD - SC — **I. SILVA-VALDERRAMA**, O. SILVA, J. BOULÉ, J.R. URBEZ-TORRES AND T.J. DAVIES. *Predicting pathogens' virulence: linking host breadth and pathogenicity of the* Botryosphaeriaceae *fungal family in grapevines (*Vitis vinifera*).*

13:45
PhD - SC

E.R.M. STORFIE, L. GALINDO-GONZÁLEZ, S.F. HWANG, AND S.E. STRELKOV. *Identification and characterization of candidate effectors common to the resistance-breaking pathotypes 3A and 5X of* Plasmodiophora brassicae.

WEDNESDAY JULY 6, 2022

7:30 – 9:15	SESSION 4 – HOST-PATHOGEN INTERACTIONS

Moderators: Jesse MacDonald and Emilee Storfie

7:30
PhD - SC
Y. WANG, S.E. SRELKOV, R. FREDUA-AGYEMAN, AND S.F. HWANG. *Exploring resistance to* Verticillium longisporum *in Brassica genotypes.*

7:45
PhD - SC
L. WU, R. FREDUA-AGYEMAN, S.E. STRELKOV, K.-F. CHANG, S.-F. HWANG. *Identification of novel genes associated with partial resistance to Aphanomyces root rot in field pea by BSR-seq analysis.*

8:00
PhD - SC
S. SUN, Y. ZHANG, C. HERRFURTH, I. FEUSSNER, AND G. BAKKEREN. *Investigating the NHP-dependent SAR pathway in common hexaploid wheat; options for broad-spectrum disease reduction?*

8:15
PhD - SC
H.T. YU, S.F. HWANG, R. FREDUA-AGYEMAN AND S.E. STRELKOV. *Host range of* Fusarium proliferatum *isolate from canola and evaluation of the reaction of Brassica genotypes*

8:30
PhD - SC
S. SONG, Z. MORALES MOREIRA, X. ZHANG, A.C. DIENER, AND C.H. HANEY. *PSKR1 helps recruit Pseudomonas fluorescens to the plant rhizosphere microbiome.*

8:45
G.A. DIAZ-CRUZ, K. TAHLAN AND **D.R.D. BIGNELL**. *Geldanamycin and nigericin are phytotoxic microbial specialized metabolites with a potential role in mediating plant-pathogen interactions.*

9:00
N. ATABAKI, **M. KALISCHUK**, B. MÜLLER, D. PRÜFER AND L. KAWCHUK. *Amplified disease resistance through a cell-surface immunity Ve receptor heterocomplex.*

9:15 – 9:45	BREAK

9:45 – 11:00	SESSION 5 – HOST-PATHOGEN INTERACTIONS

Moderators: Dr. Gurcharn Brar and Zhiyu (Fisher) Yu

9:45
J. CHUAN, W. CHEN, J. NIE, W.R. COOPER, L.R. HALE AND **X. LI**. *Transcriptome profiling of tomato plants infected by potato zebra chip pathogen* 'Candidatus Liberibacter solanacearum'*: virulence and pathway analysis.*

10:00 **J.-J. LIU**, A. ZAMANY, K. PELLOW, D. NOSHAD AND K. KLIMASZEWSKA. *Eastern white pine resistance to white pine blister rust conferred by the TIR-NBS-LRR gene PmTNL2.*

10:15 **A. NOVINSCAK**, R. R. BURLAKOTI, AND J. GRIFFITHS. *Screening tomato lines for potential resistance to tomato brown rugose fruit virus in Canada.*

10:30 **J.R. TUCKER**, A. D. BEATTIE, A.C. WOITAS, C.W. HIEBERT, A. BADEA, AND W.G.D. FERNANDO. *Genome-wide association mapping of spot blotch in elite Canadian two-row barley germplasm.*

10:45 J. COOK, J.P.M. HUI, J. ZHANG, M. KEMBER, F. BERRUE, **J.Z. ZHANG** AND Z. CHENG. *Production of quorum sensing-related metabolites and phytoalexins during* Pseudomonas aeruginosa-Brassica napus *interaction*.

11:00 – 11:15	**BREAK**

11:15 – 12:30	**SESSION 6 - DIAGNOSTICS**

Moderators: Dr. Vippen Joshi and Yishan Zhang

11:15 MSc - SC **O. HAMILA**, C.J. HENRY, M.A. HENRIQUEZ AND C.P. BIDINOSTI. *Automated Fusarium head blight detection and total number of spikelets estimation in multispectral point clouds of wheat using 3D convolutional neural networks.*

11:30 MSc - SC **J.B. PEPIN**, E. GIROUX AND G.J. BILODEAU. *Advanced pre-screening of grain and oilseed using long read sequencing for bio-surveillance of phytopathogens.*

11:45 MSc - SC **E. MCNAB** AND T. HSIANG. *A Novel Field kit to Detect DMI Fungicide Resistance in* Clarireedia jacksonii.

12:00 MSc - SC **A. RETHER**, E. MCNAB, T. HSIANG. *Comparison of an amended agar assay vs. a microplate assay for assessing fungicide sensitivity.*

12:15 PhD - SC **J. BEUTLER**, T. LI, AND G. S. BRAR. Xanthomonas translucens *isolation from barley seeds complicated by ubiquitous coinfection with* Pantoea *spp.*

12:30 – 13:15	**BREAK**

13:15 – 14:45 SESSION 7 -DIAGNOSTICS

Moderators: Dr. Wen Chen and Keisha Hollman

13:15
PhD - SC
U. ILYAS, M.N. RAIZADA, M. KALISCHUK, L. DU TOIT, AND M.R. MCDONALD. *Soil microbiome in relation to the risk of cavity spot on carrots.*

13:30
PhD - SC
V.J. JAVARAN, A. POURSALAVATI, P. MOFFETT, AND M.L. FALL. *Detection of grapevine virome (viruses and viroids) through Nanopore cDNA and direct RNA sequencing technology.*

13:45
PhD - SC
A. POURSALAVATI, V.J. JAVARAN, I. LAFOREST-LAPOINTE AND M.L. FALL. *An improved and high yielded soil eRNA extraction method to study soil microbiome using Nanopore direct RNA sequencing.*

14:00
PhD - SC
J. CHUAN, W. CHEN, L.R. HALE AND X. LI . *PolyChrome: A bioinformatics toolkit for the detection and classification of phytopathogens based on next-generation sequencing, genomics, and metagenomics.*

14:15
G. CHARRON, J. YERGEAU, G.J. BILODEAU, P. TANGUAY, C. BEAULIEU, H. VAN DER HEYDEN. *Identification of* Phytophthora europae*a as the species responsible for root-rot in Christmas tree productions and development of molecular tools for its detection.*

14:30
D. RADFORD AND W. CHEN. *IsPRIMER: a new in silico tool for predicting true coverage and off-target amplicons for metabarcoding primers.*

14:45
M. MUNAWAR, A.U. RAHMAN, P. CASTILLO AND D.P. YEVTUSHENKO. *Morphology and molecular profiling of pin nematodes (*Paratylenchus *spp.) from cultivated areas of southern Alberta, Canada.*

THURSDAY JULY 7, 2022

7:30 – 9:15	SESSION 8 – DISEASE CONTROL

Moderators: Dr. Lone Buchwaldt and Sherry Sun

7:30
MSc - SC

L. BUIRS, S. LUNG AND Z. K. PUNJA. *Epidemiology and management of* Botrytis cinerea *on greenhouse cultivated cannabis (*Cannabis sativa L.*)*

7:45
MSc - SC

J. CLEMENT, M. DELISLE-HOUDE, A. BARRADA, T.A.T. NGUYEN, M. DORAIS AND R.J. TWEDDELL. *Evaluation of plant biostimulants for their effect on baby leaf lettuce grown in a substrate colonised with* Pythium ultimum.

8:00
MSc- SC

A.C. GAHAGAN, D. RADFORD, M. MORRISON, E. GREGORICH, S. ARIS-BROSOU, AND W. CHEN. *Rotation and tillage shape soil-borne oomycetes communities.*

8:15
MSc - SC

E. JOHNSTONE AND A. FOSTER. *Detecting fungicide resistant isolates of* Fusarium graminearum *in the Maritimes.*

8:30
MSc - SC

I. THIRUGNANASAMBANDAM, T. VUCUREVICH, N. KAV, A. LAROCHE AND J. CHALLIS. *Optimization of a real-time immunoPCR assay using polyclonal antibodies for early detection of tan spot, fusarium head blight and stripe rust of wheat.*

8:45
MSc - SC

L. KING, T. FORGE, P. MUNRO, H. XU, M. JONES. *The root-lesion nematode,* Pratylenchus penetrans, *affects early growth and physiology of M.9, G.41 and G.935 apple rootstocks under field conditions.*

9:00
PhD - SC

S. SAPKOTA, R.R. BURLAKOTI, AND Z. PUNJA. *Metalaxyl sensitivity and virulence diversity of* Phytophthora rubi *population from raspberry in British Columbia.*

9:15 – 9:45	BREAK

9:45 – 11:45	SESSION 9 – DISEASE CONTROL

Moderators: Dr. Guillaume Bilodeau and Yixiao (Becky) Wang

9:45
PhD - SC

M.E.H. THOMPSON, A. SHRESTHA, E. KHALAF, J. RINNE, C. SHEARER, V. LIMAY-RIOS, L. REID AND M.N. RAIZADA. *Exploring cultured microbes of pollinated maize silks and interactions with* Fusarium graminearum *(Schwabe).*

10:00 PhD - SC
A. SHRESTHA AND M.N. RAIZADA. *Discovery and testing of pollen and silk-associated probiotic microbes from a diversity panel of maize genotypes from across the Americas to combat* Fusarium graminearum, *responsible for Gibberella ear rot (GER) in corn.*

10:15 PhD - SC
Z. YU, S.F. HWANG AND S.E. STRELKOV. *The evaluation of calcium cyanamide for clubroot management on canola.*

10:30
C. WIJEKOON, A. SABRA, J. R. TUCKER AND A. BADEA. *Comparative analysis of phenolic compounds of Canadian barley reveals potential biomarkers related to Fusarium head blight resistance.*

10:45
L. MA, J. GEDAK AND D. HENDERSON. *Development of an ultra-violet control protocol for powdery mildew in greenhouse cucumber.*

11:00
Z. MORALES MOREIRA, A. BRIGGS, D. THOMS, Y. LIU, J. CHANG, S. SONG, S. HOSSAIN, A. SRINIVAS, A. LIMAN, C. VUCUREVICH, W. ZHANG, S. CHATTERTON, C.H. HANEY. *Unraveling host-microbiome interactions for root-rot disease suppression in peas.*

11:15
Z.K. PUNJA, C. SCOTT, L. NI AND S. LUNG. *Efficacy of copper against pathogen growth and disease development on cannabis (*Cannabis sativa L.*, marijuana) plants.*

11:30
S. TAHRIRI ADABI AND D. HENDERSON. *Evaluation of the factors influencing antifungal efficacy of Black Soldier Fly waste product against soil-borne plant pathogens*

11:45 – 12:30	**BREAK**

12:30 – 13:15	**SESSION 10- DISEASE CONTROL**

Moderators: José Ramón Úrbez-Torres and Jonathan Beutler

12:30
C.L. TRUEMAN, J.C. AWREY AND L.L. VAN EERD. *Evidence that long-term cover cropping suppresses anthracnose fruit rot (*Colletotrichum *spp.) and delays defoliation in processing tomatoes.*

12:45
J.L. MacDONALD AND M.T. FRANKLIN. *Biovigilance: a more inclusive approach to disease management.*

13:00
X. NIE, M. SINGH, J. LAVOIE, V. BISHT, M. SHUKLA, A. CREELMAN AND T. MACKENZIE. *Assessment of cultivar sensitivity to potato mop-top virus induced tuber necrosis.*

13:15 – 14:30	**SESSION 11 – PATHOGEN BIOLOGY**

Moderators: Dr. Reem Aboukhaddour and Jonathan Beutler

13:15
MSc - SC

C.X. YANG, R. FREDUA-AGYEMAN, S. . HWANG, S.E. STRELKOV AND L.Y. GORIM. *Comparison of root morphological traits among Brassica accessions*

13:30
MSc - SC

M.K. LARIVIERE AND B.J. SAVILLE. *Exploring the stress response of* Ustilago maydis*: an antisense approach*

13:45
PhD - SC

M.A. JAVED AND E. PÉREZ-LÓPEZ. *Unveiling clubroot candidate effector families through ColabFold-based structural genomics.*

14:00
PhD - SC

A.M. SETO AND B.J. SAVILLE. *Exploring the functions of an RNA helicase upregulated in the* Ustilago maydis *teliospore.*

14:15
PhD - SC

M.S. McLAUGHLIN, S.N. YURGEL, P.A. ABBASI AND S. ALI. *Impacts of Abiotic Factors on the Fungal Communities of 'Honeycrisp' Apples in the Atlantic Maritime Ecozone*

FRIDAY JULY 8, 2022

8:00 – 9:00	SESSION 12 – PATHOGEN BIOLOGY

Moderators: Dr. Zayda Morales Moreira and April Mahovlic

8:00 R. GOURLIE, M. MCDONALD, M. HAFEZ, R. ORTEGA-POLO, K.E. LOW, D.W. ABBOTT, S.E. STRELKOV, F. DAAYF, **R. ABOUKHADDOUR** *Insights into the tan spot genome and its effector genes diversity.*

8:15 M. HAFEZ, M. TELFER, M.A. CARMONA, C. MOFFAT AND **R. ABOUKHADDOUR**. *Sequence analysis and structural features of the ToxB gene in* Pyrenophora tritici-repentis *and other ascomycete species.*

8:30 **S. HOLDEN**, R. BAMRAH, J. HUBENSKY, G. BAKKEREN, B.D. MCCALLUM, H.R. KUTCHER, G.S. BRAR. *Pathogenomics of Wheat Stripe Rust reveals a population shift in western Canada.*

8:45 – 9:15	BREAK

9:15 – 10:45	SESSION 13 – DISEASE/PATHOGEN EPIDEMIOLOGY

Moderators: Dr. Samuel Holden and Jared Hrycan

9:15 **T.A. FORGE**, P MUNRO, T. WATSON, M. SHARIFI, G. NEILSEN AND D. NEILSEN. *Influences of soil organic matter and irrigation management on ring nematode population growth and its relationship with growth of sweet cherry trees.*

9:30 **B.D. GOSSEN** AND M.R. MCDONALD. *Decline of* Plasmodiophora brassicae *over time in response to liming or a grass cover crop in a field trial.*

9:45 **Z.K. PUNJA**, L. NI, S. LUNG AND L. BUIRS. *The diverse and complex mycoflora present in cannabis (*Cannabis sativa L., *marijuana) inflorescences.*

10:00 **T.K. TURKINGTON**, H. KLEIN-GEBBINCK, H. KUBOTA, B. TIDEMANN, G. SEMACH, C. GEDDES, S. CHATTERTON, M. HARDING, P. LOKURUGE, A. MULENGA, E. KARPPINEN, P. MOOLEKI, D. TOMASIEWICZ, G. PENG, W. MAY, R. MOHR, G. TELMOSSE, D. PAGEAU, J. FENG, E. MCBAIN, AND S.E. STRELKOV. *Fungicide timing and assessment of risk factors for Sclerotinia stem rot of canola.*

10:15 **H. VAN DER HEYDEN**, G.J. BILODEAU, M.O. DUCEPPE, J. B. CHARRON AND O. CARISSE. *Towards improved surveillance of aerial plant pathogens using nanopore sequencing technology*

10:30 M.N. ISLAM, M. BANIK, S. SURA, J. TUCKER AND **X. WANG**. *Implications of crop rotation and fungicide on the Fusarium and mycotoxin spectra in Manitoba barley 2017-2019.*

10:45 – 11:30	**BREAK**
11:30 – 12:15	**STUDENT COMPETITION & PHOTO CONTEST AWARDS**
12:15 – 12:30	**ADJOURN**
12:45 – 14:00	**STUDENT SOCIAL**

CANADIAN PHYTOPATHOLOGICAL SOCIETY / LA SOCIÉTÉ CANADIENNE DE PHYTOPATHOLOGIE
AGENDA FOR THE 93ND ANNUAL MEETING OF MEMBERS / AGENDA ASSEMBLÉE GÉNÉRALE ANNUELLE
Monday July 4, 2022, 10 AM – 13 PM Pacific time

Please join the meeting via ZOOM link
https://ubc.zoom.us/j/61108340165?pwd=QlJmdWhHMXk5ZHlMWE83WTJTbjNoZz09

AMOM Agenda

1. Welcome remarks from the President / **Lone Buchwaldt**
2. Determination of quorum / **Tom Fetch**
3. Moment of silence for deceased CPS members / **Barry Saville**

Dr. Chuji Hiruki, Dr. William Lloyd Seaman, Dr. Blair McNeil and Dr. Marvin Weintraub.

4. Approval of the AMOM agenda / **Lone Buchwaldt**
5. Approval of minutes from the 92th AMOM on June 4, 2021 / **Tom Fetch**
6. President's report / **Lone Buchwaldt**
7. Presentation of 'CPS award for Achievement in disease management'
8. Treasurer's report / **Ken Conn**
    A) Financial statement 2021 (focus on page 4 'Statement of operations and changes in fund balances').
    B) Appointment of auditors for 2022
9. Report from the Financial Advisory Committee including a discussion of CPS five-year budget / **Barry Saville, Ken Conn**
10. Reports from Standing and Subject Matter Committees / **Lone Buchwaldt**
11. Presentation of 'CPS outstanding young scientist award' / **Lone Buchwaldt**
12. Report from the EIC of the Canadian Journal of Plant Pathology / **Stephen Strelkov**
    A) Results from a recent survey on publication preferences of authors and the new CJPP publishing model
    B) Report from the Ad Hoc Committee on a CJPP publishing contract in 2024
    C) Welcome to the new Editor-in-Chief of CJPP, Dr. Linda Jewell
13. Presentation of John Yorston graduate student scholarships
14. Presentation of 'CPS award for outstanding research'
15. Suggested Bylaw changes approved by the BOD / **Lone Buchwaldt**
    A) Modifications of wording pertaining to awards
    B) Expansion of the BOD to include the EIC of CJPP
    C) Expansion of the BOD to include the CPS Website Editor
    D) Re-numbering of certain Bylaw paragraphs for consistency
    E) Requirement for graduate students to be CPS members in order to receive CPS awards
16. New members on Standing Committees and Subject Matter Committees **/ Barry Saville**
17. New and renewed members on the Board of Directors **/ Barry Saville**
18. Installation of the Board of Directors for 2022-2023 / **Lone Buchwaldt**
19. Remarks from the President **Sheau-Fang Hwang**
20. Other business
21. Adjournment

ABSTRACTS

SESSION 1 – DISEASE ETIOLOGY

Moderators: Dr. Tom Forge and April Mahovlic

Symptomology and prevalence of Hop Latent Viroid on greenhouse grown cannabis (Cannabis sativa L.) plants. Z. K. PUNJA, K. WANG, L. NI, S. LUNG AND L. BUIRS. *Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada; and (KW) A & L Laboratories, 2136 Jetstream Rd, London, ON N5V 3P5*

Hop Latent Viroid (HpLVd) is an emerging pathogen affecting cannabis plants in Canada; little is currently known about its prevalence and symptomology. Multi-year analysis of samples submitted to a diagnostic lab (A & L Laboratories) using RT-PCR revealed that the pathogen was present in 4 provinces in 2020 and in 88.9% of total samples submitted. In 2021, the pathogen was detected in 6 provinces and in 16.2% of total samples. The provinces with highest HpLVd incidence were British Columbia and Ontario. Sampling conducted in commercial greenhouses in 2022 revealed that HpLVd affected many different cannabis genotypes. Symptoms on flowering plants included visibly reduced plant height, inflorescence stem length, inflorescence fresh weight, and root volume. The average reduction in these growth parameters was 24-33%. Symptomatic plants all tested positive by RT-PCR. Cuttings obtained from stock plants testing positive for HpLVd gave rise to plants containing the viroid, indicating that vegetative propagation was an important method of spread. The viroid was detected in leaves, petioles, inflorescence tissues, and in roots, although many plants remained asymptomatic. The viroid was also transmitted mechanically. The impact of HpLVd on total percent THC (delta-9-tetrahydrocannabinol), the most important quality and yield criterion for cannabis, was reduced by 22-39% in different cannabis genotypes. Microscopic observations indicated that glandular trichomes that produce THC were reduced in size and volume, but not density. *Hop Latent Viroid* has the potential to significantly and negatively impact the growth of the cannabis industry. The implementation of certified pathogen-free planting stock is urgently needed.

Root and soil-borne oomycetes and fungi associated with western white pine (*Pinus monticola*) mortality in British Columbia's seed orchards. S.F. SHAMOUN, K. RUFF, N. FEAU, G. BRADLEY, C. HALLDORSON, A. COSTER. *(S.F.S, KR, NF) Natural Resources Canada, Canadian Forest Service, Pacific Forestry Centre, 506 West Burnside Road, Victoria, BC V8Z 1M5 Canada; and (G.B.) BC Ministry of Forests, Lands and Natural Resources Operations and Rural Development, Vernon, BC V1B 2C7, (C.H.) BC Ministry of Forests, Lands and Natural Resources Operations and Rural Development, Saanichton, BC V8M 1W4, and (A.C.) BC Ministry of Forests, Lands, and Natural Resources Operations and Rural Development, Mesachie Lake, BC V0R 2N0*

The mortality of young and mature western white pine (*Pinus monticola* Douglas ex D. Don) trees has been recognized in British Columbia's seed orchards. Typical root-rot symptoms such as rapid

tree death, red-coloured, and bent needles, as well as, roots that are easily stripped of their epidermal and cortical tissues suggested the presence of a 'water mold' agent of the oomycete group. In order to assess the biodiversity of oomycetes and mycobiota in soil and roots associated with the mortality of western white pine trees, 52 soil and root samples were collected, of which17 were from the Okanagan and 35 from coastal Vancouver Island, BC. Soil samples were baited for oomycetes, and root samples were plated directly on selective PARPH-CMA media. These samples were assayed for oomycetes and mycobiota by sequencing PCR amplicons of the internal transcribed spacers (ITS) of the nuclear rRNA and they were identified using the NCBI nucleotides collection. For oomycetes, diverse species belonging to genera *Globisporangia*, *Pythium*, *Phytopythium* and *Phytophthora* were found, including *Phytophthora cinnamomi* Rands, a pathogen that is expected to move northwards as the climate warms. As for mycobiota diversity, species from 12 genera were identified, among which *Clonostachys, Phialocephala and Trichodermra* are well-known potential biological control agents. Ongoing research is focused on DNA-metabarcoding of the western white pine rhizosphere microbiome using second and third generation sequencing technologies, and assessing comparative aggressiveness among select oomycetes and fungi in relation to their pathogenicity on western white pine seedlings under different temperature conditions.

Crop rotation affects the structure and diversity of soil pathogenic and non-pathogenic microbial communities. M. N. ISLAM, O. MOLINA, R. KUTCHER AND X. WANG. *Agriculture and Agri-Food Canada, Morden Research and Development Centre, 101 Rte 100 #100, Morden, MB R6M 1Y5; and (R.K.) College of Agriculture and Bioresources, University of Saskatchewan, 51 Campus Dr, Saskatoon, SK S7N 5A8 Canada*

Crop rotations are one of the most desirable and sustainable disease management strategies in Canada and elsewhere in the world. At present, the information on the impact of rotations on the major soil-borne diseases/pathogens and the role of non-pathogenic microbiomes in suppressing crop diseases is limited. During the 2021 cropping season, soil samples (rhizosphere soils at crop flowering and bulk soils at crop harvest) were collected from experimental field sites in Morden, Manitoba (Black Chernozem soils) and Saskatoon, Saskatchewan (Dark Brown Chernozem soils). The soil microbiome was characterized by high-throughput targeted metagenomics sequencing of ITS (fungi) and 16S (bacteria) rRNA genes. The bioinformatics for taxonomic profiling and diversity index was performed using the QIIME 2™ platform. The effect of nine rotation combinations of cereals (wheat, barley, maize), pulses (pea, soybean), and oilseeds (canola) on the composition, abundance (frequency), Shannon diversity and operational taxonomic units/OTUs richness of microbiomes were assessed. We also evaluated the impact of two-year crop rotations (2020-2021) on the relative abundance of *Fusarium* head blight of cereals (*F. graminearum*), blackleg of canola (*Leptosphaeria maculans*), storage molds (*Alternaria* spp.), and common root rot (*Fusarium* and *Rhizoctonia* spp.) pathogens. Multivariate statistics revealed that rotational (combination of cereals-pulses-oilseeds) treatments significantly modified the structure of fungal and bacterial communities. A more in-depth analysis of the soil microbiome is currently in process to better understand the impact of crop rotations on major soil-borne pathogens and the development of diseases suppressive microbial genes/communities (e.g., bacteria), and their interactions in the prairie crop soils.

Signs and symptoms of sudden apple decline in British Columbia, impacts on tree physiology, and the potential role of environmental stressors. J.L. MacDONALD, K.D. HANNAM, AND H. XU. *Summerland Research and Development Centre, Agriculture and Agri-Food Canada, 4200 Highway 97, Summerland, BC V0H 1Z0, Canada*

Sudden apple decline (SAD) is a recent and little understood disorder, associated with wilted leaves and rapid death of apple trees. In 2018, orchard surveys were conducted in seven apple orchards in the Okanagan Valley reporting high tree mortality and potentially SAD. Of 350 trees observed, 28.4% were assessed as declining; of those, necrotic stem lesions were frequently observed (87.5%), underdeveloped foliage was observed less frequently (27.7%) and oozing wounds were rare (1.1%). A survey of a 1-10 year old apple germplasm orchard showed that the probability of trees exhibiting SAD increased with tree age, regardless of parentage. Parentage did not statistically significantly affect disease incidence. Across orchards, there appeared to be an association between infestation of apple clearwing moth (*Synanthedon myopaeformis*), the size of necrotic stem lesions, and incidence of SAD. Assessment of stem water transport showed a water-limiting bottleneck at the graft union. The trees in decline also had lower midday stem water potential, lower photosynthetic rate, and lower fruit weight and dry matter. Grid (5-m) sampling of soils in four affected orchards showed a correlation between SAD-associated tree mortality and a given soil's ability to retain water (e.g., soil depth, coarse fragment content, organic matter content). Recently, the Okanagan Valley has experienced an unprecedented drought (2017) and an increasing frequency in the number of days >35°C. We propose that heat and/or drought stress, compounded by impaired water transport across the graft union, may be a contributing factor to the incidence of SAD in this region.

SESSION 2 – HOST-PATHOGEN INTERACTIONS

Moderators: Dr. Rishi Burlakoti and Sanjib Sapkota

Summoning the ancestors: using an *Aegilops tauschii* diversity panel to improve stripe rust resistance in wheat. V. FETTERLEY, D. GILBERT, K. GAURAV, H.S. CHAWLA, G. GERARD, S. HOLDEN, H.R. KUTCHER, X. CHEN, P. HUCL, B.B.H. WULFF, C.J. POZNIAK, S. ARORA AND G.S. BRAR. *Faculty of Land and Food Systems, The University of British Columbia, 2357 Main Mall, Vancouver, BC V6T 1Z4, Canada; (D.G., K.G., B.B.H.W., S.A.) John Innes Center, Norwich Research Park, Colney Ln, Norwich NR4 7UH, United Kingdom; (H.S.C., G.G., H.R.K., P.H., C.J.P.) Department of Plant Science, The University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada; (X.C.) USDA-ARS and Department of Plant Pathology, Washington State University, Pullman, WA 99164, USA*

Wheat is the world's second largest crop after corn, yet 21.5% of the global yield is lost to pests and pathogens annually. Wheat stripe rust, caused by the fungus *Puccinia striiformis* f. sp. *tritici* (*Pst*), is responsible for more than 15 million tonnes of yield loss every year. To survive from pathogen infection, wheat and its relatives have evolved resistance genes capable of recognizing the pathogen and triggering appropriate immune or resistance responses in the host. The wild grass

Aegilops tauschii is the donor of the D sub-genome of modern bread wheat and represents a great source of genetic diversity for breeding programs. A panel composed of 151 genetically diverse *A. tauschii* accessions was genotyped using R gene Enrichment Sequencing (RenSeq) and screened against multiple races of *Pst* both at the seedling and the adult plant stages. Twenty-nine, three, and two *Pst* races from Canada, the USA, and the UK, respectively, were used to inoculate seedlings. Association genetics from the phenotype observed combined with RenSeq (AgRenSeq) identified one gene, found on chromosome 4DS (*YrAS2388*), which is present in more than 66% of the accessions, conferring a high level of resistance to all the *Pst* races used in this study. Two other race specific resistance genes, effective against Canadian *Pst* isolates, were identified through AgRenSeq. We believe those genes can and should be deployed in Canadian breeding programs to prevent stripe rust epidemics and contribute to food security.

Characterization of clubroot disease development in Arabidopsis auxin receptor mutants, and peat-based and partially-hydroponic assay systems. S. LI, H. KAUR, C. JAYASINGHEGE, D. REINECKE AND J. OZGA**.** *Plant BioSystems, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada*

Clubroot disease is a soil-borne disease of cruciferous plants including the model plant *Arabidopsis thaliana*, caused by the pathogen *Plasmodiophora brassicae*. The pathogen affects plant hormonal networks and causes swelling and abnormal growth (galling) of the roots. To assess the role of auxin receptors in the formation of clubroot disease symptoms, a quadruple auxin receptor mutant line (tir1-10, afb2-3, afb4-8, afb5-5) was compared with a wild-type (Col) *Arabidopsis* line in a peat-based growth system. Seedlings (14-d-old) were inoculated with $1x10^4$ spores/mL of *P. brassicae* and assessed at 28 days after inoculation (DAI). The 0-3 scale rating system was used for the Index of Disease (ID) calculations. The ID of the quadruple auxin receptor mutant line was 20.8%, while the wild-type line was much higher at 73.3%, suggesting that reduced auxin response in the host plant suppresses or delays root gall formation. Additionally, a partially-hydroponic root growth system was assessed for root phenotype characterization. In this study, wild-type seedlings (14-d-old) inoculated with $1x10^4$ or $1x10^5$ spores/mL of *P. brassicae* in peat-based media were transferred to a hydroponic system at 7 or 14 DAI. In the hydroponic system, seedlings were grown on filter paper wetted with 1/4 strength Hoagland's solution in plastic bags covered with foil until harvest at 27 DAI. The *P. brassicae*-infected wild-type seedlings developed prominent root galls (ID>96.7%) at both inoculum densities in the partially-hydroponic system, suggesting that this system may be useful for detailed root phenotype assessments in clubroot-infected plants.

Transcriptome analysis of rutabaga (*Brassica napus*) cultivars indicates that the indole glucosinolate pathway may play a role in inducing plant defense against clubroot disease. H. LIU, H. KAUR, S.E. STRELKOV, S.F. HWANG AND J.A. OZGA. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada*

Clubroot, caused by the obligate parasite *Plasmodiophora brassicae*, is one of the most damaging diseases of the *Brassicaceae.* Glucosinolate (GSLs) are a group of defense-related secondary metabolites in cruciferous plants that have been associated with clubroot disease. In the indole GSL pathway, 3-indolylmethyl GSL degradation leads to isothiocyanates, thiocyanate, and nitriles production, which are implicated in plant defense processes against many pathogens and herbivores. This study aims to improve understanding of the role of the indole GSL pathway in host-pathogen interactions between rutabaga (*Brassica napus* var. *napobrassica*) and *P. brassicae.* Analysis of a database from a recently published study (Zhou et al., 2020 Int J Mol Sci 21, 8381) showed that the resistant rutabaga cultivar had a different gene expression pattern in the indole GSL pathway compared with the susceptible rutabaga cultivar in response to *P. brassicae* inoculation. The presence of gene transcripts coding for specific indole GSL pathway enzyme classes was confirmed by PCR in rutabaga roots either non-inoculated or 7 days after *P. brassicae* inoculation, including those from the cytochrome P450 family 81 subfamily F2 and F4, indole glucosinolate O-methyltransferases 2 and 5, beta-glucosidase 30, nitrilases 2 and 4, nitrile specifier protein 5, and glutathione-S-transferase 13. Quantitation of these selected gene targets will be performed using qRT-PCR in the resistant and susceptible rutabaga cultivars that are either non-inoculated or 7 days after *P. brassicae* inoculation. Overall, the current analysis suggests that the indole GSL pathway may play a role in inducing enhanced plant defense against the clubroot pathogen.

Temperature regulation of plant-rhizobacteria interactions within the soil-rhizosphere-rhizoplane interface. E.J.R. MARCHETTA, K. YOSHIOKA, W. MOEDER, E. DÉZIEL AND C.D.M. CASTROVERDE. *(E.J.R.M., C.D.M.C) Department of Biology, Wilfrid Laurier University, Waterloo, ON, Canada N2L 3C5; (K.Y., W.M.) Department of Cell & Systems Biology, University of Toronto, ON, Canada M5S 3G5; (E.D.) Institut National de la Recherche Scientifique, Institut Armand-Frappier, Laval, QC, Canada H7V 1B7*

The rhizosphere is a metabolically active area of nutrient-rich soil surrounding the root. This region is home to diverse and exceptionally co-evolved rhizobacterial communities, which coordinate vital interactions to directly benefit the plant throughout their life cycle. Optimal rhizobacterial communities provide microbe-assisted protection to host plants and enhance crop resiliency. Previously, we have identified non-pathogenic soilborne bacteria isolated from Canadian soil that can enhance immunity in *Solanum lycopersicum* (tomato) against the fungal pathogen, *Botrytis cinerea*. However, the effectiveness of selecting root microbiomes for applications in agricultural regions facing suboptimal climatic conditions remain greatly underexplored. To address this knowledge gap, we have investigated the in vitro physiology of these rhizobacterial strains. Specifically, we have measured bacterial growth curves, phosphate solubilization activities and direct anti-pathogenic abilities at different environmentally relevant temperatures. We found that

these parameters are highly dependent on the specific strain and incubation temperature. In situ, we are monitoring bacterial proliferation in the rhizosphere and on the rhizoplane to establish the impacts of temperature on rhizobacterial competency and the host plant's endophytic recruitment of microbes in this region. Finally, the impacts of temperature on defense priming in tomato plants inoculated with certain rhizobacteria is being investigated using immunity-related gene expression analyses following a pathogen challenge. As global warming accelerates impacting overall plant health, it is vital to understand the effects of temperature change on host-plant interactions with beneficial microorganisms in the rhizosphere. This will contribute to global efforts assessing the durability and long-term effectiveness of these agronomic technologies.

A hydroponic based system to phenotype the clubroot pathogen. R. SALIH, J-D CÔTÉ AND E. PÉREZ-LÓPEZ. *Département of Phytology, FSAA, Université Laval, Québec, Canada. Centre de recherche et d'innovation sur les végétaux (CRIV), Université Laval, Québec, Canada. Institute de Biologie Intégrative et des Systèmes (IBIS), Université Laval, Québec, Canada.*

Clubroot caused by the obligate parasite *Plasmodiophora brassicae* is one of the devastating diseases affecting the canola industry worldwide. More than thirty *P. brassicae* pathotypes have been identified in Canada using the Canadian Clubroot Differential (CCD) system to date. However, the CCD system and other phenotyping system previously developed do not discriminate virulent and avirulent isolates of *P. brassicae* against the clubroot resistance profiles of commercially available canola cultivars. To try to solve this limitation, we have developed a hydroponic-based bioassay using *P. brassicae* single spore isolates (SSIs), and four canola inbred homozygous lines (CIH). These SSIs are representative of the virulence widely spread in the field, while CIH are representative of the resistance commercially available to growers. Through this new phenotyping scheme, we have been able to connect *P. brassicae* isolates with their ability to break down clubroot resistance in canola in shorter time and more efficiently. The successful use of this study will help to tailor the selection of resistant canola varieties to use in an infested field for the longest possible time, subsequently, empowering producers to make informed decisions about the best canola cultivar to use based on the *P. brassicae* diversity in their field.

Quantitative trait locus (QTL) mapping of aggressiveness in Fusarium graminearum, causing Fusarium head blight in durum wheat. Y. ZHANG AND G.S. BRAR. *The University of British Columbia, Department of Botany, 6270 University Blvd, Vancouver, BC V6T 1Z4, Canada*

FHB is a significant fungal disease predominantly caused by *Fusarium graminearum,* impacting the wheat industry through reduced seed quality and yield, and grain safety due to contamination with fungal toxins. It is vital to enhance the resistance level of modern varieties to reduce economic losses in Canadian wheat production. However, several FHB resistance QTL have been mapped and identified in wheat species, but few reliable markers and bread or durum wheat commercial cultivars with high resistance to FHB are available. To accelerate the development of novel durably resistant cultivars, understanding the molecular interaction between *F. graminearum* and wheat is needed. Decoding the genetic determinants of aggressiveness and its evolution in the field

populations of *F. graminearum* is necessary for studying the pathogen-host interaction. This research project aims to identify and map QTLs conferring aggressiveness in *F. graminearum.* A bi-parental population developed from a cross between PH-1 and SK-17-97 will be phenotyped on a moderately susceptible durum variety. Then the loci related to *F. graminearum* aggressiveness will be revealed, and the contribution of each QTL with aggressiveness will be estimated using QTL mapping and Pan-genome analysis. This study will provide a deeper grasp of the virulence mechanisms in *F. graminearum* and their variation in field populations, facilitating the isolation of FHB resistance/susceptibility genes in wheat.

Type of soilless mix influences the development of clubroot (*Plasmodiophora brassicae*). S. G. CHESNEY, B. D. GOSSEN, J. ROBSON AND M. R. MCDONALD. *University of Guelph, 50 Stone Road East, Guelph, ON NIG 2W1, Canada; (B.D.G.) Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK Z7N 0X2, Canada*

Clubroot is caused by the soil-borne pathogen *Plasmodiophora brassicae* Woronin which causes distinctive clubbing symptoms on infected roots of brassica crops. Soilless mixes are a common growth media used in controlled environment studies to assess pathogen biology and disease reaction to clubroot. A growth room study was conducted to assess clubroot severity that developed in two soilless mixes: LA4 (Sungro) and BM6 HP (Berger). These soilless mixes have similar characteristics, including percentage of peat moss (LA4: 63 –73%, BM6: 65 –73%) and perlite (LA4: 30%, BM6: 22%) and pH (LA4: 5.7, BM6: 5.8). However, BM6 has lower electrical conductivity (822 µS cm^{-1}) than LA4 (1148 µS cm^{-1}) based on lab testing. The effect of compaction of the growth medium was assessed by comparing dry soilless mix placed directly from the bag into tall plastic pots versus wet soilless mix saturated with water. Seedlings of canola (*Brassica napus* L.) cultivar 'L233P', 10 seedlings per experimental unit, were inoculated with 5 mL of 1×10^6 or 1×10^8 resting spores mL^{-1} of *P. brassicae* pathotype 2 (Williams' system). Clubroot severity was assessed 5 weeks after inoculation. Canola grown in LA4 exhibited above-ground symptoms within 3 weeks of inoculation while plants grown in BM6 did not develop above-ground symptoms. Across potting method and inoculum concentration, plants grown in LA4 developed high clubroot incidence and severity. Canola grown in BM6 developed few or no clubroot symptoms. These results demonstrate the importance of choosing a suitable soilless mix for studies on clubroot development.

Fusarium head blight (FHB) resistance in 'Paragon/Watkin 1190580' bi-parental mapping population. S. SINGH AND G.S. BRAR. *The University of British Columbia, Department of Botany, 6270 University Blvd, Vancouver, BC V6T 1Z4, Canada*

Fusarium head blight (FHB), caused by *Fusarium graminearum* is one of Canada's most destructive wheat diseases. It does not only result in yield loss but also compromises the grain quality by producing toxic metabolites (mycotoxins), mainly deoxynivalenol (DON). In epidemic years, FHB can cause losses of as much as 1 billion CAD. Although control measures like fungicide application and crop rotation help in managing the disease, genetic resistance is considered the most efficacious and environment-friendly strategy. To date, more than 200 QTL

have been mapped for FHB resistance across almost all the chromosomes of wheat. Chinese germplasm like 'Sumai 3' and 'Wangshuibai' has been the major contributor to FHB resistance to the breeding programs. Due to intensive selective breeding in wheat, the genetic diversity in wheat germplasm has narrowed down. Under such conditions, we have to rely upon the unexplored sources of genetic diversity such as wild relatives, and landraces. The biggest disadvantage while breeding for resistance from the secondary/tertiary germplasm of wheat is the linkage drag. To overcome this, marker-assisted selection (MAS) of resistance traits against FHB can be a valuable tool. We are utilizing a landrace namely 'Watkin 1190580' as a donor of disease resistance. A RIL population (n=90) was derived from a cross between Paragon (female parent) and Watkin 1190580 (male parent) and was screened for disease resistance in three different environments for the year 2021. The population at field nurseries i.e. Carman and Morden was screened using spray and corn spawn method of inoculation, respectively. Additionally, screening in the greenhouse (UBC) was done using the point inoculation method. Analyses of the phenotypic data from three environments revealed the presence of variation in disease response within the population. The segregation of resistance genes in the mapping population was confirmed by a few transgressive segregants. With the help of genotypic data and multi-environment phenotypic data, we will fine map the FHB resistance loci using the SNP molecular markers. As the landrace has no relation with the earlier used sources of FHB resistance, we have hypothesized that the QTL for FHB resistance in the landrace can be novel.

SESSION 3 – HOST-PATHOGEN INTERACTIONS

Moderators : Dr. Michael Cruickshank and Jared Hrycan

Regulation of nigericin and geldanamycin biosynthesis in *Streptomyces* sp. 11-1-2 by *N*-acetylglucosamine. G. A. DIAZ CRUZ AND D.R.D. BIGNELL. *Department of Biology, Memorial University of Newfoundland and Labrador, 45 Arctic Avenue, St. John's, NL A1C 5S7, Canada*

Like many other members of the *Streptomyces* genus, the plant-pathogenic strain *Streptomyces* sp. 11-1-2 can produce a myriad of specialized metabolites, including the phytotoxins nigericin and geldanamycin. The biosynthesis of these compounds is often regulated in response to changes in environmental conditions, which can provide a competitive advantage in natural settings. Under nutrient-limiting conditions, the compound *N*-acetylglucosamine (NAG), part of the bacterial cell wall, is used as a carbon and nitrogen source; additionally, it acts as an elicitor/inhibitor of specialized metabolites in *Streptomyces* strains. The current study evaluated the response of the phytotoxins nigericin and geldanamycin biosynthesis in 11-1-2 to a range of NAG concentrations added to two culture media. Organic culture extracts obtained from 14-day-old agar plates with different NAG concentrations were evaluated using reverse-phase high-performance liquid chromatography (RP-HPLC) and liquid chromatography-mass spectrometry (LC-MS). Increasing concentrations of NAG resulted in decreased biosynthesis of both phytotoxins. Moreover, two intermediates, one for each phytotoxin, were also detected. These intermediates, which are

predicted to be abierixin and 15-hydroxygeldanamycin, presented a similar trend as the main metabolites. Interestingly, nigericin and its intermediate were detected in both media, yet, the geldanamycin intermediate was found only in one medium. Altogether, these results represent a regulation mechanism at the nutritional level in 11-1-2, which can have implications for plant-microbe interactions.

Characterizing the virulence of *Plasmodiophora brassicae* on canola with 'second-generation' clubroot resistance. K. HOLLMAN, V.P. MANOLII, S.F. HWANG AND S.E. STRELKOV. *Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB T6G2P5, Canada*

Clubroot, caused by *Plasmodiophora brassicae*, is a damaging soilborne disease of canola (*Brassica napus*) first identified on the Canadian Prairies in 2003. Clubroot-resistant (CR) canola cultivars, carrying what is now known as 'first-generation' resistance, were introduced in 2009-10 and soon became the most effective and widely used clubroot management tool. Unfortunately, new pathotypes of *P. brassicae* have emerged that can overcome first-generation resistance and are found in an increasing number of fields. In response, canola breeders have developed a new set of cultivars with so-called 'second-generation' resistance. While the nature of this resistance is not in the public domain, and may differ among cultivars from different companies, it is believed to be distinct from first-generation resistance and may be conferred by a different resistance gene(s) or stacked resistance genes. Studies are underway to characterize the virulence of *P. brassicae* populations on different hosts with second-generation resistance. Isolations of the pathogen were made from symptomatic second-generation CR canola crops identified in the field and tested for their virulence on a suite of seven commercial canola cultivars carrying second-generation resistance. Preliminary results indicated that some of these cultivars developed moderate to severe levels of clubroot when challenged with isolates recovered from canola crops with second-generation resistance. This suggests that resistance-breaking isolates of *P. brassicae* may be difficult to control solely via the deployment of resistant hosts, and that a more integrated approach to clubroot management is required.

Studying the effect that ring nematode (*Mesocriconema xenoplax*) has in disease development in young grapevines infected with *Phaeomoniella chlamydospora.* J. HRYCAN, T. FORGE, P. BOWEN, M. HART, and J.R. ÚRBEZ-TORRES. *Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, Summerland, British Columbia V0H 1Z0, Canada, [2]Department of Biology; (J.H., M.H.) University of British Columbia – Okanagan, Kelowna, British Columbia V1V 1V7*

Petri disease (PD) is an important malady in young grapevines causing significant economic losses to growers around the world. Though several fungi are known to be involved on PD, *Phaeomoniella chlamydospora* (*Pc*) is the main fungus isolated from PD infected vines worldwide. It is hypothesized that *Pc* may act as a latent pathogen, transitioning from an endophytic to a pathogenic lifestyle under abiotic or biotic host stress conditions. The ring nematode *Mesocriconema xenoplax* is commonly found in vineyards in the Okanagan Valley in BC, and it has been reported to enhance disease and symptoms' development in tree fruit. Accordingly, it

may contribute to the transition of *Pc* from endophyte to pathogen in grapevines. Arbuscular mycorrhizal (AM) colonization has been proposed to suppress the effects of plant-parasitic nematodes, but results of prior research on the ring nematode-grapevine interaction, have been inconsistent. A greenhouse study to investigate the effects that ring nematode play on PD development in young 'Merlot' grapevines and the potential use of AM fungi to mitigate such stress was conducted over two growing seasons. Grapevines were vacuum inoculated with three different levels of *Pc* spores (low=1,000, medium=5,000 and high=25,000) and planted in pots containing *M. xenoplax* nematodes. Colonization by *Pc* was quantified using droplet digital PCR at the time of inoculation, planting, and end of experiment. Stem necrosis, nematode population densities, pruning, and root weights were also analyzed upon conclusion of the experiment. Preliminary results showed no dry root weight, pruning weights, or percent wood necrosis between treatments. ddPCR analysis revealed no difference in fungal growth as a result of nematode infestation.

Comparative molecular responses in lodgepole and jack pines showing differential resistance to infection by *Cronartium harknessii* reveals a non-canonical defense response to biotrophic rust fungi. S. O. OSADOLOR, M. MAYERHOFER, C. MCALLISTER, R. PEERY, L.I. ZAHARIA, S. DANG AND J.E.K. COOKE. *(S.O.O., M.M., C.M., R.P., S.D., J.E.K.C.) Department of Biological Sciences, University of Alberta, 116 St & 85 Ave, Edmonton, AB T6G 2E9, Canada; (L.I.Z.) National Research Council of Canada, 110 Gymnasium Pl, Saskatoon SK S7N 0W9, Canada; (C.M.) Department of Oncology, University of Alberta, 116 St & 85 Ave, Edmonton, AB T6G 1Z2, Canada*

Western gall rust (WGR) caused by *Cronartium* (J. P. Moore) E. Meinecke, is a fungal disease affecting a subset of pine species across North America, including lodgepole pine (*Pinus contorta* Douglas ex Loudon var. *latifolia* Engelm.) and jack pine (*Pinus banksiana* A. B. Lambert). Attack by the fungus leads to the production of galls on stems and branches of these trees. Quantitative resistance has been documented in both species, with jack pine being more resistant to *C. harknessii* than lodgepole pine. We used a comparative approach to explore the molecular mechanism conferring interspecies and intraspecies host differences in quantitative resistance to *C. harknessii*. Given that rust fungi such as *C. harknessii* are considered obligate biotrophs, we predicted that *C. harknessii* inoculation will trigger the biotroph-associated salicylate (SA)-mediated signalling network rather than the necrotroph-associated jasmonate (JA)-mediated signalling network in pines. Both hormone analyses and gene expression profiling with RNASeq indicated that SA synthesis did not increase in either lodgepole or jack pine in response to *C. harknessii* inoculation. In contrast, JA biosynthesis increased in both species, raising the possibility that JA might be induced by *C. harknessii* to suppress the host defense. Transcript abundance profiling by qRT-PCR showed that the higher resistance in jack pine relative to lodgepole pine correlates with an earlier and greater induction of genes in the biotrophic defense pathway. Our result provides a new insight into the role of JA in conifer defense against biotrophic fungal pathogens, and a potential antagonistic interaction with the SA-mediated defense network.

Predicting pathogens' virulence: linking host breadth and pathogenicity of the *Botryosphaeriaceae* fungal family in grapevines (*Vitis vinifera*). I. SILVA-VALDERRAMA, O. SILVA M., J. BOULE, J.R. URBEZ-TORRES and T.J. DAVIES. (I.S-V., T.J.D.) *University of British Columbia, Botany Department, Vancouver, BC* V6T 1Z4, *Canada.* (O.S.M.) *La Huarara, Santiago, RM 7570180, Chile.* (J.B., J.R.U-T.) *Summerland Research and Development Centre, Agriculture and Agri-Food Canada, Summerland, BC* V0H 1Z0, *Canada*

Plant diseases can have devastating effects on crops and food sources, elevating world hunger and malnutrition. Fungal pathogens are responsible for 30% of emerging plant diseases and have caused epidemics with catastrophic consequences for ecosystems and people. Previous work (Reference?) has linked host breadth and pathogen emergence, illustrating important connections with the phylogeny of the plant hosts. However, the importance of the pathogen phylogeny in shaping pathogen-host association has been under-explored, yet it may be a useful tool for describing pathogens likely to shift to novel hosts and predicting the potential for disease emergence following host jumps. Here, we describe the phylogenetic signal in host use by *Botryosphaeriaceae*, a globally distributed fungal family that infects most woody perennial plants, and explored the link between host breadth, phylogenetic relatedness, and virulence. First, we reconstructed the phylogeny of *Botryosphaeriaceae* spp. infecting grapevines (*Vitis vinifera*) and examined whether closely related pathogens infect similar host species. Second, we quantified virulence of the *Botryosphaeriaceae* known to infect *V. vinifera* using a high-throughput detached cane assay. We then modelled the relationship between host breadth and lesion size. Preliminary results show large differences in host breadth within the *Botryosphaeriaceae*, and a positive relation between the phylogenetic host breadth and pathogen virulence in *V. vinifera.* This work provides a first step towards predicting virulence of a known pathogen on a novel host following a host jump. We suggest our approach could be useful for the coordinated global monitoring of high-risk species within *Botryosphaeriaceae*.

Identification and characterization of candidate effectors common to the resistance-breaking pathotypes 3A and 5X of *Plasmodiophora brassicae*. E. R. M. STORFIE, L. GALINDO-GONZÁLEZ, S. F. HWANG, AND S. E. STRELKOV. *(E. R. M. S., S. F. H., S. E. S.) Department of Agricultural, Food and Nutritional Science, University of Alberta, 116 St & 85 Ave, Edmonton, AB T6G 2R3, Canada; (L. G. G.) Canadian Food Inspection Agency, 1400 Merivale Rd, Ottawa, ON K1A 0Y9, Canada*

Clubroot disease, caused by *Plasmodiophora brassicae*, is a major threat to Canadian canola (*Brassica napus*) production. Cultivars carrying major gene resistance represent the main clubroot management tool. The deployment of resistant cultivars exerts significant selection pressure on pathogen populations, which has led to the emergence of 'resistance-breaking' pathotypes of *P. brassicae,* including pathotypes 3A and 5X. Transcriptomic analyses were conducted on pathotype 3A at 7, 14, and 21 days after inoculation of resistant and susceptible rutabaga (*B. napus* ssp. *rapifera*) cultivars. Predicted effectors with non-redundant transcripts and low covariance were identified across time-points and cultivars, and NanoString technology was used to validate the

transcriptomic analyses. Comparisons between the pathotype 3A transcriptome and a previous study evaluating the pathotype 5X transcriptome indicated 53 effectors in common between the two pathotypes. Among these effectors, SPR01261.1, a putative serine carboxypeptidase, and SPQ99289.1, an unknown protein with a kinase domain, were characterized. Each effector had a predicted signal peptide, the function of which was confirmed by directing the secretion of invertase, whose activity was detected by a colour change in the presence of 2,3,5-triphenyltetrazolium chloride. After each effector was transformed into *Escherichia coli*, their expression was induced, and the resulting proteins were purified prior to measuring their protease (SPR01261.1) and kinase (SPQ99289.1) activities. The localization of both effectors was monitored via fluorescence microscopy after agroinfiltration of *Nicotiana benthamiana*. This study seeks to improve our understanding of the effectors deployed during the infection of the resistance-breaking pathotypes of *P. brassicae* in their *B. napus* hosts.

SESSION 4 – HOST-PATHOGEN INTERACTIONS

Moderators: Jesse MacDonald and Emilee Storfie

Exploring resistance to *Verticillium longisporum* in *Brassica* genotypes. Y. WANG, S. E. SRELKOV, R. FREDUA-AGYEMAN, AND S. F. HWANG. *Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB T6G2P5, Canada*

Verticillium stripe, caused by *Verticillium longisporum*, is an emerging disease of canola (*Brassica napus*) in Canada. First identified in Manitoba in 2014, *V. longisporum* has since been detected in most Canadian provinces. Symptoms of Verticillium stripe include half stem senescence, and the shredding and appearance of black microsclerotia on the stem. In Europe, *V. longisporum* infection can cause yield losses of up to 50%. No fungicides or soil amendments have been reported to be effective for the management of Verticillium stripe. Furthermore, no canola cultivars with resistance to this disease are registered in Canada. The objective of this study was to identify *Brassica* genotypes with resistance to *V. longisporum*. A collection of 110 rutabaga (*B. napus* ssp. *rapifera*) and 57 other *Brassica* genotypes was screened for resistance to the pathogen under greenhouse conditions in replicated experiments. Seedlings were inoculated by the root-dip method, with susceptible and moderately resistant checks included as controls. Disease development was evaluated at four different time-points on a 1-9 severity scale, and the area under disease progress curve (AUDPC) was calculated. Several *B. rapa* and *B. oleracea* genotypes developed low AUDPC values, indicating that these could serve as important sources of resistance. Broadening of the genetic basis of *V. longisporum* resistance will be important for the effective management of this pathogen in the Canadian canola crop.

Identification of novel genes associated with partial resistance to Aphanomyces root rot in field pea by BSR-seq analysis. L. WU, R. FREDUA-AGYEMAN, S.E. STRELKOV, K-F. CHANG AND S-F. HWANG**.** *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada*

Aphanomyces root rot, caused by *Aphanomyces euteiches*, causes severe yield loss in field pea (*Pisum sativum*). The identification of pea germplasm resistant to this disease is an important breeding objective. To facilitate marker-assisted selection (MAS), bulked segregant RNA-seq (BSR-seq) analysis was conducted using an F_8 RIL population derived from the cross of 'Carman' × '00-2067'. Root rot development was assessed under controlled conditions in replicated experiments. A significant genotypic effect ($P<0.05$) and significant correlation coefficient ($0.51<r<0.58$, $P<0.001$) were found for root rot severity in three greenhouse experiments. To profile the expressed resistance components in response to *A. euteiches* infection, resistant (R) and susceptible (S) bulks containing 25 individuals with three biological replicates were constructed. The BSR-seq analysis of the R bulks generated 44,595,510~51,658,688 reads, of which 98.08~99.44% were aligned, compared with 43,848,192~45,664,302 reads and alignment rates of 99.04 ~ 99.53% in the S bulks. The aligned sequences were linked to 44,757 genes in a reference genome. A total of 2,356 candidate genes were found with significant differential expression between the R and S bulks, of which 44 were used for gene annotation, including defense-related pathways (jasmonate, ethylene and salicylate) and GO biological process. Approximately 344,100 SNPs were identified between the R and S bulks, of which 395 variants were located in 31 candidate genes. The identification of novel genes associated with partial resistance to Aphanomyces root rot in field pea by BSR-seq may facilitate efforts to improve management of this important disease.

Investigating the NHP-dependent SAR pathway in common hexaploid wheat; options for broad-spectrum disease reduction? S. SUN, Y. ZHANG, C. HERRFURTH, I. FEUSSNER, AND G. BAKKEREN. *(S. S.,Y. Z.)The University of British Columbia, Department of Botany, 6270 University Blvd, Vancouver, BC V6T 1Z4, Canada; (S. S., G. B.) Agriculture and Agri-Food Canada, Summerland Research & Development Centre, Summerland, BC V0H 1Z0, Canada; (C. H., I. F.) University of Göttingen, Albrecht-von-Haller-Institute and Göttingen Center for Molecular Biosciences (GZMB), Department of Plant Biochemistry and Service Unit for Metabolomics and Lipidomics, Göttingen, D-37077, Germany*

Plant systemic acquired resistance (SAR) is a phenomenon whereby the recognition of a local microbial invasion in aerial tissue confers a 'whole-plant' immune response against a wide range of pathogens. For the model plant *Arabidopsis thaliana* and various other angiosperms, the key metabolites Pipecolic acid (Pip) and *N*-hydroxylated pipecolic acid (NHP), synthesized by the reductase SAR-Deficient 4 (AtSARD4) and Flavin-monooxygenase 1 (AtFMO1), respectively, are crucial for proper SAR establishment. However, the extent to which NHP biosynthesis contributes to SAR in common hexaploid wheat (*Triticum aestivum*) remains unclear. Here, we utilized a combination of protein homology, phylogenetic and transcriptomic analyses to elucidate functional orthologs of *AtSARD4* and *AtFMO1* in wheat. 48 *TaFMO1*-like and

three *TaSARD4* candidates were identified, from which representatives were selected for further functional characterization. All three *TaSARD4*-expressing transgenic *Δsard4 Arabidopsis* lines generated displayed dwarfism characteristic of autoimmunity, with significant reductions in rosette size (>45%) compared to the *Atsard4* deletion mutant. Two *TaFMO1*-expressing transgenic *Δfmo1 Arabidopsis* lines revealed a partial recovery in SAR when infected by the oomycete *Hyaloperonospora arabidopsidis*, indicating possible functional complementation. Furthermore, supplementing 10mM NHP to a local wheat leaf significantly and systemically reduced by 3-fold the proliferation of the biotrophic wheat fungal pathogen, *Puccinia triticina* (*Pt*); quantification of basal and *Pt*-induced NHP and Pip levels in wheat by HPLC-MS is currently underway. Altogether, our results suggest that the NHP biosynthetic pathway for pathogen defense is conserved in wheat. This underscores the value of transferring knowledge from a model plant to important non-model crop systems, potentially allowing design of broad-spectrum disease reduction.

Host range of *Fusarium proliferatum* isolate from canola and evaluation of the reaction of *Brassica* genotypes. H. T. YU, S. F. HWANG, R. FREDUA-AGYEMAN AND S. E. STRELKOV. *Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB T6G2P5, Canada*

Damping-off and root rot are major constraints to the production of canola (*Brassica napus*), one of the most economically important crops in Canada. The soilborne fungus *Fusarium proliferatum*, a common pathogen infecting numerous crop species and occurring in various climatic zones, is one of the main causes of these diseases. The host range of *F. proliferatum* isolate recovered from canola was evaluated on a suite of plant species under greenhouse conditions. The pathogen could infect most of the crops tested, causing the most severe symptoms on canola and several legume crops. Barley (*Hordeum vulgare*), wheat (*Triticum aestivum*) and faba bean (*Vicia faba*) were more tolerant to inoculation. To determine the occurrence and/or extent of resistance to *F. proliferatum* more extensively in canola and its relatives, the reaction of 42 *Brassica* genotypes to inoculation was assessed in two greenhouse experiments. The results indicated that the *Brassica* genotypes varied substantially with regard to their susceptibility to *F. proliferatum*. The canola cultivar '73-15RR' was the most susceptible to stand loss and root rot in the surviving plants. In contrast, the cultivars '74-47 CR', 'L150', 'L225PC' and 'Westar' were among the most resistant genotypes, as were the *Brassica rapa* European Clubroot Differential (ECD) 02 and ECD 05, and the *B. napus* genotypes ECD 06, ECD 08, ECD 09, 'Brutor', DKTF 98 CR, 'Mendel' and 'Laurentian'. These findings suggest the possibility of tolerance or resistance to *F. proliferatum* as a pathogen management strategy.

PSKR1 helps recruit *Pseudomonas fluorescens* to the plant rhizosphere microbiome. S. SONG, Z. M. MOREIRA, X. ZHANG, A. C. DIENER, AND C. H. HANEY. *(S. S., Z. M. M., C. H. H.)University of British Columbia, Vancouver, BC, CANADA; (X. Z., A. C. D.) Massachusetts General Hospital, Boston, MA*

Beneficial members of the rhizosphere microbiome provide diverse benefits to plants, including growth promotion and enhanced resistance. However, how plants recruit beneficial microbes while preventing microbial overgrowth remains largely unknown. By rescreening an Arabidopsis mutant collection with altered root immune signaling, combined with bulk segregant analysis and next-generation sequencing, we identified a *PSKR1* mutant allele *hsm7* that exhibits reduced beneficial *Pseudomonas fluorescens* WCS365 colonization in the rhizosphere. Microbiome sequencing with *pskr1-3* and the over-expression line *35S:PSKR1-GFP* suggests that plant *PSKR1* expression level correlates with the relative abundance of *Pseudomonas* in the rhizosphere without causing phylum-level microbiota dysbiosis. Through transcriptional profiling, we found that PSKR1 may balance growth and defence by suppressing salicylic acid (SA) responsive defense gene expression while promoting growth through photosynthesis and cell expansion. Further tests with SA biosynthesis and perception mutants suggest that SA signaling inhibits beneficial *P. fluorescens* colonization through both regulating plant defense and metabolism. Furthermore, we also found that *P. fluorescens* WCS365 strongly induces *PSKR1* expression in the root, as a potential strategy to manipulate plant response and benefit its colonization in the rhizosphere. Collectively, our data demonstrate that through suppressing SA-mediated defense responses and promoting root growth, PSKR1 recruits beneficial *P. fluorescens* to plant rhizosphere microbiome.

Geldanamycin and nigericin are phytotoxic microbial specialized metabolites with a potential role in mediating plant-pathogen interactions. G. A. DIAZ-CRUZ, K. TAHLAN AND D. R. D. BIGNELL. *Department of Biology, Memorial University of Newfoundland and Labrador, 45 Arctic Avenue, St. John's, NL A1C 5S7, Canada*

Phytopathogenic *Streptomyces* bacteria are responsible for several economically important crop diseases, the most notable of which is potato common scab. Most scab-causing pathogens produce the phytotoxic specialized metabolite thaxtomin A, which serves as the principal pathogenicity determinant involved in disease development. However, recent reports have described scab-causing *Streptomyces* strains that do not produce thaxtomin A, but instead they produce other phytotoxic specialized metabolites that may contribute to plant host colonization and disease development. *Streptomyces* sp. 11-1-2 is a highly pathogenic strain that was isolated from a common scab lesion on a potato tuber harvested in Newfoundland, Canada. The strain secretes one or more phytotoxic compounds of unknown identity, and it is hypothesized that these compounds serve as virulence factors for this organism. We analyzed the genome sequence of 11-1-2 and identified biosynthetic gene clusters for producing the known herbicidal compounds geldanamycin and nigericin. Phytotoxic culture extracts were analyzed by liquid chromatography-coupled tandem mass spectrometry, and this confirmed the presence of geldanamycin and nigericin in the extracts. Pure geldanamycin and nigericin exhibited phytotoxic effects against both radish

seedlings and potato tuber tissue, and the co-administration of the two compounds produced synergistic phytotoxic effects against potato tuber tissue compared to administration of each compound alone. Overall, our results suggest that the pathogenic phenotype of *Streptomyces* sp. 11-1-2 is due in part to the production of geldanamycin and nigericin, and that the secretion of these compounds may represent a novel mechanism of plant pathogenicity exhibited by some *Streptomyces* species.

Amplified disease resistance through a cell-surface immunity Ve receptor heterocomplex. N. ATABAKI, M. KALISCHUK, B. MÜLLER, D. PRÜFER AND L. KAWCHUK. *Department of Plant Agriculture, University of Guelph, 50 Stone Road E., Guelph, ON N1G 2W1, Canada; (B.M.) Fraunhofer Institute for Molecular Biology and Applied Ecology IME, Schlossplatz 8, 48143, Münster, Germany; (D.P.) Institute of Plant Biology and Biotechnology, University of Münster, Schlossplatz 8, 48143, Münster, Germany; (L.K.) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1st Ave S., Lethbridge, AB T1J 4B1, Canada*

Plants recognize and respond to hostile microbes by detecting molecular patterns within pathogen avirulence (*Avr*) effectors and induce cellular and systemic signaling. Many of these microbe-associated molecular pattern (MAMP) receptors confer innate immunity through the formation of cell-surface complexes that initiate signal transduction and attenuation. The immunity cell-surface receptors Ve1 and Ve2 in tomato varieties, provide excellent protection against fungi of the genus *Verticillium* causing early dying, a worldwide disease in many crops. To evaluate the synergistic effects of Ve1 and Ve2, we studied co-expression of these receptors on tomato plants against *Verticillium* spp. The results demonstrated that transgenic plants expressing Ve1 and Ve2 together, reduced pathogen titres by a further 90%, compared to plants expressing only Ve1 or Ve2, in a race-specific manner regardless of the promoter and expression levels. Confocal and immunoprecipitation experiments showed that the two receptors associate, forming heteromeric complexes in the absence of the ligand and positively regulate signaling and recycling. Results confirm immunologically that Ve1 and Ve2 form a complex with the receptor kinase BRASSINOSTEROID INSENSITIVE 1 ASSOCIATED KINASE 1 (BAK1) that activates signaling and confers innate immunity as observed with other pathogen-recognition receptors (PRRs) such as FLAGELLIN-SENSITIVE 2 (FLS2). Furthermore, receptors lacking the putative endocytosis signals E/DxxxLL and YxxΦ1, were incapable of undergoing ligand-induced internalization but this had no impact on the perception of MAMPs, complex formation, and signal transduction. These results reveal that immunity against devastating plant diseases may be amplified by optimizing the composition of a cell-surface receptor heterocomplex.

SESSION 5 – HOST-PATHOGEN INTERACTIONS
Moderator: Dr. Gurcharn Brar and Zhiyu (Fisher) Yu

Transcriptome profiling of tomato plants infected by potato zebra chip pathogen '*Candidatus* Liberibacter solanacearum': virulence and pathway analysis. J. CHUAN, W. CHEN, J. NIE, W.R. COOPER, L.R. HALE AND X. LI. *(J.C.; X.L.; J.N..).Canadian Food Inspection Agency, Charlottetown Laboratory, Charlottetown, PE, C1A5T1, Canada; (J.C., L.R.H.) Department of Biology, UPEI, Charlottetown, Canada; (W.C.) Agriculture and Agri-Food Canada, Ottawa Laboratory, Ottawa, Canada; (W.R.C.) United States Department of Agriculture, Agricultural Research Service, Wapato, WA 98951*

'Candidatus Liberibacter solanacearum' (CLso) is regulated in European and Asian countries for its infection in economically important Apiaceous and Solanaceous crops, primarily in potato. Twelve haplotypes of CLso have been identified based on rRNA, conserved genes, and host specificity. CLso haplotypes A and B are both lethal to potato, causing zebra chip disease, whereas some tomato (cvs Moneymaker and Roma) are susceptible to haplotype B, but exhibit asymptomatic to haplotype A. The virulence mechanisms of CLso to the host plants are not clearly illustrated, nor are the plant's response to the invasion of the phloem-limited pathogen. Using Illumina MiSeq, we sequenced transcriptomes of 27 tomato plants, including six infected by CLso haplotype B, ten by haplotype A, and 11 healthy plants. In comparison of haplotype B to A, 138 genes were over-expressed, and 331 genes were down-regulated. Interestingly, the gene expression profiles of healthy and haplotype A-infected tomato were similar. The results on transcriptomic expression of tomato plants infected by haplotype B, confirmed by qPCR assays of 50 selected functional genes in tomato plants, indicated that CLso affected tomato host's carbohydrate metabolic process, restrained photosynthesis and starch biosynthesis, and promoted starch degradation and consumption. In addition, the invasion of haplotype B suppressed the gene expression in steroid, phenylpropanoid, and flavonoid biosynthesis, hindering plant development, pigmentation, defense and signaling. In conclusion, this study provides insights into plants' reaction to CLso invasion. Understanding the underlying mechanisms can enhance disease control and create opportunities for breading resistant varieties of tomato and potato.

Eastern white pine resistance to white pine blister rust conferred by the TIR-NBS-LRR gene *PmTNL2*. J.-J. LIU, A. ZAMANY, K. PELLOW, D. NOSHAD, AND K. KLIMASZEWSKA. *Pacific Forestry Centre, 506 West Burnside Rd, Victoria, BC V8Z 1M5 Canada; (D.N.) British Columbia Ministry of Forests, Cowichan Lake Research Station, 7060 Forestry Rd, Mesachie Lake, BC V0R 2N0, Canada; (K.K.) Laurentian Forestry Centre, 1055 du P.E.P.S., P.O. Box 10380, succ. Sainte-Foy, Québec, Quebec, Canada*

Eastern white pine (EWP; *Pinus strobus* L.) and western white pine (WWP; *Pinus monticola* Dougl. ex D. Don) are two of the most important conifers of North America due to their economic and ecological values. Identification of disease resistance (R) genes, followed by functional verification, allows development of biotechnological strategies to enhance host resistance to plant pathogens and pests. This study evaluated long-term effects of overexpression of the WWP gene

PmTNL2 in transgenic EWP for resistance against the invasive fungal pathogen *Cronartium ribicola* (J.C. Fisch. ex Rabh.) that causes white pine blister rust. *PmTNL2* encoded a Toll/interleukin-1 receptor-nucleotide binding site-leucine rich repeat (TIR-NBS-LRR) protein. Transgenic EWP plant lines were generated through co-cultivation of an EWP somatic embryogenic cell line with *Agrobacterium tumefaciens*; and they showed high survival rates from repeated infections occurred over the last 8 years. It was observed that their needles well infected, and *C. ribicola* mycelia were transferred into branches and some cases into the main stems. Most cankered branches, however, died before the fungus spread down into main stems. In plants where cankers developed on the main stem, the top shoots above the canker either had died, or grown well; however, in both cases, the cankers did not spread further down along the main stem, had healed over and the plants had survived. Development of these resistance-related traits in transgenic EWP plants demonstrates that *PmTNL2* conferred EWP quantitative resistance against *C. ribicola* by causing extensive tissue death of the cankered stems to restrict fungal growth in-planta.

Screening tomato lines for potential resistance to tomato brown rugose fruit virus in Canada.
A. NOVINSCAK, R. R. BURLAKOTI, AND J. GRIFFITHS. *Agassiz Research and Development Centre, Agriculture and Agri-Food Canada, Agassiz, BC, Canada; (J.F.) London Research and Development Centre, AAFC, London, ON, Canada*

Tomato brown rugose fruit virus (ToBRFV) is a serious emerging threat to greenhouse tomato production in Canada. The disease has spread to several countries in Europe, Asia, and North America since it was first reported in Israel in 2014. The virus is transmitted through mechanical contact and infected plants and seeds. ToBRFV is a member of the *Tobamovirus* genus. Foliar symptoms of ToBRFV include chlorosis, mosaic pattern, mottling and occasional leaf narrowing. Fruit of diseased plants show yellow or brown patches and are often unmarketable and can cause severe economic losses to growers. The best option to manage ToBRFV is to identify novel sources of resistance that can prevent infection and spread of this disease. In this study, 60 tomato lines were evaluated under greenhouse conditions after mechanical inoculation with ToBRFV. Disease severity was assessed by evaluating symptoms on plant foliage and virus presence in plant tissue was confirmed by reverse transcriptase polymerase chain reaction (RT-PCR). Most lines showed typical symptoms of ToBRFV with a wide range of disease severity and all of the lines tested positive to ToBRFV using RT-PCR. However, two lines showed very few symptoms on the leaves. These two lines will be evaluated again and additional tomato lines will be evaluated as a continuous effort to identify potential sources of resistance to ToBRFV.

Genome-wide association mapping of spot blotch in elite Canadian two-row barley germplasm. J. R. TUCKER, A. D. BEATTIE, A. C. WOITAS, C. W. HIEBERT, A. BADEA, AND W. G. D. FERNANDO. *(J.R.T.; A.B.) Agriculture and Agri-Food Canada, Brandon Research and Development Centre, P.O. Box 1000A, R.R. 3, Brandon, MB R7A 5Y3, Canada; (A.D.B.; A.C.W.) Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada; (C.W.H.) Agriculture and Agri-Food Canada, Morden Research and Development Centre, 101 Rte 100 #100, Morden, MB R6M 1Y5, Canada; (J.R.T.; A.B.; W.G.D.F.) Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB R3T 2N2, Canada*

Spot blotch is a foliar disease of barley (*Hordeum vulgare* L.) caused by *Cochliobolus sativus* (anamorph: *Bipolaris sorokiniana* [Sacc.] Shoem.), which results in significant yield losses worldwide. Moreover, malting quality is degraded through reduced plumpness and discolouration of kernels (otherwise known as black point or kernel smudge). The disease is prevalent in warm and humid growing regions of the world. Traditionally spot blotch has been restricted to the eastern prairie region of Canada, however in recent years it has become more frequent in the major barley production regions of Saskatchewan and Alberta. The potential for a warmer climate, combined with virulent pathotypes recently isolated in western Canada, creates concern for sustainable production of barley. Two-row barley varieties now predominate the cultivated acres in Canada, but generally show higher susceptibility to spot blotch than six-row barley varieties. Thus, breeding barley varieties with resistance to spot blotch is an economical and environmentally-friendly disease management practice. Substantial breeding advancements have been made within two-row barley for spot blotch resistance, where significant variation in resistance now exists within contemporary Canadian germplasm. In this study, a panel of 200 elite Canadian genotypes was assayed with the Illumina 50K single-nucleotide polymorphism (SNP) chip and was evaluated in leaf disease nurseries at Brandon, MB and Melfort, SK. Genome-wide association analysis revealed a highly significant marker-trait association (MTA) on chromosome 3H (JHI-Hv50k-2016-156460, $P \leq 10^{-13}$) in addition to MTAs on other chromosomes. Such SNP markers could be applied in marker-assisted breeding to improve spot blotch resistance in barley.

Production of quorum sensing-related metabolites and phytoalexins during *Pseudomonas aeruginosa-Brassica napus* interaction. J. COOK, J. P. M. HUI, J. ZHANG, M. KEMBER, F. BERRUE, J. Z. ZHANG AND Z. CHENG. *Department of Microbiology and Immunology, Dalhousie University, 5850 College Street, Halifax, NS, B3H 0B3, Canada; (J.P.M.H.; F.B.; J.Z.Z.) Aquatic and Crop Resource Development Research Centre, National Research Council of Canada, Halifax, NS B3H 3Z1, Canada*

Pseudomonas aeruginosa is an opportunistic bacterial pathogen that has been shown to interact with many organisms throughout the kingdom of life, including plants. How this broad-host-range bacterium interacts with each of its diverse hosts, especially the metabolites that mediate these interactions, is not completely known. In this work, we used a liquid culture root infection system to collect plant and bacterial metabolites on days 1, 3 and 5 post *P. aeruginosa* strain PA14 infection of the oilseed plant, canola (*Brassica napus*). Using mass spectrometry-based

metabolomics approaches, we identified the overproduction of quorum sensing (QS)-related metabolites (both signaling molecules and regulated products) by *P. aeruginosa* while interacting with canola plants. On the other hand, the *P. aeruginosa* infection induced the production of several phytoalexins, which is a part of the hallmark plant defense response to microbes. While the induction of the phytoalexin brassilexin production was not significantly affected in any of the isogenic mutant strains of each of the three QS signaling branches in PA14, the induction of spirobrassinin was significantly decreased, indicating that the QS system only mediates part of the canola-*P. aeruginosa* metabolomic interactions. Interestingly, the treatment of purified QS molecules in the absence of bacteria was not able to induce any of the phytoalexin production, suggesting that active bacterial colonization is required for eliciting phytoalexin production. The production of phytoalexins can be an effective innate immunity of canola to keep potential infections by the opportunistic pathogen *P. aeruginosa* at bay.

SESSION 6 – DIAGNOSTICS

Moderator: Dr. Vippin Joshi and Yishan Zhang

Automated Fusarium head blight detection and total number of spikelets estimation in multispectral point clouds of wheat using 3D convolutional neural networks. O. HAMILA, C. J. HENRY, M. A. HENRIQUEZ AND C.P. BIDINOSTI. *(O.H., C.J.H, C.P.B) The University of Winnipeg, 515 Portage Avenue, Winnipeg, MB R3B 2E9, Canada; (M.A.H) Morden Research and Development Centre, Agriculture and Agri-Food Canada, Unit 101 Route 100, Morden, MB, R6M 1Y5, Canada*

Fusarium head blight (FHB) is one of the most significant diseases affecting wheat and other small grain cereals worldwide. The development of resistant varieties requires the laborious task of field and greenhouse phenotyping. The problem considered in this work is the automated detection of FHB disease symptoms expressed on a wheat plant and the automated estimation of the total number of spikelets in a wheat-head as a first step to calculate disease severity. The data used to generate the results are 3-dimensional (3D) multispectral point clouds (PC), which are 3D collections of points – each associated with a red, green, blue (RGB), and near-infrared (NIR) measurement. The PCs were used to develop convolutional neural networks (CNN) that excel in mapping complex input data to specific class labels. Using a multispectral 3D scanner, two datasets were created by acquiring 216 wheat plant and 80 wheat head PCs. The first dataset was used to develop novel and efficient 3D CNNs for FHB detection, and our best model achieved 100% accuracy. Moreover, the influence of the multispectral information on performance was evaluated, and our results showed the dominance of the RGB channels over both the NIR and the RGB and NIR channels combined. The second dataset was used to develop novel and efficient 3D CNNs for estimating total number of spikelets, and our best model achieved 1.13 mean absolute error. Our results suggest that replacing arduous tasks that require the input of experts and significant temporal resources with automated models is feasible and promising.

Advanced pre-screening of grain and oilseed using long read sequencing for bio-surveillance of phytopathogens. J. B. PEPIN, E. GIROUX AND G. J. BILODEAU. *Ottawa Laboratory Fallowfield, Canadian Food Inspection Agency, 3851 Fallowfield Road, Ottawa, ON K2H 8P9, Canada*

International agricultural trade creates a need for rapid and accurate detection of phytopathogens, as introducing non-native pathogens can result in significant negative socioeconomic impacts. Phytopathogen detection has traditionally been carried out through visual analysis which is slow and imprecise. Many fungal and bacterial pathogens produce similar disease phenotypes, and morphological analysis of pure cultures is unreliable as many phytopathogens are unculturable. Also, current molecular methods, such as using specific primers or probes, lack the ability to identify strains other than the ones intentionally targeted. Leading sequencing platforms typically combine short reads that are 600bp or less into longer fragments in order to cover gene regions, such as the 1500bp-long 16s rRNA gene for bacterial identification, or the 3.5kb to 6 kb rDNA regions for fungal identification. The MinION sequencing device developed by Oxford Nanopore Technologies (ONT) produces long reads capable of spanning entire barcoding regions and has been successfully used in bacterial and fungal community profiling. Through the use of long read sequencing, new testing methods for early pre-screening of pathogens on exports are currently in development. Methods being compared in our lab include PCR and PCR-free library preparation methods, benchmarking various bioinformatics pipelines for ONT data, and optimizing extractions from seed washes to evaluate the potential for bio-surveillance of soybean, wheat, and canola for detection of phytopathogens affecting these crops. Comparing whole genome versus amplicon sequencing to determine which will be used for pre-screening is also being evaluated.

A Novel Field kit to Detect DMI Fungicide Resistance in *Clarireedia jacksonii*. E. MCNAB AND T. HSIANG. *School of Environmental Sciences, University of Guelph, 50 Stone Road East, Guelph, ON N1G 2W1, Canada*

Dollar spot, caused by *Clarireedia jacksonii* Salgado, is one of the most common and costly diseases of turfgrasses in North America. It is typically managed with multiple applications of fungicides, such as DMIs (demethylation-inhibitors). In Canada, the first DMI fungicide to be registered on turfgrass was propiconazole in 1994. Since then, there has been a slow but detectable decline in sensitivity of *C. jacksonii* populations to propiconazole. Identification of DMI-resistant populations of *C. jacksonii* is time consuming and requires growing the isolated fungus on different concentrations of the target fungicide. For the field kit, we developed a medium containing a discriminatory fungicide concentration (0.5 µg/ml propiconazole) and antibiotics testing pure cultures and inoculated plants from a growth room. Field plots were inoculated with DMI-resistant or sensitive isolates, and over 1400 leaf blades were assessed with the discriminatory medium. Over 96% of the samples were correctly identified as sensitive or resistant based on the inoculated isolate, while 10% of the samples showed fungal growth, but were not *C. jacksonii* based on morphology. These other fungi were classified into 22 morphotypes, and representative isolates were identified by ITS sequencing as species such as *Microdochium bolleyi* de Hoog, *Mucor nidicola* Madden, and *Papiliotrema aspenensis* Ferreira. This field kit will allow end users to

assess isolates of *C. jacksonii* in the field and will be useful for saving time, money, and resources. This proof of concept can be used with other fungal pathogens to detect fungicide resistance.

Comparison of an amended agar assay vs. a microplate assay for assessing fungicide sensitivity. A. RETHER, E. MCNAB, T. HSIANG. *School of Environmental Sciences, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada*

Clarireedia jacksonii Salgado causes dollar spot disease on turfgrass, and frequent fungicide application is used to manage this disease. Reduced sensitivity to propiconazole has been detected in populations of this fungus. A microplate absorbance assay was developed and compared to a conventional amended agar assay to assess the sensitivity of *C. jacksonii* to the fungicide propiconazole. EC_{50} values (effective concentration required for 50% inhibition of growth) were calculated from both assays using 32 isolates of previously assessed sensitivity. Spores of bacteria and fungi have been used previously in microplate absorbance assays, but this fungus is not known to produce spores. A hyphal microplug inoculum was developed to seed the wells in the microplate, and absorbance was measured at 595 nm after 24 and 48 hr of incubation with eight replicate wells per fungicide concentration (0, 0.01, 0.1, 1.0, and 10 µg/ml). For the amended agar assay, radial growth was measured between 24 and 48 hr with three replications using the same range of concentrations. Data from three repeated experiments of each assay were subjected to Probit analysis to obtain EC_{50} values. Correlation analysis revealed a statistically significant relationship between results of the two assays ($p \leq 0.0001$); however, this relationship showed a low correlation ($R^2 = 0.06$). This relationship was improved by $\log_{10}$ transformation of EC_{50} values ($R^2 = 0.47$, $p \leq 0.0001$). The microplate absorbance assay cannot directly replace the amended agar assay for calculation of EC_{50} values, but future developments in the methods may allow for such use.

Xanthomonas translucens* isolation from barley seeds complicated by ubiquitous coinfection with *Pantoea spp. J. BEUTLER, T. LI, AND G. S. BRAR. *Crop Pathology and Genetics Lab, Faculty of Land and Food Systems, The University of British Columbia, 2357-214 Main Mall, Vancouver, BC V6J 2N6, Canada*

Xanthomonas translucens pv. *translucens* (Xtt) was isolated from diseased barley leaf tissue symptomatic of bacterial leaf streak during 2021 differential trials at an University of British Columbia research plot in Vancouver, British Columbia, Canada. Species and pathovar were confirmed via multiplex polymerase chain reaction (PCR) assays, Loop-Mediated Isothermal Amplification (LAMP), as well as targeted amplicon, and whole genome sequencing. Attempts to isolate Xtt from post-senescent barley seeds of infected plants was complicated by ubiquitous coinfection with morphologically similar *Pantoea ananatis* and *Pantoea agglomerans*. *In vitro* colonies of these common symbionts are challenging to distinguish from *Xanthomonas* spp. on Wilbrink's agar media, and may outcompete the bacterial pathogens. Further investigation is ongoing of *Pantoea spp.* performance on WBC selective media, as well as their independent pathogenic potential on barley.

SESSION 7 – DIAGNOSTICS

Moderator: Dr. Wen Chen and Keisha Hollman

Soil microbiome in relation to the risk of cavity spot on carrots. U. ILYAS, M. N. RAIZADA, M. KALISCHUK, L. DU TOIT, AND M. R. MCDONALD. *Department of Plant Agriculture, University of Guelph, Guelph, Ontario, N1G 2W1, Canada; (L.D.T.) Department of Plant Pathology, University of Washington State, Washington, 98195, United States*

Cavity spot is an economically devastating disease caused by several species of soil-borne *Pythium*. The disease appears as lesions on carrot roots making them unmarketable. The disease is widespread in Canada and around the world. Management recommendations are limited to avoiding problem fields and applying fungicides at seeding if the field has a history of cavity spot. However, there are no diagnostic tools to identify high-risk fields. It was hypothesized that poor soil health is related to higher risk of cavity spot and that the soil microbiome would reflect relative soil health. Six growers' fields having muck soils in the Holland Marsh, Ontario, were identified as low or high risk of cavity spot, based on disease history data from the local integrated pest management. Disease assessment of carrots at harvest confirmed the risk assessment. Cavity spot severity in the low-risk fields was 15-21% and 38-55% in the high-risk fields. A comparative metagenomic analysis showed that microbial communities were different in the soils with high and low risk of cavity spot. The relative abundance of fungi in the genera *Mortierella, Tetracladium, Penicillium*, *Fusarium,* and bacteria *Bauldia, Rhizobium* were greater in low-risk soils compared to high-risk. Furthermore, the low-risk soils had higher soil pH ~7 and soil calcium content ~7200 ppm compared to high-risk soils, pH ~6, and calcium content 3400 ppm. This information will help to assess the risk of cavity spot in the soil before seeding. Assessment of additional fields is continuing to verify these results.

Detection of grapevine virome (viruses and viroids) through Nanopore cDNA and direct RNA sequencing technology. V. J. JAVARAN, A. POURSALAVATI, P. MOFFETT, AND M. L. FALL. *Saint-Jean-sur-Richelieu Research and Development Centre, Agriculture and Agri-Food Canada, 430 Gouin Boulevard, Saint-Jean-sur-Richelieu, QC, J3B 3E6, Canada, and (V.J.J) (A.P) (P.M) Centre SÈVE, Département de biologie, Université de Sherbrooke, 2500 de l'Université Boulevard, Sherbrooke, QC, J1K 2R1, Canada*

Quebec's wine industry struggles with a lack of knowledge regarding the spread of viral diseases. A rapid, inexpensive, and user-friendly tool is needed for certification programs, diagnostics and management programs. This study investigated the feasibility of nanopore sequencing for viruse/viroid detection in grapevines by extracting total RNA and double-stranded RNA (dsRNA). Two library preparation kits, direct-RNA and direct-cDNA were used. Our results suggest that nanopore sequencing can be used to detect viruses and viroids. However, certain challenges remain to be optimized in terms of extraction, library preparation, and data analysis. Direct-cDNA sequencing from dsRNA produced the most accurate results in detecting grapevine viruses and viroids, compared to direct-RNA sequencing from total RNA. Additionally, direct-cDNA sequencing (dsRNA) generated more viral reads and its analysis was quicker than direct-RNA sequencing (total RNA). Also, the presence of host RNAs and rRNAs in direct total RNA

sequencing compromised the detection of low abundance viruses (e.g. Grapevine red globe virus). However, even after removing rRNA, direct total RNA sequencing yielded low viral read numbers. Nanopore sequencing results were validated using MiSeq, and the data were analyzed using Lazypipe and Virtool pipelines. The direct-cDNA sequencing method from dsRNA detected all viruses in the MiSeq experiment, and the number of detected viruses was higher in several samples. In contrast, direct RNA sequencing from total RNA samples was not sensitive enough to detect all the viruses from MiSeq. Therefore, nanopore sequencing is suitable for rapid detection of grapevine viruses, with the advantage of being portable.

An improved and high yielding soil eRNA extraction method to study soil microbiome using Nanopore direct RNA sequencing. A. POURSALAVATI, V. J. JAVARAN, I. LAFOREST-LAPOINTE AND M. L. FALL**.** *Saint-Jean-sur-Richelieu Research and Development Centre, Agriculture and Agri-Food Canada, 430 Gouin Boulevard, Saint-Jean-sur-Richelieu, QC, J3B 3E6, Canada; and (A.P , V.J.J and I.L.L) Centre SÈVE, Département de biologie, Université de Sherbrooke, 2500 de l'Université Boulevard, Sherbrooke, QC, J1K 2R1, Canada*

It is undeniable that soil microbiomes contribute to sustainable agriculture, plant health, and soil management. Next-generation sequencing has made it possible to study soil microbiomes with metagenomics and metatranscriptomics. However, several issues have slowed the progress of soil metatranscriptomics. For example, obtaining a product with high purity, quality, and yield with current RNA extraction protocols and commercial kits is still challenging. Contamination-free RNA must also be obtained in order to use methods including sequencing and real-time PCR. Furthermore, the cost-effectiveness of batch extraction also has to be considered when working with commercial kits. To overcome these limitations, we improved a phenol-chloroform method to extract environmental RNAs from mineral and organic soil samples using an optimized buffer and nucleic acid precipitation steps. This method allows the amount of DNA to be adjusted to obtain RNA that is almost DNA-free. We extracted high-quality and -quantity RNA from both soil types and successfully sequenced the extracted RNA using a Nanopore direct RNA sequencing kit. A total of 306.75 k reads were demultiplexed, quality controlled, and trimmed after the base-calling step. A customized bioinformatics workflow was used to classify and profile taxonomic groups such as bacteria, fungi, viruses and other single-celled protists. We conclude that this extraction protocol is suitable for sensitive molecular biology techniques such as Nanopore sequencingand can be used in common biological laboratories to obtain high-quality RNA from diverse soil types at a reasonable cost.

PolyChrome: A bioinformatics toolkit for the detection and classification of phytopathogens based on next-generation sequencing, genomics, and metagenomics. J. CHUAN, W. CHEN, L. R. HALE AND X. LI . *(J.C.; X.L.) Canadian Food Inspection Agency, Charlottetown Laboratory, Charlottetown, PE, C1A5T1, Canada; (J.C; L.R.H.) Department of Biology, UPEI, Charlottetown, Canada; (W.C.) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa, ON, Canada; (W.C.) Department of Biology, University of Ottawa, Ottawa, ON K1N 9A7, Canada*

Emerging outbreaks of plant diseases pose enormous threat to agricultural production and global food security. Early detection and identification of plant pathogens using next-generation sequencing (NGS) technology and bioinformatics analysis are important to cope with the increase of international trade. Here, we present the PolyChrome bioinformatics toolkit for the detection and identification of regulated plant diseases. The PolyChrome toolkit consists of two programs, PolyChrome Detector (PCD) and PolyChrome Classifier (PCC). The former detects the presence of specific species from metagenomic and meta-transcriptomic data and the latter focus on the classification of closely related microorganisms at species or subspecies levels. In the PCD workflow, adapters and low-quality reads of raw NGS sequences are removed using Atria, an in-house designed trimming program. Clean reads are mapped to individual genomes, and then assembled to larger contigs, which are aligned to databases with taxonomy assignment. At the end of the pipeline, the annotated contigs are filtered with statistics on identity, alignment lengths, and bit scores, and suspected contigs of pathogens are reported. In PCC platform analysis, we first built curated PCC databases of selected regulated agents, e.g. *Clavibacter*, *Liberibacter*, *Dickeya* and *Pectobacter*, containing the genome sequences, annotations and the pre-analysis results, including average nucleotide identity (ANI) values. Testing dataset goes through the similar pipeline as PCD for contig generation and are classified using ANI values. The PolyChrome with PCD and PCC pipelines have been used to detect and identify plant pathogens, and has great potential in the detection of potato wart pathogen in soil.

Identification of *Phytophthora europaea* as the species responsible for root-rot in Christmas tree productions and development of molecular tools for its detection. G. CHARRON, J. YERGEAU, G. J. BILODEAU, P. TANGUAY, C. BEAULIEU, H. VAN DER HEYDEN. *(G.C.; H.VDH.) Phytodata Inc. Research Company, 291 rue de la Coopérative, Sherrington, QC J0L 2N0, Canada; (J.Y.;C.B.) Département de Biologie, Université de Sherbrooke, 2500 boulevard de l'Université, Sherbrooke, QC J1K 2R1, Canada; (G.J.B.) Canadian Food Inspection Agency, 3851 Fallowfield Road, Nepean, ON K2J 4S1, Canada; (P.T.; J.Y.) Laurentian Forestry Centre, Canada Natural Resources, 1055 rue Du P.E.P.S., P.O. Box 10380, Québec, QC G1V 4C7, Canada*

Christmas trees are an economically and culturally important ornamental plant in North America. Among diseases affecting firs cultivated as Christmas trees, *Phytophthora* root-rot (PRR) causes millions of dollars in damage to plantations every year. With few available treatment options, early detection and prevention remain the best course of action to circumscribe outbreaks. The objectives of this project were to identify which *Phytophthora* species are responsible for PRR in the province of Québec and to develop an *in situ* molecular detection method for rapid diagnostic. Soils and roots samples from diseased and non-diseased trees were gathered from producers in

Chaudière-Appalache and Estrie regions. Two types of samples were obtained. First, *Phytophthora* cultures were isolated using the soil baiting approach. Second, we extracted total genomic DNA from soil samples and used a metagenomic approach to identify the community of *Phytophthora* species. Multi-locus sequencing of the isolated cutltures was used to identify and localize them along the *Phytophthora* phylogeny. We identified *Phytophthora europaea* (Hansen & Jung (2002)) as the potential culprit for PRR in the sampled plantations. *P. europaea* showed evident pathogenicity on both Fraser and balsam fir based on Koch postulates test. Using available molecular data, we developed a qPCR assay to detect *P. europaea* in various environmental samples based on the ITS1-5.8S-ITS2 sequence. While providing insights into the *Phytophthora* diversity of Christmas tree plantations, our study also provides a tool enabling the development of integrated management strategies granting producers better control over current outbreaks and providing insights when exploring suitable plantation areas.

***IsPRIMER*: a new *in silico* tool for predicting true coverage and off-target amplicons for metabarcoding primers.** D. RADFORD AND W. CHEN. *Biodiversity and Bioresources, Ottawa Research and Development Centre, Agriculture and Agri-Food Canada (AAFC), 960 Carling Ave., Ottawa, ON, K1A 0C6, Canada*

Metabarcoding has broad-reaching potential power for the survey of environmental community composition. Metabarcoding routinely enables thousands of taxa to be identified and relatively quantified within a single assay with comparatively low cost, by focusing on kingdom-wide conserved marker regions with discriminative nucleotide polymorphisms. Surveying a kingdom-level breadth of taxa often encourages generalizations and assumptions of conservation of primer target site. However, significant exceptions to these generalizations have been documented and demonstrated to skew apparent community composition. Hence, the first step is to ensure the selected primers have proper taxonomic coverage and specificity for the target taxa when using the metabarcoding approach. A new bioinformatics tool, named "*IsPRIMER*", was developed to evaluate *in silico* amplification of each given primer rather than pairs of primers in IUPAC code against both sense and antisense strands of reference sequences using a modified binary search tree algorithm and Perl regular expression pattern matching engine. *IsPRIMER* is more portable across operating systems and can handle large datasets by bypassing the dependency of third-party software such as BLAST and the requirement to simulate the complexity of actual amplification conditions. Evaluation of commonly used forward and reverse primers for metabarcoding of bacteria, fungi, and oomycetes, predicted marked variation in taxonomic coverage for major phyla and selected genera of interest. *IsPRIMER* and another in-house developed software, the Automated Oligonucleotide Design Pipeline (AODP), are critical tools to enable metabarcoding as a robust and reliable diagnostic method for phytopathogens.

Morphology and molecular profiling of pin nematodes (*Paratylenchus* spp.) from cultivated areas of southern Alberta, Canada. M. MUNAWAR, A. U. RAHMAN, P. CASTILLO AND D. P. YEVTUSHENKO. *Department of Biological Sciences, University of Lethbridge, 4401 University Drive W, Lethbridge, AB T1K 3M4, Canada; (P.C) Institute for Sustainable Agriculture (IAS), Spanish National Research Council (CSIC), Campus de Excelencia Internacional Agrolimentario, ceiA3, Avenida Menendez Pidal S/N, 14004 Cordoba, Spain*

The root system has equal importance in plant growth and development as aerial plant parts. Understanding existing nematode biodiversity in soil agroecosystems presents high interest to scientists and farmers because nematodes may divert nutrients from plants and use them for their development and reproduction. In our surveys of soil nematodes, we often observe high numbers of pin nematodes: *Paratylenchus* spp.. These nematodes are polyphagous parasitic species with ecto- and endoparasitic feeding behaviour. Diagnostics of pin nematodes at the species level were not addressed in previous studies. Hence, this study aimed to provide a comprehensive morphological and molecular characterization of the pin nematode species recovered from the cultivated areas of southern Alberta: *P. neoprojectus*, *P. tateae*, and *P. enigmaticus* sp. nov. Two species, *P. neoprojectus* and *P. tateae*, are new records from southern Alberta, whereas *P. enigmaticus* sp. nov is a newly discovered species. Our findings suggest that the known diversity of Canadian nemato-fauna has increased. However, more research is needed to further identify other genera and species of phytoparasitic nematodes that might occur in grasses, weeds, and wild plants present in arable lands. Because of limited knowledge of nematodes in these cultivated areas, it is difficult to accurately identify and assess the impact of nematode infestations problems. We anticipate that the results of this study may help to determine the cumulative effects of nematode infestation, fungal disease, and environmental factors on crop yields.

SESSION 8 – DISEASE CONTROL

Moderator: Dr. Lone Buchwaldt and Sherry Sun

Epidemiology and management of *Botrytis cinerea* on greenhouse cultivated cannabis (*Cannabis sativa L.*). L. BUIRS, S. LUNG AND Z. K. PUNJA. *Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada; (S.L.)Pure Sunfarms, 4431 80th Street, Delta, BC V4K 3N3, Canada*

Botrytis cinerea is a necrotrophic plant pathogen that causes bud rot on cannabis, significantly reducing yield and quality. Little is currently known about the timing of infection, impact of growing season or cannabis genotype, and disease management strategies. This study was conducted during 2020-2022 to obtain a better understanding of these factors. To establish timing of infection, a spore suspension of *B. cinerea* ($1x10^5$ spores/mL) was applied weekly to developing inflorescences of genotype 'Pink Kush' from 7 to 35 days into the flowering period. The extent of bud rot was rated in subsequent weeks. Results showed that disease developed as early as 30 days into this period; the infection level varied depending on the inoculation timing and season. The season in which *B. cinerea* naturally proliferates was identified to be July to October; this

correlated with a rise in outdoor absolute humidity. Disease levels as high as 40% were observed on susceptible genotypes. These genotypes produced large inflorescences and abundant inflorescence leaves, creating a microclimate that favored infection by spores. The impact of cultural, environmental, and biological control approaches on disease was evaluated over two July-October periods. The following significantly ($P < 0.01$) reduced bud rot development: decreased planting density from 2 to 1 plants/m^2, increased greenhouse air circulation with air mix fans, and applications of Rootshield HC (*Trichoderma harzianum*) or Regalia Maxx (*Reynoutria sachalinensis*) made weekly between 14-28 days of the flowering period. These treatments reduced percent bud rot on 'Pink Kush' by 71%, 27%, 72%, and 59%, respectively.

Evaluation of plant biostimulants for their effect on baby leaf lettuce grown in a substrate colonised with *Pythium ultimum*. J. CLEMENT, M. DELISLE-HOUDE, A. BARRADA, T. A. T. NGUYEN, M. DORAIS AND R. J. TWEDDELL. *Département de phytologie, Faculté des sciences de l'agriculture et de l'alimentation, Pavillon Paul-Comtois, Université Laval, 2425, rue de l'Agriculture, Québec, QC G1V 0A6, Canada*

Plant biostimulants are substances or microorganisms used to stimulate natural processes and enhance nutrient uptake, nutrition use efficiency, crop quality traits and/or abiotic stress tolerance regardless of their nutrient content. Recent work suggests that biostimulants could also improve plant tolerance to biotic stress, generating an increasing amount of interest from scientists, plant pathologists and agricultural sector stakeholders. The objective of the study was to evaluate a variety of plant biostimulants for their effect on the development of baby leaf lettuce (*Lactuca sativa* L. cv. Garrisson) grown in the presence of the soilborne pathogen *Pythium ultimum* Trow using either conventional or organic practices. Biostimulants were applied before seeding or at seeding to a growing medium previously inoculated with a zoospore suspension of *P. ultimum*. The results obtained show that biostimulants did not significantly ($p \leq 0.05$) influence germination rate and the percentage of healthy plants in both conventional and organic management systems. Above-ground biomass of baby leaf lettuce treated with biostimulants was not significantly different than that of untreated controls in both conventional and organic management systems. In this study, no beneficial effect of plant biostimulants was observed on the development of baby leaf lettuce grown in a substrate colonised with *P. ultimum*.

Rotation and tillage shape soil-borne oomycetes communities. A. C. GAHAGAN, D. RADFORD, M. MORRISON, E. GREGORICH, S. ARIS-BROSOU, AND W. CHEN. *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Ave., Ottawa, ON K1A 0C6, Canada; (D.R., M.M, E.G., W.C.) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Ave., Ottawa, ON K1A 0C6, Canada; (A.C.G, S.A, W.C.) Department of Biology, University of Ottawa, Ottawa, Marie-Curie Private, Ottawa, ON K1N 9A7, Canada*

The *Oomycetes* are fungus-like eukaryotic microorganisms that include devastating plant pathogens causing substantial losses in the quality and yield of important crops. To better manage soil-borne oomycetes, it is critical to understand how they respond to common agricultural

practices, such as tillage and crop rotation. We used amplicon sequencing of the Internal Transcribed Spacer 1 region (ITS1) to characterize the soil oomycetes communities over three consecutive years (2016-2018). The field experiment utilized a two-way factorial design with tillage (2 levels) and rotation (4 levels) regimes. The ITS1 metabarcodes were processed using the DADA2 pipeline, and 592 Amplicon Sequence Variants (ASV) were assigned to oomycetes based on a custom oomycete ITS1 reference database compiled from GenBank. Conventional tillage (CT) increased the community structure heterogeneity and it's diversity compared to no till (NT), especially under soybean monoculture, while the community was least diverse under NT with wheat monoculture or a corn-soybean-wheat rotation. Of the 16 genera recovered, *Globisporangium* (71.9% in abundance, 337 ASVs), *Pythium* (23.3%, 158), and *Wilsoniana* (1.1%, 11) were most abundant. Nonparametric tests of the main and interaction effects of tillage and rotation treatments showed that 36 species differed significantly in abundance between CT and NT, including *Globisporangium ultimum*, an aggressive pathogen for soybean and corn that was more abundant under CT than NT. The interaction effects of tillage and rotation on most oomycetes species accentuated the complexity of managing this important group of pathogens.

Detecting fungicide resistant isolates of *Fusarium graminearum* in the Maritimes. E. JOHNSTONE AND A. FOSTER. *Agriculture and Agri-Food Canada, Charlottetown Research and Development Centre, 440 University Avenue, Charlottetown, PE C1A 4N6, Canada*

Fusarium graminearum Schwabe (teleomorph *Gibberella zeae* (Schwein.) Petch.) is one of many *Fusarium* spp. causing Fusarium head blight (FHB) of small grain cereals in the Maritime provinces of Canada. FHB is managed through an integrated approach often including triazole fungicides to reduce quality losses and mycotoxin contamination. Continued use of these products is cause for concern in the development of fungicide resistance. The objective of this study was to determine if fungicide resistance is present in *F. graminearum* found in the Maritime provinces. *F. graminearum* isolates were collected in 2021 from wheat and barley samples from Nova Scotia (NS), New Brunswick (NB) and Prince Edward Island (PE). Isolates were grown on media control or amended with one of each commercial fungicide product including Prosaro® XTR, Miravis® Ace, Folicur® at 0.1µg mL^{-1} and Tilt® at 1.0µg mL^{-1}. Mycelial growth rate was measured and the percent reduction was calculated. Susceptibility of isolates to fungicides varied among province and treatment. Isolates collected from wheat were significantly -slower growing to Prosaro® XTR and Miravis® Ace. There was a difference in susceptibility to Prosaro® XTR by province, with isolates from NB significantly more susceptible than those collected from PE. The association between isolate phenotype and fungicide resistance will also be discussed. Fungal resistance monitoring could provide valuable information for the management of FHB in the Maritimes.

Optimization of a real-time immunoPCR assay using polyclonal antibodies for early detection of tan spot, fusarium head blight and stripe rust of wheat. I. THIRUGNANASAMBANDAM, T. VUCUREVICH, N. KAV, A. LAROCHE AND J. CHALLIS. *(I. T., N. K.)Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada; (I. T., T. V., A. L., J. C.) Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre, Lethbridge, AB, T1J 4B1, Canada*

Wheat is a staple food crop with 760 million tonnes consumed globally in 2020 out of which Canada produced 35 million tonnes. However, airborne fungal pathogens pose a serious threat to wheat growers. Tan spot (TS), caused by *Pyrenophora tritici-repentis* (Died.) Drechs, fusarium head blight (FHB), caused by *Fusarium graminearum* (Schwein) Petch, and stripe rust (SR) caused by *Puccinia striiformis* Westend. f. sp. *tritici* Erikss, are important wheat diseases that impact crop quality and yield. To mitigate these fungal diseases and minimize their damage, a detection assay to predict early infection is needed. In this study, we aim to detect these three pathogens by developing polyclonal antibody assays. These antibodies were validated and optimized against TS, FHB, and SR spores through indirect enzyme-linked immunosorbent assay (ELISA) and real-time immunoPCR (RT-iPCR) assays. The RT-iPCR sensitivity was compared to that of an indirect ELISA. RT-iPCR assay showed improved sensitivity by 25-times for TS, 5-times for FHB, and 6-times for SR spores when compared to ELISA. These results suggest that RT-iPCR quantification using specific antibodies can be a very useful tool in antigenic detection of TS, FHB and SR spores. These early detection measures could ensure sustainable yield by reducing crop losses due to the presence of airborne fungal spores of TS, FHB and SR. Future experiments will focus on quantifying TS, FHB, and SR spores in real time air samples using the validated RT-iPCR assays. Experiments to test cross-reactivity of the spores and antibodies against closely related pathogens are ongoing.

The root-lesion nematode, *Pratylenchus penetrans,* affects early growth and physiology of M.9, G.41 and G.935 apple rootstocks under field conditions. L. KING, T. FORGE, P. MUNRO, H. XU AND M. JONES. *Agriculture and Agri-Food Canada, Summerland Research and Development Centre, 4200 Hwy 97, Summerland, BC V0H 1Z0, Canada; and (M.J.) Biology Department, The University of British Columbia – Okanagan Campus, Kelowna V1V 1V7, British Columbia, Canada*

The root-lesion nematode, *Pratylenchus penetrans*, parasitizes roots of temperate fruit trees. It affects early growth of trees replanted into old orchard sites where populations have built up, and is suspected of contributing to decline complexes of mature trees. Most British Columbia, Canada apple acreage is planted with M.9 rootstock. Growers are increasingly planting Geneva-series rootstocks such as G.41 and G.935. Among these rootstocks, responses to *P.penetrans*, specifically, are poorly known. To compare the resistance and tolerance of G.41, G.935 and M.9 rootstocks ('Ambrosia' scion) to *P.penetrans*, a field microplot experiment was established in spring of 2020 at the Summerland Research and Development Centre. The experimental design is a 2 x 3 factorial combination of: *P.penetrans* inoculation (+/-) and rootstock (G.41, G.935, M.9), with 20 replicate microplots of each of the six treatment combinations arranged in a randomized

complete block design. The *P.penetrans* inoculum was 5400 *P.penetrans*/microplot or 54/L soil. In the establishment year (2020), vegetative growth parameters (TCSA, shoot growth, leaf surface area) were suppressed by *P.penetrans*. In 2021, *P.penetrans* suppressed shoot growth, tree physiological parameters (stomatal conductance, transpiration, photosynthesis, stem water potential), and root length and surface area. These findings indicate that *P.penetrans* has modest but chronic effects on growth and physiological processes relating to water relations and carbon balance, suggesting mechanisms by which *P.penetrans* may predispose trees to other stresses. In both years, trees were equally affected by *P.penetrans*, regardless of rootstock, suggesting that while these updated rootstocks may have other benefits, they are equally susceptible to *P.penetrans*.

Metalaxyl sensitivity and virulence diversity of *Phytophthora rubi* population from raspberry in British Columbia. S. SAPKOTA, R. R. BURLAKOTI, AND Z. PUNJA. *(S.S.; R.R.B.) Agassiz Research and Development Centre, Agriculture and Agri-Food Canada, Agassiz, BC V0M 1A0, Canada*; *(S.S.; Z.K.P.) Department of Biological Sciences, Simon Fraser University, Burnaby, BC V5A 1S6, Canada*

*Phytophthora rubi (*scientific authority for name *?)*is a major pathogen associated with raspberry root rot and wilting complex in British Columbia. The disease complex is the most important biotic constraint for raspberry growers. Metalaxyl is a major group of fungicides used by growers in BC to manage the disease complex; however, the sensitivity of *P. rubi* population on metalaxyl is unknown. Thirty strains of *P. rubi* collected from diverse raspberry fields in BC were evaluated *in vitro* for metalaxyl sensitivity using the radial growth method. Metalaxyl was amended to 20% clarified V8 agar to yield final concentrations of 0, 0.001, 0.01, 0.1, 1, 10 µg ml^{-1}. Each strain was tested in triplicate and experiments were repeated twice independently. Fifty percent effective concentration (EC_{50}) values and dose response curves were determined for each strain. The majority (80%) of *P. rubi* strains were sensitive to metalaxyl with mean EC_{50} values of 0.19 (range from 0.037 to 0.90). We also confirmed the pathogenicity of these strains and assessed their virulence diversity by inoculating raspberry seedlings in the greenhouse. Days to first symptom development, plant wilt progression, and root assessment were recorded. All strains (n = 24) were pathogenic, 70% of them were highly virulent and 30% were moderately virulent. Results from this study will help in developing strategies for managing fungicide resistance and exploiting host resistance in a raspberry breeding program.

SESSION 9 – DISEASE CONTROL

Moderator: Dr. Guillaume Bilodeau and Yixiao (Becky) Wang

Exploring cultured microbes of pollinated maize silks and interactions with *Fusarium graminearum* (Schwabe). M. E. H. THOMPSON, A. SHRESTHA, E. KHALAF, J. RINNE, C. SHEARER, V. LIMAY-RIOS, L. REID, M.N. RAIZADA. *Department of Plant Agriculture, University of Guelph, 50 Stone Rd E, Guelph, ON, N1G 2W1; (V. L-R.) Department of Plant Agriculture, Ridgetown Campus, University of Guelph, 120 Main St E, Ridgetown, ON, N0P 2C0; (L. R.) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON, K1A 0C6*

The female reproductive tract of plants must be exposed to the environment to receive pollen, which also makes it susceptible to toxin-forming fungi. In maize, *Fusarium graminearum* (Schwabe) (*Fg*) invades through styles, known as silks, and deposits dangerous mycotoxins in grain. The corresponding disease is called Gibberella ear rot. Naturally occurring microbes may have co-evolved in styles to protect plants from pathogens. Styles are a novel tissue for microbiome research. We found that pollinated maize silks contain diverse, culturable microbes. We cultured a library of >1000 microbes from 14 maize genotypes; half the samples had been *Fg*-treated. Three bacterial genera, *Pantoea*, *Stenotrophomonas*, and *Klebsiella*, dominated the cultured silk microbiome, constituting 46% of the community. Some bacteria had an increased presence in *Fg*-treated silk tips. The cultured microbiome followed similar patterns as parallel MiSeq 16S-metagenomics data, with *Fg*-treated silks experiencing overall diversity decline but an increase in certain remaining genera. We used MiSeq data to bioinformatically predict which bacteria may be up-regulated in response to *Fg* infection, and tested them against *Fg in-vitro*. Forty-seven unique silk-derived strains were indeed antifungal. Whole-genome mining revealed the presence of putative anti-fungal genes. Five low-risk silk-associated strains were tested in greenhouse trials against *Fg in-vivo* which included mycotoxin measurements. Innovative confocal microscopy revealed a close-up examination of microbiome-pathogen-host relationships. Overall, the silk microbiome may "respond" to, or be shaped by *Fg* infection. This exploration of the style tissue yielded a fascinating array of microbes, some of which show potential to protect our crops from mycotoxins.

Discovery and testing of pollen and silk-associated probiotic microbes from a diversity panel of maize genotypes from across the Americas to combat *Fusarium graminearum*, responsible for Gibberella ear rot (GER) in corn. A. SHRESTHA AND M. N. RAIZADA. *Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON N1G 2W1, Canada*

Gibberella Ear Rot (GER) is a globally devastating disease in corn/maize (*Zea mays* L.), caused by the fungal pathogen *Fusarium graminearum* (*Fg*). In grain, GER results in the accumulation of mycotoxins such as deoxynivalenol (DON) which are toxic to both humans and livestock. *Fg* enters corn ears via silk channels (the female reproductive tract) that, at the time of *Fg* transmission, contain elongated pollen tubes intended to transmit sperm nuclei to awaiting egg sacs. Previous studies in our lab showed that pollinated silks of some North American maize genotypes harbor beneficial microbes. Furthermore, we showed that some wild and ancient relatives of modern maize host microbes that combat *Fg.* Therefore, we hypothesized that unpollinated silks and pollen of wild and ancient maize possess probiotic microbes that suppress *Fg*. To test this, bacteria were isolated from these tissues collected from a diverse panel of maize assembled from across the Americas including wild teosintes and traditional landraces. The pollen and unpollinated silk-associated bacteria were taxonomically classified and tested for their ability to antagonize *Fg in vitro* using dual culture assays. The positive candidates were then sprayed onto silks of hybrid corn to test their ability to suppress GER *in planta* in replicated greenhouse trials. All the tested candidates resulted in significant reductions in GER disease infection, increased grain yield, and reduced DON mycotoxins in both greenhouse trials. This study shows that pollen and unpollinated silk-associated bacteria can be used as biocontrol agents to control GER in corn.

The evaluation of calcium cyanamide for clubroot management on canola. Z. YU, S. F. HWANG AND S. E. STRELKOV. *Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB, T6 G2P5*

Clubroot, caused by *Plasmodiophora brassicae,* is an important disease of cruciferous crops worldwide and threatens the production of canola (*Brassica napus*) in western Canada. Calcium cyanamide (commercialized as Perlka) has been used as a soil amendment for the control of clubroot on *Brassica* vegetables. To evaluate its efficacy for the management of clubroot of canola, Perlka was applied at rates of 0, 0.5, 1, and 2 t/ha at 7-10 days prior to planting of two canola hybrids, '45H31' (susceptible) and 'CS2000' (moderately resistant) in greenhouse and field experiments. Under greenhouse conditions, the cultivars and treatments were tested with concentrations of 1×10^5 (low) or 1×10^7 (high) *P. brassicae* resting spores g^{-1} soil. The application of Perlka at any rate from 0.5 to 2 t/ha resulted in significant reductions in clubroot severity index (DSI) relative to the untreated controls. The greatest effects were obtained with a rate of 2 t/ha, resulting in a DSI of <10% on '45H31' at the low spore concentration and on 'CS2000' at both spore concentrations. Under field conditions, reductions in DSI and increases in yield were also observed in the Perlka-treated plots over the two field seasons of the study, with the lowest ID (<10%) and highest yield obtained at 2 t/ha. The application of Perlka has potential as a useful component of an integrated strategy for the management of clubroot of canola.

Comparative analysis of phenolic compounds of Canadian barley reveals potential biomarkers related to Fusarium head blight resistance. C. WIJEKOON, A. SABRA, J. R. TUCKER AND A. BADEA. *Morden Research and Development Centre, Agriculture and Agri-Food Canada, Route 100, Unit 100-101 Morden, MB R6M 1Y5, Canada and Canadian Centre for Agri-Food Research in Health and Medicine, 351 Taché Avenue, Winnipeg, MB R2H 2A6, Canada; (J.R.T and A.B) Brandon Research and Development Centre, Agriculture and Agri-Food Canada, 2701 Grand Valley Road, P.O. Box 1000A, Brandon, MB R7A 5Y3, Canada*

Fusarium head blight (FHB) in barley (*Hordeum vulgare* L.) is the most devastating disease worldwide including Canada. This disease is primarily problematic due to deterioration in grain quality, as a result of several mycotoxins such as deoxynivalenol (DON) that are detrimental to human and animal health. Developing FHB resistant cultivars is difficult due to lack of reliable molecular markers and laborious testing. Moreover, specific biomarkers designed to distinguish the FHB resistance in barley genotypes are limited. In this study, several Canadian barley genotypes with different resistance to FHB have been grown in FHB artificially infected and adjacent, non-infected field trials with the aim of investigating their phenolic compound profile and to identify potential biomarkers for selection of barley with resistance to FHB. Grains of each variety tested were harvested and assessed for the presence of DON (infected samples) via the enzyme-linked immunosorbent assay (ELISA). High-performance liquid chromatography (HPLC) analysis was performed using both infected and non-infected samples. Quantitative analysis of bound phenolic compound revealed differences among genotypes tested in non-infected samples, but in general the resistant genotypes showed higher amounts of ρ-coumaric acid (PCA), ferulic acid, caffeic acid, catechin and vanillin compared to the susceptible ones. In addition, FHB infected samples of the most susceptible genotype showed a significant increase in the accumulation of PCA and ferulic acid suggesting the involvement of these two compounds in the resistance response against FHB.

Development of an ultra-violet control protocol for powdery mildew in greenhouse cucumber. L. MA, J. GEDAK AND D. HENDERSON. *Institute for Sustainable Horticulture, Kwantlen Polytechnic University, 12666 72 Avenue Surrey, BC V3W 2M8, Canada*

Powdery mildew caused mainly by *Sphaerotheca fuliginea* (Schlechtend.) Pollacci, is one of the most problematic fungal diseases in greenhouse-grown cucumbers (*Cucumis sativus* L.) in Canada and many other countries, which requires intensive application of fungicides for control. UV-C radiation provides an alternative control measure to decrease both fungicide input and the risk of resistance development in greenhouse-grown crops. A phase-I research project was conducted at the Institute for Sustainable Horticulture at Kwantlen Polytechnic University to examine the effect of UV-C radiation (254 nm) against cucumber powdery mildew including fungal application dose and frequency, and dark period under laboratory conditions. Experiments were conducted on detached infected and uninfected cucumber leaves that were kept alive in fertilizer water in moist sandboxes for up to 12 days. Different UV-C regimes (control, 29.4, 48.4, 58.8, and 96.8 mJ/cm^2 with weekly exposure; control, 5.15, 10.3, 15.45, 20.6 mJ/cm^2 with daily exposure; daily exposure of 30.6 mJ/cm^2 with 0, 2, and 4 hours of dark periods) were tested. Our results showed that UV-C radiation applied as low as 5.15 mJ/cm^2 daily can suppress powdery mildew. Leaves kept in

darkness for 4h following UV-C treatment had the fewest mildew lesions when treated preventatively. This study has provided valuable information for a phase-II project where UV-C treatment will be delivered by robotics in a commercial greenhouse. UV-C light promises to provide an environmentally-friendly nonchemical option to control powdery mildew in greenhouse cucumbers.

Unraveling host-microbiome interactions for root-rot disease suppression in peas. Z. MORALES MOREIRA, A. BRIGGS, D. THOMS, Y. LIU, J. CHANG, S. SONG, S. HOSSAIN, A. SRINIVAS, A. LIMAN, C. VUCUREVICH, W. ZHANG, S. CHATTERTON AND C.H. HANEY. *Dept. of Microbiology and Immunology, The University of British Columbia, Vancouver, BC, V6T 1Z4, Canada; (W.Z.) Aquatic and Crop Resource Development, National Research Council Canada, 110 Gymnasium Place, Saskatoon, SK, S7N 0W9, Canada; (C.V., S.C.) Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre, Lethbridge, AB, T1J 4B1, Canada*

Root rot diseases are a major problem for crops worldwide. Depending on the causal agent and host, crop losses can reach devastating levels that impact economies and threaten food security. Diverse plant species, including legumes, are affected by fungi and oomycete complexes causing root rot. In peas (*Pea sativum*), for example, the *Fusarium-Aphanomyces* complex causes losses each year in several countries including the largest producer in the world, Canada. Disease management strategies including chemical application, crop rotation, and the use of cultivars with partial resistance are not sufficient to reduce disease levels and yield loss. Plants species form associations with a plethora of microorganisms (the microbiome) that affect plant health and fitness. *Pseudomonas fluorescens* and related species are broadly plant-associated bacteria that are able to provide benefits to the host, including pathogen control. We are studying the potential of *Pseudomonas fluorescens* and related species to control *Aphanomyces euteiches* of pea. We have chosen to focus on the pea-*Aphanomyces* model both for its economic importance in Canada and ease of manipulation in the lab. Our goal is to identify genes and mechanisms by which *Pseudomonas* decrease pathogen growth and consequently disease severity. We are performing experiments *in vitro* and *in planta* and comparing the genomes of protective and non-protective strains to identify genes that are unique to strains able to control the pathogen. In addition, transcriptomics and metabolomics approaches will allow us to detect bacterial biocontrol genes and molecules that are specifically induced in the root and rhizosphere compartments. Our research represents an important step toward the identification of strains and mechanisms to control a wide range of important root rot pathogens in a sustainable way.

Efficacy of copper against pathogen growth and disease development on cannabis (*Cannabis sativa* L., marijuana) plants. Z. K. PUNJA, C. SCOTT, L. NI AND S. LUNG. *Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada.*

Cannabis (*Cannabis sativa* L.) grown under greenhouse conditions is affected by root rots caused by *Fusarium* and *Pythium* species, bud rots caused by *Botrytis cinerea*, *Alternaria alternata* and *Penicillium olsonii*, and powdery mildew (*Golovinomyces ambrosiae*). There are no synthetic fungicides currently registered on cannabis to manage these diseases. The objective of this study was to determine if copper sulfate pentahydrate (PT81, Ocion Water Sciences) could reduce growth of these pathogens and provide disease protection. Levels of 25, 50 and 100 ppm copper were dispensed into potato dextrose broth and inoculated with the pathogens. Mycelial growth was measured after 7 days. Significant reduction of all pathogens except *F. oxysporum* was observed at 25 ppm copper; the latter was inhibited at 150-200 ppm. Further studies showed that *P. myriotylum* was inhibited at 10 ppm. Applications of copper at 100 ppm were made weekly on cannabis plants showing symptoms of powdery mildew infection. Disease severity was significantly reduced by four applications. Applications of 100 ppm copper to cannabis inflorescences followed by inoculation with *B. cinerea* did not reduce bud rot development. Addition of 3 ppm copper to a hydroponic nutrient solution in which cannabis plants were grown and infected with *P. myriotylum* significantly reduced disease and increased plant height and root and shoot fresh weights compared to the untreated control. Levels of copper in leaf tissues were increased to >200 ppm compared to 6 ppm in control leaves. These results show that copper is effective against a number of important diseases affecting cannabis.

Evaluation of the factors influencing antifungal efficacy of Black Soldier Fly waste product against soil-borne plant pathogens. S. TAHRIRI ADABI AND D. HENDERSON.
Institute for Sustainable Horticulture, Kwantlen Polytechnic University, 12666 72 Avenue Surrey, BC V3W 2M8, Canada

Black soldier fly (BSF) larvae (*Hermetia illucens* L.) consume and decompose food and agricultural waste, producing frass – excrement which harbors a unique microbial community, chitin, and essential nutrients for plant growth and development. The objective of this study was to assess the impact of soaking time in the water, heating, and filtration on the ability of frass to suppress *Fusarium oxysporum, Rhizoctonia solani, Sclerotinia sclerotiorum, Phytophthora cinnamomi*, and *Pythium* spp. *in vitro*. Moreover, microbial communities of frass, which are responsible for plant-pathogen suppression, were evaluated. Examination of soaking frass in water from one hour to 20 days at concentrations ranging between 0.25% and 10% demonstrated that soaking the frass for 7 days at 0.5%, 0.75%, and 1% concentrations significantly suppressed plant-pathogen growth. The antifungal activity of the frass was reduced when it was heated at 121°C, 15 psi for 30 minutes, and also when it was passed through 0.1 µM filter. Heating the frass at 70°C for 30 minutes had no effect on the ability of the frass to suppress the plant pathogens. Among the beneficial bacteria identified in frass by PCR and NGS, the dominant species belong to the families Pseudomonadaceae, Bacillacea, Paenibacillaceae, Sphingobacteriaceae, and Corynebacteriaceae. The results of the current study provided a framework for improving the frass efficacy and

understanding of the frass mechanisms to suppress plant pathogens and also to generate a sustainable bioproduct that supports the IPM programs and plant growth.

SESSION 10 – DISEASE CONTROL

Moderator: José Ramón Úrbez-Torres and Jonathan Beutler

Evidence that long-term cover cropping suppresses anthracnose fruit rot (*Colletotrichum* spp.) and delays defoliation in processing tomatoes. C. L. TRUEMAN, J. C. AWREY AND L. L. VAN EERD. *Department of Plant Agriculture, University of Guelph – Ridgetown Campus, 120 Main Street East, Ridgetown, ON N0P 2C0, Canada; (J.C.A. & L.L.V.E) School of Environmental Sciences, University of Guelph – Ridgetown Campus, 120 Main Street East, Ridgetown, ON N0P 2C0, Canada*

While links between soil and plant health are implied, there are few opportunities to empirically evaluate this due to inherent differences among sites. An exception is a long-term experiment established in 2007 (repeated in 2008) in Ridgetown, ON, where 22% greater organic matter and improved soil health scores were observed when annual cover crops (CC) were grown 6 times over 8 years. This led us to hypothesize that CC-induced changes in soil health might affect bacterial spot (*Xanthomonas* spp.) and anthracnose (*Colletotrichum* spp.) development in processing tomato. Five CC treatments (no CC control, winter cereal rye, oat, radish, and radish+rye) planted after winter wheat harvest were evaluated in 2019 and 2020 (CC grown 9 times over 12 years). Fruit yields were similar or greater with CC than without. In 2019, there was greater defoliation (area under the disease progress stairs = 4370±204), percent red fruit (71.0%±5.38) and rots (1.91%±0.5) in no CC than with radish (3410, 39.1%, 0.62%, respectively, $P \leq 0.0366$), indicating earlier fruit maturity in no CC plots. Similarly, no CC had a greater incidence of red fruits with anthracnose (25.8%±2.89) compared with all CCs but rye (7.4 to 12.1%±2.89) (P=0.0029), but no effect on bacterial spot (P=0.5009). Environmental conditions in 2020 were less favourable for disease development. Defoliation was not affected by CC treatment (P=0.1254) and anthracnose incidence was low (≥90.3±1.22% healthy fruit), which may have limited the ability to detect treatment effects (P=0.2922). Long-term CCing, perhaps mediated through enhanced soil and plant health, can suppress anthracnose in processing tomato when disease intensity is high.

Biovigilance: a more inclusive approach to disease management. J. L. MacDONALD AND M. T. FRANKLIN. *Summerland Research and Development Centre, Agriculture and Agri-Food Canada, 4200 Hwy 97, Summerland, BC V0H 1Z0, Canada; (M.T.F.) Agassiz Research and Development Centre, Agriculture and Agri-Food Canada, 6947 Hwy 7, Agassiz, BC V0M 1A2, Canada*

Biovigilance is an ecosystems-based approach to understand and reduce the negative effects of climate change, pest movements and changes in behavior and disease dynamics, and new crops and farming practices on plant health. Anticipating and understanding how disease and environmental conditions will evolve allows for adapting agricultural practices to cope with

changing conditions, and results in increased agroecosystem and crop health. This approach relies on a continuum of science-based activities to ensure that mitigation strategies are efficient and do not create new problems. These steps start with awareness and build towards understanding, mitigating, and anticipating unintended consequences. Biovigilance requires a holistic, de-silo's approach in order to be successful. Fundamentally, this means monitoring and understanding the effects of invasive insects, disease, and reactionary management practices beyond our agro-ecosystems, into the broader landscape. A pilot project in British Columbia applies biovigilance principles to the establishment and management of the strawberry blossom weevil (*Anthonomus rubi*), and involves a diverse group of stakeholders to collectively address the issues surrounding it. This presentation will summarize this ongoing work and the current results of this effort, and discuss how it can be applied in a phytopathological context.

Assessment of cultivar sensitivity to potato mop-top virus induced tuber necrosis. X. NIE, M. SINGH, J. LAVOIE, V. BISHT, M. SHUKLA, A. CREELMAN AND T. MACKENZIE. *Fredericton Research and Development Centre, Agriculture and Agri-Food Canada, Fredericton, New Brunswick, Canada E3B 4Z7; (M.S. and T.M.) Agricultural Certification Services, Fredericton, New Brunswick, Canada E3B 8B7; (J.L.) New Brunswick Department of Agriculture, Aquaculture and Fisheries, Potato Development Centre, Wicklow, NB, Canada E7L 3S4; (V.B.) Manitoba Agriculture, Box 1149, #65 - 3rd Avenue NE, Carman, Manitoba, Canada R0G 0J0*

Potato mop-top virus (PMTV, genus *Pomovirus*, family *Virgaviridae*) is a soil-borne virus that causes a severe tuber disease called spraing, which is characterized by internal necrotic arcs or rings in infected potato tubers. The disease can result in significant economic losses to the potato industry when disease incidence becomes sufficiently high. Since its first discovery in North America in 2003, the virus has been reported in many potato production areas in USA and Canada. PMTV is transmitted by *Spongospora subterranea* f.sp. *subterranea* (Sss, the causal agent of powdery scab disease in potato), and infested soil is the major source leading PMTV infection in potato. Here we report the preliminary assessment of potato cultivar sensitivity to PMTV-infection and the infection-induced spraing disease by trials in a PMTV-infested field identified by our newly developed high resolution DNA melting (HRM) assay. Of 15 cultivars/clones tested in 2019, the red-skinned cultivars Dark Red Norland and Chieftain showed the highest susceptibility to PMTV-associated tuber necrosis with an occurrence of ca. 7.8% and 6.5%, respectively, followed by Kennebec (5.3%), Snowden (3.4%), Yukon Gold (2.5%), Atlantic (1.6%), Shepody (1.3%), Russet Norkotah (1.3%), Goldrush (0.9%), Lamoka (0.9%), and Russet Burbank (0%). Among the four advanced clones, F13014 showed the most susceptibilities to PMTV-associated tuber necrosis with an occurrence of 2.2%, followed by F13007 (1.3%), F13015 (0.9%) and F13049 (0.6%). A similar trend was observed from tubers of different cultivars in a trial carried out in the 2021 cropping year.

SESSION 11 – PATHOGEN BIOLOGY

Moderators: Dr. Reem Aboukhaddour and Jonathan Beutler

Comparison of root morphological traits among *Brassica* accessions. C. X. YANG, R. FREDUA-AGYEMAN, S. F. HWANG, S. E. STRELKOV AND L. Y. GORIM**.** *Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB T6G 2P5, Canada*

Brassica is an important plant genus containing many cash crops and vegetables grown worldwide. Root architectural traits can vary among *Brassica* genotypes and may influence the host response to soilborne root pathogens, the efficiency of nutrient and water uptake from the soil, as well as other important biological and ecological processes. However, comparative studies including both morphological and genetic analyses of root architecture in *Brassica* are limited. Thus, we are comparing 11 root architectural traits in a collection of 242 *Brassica* accessions including *B. napus*, *B. rapa*, *B. nigra*, *B. oleracea*, *B. juncea*, and *B. carinata*. The traits examined include root length, total root surface area, average root diameter, number of root tips, total primary root length, total lateral root length, total tertiary root length, basal link length, and the proportion/distribution of total tertiary root length, surface area and volume within seven root diameter classes (0 mm - 3.5 mm). Preliminary results indicate significant differences among *Brassica* genotypes with respect to root morphological traits and root distribution within different diameter classes. This work will serve as a foundation for understanding *Brassica* root architecture, genetic diversity and its influence on disease resistance and other biotic and abiotic stresses.

Exploring the stress response of *Ustilago maydis*: an antisense approach. M. K. LARIVIERE AND B. J. SAVILLE. *Environmental & Life Sciences Graduate Program, Trent University, DNA Building, 2140 East Bank Drive, Peterborough, ON, K9J 7B8, Canada; and (B.J.S) Forensic Science Program, Trent University, DNA Building, 2140 East Bank Drive, Peterborough, ON, K9J 7B8, Canada*

As climate variability and the global population increase, worldwide hunger continues to rise. Efforts to mitigate this require a multipronged approach, as increased crop production is still vulnerable to the impacts of plant pathogens. Fungal pathogens adapt faster to these changes in climate compared to their hosts, due in part to their short generation times and a variety of adaptive mechanisms exhibited in response to abiotic and biotic stressors. We hypothesize that RNA-mediated mechanisms enhance fungal adaptation to stress. We will present work that explores the modulation of stress response in the model fungus *Ustilago maydis* through natural antisense transcripts (NATs). In a previous study, RNA-sequencing data identified 349 NATs that are conserved among three distinct smut species. This suggested NATs have important functional roles. In this study, we analyzed 28 NATs that are complementary to genes encoding proteins with documented roles in stress response. RNA was isolated from *U. maydis* haploid cells exposed to various stressors, and mRNA/NAT transcript levels were determined through RT-PCR. That screen identified five NATs with altered transcript levels in multiple stressed environments, and those results were supported using RT-qPCR. Antisense transcript expression vectors were created and transformed into *U. maydis* haploid cells. Initial results showing the impact of antisense

expression on cell growth and structure, the levels of the complementary mRNAs, and stress response will be presented. Overall, identifying and describing RNA-mediated fungal responses to stress may provide a better understanding of emerging plant pathogens.

Unveiling clubroot candidate effector families through ColabFold-based structural genomics. M. A. JAVED and E. PÉREZ-LÓPEZ. *Département of Phytology, FSAA, Université Laval, Québec, Canada. Centre de recherche et d'innovation sur les végétaux (CRIV), Université Laval, Québec, Canada. Institute de Biologie Intégrative et des Systèmes (IBIS), Université Laval, Québec, Canada.*

Plasmodiophora brassicae is one of the most catastrophic pathogens causing clubroot disease in cruciferous crops worldwide. Although several subsets of protein effector candidates have been identified in the genomes and/or transcriptomes of *P. brassicae*, the full prediction of effectors based on conserved motifs has been very challenging for this pathogen. To date, only three *P. brassicae* effectors have been fully characterized, calling for new tools for functional gene assessment. Structural genomics has become a very important strategy to help to understand pathogens effector repertory. In this study we analyze *P. brassicae* secretome using AlphaFold2 to predict protein families based on predicted 3D fold. After analyzing 476 putative secreted proteins from *P. brassicae*, we identified many effector candidates with a predicted structure like well-known fungal effectors, and high representation of alpha helices and beta sheet structures. Our analysis highlighted new evidence for a secretome rich in proteins with DNA binding domains, pointing to the probable ability of the clubroot pathogen to reprogram the plant cell at the transcription level. Although a high portion of *P. brassicae* secretome is formed by proteins with unknown domains and functions, our analysis has allowed prediction of effector families that could help us to identify new features of this unique plant pathogen.

Exploring the functions of an RNA helicase upregulated in the *Ustilago maydis* teliospore. A.M. SETO AND B.J. SAVILLE. *Environmental and Life Sciences Graduate Program, Trent University, 1600 West Bank Drive, Peterborough, ON, K9L 0G2, Canada; and (B.J.S.) Department of Forensic Science, Trent University, 2140 East Bank Drive, DNA Building, Peterborough, ON, K9L 0G2, Canada*

Fungal spores are responsible for the spread of plant diseases. They enable dispersal and protect fungi from environmental stresses outside the plant. We used *Ustilago maydis* D.C. Corda teliospores as a model for the molecular aspects of spore germination. The components necessary for spore germination are present inside the dormant teliospore, which include mRNAs and other RNAs. We hypothesize that mRNAs are stabilized during spore dormancy through binding with complementary antisense RNAs, to form double-stranded RNAs (dsRNAs). This hypothesis requires mechanisms to stabilize RNA:RNA interactions and to unwind the mRNAs for subsequent translation. RNA helicases belong to an enzyme class capable of both these functions. We identified 46 *U. maydis* RNA helicases and detected five that have increased transcript levels in dormant teliospores, but decreased levels during germination. The helicase with the greatest transcript level increase in the teliospore is an ortholog to *Saccharomyces cerevisiae DED1*, which we have named *uded1*. As direct molecular analysis of the thick-walled teliospore is difficult, we created several *uded1* deletion and *uded1* expression mutants in haploid cells to investigate its

function. The strain construction and findings that *uded1* has a role in growth, stress response, dikaryon formation, pathogenesis, and teliospore development will be presented, along with data on the impact of *uded1* expression on dsRNA stability. The latter research supports Uded1 having both RNA clamp and RNA unwinding capabilities. Overall, determining the roles of RNA helicases provides insight into the molecular events involved in fungal disease spread through spore dormancy and germination.

Impacts of Abiotic Factors on the Fungal Communities of 'Honeycrisp' Apples in the Atlantic Maritime Ecozone. M.S. MCLAUGHLIN, S.N. YURGEL, P.A. ABBASI AND S. ALI. *(M.S.M., P.A.A., S.A.) Kentville Research and Development Centre, Agriculture & Agri-Food Canada, Kentville, Nova Scotia, B4N 1J5, Canada; (M.S.M.) Department of Plant, Food, and Environmental Sciences, Faculty of Agriculture, Dalhousie University, Truro, Nova Scotia, B2N 5E3, Canada; (S.N.Y.) USDA, ARS, Grain Legume Genetics and Physiology Research Unit, Prosser, WA, 99350, USA*

The maintenance of the plant microbiome to control pathogens is an emerging concept of disease management, and necessitates a clear understanding of these indigenous microbial communities and environmental factors that affect their diversity and compositional structure. In apple fruit, numerous biotic and abiotic factors such as management strategies, tissue type, growing season, geographical location and plant genotype can significantly influence host microbial communities. However, the relative impact of these variables is difficult to discern from the literature, as studies typically target a single variable. Additionally, due to the significant impacts of geographical location and cultivar on the microbiome, the microbiome of the most economically significant apple cultivar may vary by location. Here we discuss the fungal microbiome of the most economically significant cultivar in the Atlantic Maritime Ecozone - 'Honeycrisp', and compare the effect of management practices, geographical location (province of origin) and weather conditions on the fungal microbial communities on and in apple fruit tissues at harvest, including shifts in genera with plant-associated (symbiotic or pathogenic) lifestyles. We demonstrate that while all environmental factors significantly impacted the microbiome of apple, weather conditions are the most significant factor affecting fungal community structure and diversity of apple fruit, suggesting that future microbiome studies should take place over multiple growing years to better represent the host-microbiome of perennial crops under changing environmental conditions.

SESSION 12 – PATHOGEN BIOLOGY

Moderators: Dr. Zayda Morales Moreira and April Mahovlic

Insights into the tan spot genome and its effector genes diversity. R. GOURLIE, M. MCDONALD, M. HAFEZ, R. ORTEGA-POLO, K. E. LOW, D. W. ABBOTT, S. E. STRELKOV, F. DAAYF, R. ABOUKHADDOUR. *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1 Ave S, Lethbridge, AB T1J 4B1, Canada; (M.M) University of Birmingham, School of Biosciences, Edgbaston, Birmingham, United Kingdom; (S.E.S) University of Alberta, Faculty of Agricultural, Life, and Environmental Sciences, Edmonton, Alberta, Canada; (F.D.) University of Manitoba, Faculty of Agricultural and Food Sciences, Winnipeg, Manitoba, Canada*

Tan spot of wheat is one of the most destructive foliar wheat diseases worldwide, and is caused by the fungal pathogen *Pyrenophora tritici-repentis* (Ptr). Ptr serves as a model system for foliar necrotrophic pathogens following the inverse gene-for-gene interaction. Its genome is characterized by the presence and absence of necrotrophic effectors. In our Lab we have sequenced a global collection of Ptr isolates and followed by a comparative genome analysis. The results showed that the Ptr genome is about 39 Mb in size with extensive portion of its genes defined as accessory (56%) and about 17% defined as transposable elements. In addition to the major chromosomal rearrangements, the mobility of its effector genes as a nested transposon within a new class of large 'starship' transposon is indicative of a rapidly evolving genome. Similarly, the various and novel haplotypes detected for both *ToxA* and *ToxB* effector-encoding genes from a worldwide isolates revealed a high rate of nonsynonymous mutations, which suggests a high selection pressure driving its evolution.

Sequence analysis and structural features of the *ToxB* gene in *Pyrenophora tritici-repentis* and other ascomycete species. M. HAFEZ, M. TELFER, M. A. CARMONA, C. MOFFAT AND R. ABOUKHADDOUR. *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 1 Ave S, Lethbridge, AB T1J 4B1, Canada; (M.A.C.) Cátedra de Fitopatología, Facultad de Agronomía, Universidad de Buenos Aires, Buenos Aires, Argentina; (C.M.) Centre for Crop and Disease Management, Department of Environment and Agriculture, Curtin University, Bentley, WA, Australia*

Pyrenophora tritici-repentis is a destructive foliar pathogen of wheat worldwide, the fungus produces several necrotrophic effectors, including ToxB, which causes chlorophyll degradation and induce chlorosis on sensitive wheat genotypes. ToxB is a 6.5 KDa protein and is encoded by the multi-copy *ToxB* gene. The *ToxB* gene has several homologs, and in *P. tritici-repentis*, these homologs render the toxin inactive and therefore the development of the corresponding chlorosis is inhibited upon infection. Homologs of *ToxB* gene have been previously identified in the closely related species *Pyrenophora bromi*, the causal agent of brown leaf spot of bromegrass and in other distantly related species within Dothidiomycetes. Here, we have investigated the sequence

homology of *ToxB* in a collection of 268 *P. tritici-repentis* isolates. These isolates were obtained from various regions worldwide, and some have dated back to 1950s. The *ToxB* gene ORF and its flanking regulatory sequences were analysed to reveal the presence of nine unique haplotypes in *P. tritici-repentis*. In addition to *P. tritici-repentis* and *P. bromi*, BLASTn searches identified the presence of *ToxB* homologs in additional two species: *Pyrenophora teres* and *Pyrenophora seminiperda*. Altogether, the *ToxB* sequences were aligned and collapsed to 18 different *ToxB* haplotypes. These haplotypes were then used to generate a haplotype network to predict genetic and evolutionary relationships between these various haplotypes. Furthermore, BLASTp searches showed that the distribution of ToxB-like protein sequences extends throughout the genus *Pyrenophora* into other genera of the class Dothidiomycetes. Additionally, a BLASTp search of available fungal genomes revealed that putative ToxB protein homologs is not restricted to Dothidiomycetes, but also identified in member of another classes of the Ascomycetes (Sordariomycetes and Leotiomycetes). Finally, the evolutionary conservation of each amino acid position in ToxB protein was analysed in these three classes. Results uncovered a conserved structural features like the conserved position of four cysteine residues that form disulfide bonds and a conserved β1-β2 loop sequence which represent the proposed site of interaction with putative host targets.

Pathogenomics of Wheat Stripe Rust reveals a population shift in western Canada. S. HOLDEN, R. BAMRAH, J. HUBENSKY, G. BAKKEREN, B.D. MCCALLUM, H.R. KUTCHER, G.S. BRAR**.** *Faculty of Land and Food systems, University of British Columbia, 2357 Main Mall, Vancouver, BC, Canada, V6T 1Z4. (G.B) Agriculture and Agri Food Canada, Summerland, BC, Canada, V0H 1Z0. (B.D.M) Morden Research and Development Centre, Agriculture and Agri-Food Canada, Morden, MB, Canada, R6M 1Y5. (H.R.K) Crop Development Centre, Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada, S7N 5A8*

Despite the status of wheat stripe rust (*Puccinia striiformis* f. sp. *tritici.* Eriksson - *Pst*) in Canada as a Priority 1 Disease of wheat; one of the nation's most important agricultural products, little is known about which lineages are prevalent in different Canadian provinces, and many studies simply group the entire North American continent into a single locale. Previous work in Brar et al. (2018) used microsatellite markers to identify at least four distinct linages in Canada: PstS0 (European), PstS1 and PstS1-related (Canadian), and PstPr (Warrior).

To continue this work we sampled *Pst* from wheat fields in four provinces (BC, AB, SK, MB) in 2019, 2020, and 2021 (N=45) and performed RNAseq, race typing and MARPLE diagnostics (Radhakrishnan et al. 2019). We also evaluated WGS data from isolates collected between 2010 and 2013 (N=23), and from published *Pst* genomes and transcriptomes (N=96). We assess the suitability of the published MARPLE diagnostic protocol and alternative genomic techniques for identifying Canadian field isolates, and use the breadth of our sequencing data to place our field samples in their global context. We also identify a population shift in Canadian field isolates from 2010 to 2020, where isolates derived from Ethiopian and European populations have been outcompeted by the PstS1-related strain, now present in all sampled provinces.

This work demonstrates the benefits of modern field pathogenomics approaches for quickly identifying pathogen races from field samples, as well as underscoring the necessity for monitoring the field population of this rapidly evolving pathogen.

SESSION 13 – DISEASE/PATHOGN EPIDEMIOLOGY

Moderators: Dr. Samuel Holden and Jared Hrycan

Influences of soil organic matter and irrigation management on ring nematode population growth and its relationship with growth of sweet cherry trees. T.A. FORGE, P MUNRO, T. WATSON, M. SHARIFI, G. NEILSEN AND D.NEILSEN. *Summerland Research and Development Centre, Agriculture and Agri-Food Canada, 4200 Highway 97, Summerland, British Columbia, V0H 1Z2, Canada; and (T.W.) Department of Plant Pathology and Crop Physiology, Louisiana State University, Baton Rouge, Louisiana, USA*

The ring nematode, *Mesocriconema xenoplax* (Raski 1952) Loof and De Grisse 1989, has been found to be widespread but at variable population densities in sweet cherry orchards in the Okanagan Valley of British Columbia. Little is known of factors governing variation in *M. xenoplax* population densities or its impacts on cherry trees. In spring of 2014 a field experiment was established at the Summerland Research and Development Centre to assess interactive effects of irrigation systems (drip vs micro-sprinkler) and soil treatments (non-treated control, compost, bark mulch, compost+mulch, fumigation) on nematode populations and early growth of cherry trees planted into an old apple orchard site. *M. xenoplax* was not detected at the site prior to planting. By fall of 2021, *M. xenoplax* was present in 55% of the 60 plots with an average population density of 52 *M. xenoplax*/100 cm^3 soil. Multi-year *M. xenoplax* population data were converted to Area Under Population Curve (AUPC) by plot for further analyses. *M. xenoplax* AUPC was greater ($p = 0.016$) under drip irrigation than micro-sprinkler, and in compost treated soil than in mulched and non-treated soil ($p \leq 0.05$). Among compost treated plots there was a significant negative relationship between *M. xenoplax* AUPC and tree cross sectional area ($p = 0.006$). Our data demonstrate the development of a natural *M. xenoplax* infestation in a new cherry orchard, that irrigation and soil management can influence infestation development, and that effects of the nematode on tree growth may vary with soil management.

Decline of *Plasmodiophora brassicae* over time in response to liming or a grass cover crop in a field trial. B. D. GOSSEN, M. R. MCDONALD. *Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada and (M.R.M.) University of Guelph, 50 Stone Road East, Guelph, ON NIG 2W1, Canada*

Resting spores of the soil-borne pathogen *Plasmodiophora brassicae* Woronin, which causes clubroot of brassica crops, can persist in soil for many years. High concentrations of spores are

associated with rapid breakdown of genetic resistance to clubroot. Application of lime has been shown to reduce clubroot severity, likely by inhibiting spore germination. In contrast, perennial ryegrass (*Lolium perenne*) has been shown to reduce spore concentration under controlled conditions, possibly by stimulating spore germination. A replicated field trial was initiated in 2018 in a heavily infested commercial field near Edmonton, Alberta (deep black chernozem, pH 5.5) to assess changes in spore concentration over time in response to application of lime (target pH = 7.5, applied as standard lime, hydrated lime or mixture, incorporated by rototilling) or a ryegrass cover crop. Five soil cores per plot (15-cm depth) were collected, air-dried and spore concentration was assessed using ddPCR. The pH target as not achieved in 2018, so additional lime was applied in spring 2019. The trial was sampled each year until spring 2022. As expected, application of hydrated lime initially had a stronger impact on pH relative to standard lime, but its effect on pH dropped off more quickly over time. Resting spore concentration was highly variable throughout the study. Initial resting spore numbers averaged 1.9×10^7 spores g^{-1} soil and declined by 80% over time, but remained high enough to produce severe symptoms in a susceptible crop. The hypothesis that a grass cover crop would reduce spore concentration was not supported.

The diverse and complex mycoflora present in cannabis (*Cannabis sativa* L., marijuana) inflorescences. Z. K. PUNJA, L. NI, S. LUNG AND L. BUIRS. *Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada*

Cannabis is cultivated in greenhouses throughout Canada for the medicinal and recreational markets. Regulatory guidelines established by Health Canada require that microbial contamination by total yeasts and molds (TYM), expressed as total colony-forming units per g of dried flower, do not exceed recommended thresholds. The nature of TYM populations occurring within developing cannabis inflorescences was investigated during 2020-2022. Inflorescences of several genotypes of cannabis grown under commercial greenhouse conditions were randomly sampled at various times during plant development up until harvest time (8 weeks duration). The experiment was repeated over several cycles of plant production. The inflorescence tissues were weighed (10 g fresh weight), blended in water for 30 s, and dilution-plated onto potato dextrose agar containing 140 mg/l of streptomycin sulfate. This medium was selected after comparisons to several other nonselective agar media. Colonies of all fungi and yeasts were identified by PCR of the ITS1-5.8S-ITS2 region of rDNA. Up to 35 different species of fungi were recovered, with *Penicillium* represented by 10 species, *Fusarium* by 4 species, *Aspergillus* by 3 species and *Mucor* by 2 species. Other fungi present in inflorescences included species of *Cladosporium*, *Alternaria*, *Trichoderma* and *Botrytis*. The yeasts identified included species of *Pseudozyma*, *Rhodotorula*, *Candida* and *Meyerozyma* (*Pichia*). The population levels of TYM in inflorescences were positively influenced by several factors, including the cannabis genotype, growing season (summer vs. winter), relative humidity levels in the greenhouse, and handling procedures of the inflorescences. Drying of inflorescences after harvest negatively influenced population levels as did electron-beam irradiation.

Fungicide timing and assessment of risk factors for sclerotinia stem rot of canola. T.K. TURKINGTON, H. KLEIN-GEBBINCK, H. KUBOTA, B. TIDEMANN, G. SEMACH, C. GEDDES, S. CHATTERTON, M. HARDING, P. LOKURUGE, A. MULENGA, E. KARPPINEN, P. MOOLEKI, D. TOMASIEWICZ, G. PENG, W. MAY, R. MOHR, G. TELMOSSE, D. PAGEAU, J. FENG, E. MCBAIN, AND S.E. STRELKOV. *(T.K.T., H.K., B.T.) Lacombe Research and Development Center, Agriculture and Agri-Food Canada, Lacombe, AB T4L 1W1, Canada; (H.K.-G., G.S.) Beaverlodge Research Farm, Agriculture and Agri-Food Canada, Beaverlodge, AB T0H 0C0, Canada; (C.G., S.C.) Lethbridge Research and Development Center, Agriculture and Agri-Food Canada, Lethbridge, AB T1J 4B1, Canada; (M.H.) Alberta Agriculture and Forestry, Crop Diversification Centre South, Brooks, AB T1R 1E6, Canada; (P.L., A.M., retired) Scott Research Farm, Agriculture and Agri-Food Canada, Scott, SK S0K 4A0, Canada; (E.K., P.M., D.T., retired) Canada-Saskatchewan Irrigation Diversification Centre, Agriculture and Agri-Food Canada, Outlook, SK S0L 2N0, Canada; (G.P.) Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, Saskatoon, SK S7N 0X2, Canada; (W.M..) Indian Head Research Farm, Agriculture and Agri-Food Canada, Indian Head, SK S0G 2K0, Canada; (R.M.) Brandon Research and Development Center, Agriculture and Agri-Food Canada, Brandon, MB R7A 5Y3, Canada; (G.T., D.P., retired) Normandin Experimental Farm, Agriculture and Agri-Food Canada, Normandin, QC G8M 4K3, Canada; (J.F.) Alberta Agriculture and Forestry, Crop Diversification Centre North, Edmonton, AB T5Y 6H3, Canada; and (E.B., S.E.S) Department of Agricultural, Food and Nutritional Science, 410 Agriculture/Forestry Center, University of Alberta, Edmonton, AB T6G 2P5, Canada*

Fungicide decisions can be challenging when trying to manage sclerotinia stem rot (SSR) of canola (caused by *Sclerotinia sclerotiorum*). The objective of this work was to assess fungicide timings in relation to growth stage, weather and inoculum load. An experiment was conducted in 2019 and 2021 at 10 locations across Canada and included two seeding rates (60 and 120 seeds m^{-2}) and nine fungicide timings arranged in a four-replicate factorial design. Applications included a check and single or dual fungicide applications (prothioconazole) starting at the yellow bud (YB) stage and then 1-4 weeks after YB. Rainfall, and in-canopy and ambient temperature and relative humidity were monitored along with assessment of aerial inoculum load. Weather conditions and reduced inoculum load at most sites limited SSR, except Beaverlodge, AB and Outlook, SK in 2019. The greatest reduction in SSR at Beaverlodge tended to occur for the single fungicide application three weeks after YB and the dual application at YB and again three weeks later. At Outlook, the one week after YB tended to have the lowest SSR. No yield data were available at Beaverlodge due to an early onset of winter and subsequent deer damage, while at Outlook no yield differences occurred, likely due to low SSR levels (<4% incidence in the check treatments). Dry conditions in 2021 precluded SSR development and yield differences due to fungicide timing. Preliminary results suggest optimal fungicide timing for SSR will vary based on growth stage, weather conditions, and inoculum loads prior to and during flowering.

Towards improved surveillance of aerial plant pathogens using nanopore sequencing technology. H. VAN DER HEYDEN, G. J. BILODEAU, M.O. DUCEPPE, J. B. CHARRON AND O. CARISSE. *Compagnie de recherche Phytodata Inc., Sherrington, QC J0L2N0, Canada; Department of Plant Science, McGill University, Macdonald Campus, 21,111 Lakeshore Road, Ste-Anne-de-Bellevue, Quebec, Canada, H9X 3V9; (G.J.B. AND J.B.C.) Canadian Food Inspection Agency, 3851 Fallowfield Road, Ottawa, ON, Canada, K2H 8P9; (O.C.) Agriculture and Agri-Food Canada, 430 Gouin, St-Jean-sur-Richelieu, Qc, Canada, J3B 3E6*

Internal (e.g., agricultural practices) and external (e.g., agricultural systems) pressures influence the composition of aerobiota and the dynamics of plant pathogens. Thus, predicting plant disease risk is becoming more and more complex. Monitoring of airborne pathogens by spore collector has been proven in the last decades, and the development of molecular quantitative tools has contributed to the deployment of large-scale monitoring networks that provide very accurate information at the landscape scale. However, our ability to be rapidly informed about the occurrence of specific species or genotypes is now critical to perform active and efficient biosurveillance. As a first step towards improved biosurveillance, we used Nanopore sequencing technology to study the aerobiota at the landscape scale. We took advantage of spore sampling networks in place among onion growers in southern Quebec. Samples from six samplers were collected three times per week from June 1 to August 20. Following total DNA extraction using a Chelex-based protocol, the ITS region (a ~700 bp and/or a ~3.5kb fragment) and cytochrome oxidase (COI) regions were amplified by PCR. Sequencing of the amplicons was performed on R10.4 flowcells using Q20+ chemistry. The data analysis was performed with Kraken2 and the Unite database supplemented with a custom database. This approach allowed us to detect the main onion diseases (e.g., *Stemphylium vesicarium*, *Botrytis* spp. *Peronospora destructor*) and various pathogens of neighbouring crops (e.g., *Peronospora manshurica* or *P. camelinae*). Moreover, it was possible to describe their relative abundance and patterns of diversity over time.

Implications of crop rotation and fungicide on the *Fusarium* and mycotoxin spectra in Manitoba barley 2017-2019. M.N. ISLAM, M. BANIK, S. SURA, J. TUCKER AND X. WANG. *(M.N. I., M. B., S. S., and X. W.) Agriculture and Agri-Food Canada (AAFC), Morden Research and Development Centre, 101 Route 100, Morden, MB R6M 1Y5, Canada; (J. K.) Agriculture and Agri-Food Canada (AAFC), Brandon Research and Development Centre, 2701 Grand Valley Road, P. O. Box 1000A, Brandon, MB R7A 5Y3, Canada*

Fusarium head blight (FHB) is one of the most important diseases on barley in Manitoba. Little is known about the *Fusarium* species and mycotoxin spectra associated with FHB of barley in this region. Hence, barley grain samples were collected from 149 commercial fields from 2017 to 2019, along with information on respective cropping history, and analyzed with respect to *Fusarium* species spectra, abundance, chemotype composition, and mycotoxin profiles. The results show *Fusarium poae* is the predominant Fusarium species associated with FHB of barley in Manitoba, followed by *F. graminearum* and *F. sporotrichioides*; *F. equiseti* and *F. avenaceum* were also detected but only at low levels. *F. poae* strains with the NIV chemotype and *F. graminearum* strains with 3-ADON and 15-ADON chemotypes were commonly detected in the barley grain samples. Nivalenol (NIV) and deoxynivalenol (DON) were the two most important mycotoxins contaminating Manitoba barley. A substantially higher DON content was detected in grain samples

from barley fields with cereals, compared to canola and flax, as the previous crop. Furthermore, *F. poae* proved less sensitive to four triazole fungicides (Caramba, Prosaro, Folicur, and Proline) than *F. graminearum*. Results from the current study can assist Manitoba barley producers in better understanding FHB threat levels and optimizing practices for the management of barley FHB.