CPS-QSPP joint meeting • Réunion conjointe **SCP-SPPQ**

The future of pesticides and the 'omics' era: will plant pathogens have the last word?

L'avenir des pesticides et l'ère des 'omiques": les agents pathogènes auront-ils le dernier mot ?

Hotel Delta Québec, Québec
June 17 to June 20, 2018 • 17 au 20 juin 2018

THE CANADIAN PHYTOPATHOLOGICAL SOCIETY
LA SOCIÉTÉ CANADIENNE DE PHYTOPATHOLOGIE

Société de protection des plantes du Québec
Quebec Society for the Protection of Plants

The Organizers of the 2018 Annual Meeting of the Canadian Phytopathological Society and the Quebec Society for Plant Protection acknowledge the generous support of the following sponsors!

Les organisateurs de la Réunion conjointe de la Société Canadienne de Phytopathologie et de la Société de Protection des Plantes du Québec 2018 tiennent à remercier le soutien généreux de nos commanditaires!

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Abstract/résumés	Mamadou Lamine Fall and Odile Carisse
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CPS-QSPP joint meeting
Hotel Delta Québec, Québec June 17 to June 20, 2018.

Réunion conjointe SCP-SPPQ
Hôtel Delta Québec, Québec, 17 au 20 juin, 2018.

The future of pesticides and the Omics era: will plant pathogens have the last word?

L'avenir des pesticides et l'ère des 'omiques': les agents pathogènes auront-ils le dernier mot ?

Program / Programme

Preconference meeting: Saturday June 16, 2018 / Réunion pré-conférence: Samedi 16 juin 2018

18:00-22:00 CPS-Financial advisory meeting (FAC) / SCP-comité consultatif finance-(CAF) ROOM/SALLE BUADE

Day 1: Sunday June 17, 2018 / Jour 1: Dimanche 17 juin 2018

08:00-13:00 CPS Outgoing board meeting / CA sortant de la SCP
ROOM/SALLE BUADE

13:00-19:00 ►Registration desk open / Table d'inscription ouverte
Poster setup/ Installation des affiches
ROOM/SALLE DU QUESNE

13:00-15:30 Workshop on pathogen identification: Accurate identification of plant pathogens using? high-throughput sequencing (HTS) data. / Atelier sur l'identification des pathogènes: Identification précise des agents phytopathogènes à partir des données de séquençage à haut débit (en anglais). ROOM/SALLE CREMAZIEGARNEAU

Sponsored by /commandité par: Phytodata Inc. and BioWorks Inc..
Instructor: Dr. Wen Chen, Agriculture and Agri-Food Canada Ottawa R&D Center and
Dr. Manuel Zahariev, Skwez Technology Corp.

Topics: Metabarcoding and metagenomics overview (Dr. Wen Chen); Tutorials on generic data processing pipelines (Dr. Wen chen); Automated oligonucleotide design pipeline for pathogen detection from metabarcodes (Drs. Manuel Zahariev, Wen Chen).

16:00-18:00 Workshop on scientific communication / Atelier de communication scientifique (en anglais). ROOM/SALLE CREMAZIEGARNEAU

Sponsored by /commandité par: CENTRE SÈVE

Instructor: Dr. Olivia Wilkins, McGill University, Québec, Canada and Kavli Foundation Scientist-Writer Fellow.
'The best scientists don't just write technical papers for their immediate colleagues; they reach colleagues in other fields and communicate the joy of discovery to the larger public' (Kavli Scientist-Writer Workshops).

18:30- 21:00 Opening reception / Réception de bienvenue
ROOM/SALLE WOLFE-MONTCALM

Day 2: Monday June 18, 2018 / Jour 2: Lundi 18 juin 2018

7:30-12:00 ►Registration desk open / Table d'inscription ouverte
Poster setup/ Installation des affiches
ROOM/SALLE DUQUESNE

08:00-08:15 Opening remarks by / Allocution d'ouverture par **Hervé Van Der Heyden (QSPP) and Odile Carisse (CPS)** ROOM/SALLE JONQUIÈRE-LAUZON

08:15-10:30 Symposium I: Bridging plant disease management and 'Omics' technologies.
ROOM/SALLE JONQUIÈRE-LAUZON

Sponsored by /commandité par: the CENTRE SÈVE

08:15-08:30 Opening remarks by / Allocution d'ouverture par **Mamadou L. Fall**, Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu, Quebec, Canada.

08:30-09:00 **(SI-1)** Systems approaches for resilient crop development. **Olivia Wilkins,** McGill University, Quebec, Canada.

09:00-09:30 **(SI-2)** RKS1, a starting point to decipher the gene regulatory network controlling quantitative disease resistance against *Xanthomonas campestris* - an example for systems biology perspectives. **Dominique Roby,** CNRS/INRA, Toulouse, France.

09:30-10:00 **(SI-3)** 'Omic Analyses of Fungal Plant Pathogens: Discovery to Application. **Dr. Barry Saville**, Trent University, Ontario, Canada

10:00-10:30 Open discussion**, Chairs: Barry Saville**, Trent University, Ontario, Canada and **Mamadou L. Fall**, Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu, Quebec, Canada

10:30-11:00: Health break / Pause santé
Sponsored by /commandité par: Western Grains Research Foundation and Corteva Agriscience TM, Agriculture Division Semences Prograin Inc.

11:00-12:30 Contributed session 1 Epidemiology I (Student competition)
ROOM/SALLE JONQUIÈRE-LAUZON
Chairs: Syama Chatterton, Agriculture and Agri-Food Canada and Romaric Armel Mouafo Tchinda, Sherbrooke University, Québec, Canada

CS1-1. Effet de la température sur l'éclosion des sporanges et l'agressivité des deux *formae specialis* de *Plasmopara viticola (P.v. riparia* et *P.v. aestivalis)* responsable du mildiou de la vigne dans l'Est du Canada. R.A. MOUAFO TCHINDA, C. BEAULIEU, M.L. FALL. AND O. CARISSE. (RAMT, CB) *Centre SEVE, Département de biologie, Université de Sherbrooke, 2500 Boulevard de l'Université, Sherbrooke, Quebec, J1K 2R1, Canada;* (MLF, OC) *Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu Research and Development Centre, 430 Gouin Boulevard, Saint-Jean-sur-Richelieu, QC, J3B 3E6, Canada.*

CS1-2. Impact of *Brassica napus-Leptosphaeria maculans* interaction in the emergence of virulent isolates of *L. maculans*, the causal agent of blackleg disease in canola. M. H. RASHID, S. LIBAN, X. ZHANG, P. PARKS, Z. ZOU, H. BORHAN, AND W.G. D. FERNANDO. *Department of Plant Science, University of Manitoba, MB, R3T 2N2, Canada; (H.B) AAFC, Saskatoon Research Centre, SK, S7N 0X2, Canada.*

CS1-3. Interaction between soybean cyst nematode (*Heterodera glycines*) and Phytophthora root rot (*Phytophthora sojae*) on soybean. C. AUDETTE, R.R. BÉLANGER AND B. MIMEE. *(C.A.)(B.M.) Saint-Jean-sur-Richelieu Research and Development Centre, Agriculture and Agri-Food Canada, 430 boulevard Gouin, Saint-Jean-sur-Richelieu, QC, J3B 3E6, Canada; (C.A.) (R.R.B.) Département de phytologie, Faculté des Sciences de l'Agriculture et de l'Alimentation, Université Laval, Québec, QC, G1V 0A6, Canada.*

CS1-4. Survival and detection of *Colletotrichum* species on celery and common weeds species. S. REYNOLDS, M. J. CELETTI, K. S. JORDAN AND M. R. MCDONALD. *Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1, Canada; (M.J.C.) Ontario Ministry of Agriculture, Food and Rural Affairs, Guelph, ON, N1G 4Y2, Canada.*

CS1-5. Identification of critical time-points of *Colletotrichum lentis* infection on lentil for transcriptomic studies. P. BAWA, J. HALLIDAY, C. CHO, V. BHADAURIA, K. BETT, A. VANDENBERG, S. BANNIZA. *Department of Plant Sciences/ Crop Development Centre, 51 Campus Drive, University of Saskatchewan, Saskatoon, SK, S7N 5A8, Canada; (V.B.) AAFC, Swift Current Research and Development Centre, 1030, Swift Current, SK, S9H 3X2, Canada.*

12:30-13:30 Lunch (included) / déjeuner (inclus)

Sponsored by /commandité par: Thermo Fisher Scientific and OMEX Agriculture Inc.
ROOM/SALLE WOLFE-MONTCALM

13:30-15:15 Contributed session 2: Omics, genomic and transcriptomic (regular and student competition)
ROOM/SALLE JONQUIÈRE-LAUZON
Chairs: David Joly, Moncton University and Lauriane Giroux, Sherbrooke University

CS2-1. Battling biology – Overcoming challenges with spore germination. A.M. SETO, M.E. DONALDSON, B.J. SAVILLE. *Environmental and Life Sciences Graduate Program, Trent University, 1600 West Bank Drive, Peterborough, ON, K9L 0G2, Canada; (B.J.S.) Forensic Science Program, Trent University, 2140 East Bank Drive, DNA Building, Peterborough, ON, K9L 0G2, Canada.*

CS2-2. CRISPR/Cas9 gene editing of the Dutch elm disease pathogen *Ophiostoma novo-ulmi.* P. TANGUAY. *Natural Resources, Canadian Forest Service, Laurentian Forestry Centre, 1055 rue du PEPS, P.O. 10380 Ste-Foy stn., Quebec, QC, G1V 4C7, Canada.*

CS2-3. Gene flow as a character in polyphasic classification of phytopathogenic fungi: a case study in wheat leaf rust species complex. M. LIU, S. HAMBLETON, Y. ANIKSTER, AND J. KOLMER. *Biodiversity and Bioresources, Ottawa Research and Development Centre (ORDC), Agriculture and Agri-Food Canada, 960 Carling Ave. Ottawa. ON K1A 0C6, Canada; Institute for Cereal Crops Improvement, George S. Wise Faculty of Life Science, Tel Aviv University, Tel Aviv 69978, Israel; and U. S. Department of Agriculture (USDA), Cereal Disease laboratory, 1551 Lindig Street, St. Paul, MN 55108, U. S. A.*

CS2-4. Molecular Management of Fungal Phytopathogens via RNAi. N. WYTINCK, A. G. MCLOUGHLIN, J. C. WAN, K. T. BIGGAR, M. F. BELMONTE, AND S. WHYARD *Department of Biological Sciences, 50 Sifton Road, University of Manitoba, MB, R3T 2N2, Canada.*

CS2-5. Transcriptomic analysis of *Brassica napus*- *Leptosphaeria maculans* pathosystem by dual RNA-seq using a single-*R*-gene cultivar and a single-*Avr*-gene isolate. K. R. E. PADMATHILAKE, H. SONAH, Z. ZOU, J.R. TUCKER, A, CARTER, R.R. BELANGER AND W.G. DILANTHA FERNANDO. *Department of Plant Science, University of Manitoba, Winnipeg, MB, R3T2N2, Canada; (H.S. and R.R.B.) Department of Plant Science, Laval University, Québec, G1V0A6, Canada; and (A.C.) Brandon Research and Development Centre, Agriculture and Agri-Food Canada, Brandon, MB, R7A5Y3, Canada.*

CS2-6. Tissue specific RNA sequencing of *Brassica napus* in response to *Sclerotinia sclerotiorum* infection. P.L. WALKER, I.J. GIRARD, M.G. BECKER, S. SAIKIA, T.R. de KIEVET, W.G.D. FERNANDO, M.F. BELMONTE. *Department of Biological Sciences, University of Manitoba, 50 Sifton Road, Winnipeg, MB, R3T 2N2, Canada; (S.S, T. de K.) Department of Microbiology, 213 Buller Building, University of Manitoba, MB R3T 2N2, Canada; (W. G. D. F.) Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB, R3T 2N2, Canada.*

CS2-7. Proteome analysis of *Streptomyces scabies* grown in the presence of potato tuber. L. GIROUX, I. ISAYENKA, N. BEAUDOIN AND C. BEAULIEU**.** *Centre SÈVE, Département de biologie, Faculté des sciences, Université de Sherbrooke, Sherbrooke, QC, J1K 2R1, Canada.*

15:15-15:30 Health break / Pause santé
Sponsored by /commandité par: Cargill and Semences Prograin Inc.

15:30-17:15 Contributed session 3: Disease management I (Student competition)
ROOM/SALLE JONQUIÈRE-LAUZON
Chairs: Khalid Youssef Rashid, Agriculture and Agri-Food Canada and Adele Bunbury-Blanchette, Acadia University

CS3-1. Efficacy testing of low risk products for the control of dollar spot (*Sclerotinia homoeocarpa*). K. STONE AND T. HSIANG. *Environmental Sciences, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada.*

CS3-2. Evaluation of lime products as a clubroot management tool in canola. N.M. FOX, S.F. HWANG, V.P. MANOLII, G. TURNBULL, AND S.E. STRELKOV. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada; and (S.F.H., G.T) Crop Diversification Centre North, Alberta Agriculture and Forestry, Edmonton, AB, T5Y 6H3, Canada.*

CS3-3. Evaluating the potential of arbuscular mycorrhizae to manage carrot leaf blight
U. ILYAS, M. N. RAIZADA, L. DU TOIT, AND M. R. MCDONALD. *Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W, Canada; (U.I., M.N.R., M.R.M.) and (Department of Plant Pathology, University of Washington State, Washington, WA, 98273-4768 USA, (L.T.).*

CS3-4. An investigation of Fusarium basal rot of onion and candidate biocontrol agents in the Annapolis Valley, Nova Scotia. A. L. BUNBURY-BLANCHETTE AND A. K. WALKER**.** *Acadia University, Department of Biology, 33 Westwood Avenue, Wolfville, NS, B4P 2R6, Canada.*

CS3-5. Identification of non-host crops for the management of stem and bulb nematode (*Ditylenchus dipsaci*) in garlic (*Allium sativum*). L. IVES, M. J. CELETTI, K. JORDAN AND M. R. MCDONALD. *Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada; and (M.J.C.) Ontario Ministry of Agriculture, Food and Rural Affairs (OMAFRA), University of Guelph, Guelph, ON, N1G 2W1, Canada.*

17:15-18:30 POSTERS /AFFICHES
ROOM/SALLE DUQUESNE

18:00-19:00 QSPP Outgoing board meeting/SPPQ conseil d'administration sortant

19:00-21:00 CPS President Reception (by invitation only) / Réception du président de la SCP (sur invitation seulement)
ROOM/SALLE FOYER

19:00 Evening Graduate Student Social / Soirée étudiante

Day 3: Tuesday June 19, 2018 / Jour 3: Mardi 19 juin 2018

8:00-10:00 ►Registration desk open / Table d'inscription ouverte

08:15-10:30 Symposium II: The future of pesticides in globally and locally changing agricultural environments. ROOM/SALLE JONQUIÈRE-LAUZON

08:15-08:30 Opening remarks by **Odile Carisse**, Agriculture and Agri-Food Canada.

08:30-09:00 **(SII-1)** The future of plant disease management: environmental, biological, economic, and social constraints. **George Sundin,** Michigan State University, U.S.A.

09:00-09:30 **(SII-2)** The future of biopesticides in crop protection. **Sue Boyetchko,** Agriculture and Agri-Food Canada.

09:30-10:00 **(SII-3)** Combining technologies, new and old, to reduce pesticide use. **Mary Ruth McDonald**, University of Guelph, **Bruce D. Gossen** Agriculture and Agri-Food Canada.

10:00-10:30 Open discussion.

10:30-11:00 Health break / Pause santé

Sponsored by /commandité par: Novozymes BioAg Limited

11:00-12:30 Contributed session 4 Genetics and resistance I
ROOM/SALLE JONQUIÈRE-LAUZON
Chairs: Guillaume Bilodeau, Canadian Food Inspection Agency and Valérie Gravel, McGill University.

CS4-1. Contrasting aboveground and belowground responses to PAMP-triggered immunity
A. LACAZE, A. CULL AND D. L. JOLY. *Université de Moncton, 18 avenue Antonine-Maillet, Moncton, NB, E1A 3E9, Canada.*

CS4-2. Compartmentalization barriers in trees: some reflections on possible routes exploited by pathogens to overcome these defensive tissues. D. RIOUX and M. BLAIS. *Natural Resources Canada, Canadian Forest Service, Laurentian Forestry Centre, 1055 du P.E.P.S., P.O. Box 10380, Stn. Sainte-Foy, Québec, QC, G1V 4C7, Canada.*

CS4-3. Integrated genomics, plant pathology and breeding research for improvement of Fusarium head blight, leaf rust and stripe rust resistance in Canadian cereals. M.A. HENRIQUEZ, G. HUMPHREYS, B.D. MCCALLUM, H.S. RANDHAWA, T. FETCH, J.M. FETCH, X. WANG, M.F. BELMONTE, C.A. MCCARNTNEY, M. KANG-CHOI
(M.A.H, B.D.M., C.A.M., X.W., T.F) Morden Research and Development Centre, Agriculture and Agri-Food Canada, Unit 101 Route 100, Morden, MB, R6M 1Y5, Canada; (G.H., M.KC) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Ave, Ottawa, ON, K1A 0C6, Canada; (H.S.R.) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 – 1st Avenue South, PO Box 3000, Lethbridge, AB, T1J 4B1, Canada; (J.M.F.) Brandon Research and Development Centre, Agriculture and Agri-Food Canada, , 2701 Grand Valley Road, Brandon, MB, R7A 5Y3, Canada; (M.F.B.) Department of Biological Sciences, University of Manitoba, 50 Sifton Road, Winnipeg, MB, R3T 2N2, Canada.

CS4-4. Ethylene-mediated resistance to fusarium head blight of wheat. N.A. FOROUD, R.K. GOYAL, D. RYABOVA, A. ERANTHODI, D. GONZÁLEZ-PEÑA FUNDORA, Y. PAN, R. PORDEL, I. KOVALCHUK AND S. CHATTERTON. *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, T1J 4B1, Canada; Information and Communications Technologies, National Research Council of Canada, Ottawa, ON, K1A 0R6 Canada (Y.P.); Department of Biological Sciences, University of Lethbridge, Lethbridge, AB, T1K 3M4, Canada (I.K.).*

CS4-5. Adoption of major-gene resistance groups for managing blackleg (*Leptosphaeria maculans*) of canola in Canada. J. E. J. CORNELSEN, C. JURKE AND C. REMPEL. *Canola Council of Canada, 400-167 Lombard Avenue, Winnipeg, MB, R3B 0T6, Canada.*

12:30-13:30 Lunch (included)-presentation of the video competition / déjeuner (inclus)-présentation des vidéos étudiants.

ROOM/SALLE WOLFE-MONTCALM

13:30-16:30 Special session on soybean diseases.
ROOM/SALLE JONQUIÈRE-LAUZON

Sponsored by /commandité par: SOYAGEN

Chair Dr. Richard Bélanger, Université de Laval, Québec, Canada

13:30-14:00 **(SS-1)** "Soybean Diseases – An Eye Towards the Future**"/** "Les maladies du soja - Un regard vers l'avenir", **Daren Mueller,** Iowa State University.

14:00-14:30 **(SS-2)** "Genotypic and phenotypic diversity of *Phytophthora sojae* isolates in Canadian soybean fields"/ "Diversité génotypique et phénotypique des isolats de *Phytophthora sojae* dans les champs de soja canadiens", **Richard Bélanger**, Université Laval.

14:30-15:00 **(SS-3)** "Soybean cyst nematode: genomics applied to biovigilance"/ "Nématode à kyste du soya: la génomique au service de la biovigilance" **Benjamin Mimee**, Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu.

15:00-15:30 **(SS-4)** "Soybean Sudden Death Syndrome: Know the enemy"/ "Syndrome de la mort subite du soja: Connaître l'ennemi", **Owen Wally**, Agriculture and Agri-Food Canada, Harrow, ON.

15:30-15:45 Health Break / Pause santé.
Sponsored by /commandité par: NUTRIEN

15:45-17:30 Contributed session 5: Genetics and resistance II (Student competition)
ROOM/SALLE JONQUIÈRE-LAUZON
Chairs: Benjamin Mimee, Agriculture and Agri-Food Canada and Vincent-Thomas St-Amour, Université Laval.

CS5-1. The Cross-Kingdom Biosynthesis and Signaling of Cytokinins during the Formation of Tumors in the *Ustilago maydis-Zea mays* Pathosystem I. O. ALIMI, R. J. N. EMERY and B. J. SAVILLE. *Environmental and Life Sciences Graduate Program, Trent University, 1600 West Bank Drive, Peterborough, ON, K9J 0G2, Canada; (R.J.N.E.) Biology Department, Trent University, 1600 West Bank Drive, Peterborough, ON, K9J 0G2, Canada; and (B.J.S.) Forensic Science Program, Trent University, 1600 West Bank Drive, Peterborough, ON, K9J 0G2, Canada.*

CS5-2. QTL mapping of PI 494182, a new source of resistance to soybean cyst nematode.
V. T. ST-AMOUR, F. BELZILE, B. MIMEE AND L. S. O'DONOUGHUE. *Département de phytologie and Institut de Biologie Intégrative et des Systèmes, Université Laval, 1030 avenue de la Médecine, Québec, QC, G1V 0A6, Canada; (L.O.) Le Centre de recherche sur les grains (CÉROM), 740 chemin Trudeau, Saint-Mathieu-de-Beloeil, QC, J3G 0E2, Canada; (B.M) Saint-Jean-sur-*

Richelieu Research and Development Centre, Agriculture and Agri-Food Canada, 430 Gouin Boulevard, Saint-Jean-sur-Richelieu, QC, J3B 3E6, Canada.

CS5-3. Effects of over-expressing the Mgv1 mitogen-activated protein kinase in *Fusarium graminearum*. D. GONZÁLEZ-PEÑA FUNDORA, A. ERANTHODI, R.K. GOYAL, R.G. SUBRAMANIAM, C. RAMPITSCH, N. THAKOR AND N. A. FOROUD. *(D.G.F., A.E, R.K.G., N.A.F.) Agriculture and Agri-Food Canada (AAFC)-Lethbridge, 5403 1st Avenue South, Lethbridge AB, T1J 4B1, Canada; (D.G.F., N.T.) University of Lethbridge, Department of Chemistry and Biochemistry, 4401 University Dr W, Lethbridge, AB, T1K 6T5, Canada; (A.E.) University of Lethbridge, Department of Biological Sciences, 4401 University Drive West, Lethbridge, AB, T1K 6T5, Canada; (R.G.S.) AAFC-Ottawa. 960 Carling Avenue, Ottawa, ON, K1A 0C6, Canada; and (C.R.) AAFC-Morden, 101 Route 100, Morden, MB, R6M 1Y5, Canada.*

CS5-4. Deoxynivalenol-3-Glucoside content of two-row barley infected with *Fusarium graminearum* measured by ultra-performance liquid chromatography - tandem mass spectrometry. J. R. TUCKER, A. BADEA, R. BLAGDEN, K. PLESKACH, S. A. TITTLEMIER AND W. G. D. FERNANDO. *Agriculture and Agri-Food Canada, Brandon Research and Development Centre, 2701 Grand Valley Road, P.O. Box 1000A, R.R. 3, Brandon, MB R7A 5Y3, Canada; (R.B, K.P., S.A.T.) Grain Research Laboratory, Canadian Grain Commission, 303 Main St., Winnipeg, MB, R3C 3G8, Canada; and (J.R.T., W.G.D.F) Department of Plant Science, 222 Agriculture Building, University of Manitoba, Winnipeg, MB, R3T 2N2, Canada.*

CS5-5. Mutations in the *os-1* gene of *Microdochium nivale* (*mnos-1*) confer resistance to the dicarboximide fungicide iprodione. R. GOURLIE AND T. HSIANG. *University of Guelph, School of Environmental Sciences, Guelph, ON, N1G 2W1, Canada.*

CS5-6. Identification of QTLs associated with horizontal resistance against *Phytophthora sojae* in early maturing soybeans. M. DE RONNE, A. LEBRETON, C. LABBÉ, J. LAUR, A. RASOOLIZADEH, C. DUSSAULT-BENOIT, D. GOVARE-MONROE, F. BELZILE, L. O'DONOGHUE, R.R. BÉLANGER. *Envirotron, Université Laval, 2480 Boulevard Hochelaga, Québec, QC, G1V 0A, Canada; (F.B.) Pavillon Charles-Eugène-Marchand, 1030 Rue de la Médecine, Québec, QC, G1V 0A6, Canada; (L. O.) CEROM, 740 Chemin Trudeau, Saint-Mathieu-de-Beloeil, QC, J3G 0E2, Canada.*

17:15-18:00 POSTERS/ AFFICHES
ROOM/SALLE DUQUESNE
Silent auction by QSPP /encan silencieux de la SPPQ

19:00-22:00 Banquet / Banquet
Awards/prix / encan silencieux de la SPPQ
Entertainment/Divertissement
ROOM/SALLE DUQUESNE-JONQUIERE/

Sponsored by /commandité par: BASF Canada Inc. and CEROM

Day 4: Wednesday June 20, 2018 / Jour 4: Mercredi 20 juin

08:00-9:45 CPS-AGM/SPPQ-AGA / SCP-AGA/SPPQ-AGA
ROOM/SALLE WOLFE-MONTCALM

Breakfast included/petit-déjeuner inclus
Sponsored by / commandité par: Bayer Crop Science Inc.

9:45-11:15 Contributed session 6 Epidemiology II
ROOM/SALLE JONQUIÈRE-LAUZON
Chair: Philippe Tanguay, Natural Resources Canada

CS6-1. Introducing an odd pathogen of coriander: *Heterosphaeria.* C. L. ARMSTRONG-CHO and S. BANNIZA. *Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK, S7N 5A8, Canada.*

CS6-2. Inoculum threshold and quantification of *Aphanomyces euteiches*, causal agent of root rot of peas. S. CHATTERTON, S. BANNIZA, R. BOWNESS, AND M.W. HARDING. *Agriculture and Agri-Food Canada, Lethbridge Research Centre, 5403 1st Ave S, Lethbridge, AB T1J 4B1, Canada; (S.B.) Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada; (R.B.) Alberta Agriculture and Forestry (AAF), Lacombe Research Centre, 6000 C & E Trail, Lacombe, AB, T4L 1W1, Canada; and (M.W.H.) Crop Diversification Centre South, AAF, 301 Horticultural Station Road East, Brooks, AB, T1R 1E6, Canada.*

CS6-3. Modelling and mapping the suitability of Canada's climate for an insect-vectored, exotic blue-stain fungal pathogen, *Endoconidiophora polonica*. K. R. Sambaraju, R. Saint-Amant, C. Côté, and B. Filion. *Natural Resources Canada, Canadian Forest Service, Laurentian Forestry Centre, 1055 du P.E.P.S., P.O. Box 10380, Stn. Sainte-Foy, Québec, QC,, G1V 4C7, Canada*.

CS6-4. Distribution of viable resting spores of *Plasmodiophora brassicae* in infested fields. F. AL-DAOUD, B.D. GOSSEN, AND M.R. MCDONALD. *Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1, Canada; (B.D.G.) Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, Saskatoon, SK, S7N 0X2, Canada.*

CS6-5.-1. Genomic profiling of Sudden Oak Death (SOD) populations. G. J. BILODEAU, R. HEINZELMANN, N. FEAU, A. DALE and R.C. HAMELIN. *(G.J.B.) Canadian Food Inspection Agency (CFIA), 3851 Fallowfield Road, Ottawa, ON, K2H 8P9, Canada; (R.H.; N.F.; A.D.) University of British Columbia (UBC), 2424 Main Mall, Vancouver, BC, V6T 1Z3, Canada; (R.C.H.) UBC and Universite Laval, 1030, avenue de la Médecine, Quebec, QC, G1V 0A6, Canada.*

CS6-5. Identification and Characterization of Verticillium isolates from *Brassica* crops in Manitoba, Canada. Z. Zou, V. Bisht, and W.G. D. Fernando. *Department of Plant Science, University of Manitoba, Winnipeg, MB, R3T 2N2, Canada*.

11:15- 11:30 Health break / Pause santé

11:30-13:15 Contributed session 7: Disease management II
ROOM/SALLE JONQUIÈRE-LAUZON
Chair: James G. Menzies, Agriculture and Agri-Food Canada

CS7-1. Selection of antagonistic bacteria from pea root and rhizosphere to manage aphanomyces root rot. Z. HOSSAIN, L.D. BAINARD and Y. GAN. *Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, 1 Airport Road East, Swift Current, SK, S9H 3X2, Canada*.

CS7-2. Plant growth promotion by bacterial consortia. L. EMAD, P. BEAUREGARD AND C. BEAULIEU. *Centre SÈVE, Département de biologie, Faculté des sciences, Université de Sherbrooke, Sherbrooke, QC, J1K 2R1, Canada*.

CS7-3. The elusive *Puccinia tritici-duri* – pathology, taxonomy and relationship to *Puccinia recondita*. S. HAMBLETON AND M. LIU. *Ottawa Research and Development Centre (ORDC), Agriculture and Agri-Food Canada, 960 Carling Ave. Ottawa ON, K1A 0C6, Canada.*

CS7-4. Practical solutions for managing clubroot (*Plasmodiophora brassicae*) on canola in western Canada. DAN ORCHARD, BRUCE D. GOSSEN, MARY RUTH MACDONALD, AND STEPHEN E. STRELKOV. *Canola Council of Canada, 400-167 Lombard Avenue, Winnipeg, MB R3B 0T6, Canada; (BDG) Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada; (MRM) Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada; and (SES) Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada.*

CS7-5. Évaluation de la détection moléculaire et de l'observation visuelle pour établir le seuil de nuisibilité de la tache argentée et de la dartrose sur les semences de pommes de terre. J. D'ASTOUS-PAGÉ[a], S. MORISETTE[b], A. GAGNON[c] ET R. HOGUE[a]. (JDP, RH) *Institut de recherche et de développement en agroenvironnement, 2700 rue Einstein, Québec, QC, G1P 3W8, Canada; (SM) Groupe Pousse-Vert, 301-49 rue de l'Église, Saint-Arsène, QC, G0L 2K0, Canada; (AG) Progest2001, 6833 route Marie-Victorin, Sainte-Croix, QC, G0S 2H0, Canada.*

CS7-6. Resistance characterization of potato *Fusarium* dry rot. D. Chen[1], H. H. Tai[1], K. Gardner[1], B. Bizimungu[1], Sylvia Soucy[1], and R. Peters[2]. [1] Fredericton Research and Development Centre, Agriculture and Agri-Food Canada, 850 Lincoln Road, Fredericton, NB, E3B 4Z7, Canada[2]; Charlottetown Research and Development Centre, Agriculture and Agri-Food Canada, 440 University Avenue, Charlottetown, PEI, C1A 4N6, Canada.

CS7-7. Control of pathogens of *Triticum aestivum* using endophytic fungal isolates. A. Abaya and T. Hsiang. *Environmental Sciences, Bovey 3224, University of Guelph, 50 Stone Rd E, Guelph, ON N1G 2W1, Canada*".

13:15-13:30 closing remark

13:30-17:00 Field trip to Ile d'Orléans (lunch included)/ excursion à l'Ile d'Orléans (lunch compris)

18:00-21:00 CPS Incoming board meeting/ Conseil d'administration entrant SCP.
ROOM/SALLE BUADE

----------CPS-SPPQ-Notes ----------

----------CPS-SPPQ-Notes ----------

----------CPS-SPPQ-Notes ----------

----------CPS-SPPQ-Notes ----------

Abstracts/Résumés

Symposium I: Bridging plant disease management and 'Omics' technologies.

SI-1. Systems approaches for resilient crop development. O. WILKINS. *McGill University, Quebec, Canada.*

Improvements in the availability and accuracy of genome scale technologies have changed the ways we study plant responses to the environment. High-throughput and low-input surveys of genomes, transcriptomes, metabolomes and proteomes are now routine. The present challenge is to move from descriptive interpretations (molecular abundance, genetic markers) of these data to mechanistic ones (prediction of phenotype from genotype, genome editing to improve stress resilience). Systems biology, the study of the emergent properties of biological systems, offers a framework for doing this. In this talk, I will address some strategies for designing experiments for maximizing the information content for systems analyses with a focus on transcriptional regulation and will present some examples how the interpretation of these data might be used to develop stress resilient crops.

SI-2. RKS1, a starting point to decipher the gene regulatory network controlling quantitative disease resistance against Xanthomonas campestris -an example for systems biology perspectives. F. DELPLACE, C.HUARD-CHAUVEAU, U. DUBIELLA, M. INVERNIZZI, F. ROUX, R. PEYRAUD AND D. ROBY. *Laboratory of Plant-Microrganism Interactions (LIPM), University of Toulouse, UMR CNRS-INRA, 31326 Castanet-Tolosan, France*

The importance of pathogen perception and signaling pathways in the regulation and execution of plant immune responses have become apparent during the last years. Notably, *R* gene-mediated immunity has been shown to be the most efficient form of resistance in plants, but it is also not durable. Additional forms of resistance have gained increasing attention for breeding purposes, such as quantitative disease resistance (QDR) that is considered a more durable type of resistance with partial effects on plant immunity. The identification of genes underlying QDR might have practical implications to increase crop yield and quality. However, there is still very limited information about the molecular mechanisms controlling QDR. One of the most important disease of crucifers (including cabbage, broccoli and rapeseed), is the black rot, caused by the bacterial plant pathogen *Xanthomonas campestris* pv. *campestris* (*Xcc*). Based on results obtained by genome wide associating (GWA) mapping and

functional approaches, we were able to clone Resistance related KinaSe 1 (RKS1) as the gene underlying a major QTL conferring approximately 50% resistance in *Arabidopsis thaliana* against the strain *Xcc568* (Huard-Chauveau et al., 2013). Our main objective is now to decipher the regulatory pathway(s) controlling and controlled by RKS1. In our study, we used two complementary approaches: (i) comparative transcriptome analysis of mis-expressing *RKS1* lines, and (ii) identification of proteins interacting with RKS1 by Yeast-two-Hybrid assays, to identify candidate genes involved in QDR. We then reconstructed the molecular network involving RKS1 using our dataset and published interactions. The network was converted in a mathematical model to predict interactions among the genes and we are now performing mutant-based experiments to validate those predictions. The results and perspectives of this work based on a combination of molecular biology, computational biology, mathematical modeling and genetics for the identification of candidate components of QDR, will be presented.

SI-3. Omic Analyses of Fungal Plant Pathogens: Discovery to Application. B. SAVILLE, G. BAKKEREN AND O. CARISSE. *(BS) Trent University, 1600 West Bank Drive, Peterborough, ON, Canada K9L 0G2; (GB) Agriculture and Agri-Food Canada, 4200 Highway 97Box 5000, Summerland, BC, Canada, V0H 1Z0; (OC) Agriculture and Agri-Food Canada, Research Centre, 430 Gouin Blvd., Saint-Jean-sur-Richelieu, QC, Canada, J3B 3E6*

The world's population is predicted to reach ~ 10 billion by 2050 and this increasing population will require a continual expansion in agricultural crop production. Yet this production is under siege by existing, changing, and emerging fungal pathogens. To provide insight regarding the use of omics to mitigate this fungal threat we will outline discoveries made and applications initiated as a result of these analyses. Discoveries will be highlighted in four areas: 1) uncovering coding potential, 2) identification of gene expression change, 3) functional analysis of fungal genes, and 4) the detection of fungal gene expression networks during disease development. We will also touch on some ongoing work by us and others targeting the identification of variation in coding potential. We will focus on the biotrophic fungal pathogens *Ustilago maydis* and *Puccinia triticina* to illustrate these discoveries. The applications enabled through genomic analyses have primarily been through the use of knowledge obtained. We will present data on the use of genome sequences to develop assays for species, genotype and race identification, as well as the detection of fungicide resistance genes. Examples of the use of identification in disease management will also be presented. Further, we will present some omics derived intervention strategies including the development of RNAi-based antifungal technologies, using knowledge of fungal pathogens to inform plant breeding and the potential to identify new antifungal targets. Then close by discussing the potential of using omics directly to monitor the status of fungal threats and how such knowledge may aid disease management.

Symposium II: The future of pesticides in globally and locally changing agricultural environments.

SII-1. The future of plant disease management: environmental, biological, economic, and social constraints. G. SUNDIN, *Michigan State University, U.S.A.*

Future predictions of global food needs by 2050 highlight a need for significantly-increased crop production on ever-shrinking hectarage of available arable land. Context framing strategies designed to ramp up production must always account for plant diseases, as diseases place major constraints on crop production and cause significant, consistent yearly losses on a global scale that can spike in epidemic years. When considering the future of plant disease management and crop production, growers are faced with a wide range of uncertainties. For example, climate change effects such as warming temperatures will likely expand the geographic range of some potentially devastating plant pathogens; however, other aspects of climate change such as the increased frequency of severe storms could have the most important impacts on disease epidemiology. Limitations in the number and diversity of efficacious chemical control compounds, as well as pathogen resistance, can have disastrous consequences in years when the environment favors pathogen growth, infection, and dissemination. The introduction of pathogens into new geographic regions due to human activity can decimate a regional industry in a short time frame. Overlaying these newly-developing issues, the correlation of desirable crop traits with high disease susceptibility, most notably with many specialty crops, puts growers at significant risk even before considering other factors that can go wrong during the growing season. Manipulation of host populations through addition of disease resistance and/or tolerance traits promises to be the most impactful pathology solution; however, continued deployment of such prized cultivars in monocultures may quickly tarnish that silver bullet. Creativity, high risk – high reward, novel interdisciplinary approaches etc. are buzzwords that are frequently desired in large grant proposals but infrequently generate meaningful field research that results in near-term implementation of truly novel, viable, efficacious strategies. This is likely because what is lacking in current largescale plant pathology initiatives is the integration of applied experience and direction with the basic science. This collaboration is fully necessary and will underlie the future contribution of plant pathology to world food production.

SII-2. The Future of Biopesticides in Crop Protection. S.M. BOYETCHKO, T. DUMONCEAUX, AND C. OLIVIER. *Saskatoon Research and Development Centre, Saskatoon, SK, S7N 0X2 Canada*

Investment in biopesticide research globally has progressed during the last 35 years, with a significant number of products registered since 2000. Greater consumer awareness and demand for safer foods and recent government legislation have spurred the development of reduced risk pest control products and renewed interest in biopesticides. The synthetic pesticide market has decreased by 12% over the last 10 years, but demand for biopesticides is expected to exceed $1 Billion in sales. In Canada, banning of chemicals in urban municipalities, development of pesticide resistance in crop pests, demand for new products by organic farmers, and the recognition of hidden costs to human health and the environment are further fueling the need for biological alternatives. The discovery of new microbial candidates for development as biopesticide active ingredients has far out-paced the knowledge and related technology required to bring these products to commercialization. Although there are numerous biopesticides registered for use globally, the public wonders why there are "so few" biopesticides available in the marketplace. It has become apparent that biopesticide research needs to be demonstrated to have evolved beyond the lab bench and there is a clear process for implementation and commercialization. The importance of regulatory and market considerations cannot be underestimated. Understanding the microbial community and focusing on the phytobiome will result in a better comprehension for tackling crop health. New techniques in DNA sequencing will be a useful tool for selection of superior isolates with a known mode of action and the emergence of nanotechnology is contributing to advancing biopesticide formulation. Discovery of bioactive compounds from microbes and botanical sources is facilitated by sophisticated techniques using NMR and UPLC-MS. The future of biopesticides is in the –omics age has come to realization.

SII-3. Opportunities for technology, new and old, to reduce, improve or replace pesticides. M. R. MCDONALD, AND B. D. GOSSEN. *Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1, Canada; and (B.D.G.) Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, 107 Science Place, Saskatoon, SK S7N 0X2, Canada.*

A consistent shift to larger farms, bigger equipment and reduced crop diversity has been occurring in Canadian agriculture from many years. As a result, the natural biological control provided by i) crop rotation and ii) biological diversity from wetlands, headlands, fencerows, and windbreaks has been replaced by increased reliance on genetic resistance and pesticides. This has often resulted in rapid erosion of cultivar resistance and loss of sensitivity to single-site pesticides. The increasing expense of finding new genetic resistance and pesticides indicates that this approach is not sustainable in the long-

term. Fortunately, several new technologies may help to change this balance. Gene editing (e.g., using CRISPR/Cas 9) will provide a source of novel resistance, and marker-assisted selection will facilitate selection for complex traits. RNA interference (gene silencing) may provide effective reductions in some pests and pathogens. A shift to autonomous field equipment has the potential to reverse the trend for larger farm equipment. Smaller autonomous equipment could seed and harvest small areas, making intercropping, deployment of multi-lines, and variable plant spacing easier and cost-effective. Remote sensing of the host, microenvironment and individual pests, combined with autonomous, targeted application of pesticides, could improve the efficacy of both biocontrol agents and synthetic pesticides in these small crop areas. Robots may also remove or treat individual weeds, insects or infected plants. These changes could shift the balance back towards natural biological control and biological diversity, and so reduce the need for large-scale pesticide application.

Special session on soybean diseases.

SS-1. Soybean Diseases – An Eye Towards the Future. D. MUELLER**,** *Iowa State University,USA.*

Soybean diseases cause substantial yield loss and reduce seed and grain quality throughout North American soybean growing regions each year. For example, economic losses caused by soybean diseases were estimated to be $26 billion from 2010 to 2014 in the U.S. and Ontario, Canada. This is an average loss of more than $60 per acre annually and does not take into consideration disease-management costs incurred by farmers and agribusiness. Despite advances in fungicide technology, improved soybean genetics, and increased understanding of pathogens, diseases continue to threaten soybean production, and losses have remained relatively consistent over the past two decades. This occurs for numerous reasons including changes in genetics of pathogen populations, soybean varieties, and environment (production practices, climate, etc.). Soybean cyst nematode (*Heterodera glycines*) is an example of a pathogen with recently observed genetic shifts in populations. The number of soybean varieties with soybean cyst nematode resistance has increased dramatically over the past 25 years. However, nearly all varieties have the same resistance gene (PI88788) and SCN populations are showing increased reproduction on varieties with this source of resistance. Also, alternative management such as nematicide seed treatments have yet to provide the necessary control. Soybean varieties are continually changing as seed and chemical companies produce new technologies and vie for market share. Although new varieties may have beneficial traits, such as herbicide resistance to dicamba (Xtend soybeans), these varieties may be more susceptible to diseases than previous soybeans. In university research, Xtend varieties have shown increased susceptibility to white mold (caused by *Sclerotinia sclerotiorum*) and southern stem canker (caused by *Diaporthe aspalathi*). Thus, solving one issue (herbicide resistant weeds) has increased risk of disease related production issues.

SS-2. Genotypic and phenotypic diversity of *Phytophthora sojae* isolates in Canadian soybean fields. G. ARSENAULT-LABRECQUE, C. DUSSAULT-BENOIT, H. SONAH, F. BELZILE AND R.R. BELANGER. *Département de phytologie, Université Laval, 2425 rue de l'Agriculture, Québec, Qc, G1V0A6, Canada*.

Phytophthora sojae, causing Phytophthora Root Rot (PRR), has been present in Canada since 1950. The expansion of Canadian soybean in the last years gave this pathogen a new niche to establish its devastating presence. The best method to control it is through the use of soybean varieties carrying resistance genes (*Rps*) that provide immunity against *P. sojae* isolates carrying the corresponding

avirulence genes (*Avr*). Breeders are thus confronted with the need to introgress *Rps* genes based on the *P. sojae* pathotypes found in the environment, while this information is constantly incomplete because of the rapid evolution of the pathogen versus the unwieldiness of phenotyping methods. This project aimed to determine the presence and distribution of virulence profile (pathotypes) of *P. sojae* in Canada, based on the seven most important *Rps*/*Avr* genes relationships. For this purpose, a collection of 31 *P. sojae* isolates representing the most common pathotypes found in Canadian fields were targeted for whole-genome-sequencing. Different gene mutations directly linked to those seven *Avr* genes from *P. sojae*, mostly gene suppression and SNPs, were discovered. These findings corroborate some previous reports, and highlight new findings, while demonstrating the reliability of genomic markers to predict phenotypes of *P. sojae* isolates.

SS-3. Soybean cyst nematode in Canada: genomics applied to biovigilance. B. MIMEE. *Saint-Jean-sur-Richelieu Research and Development Centre, Agriculture and Agri-Food Canada, 430 boul. Gouin, Saint-Jean-sur-Richelieu, QC J3B 3E6, Canada*

Soybean production has had a spectacular growth over the last five years in Canada. One of the main soybean pest, *Heterodera glycines*, responsible for over a billion-dollar yield loss in the U.S. annually, is already well established in Southwestern Ontario. Is this microscopic worm a real threat to soybean production in northern latitudes? Climate warming will promote the expansion of soybean to northern areas but will also increase the number of generation the nematode can produce in a single year, thus speeding up its establishment and spread in new areas. Even if the nematode was found in all regions of Quebec, population densities are still very low and it is anticipated that yield limiting populations will not be reached until several years. However, the adaptive potential of this alien invasive species to new environments was found to be very high. Winter, drought or high precipitations will not stop its spread. Worst, it appears that strong selective pressure resulting from the overuse of resistant cultivars in the Midwest is causing a large scale homogenization with virulent populations. Thus, these cultivars will become increasingly ineffective more rapidly in new areas than before. It is therefore critical to include new promising parental lines with new resistance genes in breeding programs. Even more important is the comprehension of the mechanisms used by the nematode to overcome plant resistance. To this end, recent advances in SCN genomics suggest that gene duplication and transposition could be responsible for the rapid adaptation and evolution of the pest.

SS-4. Sudden Death Syndrome of Soybean: Know your enemy. O.S. WALLY AND A. TENUTA. *(OSW)Harrow Research and Development Centre, Agriculture and Agri-Food Canada, Harrow ON, Canada N0R 1G0*; (A.T) *Ontario Ministry of Agriculture, Food and Rural Affairs, Ridgetown, Ontario, Canada*

The fungal pathogen *Fusarium virguliforme* causes soybean Sudden Death Syndrome (SDS) in North America. The disease was first observed in Arkansas and has spread in a general northern direction through the majority of soybean growing areas in North America being first identified in Ontario in 1998. *F. virguliforme* colonizes the roots of soybeans during seed germination, as the soybeans mature the fungi produces toxins that translocate up the xylem causing the classic interveinal chlorosis and leaf cupping eventually leading to premature defoliation and seed abortion. Disease is rated as a disease index (DX) which is a measure of severity (0-9, 0=asymptomatic, 9=defoliation) multiplied by the incidence (%) divided by 9, giving a DX from 0-100. Yield losses from SDS are directly correlated to DX, with an increase of 10 DX resulting in ~10% reduction in yield, losses due to SDS make it the 2nd or third most damaging soybean pest in the northern USA and Ontario depending on the year. There are a number of factors that influence the disease which includes; varietal resistance, soil composition, soil moisture and interactions with the soybean cyst nematode (SCN). Control measures for mitigating SDS damage include planting tolerant varieties as there currently are no completely resistant varieties, delaying planting date and the use of certain seed treatments have proven effective under moderate SDS pressure. Additional control may be obtained through the study of soils grown under continuous soybeans which have been discovered to be highly suppressive to SDS in southwestern Ontario.

ORAL PRESENTATION.

Contributed session 1 Epidemiology I (Student competition)

CS1-1. Effet de la température sur l'éclosion des sporanges et l'agressivité des deux *formae specialis* de *Plasmopara viticola (P.v. riparia* et *P.v. aestivalis)* responsable du mildiou de la vigne dans l'Est du Canada. R.A. MOUAFO TCHINDA, C. BEAULIEU, M.L. FALL. AND O. CARISSE. (RAMT, CB) *Centre SEVE, Département de biologie, Université de Sherbrooke, 2500 Boulevard de l'Université, Sherbrooke, QC, Canada, J1K 2R1;* (MLF, OC) *Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu Research and Development Centre, 430 Gouin Boulevard, Saint-Jean-sur-Richelieu, QC, J3B 3E6, Canada.*

Originaire de l'Amérique du Nord, le mildiou de la vigne causé par *Plasmopara viticola*, est l'une des plus dévastatrices maladies de la vigne. En effet, lorsque les conditions sont favorables, les épidémies de mildiou entrainent des pertes de production pouvant atteindre 100%. Des études récentes sur la génétique des populations de *P. viticola* ont démontré qu'il existe quatre sous-espèces, dont deux (*P. viticola aestivalis* et *P. viticola riparia)* sont responsables des épidémies dans l'est du Canada. L'objectif de ce travail était d'évaluer l'influence de la température sur l'éclosion des sporanges et l'agressivité des deux *formae specialis* de *P. viticola*. L'évaluation de l'effet de la température sur l'éclosion des sporanges et sur l'agressivité a été effectuée à différentes températures (5, 10, 15, 20, 25 et 30 ^{o}C) en fonction du temps. Les sporanges des deux génotypes montraient un maximum d'éclosion entre 15 et 20 ^{o}C, 3h après le début de l'incubation. Le taux d'éclosion de *P.v. aestivalis* était significativement supérieur à celui de *P.v. riparia* après 24h à 25 ^{o}C. Tous les paramètres d'agressivité évalués (incidence de contamination; temps de latence; efficacité d'infection; sporulation) suggèrent que *P.v. aestivalis* est plus agressif que *P.v. riparia*.

CS1-2. Impact of *Brassica napus-Leptosphaeria maculans* interaction in the emergence of virulent isolates of *L. maculans*, the causal agent of blackleg disease in canola. M. H. RASHID, S. LIBAN, X. ZHANG, P. PARKS, Z. ZOU, H. BORHAN, AND W.G. D. FERNANDO. *Department of Plant Science, University of MB, R3T 2N2 Canada; (H.B) AAFC, Saskatoon Research Centre, SK, S7N 0X2, Canada.*

Canola (*Brassica napus* L.) is one of the major oilseed crops grown in Canada and other temperate parts of the world. Blackleg, caused by the fungus *Leptosphaeria maculans* causes sever yield losses. In Canada, farmers have begun to grow canola more intensively because of the market demand and the

development of cultivars harbouring single resistance (*R*) genes. However, the industry has suffered some losses due to breakdown of blackleg *R* genes in grower's fields. A 4-year study from 2014 to 2017 at the Ian N. Morrison Research Station Carman Manitoba investigated the impact of *B. napus*-*L. maculans* interaction in the emergence of virulent isolates toward specific *R* genes, using Topas introgressed lines carrying single *R*-genes, under field conditions with a 2-year rotation with wheat. Blackleg incidence was reduced up to a maximum of 40% in 2017 compared to 2014 for all *R* genes tested except *Rlm4*. Disease severity of 52-21% was reduced in 2017 compared to 2014 regardless of *R* genes tested except *Rlm2*. In 2017 there was a shift from *AvrLm2* and *AvrLm4* to virulent alleles that is *avrLm2* and *avrLm4* respectively which led to the gain of virulence toward *Rlm2* and *Rlm4* within a year. Sequencing of the *AvrLm2* gene from 2014- and 2015-isolates revealed a shift of *AvrLm2* to *avrLm2* allele due to accumulation of point mutations. In addition, as reported previously, masking of *AvrLm3* phenotype by the presence of the *AvrLm4-7* allele was also confirmed by analysing phenotypes and genotypes of the isolates collected from 2014 to 2017. Based on previous and this study, we predict that alternating *Rlm3*, *Rlm4*, and *Rlm7* carrying cultivars offers an opportunity to increase the durability of those *R* genes in a 2-year crop rotation in Canada. Additionally, we propose to develop an epidemiological model that takes into account complex molecular mechanisms allowing plant breeders to select appropriate *R* genes in the proposed cultivar rotation strategies introduced on the Prairies.

CS1-3. Interaction between soybean cyst nematode (*Heterodera glycines*) and Phytophthora root rot (*Phytophthora sojae*) on soybean. C. AUDETTE, R.R. BÉLANGER AND B. MIMEE. *(C.A.)(B.M.)Saint-Jean-sur-Richelieu Research and Development Centre, Agriculture and Agri-Food Canada, 430 boulevard Gouin, Saint-Jean-sur-Richelieu, QC, J3B 3E6, Canada; (C.A.) (R.R.B.) Département de phytologie, Faculté des Sciences de l'Agriculture et de l'Alimentation, Université Laval, Québec, QC, G1V 0A6, Canada.*

In Canada, soybean acreage has been increasing steadily in recent years. However, this broad expansion has contributed to the establishment and spread of several diseases and pests. The soybean cyst nematode (SCN), *Heterodera glycines*, is the leading cause of economic losses in the United States. It is present in Ontario since 1987 and was reported in Quebec in 2013. Currently, Phytophthora Root Rot (PRR) caused by *Phytophthora sojae* is still the most problematic disease of soybean in Canada. The best tool to control these pathogens is the use of resistant cultivars. It is known that SCN may facilitate the development of certain diseases (e.g. *Fusarium virguliforme*) or repress some host resistance genes (e.g. *Cadophora gregata*). Thus, the objective of this project was to determine if cultivars with resistance to PRR and SCN will remain effective if both pathogens are present. This study revealed that the presence of *P. sojae* negatively affected the number of cysts produced by SCN

on susceptible host (more than 50% reduction). This suggests that *P. sojae* may activate host defense mechanisms that could be effective against SCN or directly decrease SCN virulence. On the other hand, plant resistance was not affected by the presence of either pathogens and remained effective against both pathogens. This confirms that the use of resistant cultivars is a valid option for controlling and preventing SCN and PRR even when both organisms co-occur in a field.

CS1-4. Survival and detection of *Colletotrichum* species on celery and common weeds species. S. REYNOLDS, M. J. CELETTI, K. S. JORDAN AND M. R. MCDONALD. *Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1, Canada; (M.J.C.) Ontario Ministry of Agriculture, Food and Rural Affairs, Guelph, ON, N1G 4Y2, Canada.*

Fungal pathogens *Colletotrichum fioriniae* and *C. nymphaeae* cause anthracnose on several agriculturally important crops but can also asymptomatically colonize non-host species. The objective of this study was to evaluate the pathogenicity of *C. fioriniae* and *C. nymphaeae* and determine their survival on common weed species of Ontario. Conidia of one isolate of *C. fioriniae* from celery and apples and one isolate of *C. nymphaeae* from strawberry were inoculated onto the foliage of celery (cv. 'TZ 9779') and five weed species: *Amaranthus retroflexus*, *Chenopodium album*, *Chenopodium glaucum*, *Cyperus esculentus*, and *Senecio vulgaris*. Leaf tissue sections were excised 10 and 20 days post inoculation (dpi), and were either plated directly or surface-sterilized and plated on semi-selective media to determine percent pathogen recovery. Quantitative PCR was also used to detect and quantify the pathogen from leaf samples, and conidia germination was characterized by light microscopy. *C. fioriniae* caused typical anthracnose symptoms on celery, whereas *C. nymphaeae* only caused minor lesions on young leaves. Weeds remained asymptomatic, however, plated leaf segments from all weeds and celery showed *Colletotrichum* growth. Growth was observed from surface-sterilized leaves, suggesting endophytic or latent infection. On all plant species tested, most conidia germinated, developed melanised appressoria and produced secondary conidia by 4 dpi. Quantitative PCR was able to detect *C. fioriniae* and *C. nymphaeae*, and therefore can be used as a tool for rapid detection of the pathogen on asymptomatic leaves. Both *Colletotrichum* species colonized and reproduced on weeds, which could be a potential inoculum source for surrounding hosts.

CS1-5. Identification of critical time-points of *Colletotrichum lentis* infection on lentil for transcriptomic studies. P. BAWA, J. HALLIDAY, C. CHO, V. BHADAURIA, K. BETT, A. VANDENBERG, S. BANNIZA. *Department of Plant Sciences/ Crop Development Centre, 51 Campus Drive, University of SK, Saskatoon, SK S7N 5A8, Canada; (V.B.) AAFC, Swift Current Research and Development Centre, 1030, Swift Current, SK S9H 3X2, Canada.*

Anthracnose is one of the major foliar diseases of lentil in western Canada and remains an impediment to the production of high quality seeds and yields of lentil. Two pathogenic races (races 0 and 1) have been differentiated in western Canadian populations of the causal pathogen of anthracnose, *Colletotrichum lentis*. Previous microscopic studies revealed that race 1 isolates had lower conidial germination, fewer appressoria, and a slower and less destructive necrotrophic phase compared to isolates of the more virulent race 0 after inoculation on lentil cultivar CDC Robin with partial resistance to the less virulent race 1. Consistent with this, we found that fungal biomass of a race 0 isolate in CDC Robin assessed at different time points through quantitative real-time PCR (qPCR) was higher than that of the race 1 isolate. Accessions of *Lens ervoides*, a wild relative of lentil, have been identified with high levels of resistance to both pathogenic races of *C. lentis*. An intraspecific *L. ervoides* population (LR-66) was previously developed from accessions L01-827A × IG 72815 to study the genetic control of resistance to *C. lentis*. The growth and development of a virulent race 0 isolate in the most resistant and the most susceptible recombinant inbred lines through qPCR has been assessed to identify critical time-points for in-depth gene expression studies.

Contributed session 2: Omics, genomic and transcriptomic (all)

CS2-1. Battling biology – Overcoming challenges with spore germination. A.M. SETO, M.E. DONALDSON, B.J. SAVILLE. *Environmental and Life Sciences Graduate Program, Trent University, 1600 West Bank Drive, Peterborough, ON, K9L 0G2, Canada; (B.J.S.) Forensic Science Program, Trent University, 2140 East Bank Drive, DNA Building, Peterborough, ON, K9L 0G2, Canada.*

Fungal diseases are a major threat to sustainable crop production. The success of these fungal pathogens stems from their production of spores, which allows them to disperse over long distances and survive for extended periods of time outside the host. The processes of spore dormancy, dispersal, and germination are integral to the emergence of infectious fungal diseases. Despite their importance, studies on fungal spores have been limited. We use *Ustilago maydis* D.C. Corda as a model for studying plant-pathogen interactions. This fungus is dispersed as thick-walled dormant teliospores, which germinate, and complete meiosis to initiate new rounds of *Zea mays* infection. Teliospore germination is asynchronous, which presents a challenge when identifying changes in gene expression. To overcome this challenge, we used RNA-seq to analyze transcript level changes at 0, 9, and 18 hours after teliospore germination was induced. These analyses identified 18 patterns of transcript level change, nine for genes up regulated in the teliospore and nine for genes down regulated in the teliospore. These patterns suggest transcriptional and post-transcriptional control of gene expression during teliospore development and germination. Reverse transcriptase quantitative PCR (RT-qPCR) confirmed some of the patterns of transcript level change. Gene ontology (GO) enrichment analysis identified biological processes that were enriched for in each pattern. A summary of the GO enrichment and RT-qPCR analysis will be presented, along with a model of functional changes during teliospore development and germination. This model can be used to inform future investigations of smut and rust teliospore germination.

CS2-2. CRISPR/Cas9 gene editing of the Dutch elm disease pathogen *Ophiostoma novo-ulmi.* P. TANGUAY. *Natural Resources, Canadian Forest Service, Laurentian Forestry Centre, 1055 rue du PEPS, P.O. 10380 Ste-Foy stn., Quebec, QC, G1V 4C7, Canada.*

Strategies employed to establish a CRISPR/Cas9 system to efficiently disrupt target genes in the tree pathogen *Ophiostoma novo-ulmi* are being described. We achieved successful CRISPR/Cas9 knock-out of the *ADE2* gene. *O. novo-ulmi* protoplasts were co-transformed by PEG/CaCl2 using synthetic sgRNAs and a plasmid expressing a *O. novo-ulmi* codon-optimized Cas9 nuclease. Furthermore, we

are testing, in *O. novo-ulmi*, the ability of a linear plasmid with telomeric ends to behave as an artificial acentric minichromosome, rapidly lost under non-selective conditions. This would allow recycling of the selection marker, and prevent the potential negative effects of constitutive Cas9 expression. A CRISPR/Cas9 gene editing system is an important advance to investigate gene function in *O. novo-ulmi*, a species with extremely low rates of homologous recombination.

CS2-3. Gene flow as a character in polyphasic classification of phytopathogenic fungi: a case study in wheat leaf rust species complex. M. LIU, S. HAMBLETON, Y. ANIKSTER, AND J. KOLMER. *Biodiversity and Bioresources, Ottawa Research and Development Centre (ORDC), Agriculture and Agri-Food Canada, 960 Carling Ave. Ottawa. ON K1A 0C6, Canada; Institute for Cereal Crops Improvement, George S. Wise Faculty of Life Science, Tel Aviv University, Tel Aviv 69978, Israel; and U. S. Department of Agriculture (USDA), Cereal Disease laboratory, 1551 Lindig Street, St. Paul, MN 55108, U. S. A.*

The combination of phylogenetics and molecular technologies has dramatically increased the resolution of fungal classification over the past 30 years. Numerous species defined by morphology turn out to be complexes. Along with the achievements of more refined species recognition, a commonly encountered dilemma and debate is whether paraphyletic species should be recognized. Topology based species recognition considers that species must be supported by evidence of monophyly. A study of four host-associated forms of *P. triticina* Erikss. by Liu et al 2013 showed that tree topologies varied when different loci and analytical methods were used. The combined ITS and EF1-α analyses grouped all four forms as one clade whereas phylogenetic analysis of 239 SNPs from 15 loci resolved two strongly supported monophyletic groups and coalescence-based analysis (BEAST) resolved three monophyletic groups. In this case, 1, 2 or 3 species could be recognized based on various tree topologies. The form on *Aegilops speltoides* Tausch was previously recognized as a *forma speciales* based on infection experiments by Anikster et al 2005, which showed that *A. speltoides* was resistant *to P. triticina* isolated from wheat. Gene flow analysis (IMa2) indicated that there was no detectable gene flow between the *Aegilops* form and any other forms while constant gene flow was detected among other forms. We consider the lack of gene flow as strong evidence of genetic separation and propose to recognize *Aegilops* form as a separate species: *Puccinia speltoides* sp. nov., while other forms belong to one species.

CS2-4. Molecular Management of Fungal Phytopathogens via RNAi. N. WYTINCK, A. G. MCLOUGHLIN, J. C. WAN, K. T. BIGGAR, M. F. BELMONTE, AND S. WHYARD *Department of Biological Sciences, 50 Sifton Road, University of Manitoba, MB, R3T 2N2, Canada.*

Necrotrophic fungal phytopathogens, such as *Sclerotinia sclerotiorum and Botrytis cinerea,* devastate a wide range of important crop species. These fungi are capable of infecting more than 500 plant species worldwide, including economically significant crops such as canola, pulses and fruits. In particular, canola, which contributes 27 billion dollars to the Canadian economy annually, is especially susceptible to infection from necrotrophic fungi. Control practices currently used by producers predominantly involve broad spectrum fungicides. Unfortunately, these chemicals are becoming increasingly ineffective due to resistance developing, in addition to the damage they cause to beneficial species and the environment. A novel, species specific, and effective solution is therefore needed to control these evermore difficult pests. Through the use of RNA interference, we can drastically reduce fungal pathogenesis by targeting specific transcripts through careful design of double stranded RNA molecules (dsRNA). Through a rigorous bioinformatics pipeline, our lab has identified dsRNAs in *Sclerotinia* that have proven effective in limited fungal growth in canola. Specifically, we were able to reduce *Sclerotinia* infection significantly by using RNAi technology both as a foliar spray as well as through transgenic canola expressing dsRNA molecules. Additionally, we have used this technology to effectively target a related phytopathogen, *Botrytis cinerea*. The mechanism by which dsRNA is taken intracellularly in fungal cells is also being investigated and has been shown to occur through endocytotic processes. Ultimately, using leading-edge molecular technologies, we developed novel, species specific fungicides that will be of utility to both producers and researchers in Canada and abroad.

CS2-5. Transcriptomic analysis of *Brassica napus- Leptosphaeria maculans* pathosystem by dual RNA-seq using a single-*R*-gene cultivar and a single-*Avr*-gene isolate. K. R. E. PADMATHILAKE, H. SONAH, Z. ZOU, J.R. TUCKER, A, CARTER, R.R. BELANGER AND W.G. DILANTHA FERNANDO. *Department of Plant Science, University of Manitoba, Winnipeg, MB R3T2N2, Canada; (H.S. and R.R.B.) Department of Plant Science, Laval University, Québec, G1V0A6 Canada; and (A.C.) Brandon Research and Development Centre, Agriculture and Agri-Food Canada, Brandon, R7A5Y3 Canada.*

Blackleg disease caused by *Leptosphaeria maculans* remains a significant threat to canola (*Brassica napus*) cultivation. Understanding plant resistant mechanisms is crucial to counter this disease effectively. Qualitative resistance of the plant, which is controlled by a single resistant *(R)* gene

activates when the infecting pathogen contains the corresponding avirulence *(Avr)* gene. The R-Avr incompatible interaction, leads to a hypersensitive reaction as the plant recognizes the pathogen at early onset. This study focused on identifying genes associated with the *B. napus – L. maculans* pathosystem using dual RNA-sequencing. *B. napus* genotype, '01-23-2-1' that carries only *Rlm7* was inoculated with a *L. maculans* isolate UMAvr7 that carries only *AvrLm7,* and with the *AvrLm7* knockout mutant umavr7 of the same isolate in order to study incompatible and compatible interactions, respectively. This study will investigate differential gene expression during biotrophic over necrotrophic stage, differentially expressed effector genes in the pathogen, receptor-genes and genes associated with signal transduction of the host. Plants were inoculated followed by sample collection at time of inoculation, 1d, 3d, 7d, and 11d after inoculation. Total RNA was extracted and sequenced on an Illumina 4000 HiSeq. The results will be presented at the conference.

CS2-6. Tissue specific RNA sequencing of *Brassica napus* in response to *Sclerotinia sclerotiorum* infection. P.L. WALKER, I.J. GIRARD, M.G. BECKER, S. SAIKIA, T.R. de KIEVET, W.G.D. FERNANDO, M.F. BELMONTE. *Department of Biological Sciences, University of Manitoba, 50 Sifton Road, Winnipeg, MB R3T 2N2, Canada; (S.S, T. de K.) Department of Microbiology, 213 Buller Building, University of Manitoba, MB R3T 2N2, Canada; (W. G. D. F.) Department of Plant Science, University of Manitoba, 66 Dafoe Road, Winnipeg, MB R3T 2N2, Canada.*

White mold in *Brassica napus* (canola) is caused by the fungal pathogen *Sclerotinia sclerotiorum* and is responsible for significant losses in crop yield across the globe. With advances in high-throughput transcriptomics and computational biology, our understanding of canola's defense response to *S. sclerotiorum* is becoming clearer; however, the response of individual cell and tissue layers directly at the site of infection has yet to be explored. Using cutting edge laser-capture microdissection coupled with high-throughput RNA sequencing we have profiled epidermal, mesophyll and vascular leaf tissues in response to *S. sclerotiorum* infection. This strategy increases the number of genes detected compared to whole leaf assessment and provides information on cell and tissue-specific gene expression profiles. For example, the epidermis contains genes associated with increased defense hormone expression, the mesophyll is key in cell wall reinforcement and the vascular tissue is involved in phenylpropanoid biosynthesis and cell death. Our findings indicate distinct roles for each tissue layer in response to infection and our bioinformatics approach has identified novel transcriptional regulators predicted to guide plant immunity. We further discuss how this information will play a role in protecting one of Canada's most important cash crops against white mold disease.

CS2-7. Proteome analysis of *Streptomyces scabies* grown in the presence of potato tuber

L. GIROUX, I. ISAYENKA, N. BEAUDOIN AND C. BEAULIEU**.** *Centre SÈVE, Département de biologie, Faculté des sciences, Université de Sherbrooke, Sherbrooke, QC, J1K 2R1, Canada.*

Streptomyces scabies is the major causal agent of potato common scab.The disease is characterized by suberized lesions on potato tubers that decrease their market value. A proteomics study aiming to identify *S. scabies* proteins produced during potato infection was carried out. Potato microtubers from the resistant cultivar Russet Burbank (RB) and the sensitive cultivar Yukon Gold (YG) were produced on Murashige-Skoog medium with 8% sucrose. *S. scabies* was then grown in a liquid growth medium in the absence or presence of 6-week-old potato microtubers of each cultivar. After 5 days of growth, *S. scabies* proteins were extracted and analysed by LC-MS/MS. The similarity index of *S. scabies* proteome profiles between a culture grown in the absence or presence of microbuters was of 48 and 54% for the cultivars RB and YG, respectively. The proteomes of *S. scabies* grown in the presence of YG or RB exhibited a higher similarity index (70%). Proteins linked to the production of the toxins concanamicyns and the siderophore pyochelin were detected only in the presence of tubers. These proteins were found more abundant when the bacterium was grown with the resistant cultivar than with the sensitive one. The production of concanamycins and the ability to scavenge iron thus appear to participate in the infection process. Proteins involved in the SOS response and DNA repair were also found to be more abundant in the presence of microtubers than when the bacterium was grown in pure culture suggesting a bacterial stress adaptation during host infection.

Contributed session 3: Disease management I (Student competition)

CS3-1. Efficacy testing of low risk products for the control of dollar spot (*Sclerotinia homoeocarpa*). K. STONE AND T. HSIANG. *Environmental Sciences, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada.*

Dollar spot is a disease of turfgrass caused by the fungus *Sclerotinia homoeocarpa* (F.T.Benn.) which causes significant aesthetic and economic damage to lawns and golf courses. Dollar spot management is complicated as some jurisdictions have pesticide regulations limiting pesticide use for cosmetic purposes. The Pest Management Regulatory Agency defines Class 11 products as 'low risk' and the Ontario provincial government allows Class 11 products for cosmetic use. The objective of this research was to investigate whether select Class 11 products could inhibit damage caused by dollar spot on lab and field grown creeping bentgrass (*Agrostis stolonifera* L.) in comparison to the conventional fungicide propiconazole. For lab trials, creeping bentgrass cv. 'Penncross' was grown in Cone-tainers containing ~150 g of a sand mixture. For field trials, 0.25 m^2 plots consisting of 75% creeping bentgrass and 25% annual bluegrass (*Poa annua* L.) were established at the Guelph Turfgrass Institute (Guelph, ON). Lab samples and field plots were treated with ten Class 11 compounds, Banner Maxx as a fungicide control, and water as a control. Grasses were inoculated with *S. homoeocarpa*. Lab tests were visually evaluated for percent yellowing at 7 and 14 days post inoculation (DPI), and field plots weekly following inoculation. Lab treatments were more effective at 14 DPI with significant suppression by Banner Maxx, Sunlight dish soap, acetic acid, sodium chloride, hydrogen peroxide, phosphite, garlic powder, and ferric sulfate, but not citric acid, Borax, and sulphur. For field trials, only Banner Maxx and ferric sulfate gave significant reductions in disease.

CS3-2. Evaluation of lime products as a clubroot management tool in canola. N.M. FOX, S.F. HWANG, V.P. MANOLII, G. TURNBULL, AND S.E. STRELKOV. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada; and (S.F.H., G.T) Crop Diversification Centre North, Alberta Agriculture and Forestry, Edmonton, AB, T5Y 6H3, Canada.*

Clubroot, caused by *Plasmodiophora brassicae* Wor., is a soil-borne disease that has become a constraint to canola (*Brassica napus* L.) production in Alberta, Canada. The disease is managed primarily by the planting of clubroot resistant cultivars, but this resistance already has been overcome in over 60 fields in the province. Disease development is favoured in acidic soils; therefore, increasing soil pH could reduce clubroot severity in infested soils and serve as another management tool. The

efficacy of hydrated lime products in reducing clubroot severity was assessed in replicated field plot experiments in central Alberta in 2017. The addition of moderate to high rates of hydrated lime significantly reduced clubroot severity and increased above-ground biomass in a susceptible canola cultivar at 8 weeks after planting. At the highest application rate, lime treatment reduced the clubroot disease severity index by 35-91%, while increasing above-ground plant biomass by 58-116%. A supplemental greenhouse study was conducted to assess the efficacy of hydrated lime in reducing clubroot severity in susceptible and moderately resistant canola cultivars, under different application rates and concentrations of inoculum. Under all inoculum levels, there was a high degree of infection (92-100%) in the susceptible canola and very low infection (9-13%) in the moderately resistant canola. All four rates of hydrated lime application completely eliminated visible signs of infection in both cultivars. Further quantitative PCR analysis is underway to measure the impact of the treatments on pathogen inoculum and disease development in 10-day old seedlings.

CS3-3. Evaluating the potential of arbuscular mycorrhizae to manage carrot leaf blight

U. ILYAS, M. N. RAIZADA, L. DU TOIT, AND M. R. MCDONALD**.** *Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W Canada; (U.I., M.N.R., M.R.M.) and (Department of Plant Pathology, University of Washington State, Washington, WA 98273-4768 USA; (L.T.)*

The symbiosis of plants and arbuscular mycorrhizae (AM) is known to increase nutrient uptake and improve resistance to biotic and abiotic stresses. Commercial AM products are available and carrot growers are using these products. However, the ability for AM to suppress disease or increase yield in carrots in Ontario is currently unknown. The present study evaluated the efficacy of AM inoculant *Glomus intraradices*, on carrot seeds, to manage carrot leaf blight. Leaf blight is caused by one or both fungi *Alternaria dauci* Kühn and *Cercospora carotae* Pass. Field trials were conducted on high organic matter soils at two sites, one with low phosphorous (P) content (46 ppm) and one with high P content (68 ppm) near Bradford, ON in 2017. Mono-ammonium phosphate was applied at 100 kg actual P/ha to high P soils only. Fungicide was applied biweekly in August and September. Disease severity was assessed throughout the growing season and canopy health and yield was determined at harvest. There were no differences in disease progress among the treatments during the growing season. At harvest, the treatment with AM applied to low P soils had less disease (25 %), more healthy leaves per plant (22 %), and higher canopy fresh (46 %) and dry weight (55 %) compared to the no AM check. However, there were no differences in yield or the percentage of AM colonization in roots of AM treated and untreated carrots. Results suggest that AM association might beneficial in low P soils.

CS3-4. An investigation of Fusarium basal rot of onion and candidate biocontrol agents in the Annapolis Valley, Nova Scotia. A. L. BUNBURY-BLANCHETTE AND A. K. WALKER**.** *Acadia University, Department of Biology, 33 Westwood Avenue, Wolfville, NS, B4P 2R6, Canada.*

The fungal pathogen *Fusarium oxysporum* f. sp. *cepae* (Hanzawa) W.C. Snyder & H. N. Hansen (FOC) causes Fusarium basal rot (FBR) of bulb onions. Disease incidence and severity of symptoms are increasing in the Annapolis Valley, Nova Scotia, leading to declined crop yield and quality, at an annual loss of $600 000, or 20%. Current control strategies have not reduced symptoms, prompting research to characterize local FOC and to identify and test local fungi for potential as biocontrol agents. Fungi from soil collected from onion fields in the Annapolis Valley were isolated and identified using DNA barcoding; seven belonged to the genus *Trichoderma*. Dual culture trials were conducted to determine possible antagonism between FOC and the identified *Trichoderma* species. Virulence of FOC on onion was determined using greenhouse assays; candidate *Trichoderma* species were then also tested in the greenhouse to determine effect on presence and severity of FOC symptoms. All *Trichoderma* species tested showed signs of antagonism against FOC in dual culture; *T. hamatum* P. Karst and *T. harzianum* Rifai most commonly outcompeted FOC. The local FOC strain was demonstrated to produce 50% mortality in seedlings at a concentration of approximately 1000 spores per gram of soil, and *T. atroviride* P. Karst and *T. harzianum* reduced basal rot symptoms in onion seedlings. This is the first research to focus on Fusarium basal rot of onion in the Annapolis Valley, and supports the consideration of fungal biocontrol agents such as *Trichoderma* species as part of a control program for FBR.

CS3-5. Identification of nonhost crops for the management of stem and bulb nematode (*Ditylenchus dipsaci*) in garlic (*Allium sativum*). L. IVES, M. J. CELETTI, K. JORDAN AND M. R. MCDONALD. *Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON N1G 2W1, Canada; and (M.J.C.) Ontario Ministry of Agriculture, Food and Rural Affairs (OMAFRA), University of Guelph, Guelph, ON N1G 2W1, Canada.*

Stem and bulb nematode (SBN), *Ditylenchus dipsaci* (Kuhn, 1857) Filip'ev, 1936, is problematic for garlic (*Allium sativum* L) growers in Ontario, where this nematode reduces yield and infests seed cloves for successive planting. There are no garlic cultivars with resistance to SBN, and no nematicides are registered for use on garlic seed cloves. Rotating garlic with nonhost crops could reduce the soil population between cropping seasons. However, the susceptibility of rotation crops to the SBN strain affecting Ontario garlic is unknown. In growth room trials, six potential rotation crops: carrot, corn, potato, onion, soybean and wheat were evaluated for their response to infection by SBN. The experiment contained a positive (susceptible garlic cv. 'Music') and negative (inoculated soil without

vegetation) control. At planting, each pot was inoculated using 100 nematodes of mixed developmental stages. Plants were harvested six weeks post-inoculation, and nematodes were recovered from soil and plant tissue using the Baermann funnel method. Nematode reproduction factor (RF) was calculated to identify nonhost crops. Soil RF values suggest that potato (RF=7.3), carrot (RF=6.1), onion (RF=4.3), and corn (RF=3.5) were hosts. However, based on plant tissue extraction, onion appeared to be a very susceptible host (RF=23.8) compared to corn (RF=1.1), garlic (RF=1.0), and potato (RF=0.6). Soybean and wheat were nonhosts, since no nematodes were recovered from plant tissue, and fewer nematodes were recovered from soil than were used for inoculation. Wheat and soybean may be good choices of crops to rotate with garlic to reduce SBN population levels in the soil.

Contributed session 4 Genetics and resistance I

CS4-1. Contrasting aboveground and belowground responses to PAMP-triggered immunity
A. LACAZE, A. CULL AND D. L. JOLY. *Université de Moncton, 18 avenue Antonine-Maillet, Moncton, NB E1A 3E9, Canada.*

Deciphering the molecular responses to pathogen-associated molecular patterns (PAMPs) is an active research area in the field of plant–microbe interactions. Much of the progress that has been made in puzzling out PAMP-triggered immunity (PTI) pathways and the microbial factors involved in the elicitation or suppression of PTI has relied solely on aerial parts to generate insights, despite the organ-specificity of plant defenses. In this study, we focus on one oomycete PAMP, Pep-13/Pep-25, and contrast it to the well-characterized bacterial PAMP flg22 in aerial and belowground organs of *Solanum tuberosum* L. and *Arabidopsis thaliana* (L.) Heynh. By systematic analyses of defense responses such as ROS burst, transcript changes or accumulated hormones, we found that flg22 triggers fast and strong responses in the different organs tested, while Pep-13/Pep-25 treatments elicit organ-specific responses. Using measurement of PAMP-induced ROS generation, we screened collections of *A. thaliana* T-DNA insertional mutants for those suppressed for Pep-25 responsiveness, including the regulatory leucine-rich repeat-receptor-like kinases BAK1 and SOBIR1. This study will improve our global understanding of PAMP-triggered immunity and allow the discovery of novel components of the plant immune system.

CS4-2. Compartmentalization barriers in trees: some reflections on possible routes exploited by pathogens to overcome these defensive tissues.
D. RIOUX and M. BLAIS. *Natural Resources Canada, Canadian Forest Service, Laurentian Forestry Centre, 1055 du P.E.P.S., P.O. Box 10380, Stn. Sainte-Foy, Québec, QC, G1V 4C7, Canada.*

Compartmentalization barriers (CBs), in the broad sense, occur as nonspecific defensive responses in the bark and xylem of trees reacting to various injuries or attacks by pathogens. Many studies report that the entry of air which accompanies these damages would be the main trigger to the formation of CBs. Canker pathogens can directly penetrate necrophylactic periderms, the main CBs in the bark. However, it has also been proposed that they can colonize beyond these CBs indirectly, through disruptions in them or by bypassing these defensive tissues. As we showed in a recent study involving artificial inoculations with the butternut canker pathogen, and no matter the route taken, fungal colonization that occurs during dormancy seems to be crucial in disease development. In some cases, when the pathogen is already present in the xylem, or when it can reach it, propagules can be transported

over long distances beyond the CBs through the long open vessels. Time-course microscope studies are needed to follow the path of these pathogens and promising insights will likely be gained using fluorescent species-specific markers, but this only when coupled with the use of reagents capable of quenching the autofluorescence of the numerous compounds present in trees.

CS4-3. Integrated genomics, plant pathology and breeding research for improvement of Fusarium head blight, leaf rust and stripe rust resistance in Canadian cereals. M.A. HENRIQUEZ, G. HUMPHREYS, B.D. MCCALLUM, H.S. RANDHAWA, T. FETCH, J.M. FETCH, X. WANG, M.F. BELMONTE, C.A. MCCARNTNEY, M. KANG-CHOI
(M.A.H, B.D.M., C.A.M., X.W., T.F) Morden Research and Development Centre, Agriculture and Agri-Food Canada, Unit 101 Route 100, Morden, MB, R6M 1Y5, Canada; (G.H., M.KC) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Ave, Ottawa, ON, K1A 0C6, Canada; (H.S.R.) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403 – 1st Avenue South, PO Box 3000, Lethbridge, AB, T1J 4B1, Canada; (J.M.F.) Brandon Research and Development Centre, Agriculture and Agri-Food Canada, , 2701 Grand Valley Road, Brandon, MB, R7A 5Y3, Canada; (M.F.B.) Department of Biological Sciences, University of Manitoba, 50 Sifton Road, Winnipeg, MB, R3T 2N2, Canada.

Development of cereal crop varieties with resistance to Fusarium head blight (FHB) (*Fusarium sp.)* and rust (*Puccinia sp.)* is a main breeding goal worldwide. This project objectives are; 1) development and genotyping of a winter wheat germplasm collection, 2) development of a doubled haploid mapping population from the winter wheat cross: AC Morley x Emerson, 3) phenotyping of the DH population for its response to Fusarium head blight, 4) genotype the AC Morley x Emerson doubled haploid population to provide SNPs to generate a molecular map of the population, 5) QTL mapping of FHB resistance, 6) identify and characterize *Fusarium* species from FHB infected winter wheat crops, 7) transcriptome analyses of winter wheat - *F. graminearum* interaction, 8) validation of differentially expressed genes, 9) development/validation of SNP markers diagnostic for FHB resistance of winter wheat, 10) development of FHB, leaf rust and stripe rust resistant germplasm, and linked molecular markers, that can be used by wheat breeding programs, and 11) analysis of *Fusarium* species complex in oat and screening of oat germplasm for resistance to major *Fusarium* species found in western Canada. This knowledge will be transferred to breeding programs for marker assisted selection and will be an important resource for breeding new elite disease resistant wheat and oat cultivars for Canada.

CS4-4. Ethylene-mediated resistance to fusarium head blight of wheat. N.A. FOROUD, R.K. GOYAL, D. RYABOVA, A. ERANTHODI, D. GONZÁLEZ-PEÑA FUNDORA, Y. PAN, R. PORDEL, I. KOVALCHUK AND S. CHATTERTON. *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB T1J 4B1, Canada; Information and Communications Technologies, National Research Council of Canada, Ottawa, ON, K1A 0R6 Canada (Y.P.); Department of Biological Sciences, University of Lethbridge, Lethbridge, AB T1K 3M4, Canada (I.K.)*

Ethylene is a gaseous plant hormone involved in both plant defence and development. Often ethylene-mediated plant defence responses to necrotrophic fungi involve synergistic interactions with the jasmonate signalling pathway. On the other hand, ethylene is also an inducer of senescence and cell death, which could be beneficial for some invading necrotrophic pathogens. *Fusarium graminearum* is a hemibiotrophic pathogen, with both biotrophic and necrotrophic phases, that can infect the wheat inflorescence and cause a disease known as fusarium head blight (FHB). Interestingly, the role of ethylene signalling in the host-response to FHB is unclear: some studies indicate that ethylene mediates resistance, while others have shown that it is associated with susceptibility. Preliminary results in our group suggested that there may be a genotype-dependent role for ethylene, explaining some of these discrepancies. To test this hypothesis, FHB experiments were carried out in six wheat genotypes with different levels of resistance or susceptibility. Detached wheat heads from each genotype were treated with ethylene inhibitors or enhancers and then inoculated with *F. graminearum* to assess both resistance to initial infection and disease spread. The results suggest that ethylene signalling promotes resistance, regardless of genotype: ethylene inhibition broke down resistance in three resistant wheat genotypes, whereas enhancer treatments resulted in reduced susceptibility in three susceptible genotypes. Additional work is underway to determine whether time-dependent expression of ethylene signalling or cross-talk with other hormone pathways can affect ethylene-mediated resistance to FHB.

CS4-5. Adoption of major-gene resistance groups for managing blackleg (*Leptosphaeria maculans*) of canola in Canada. J. E. J. CORNELSEN, C. JURKE AND C. REMPEL. *Canola Council of Canada, 400-167 Lombard Avenue, Winnipeg, MB, R3B 0T6, Canada.*

The fungal pathogen *Leptosphaeria maculans* (Desmaz.) Ces. & de Not. causes blackleg, one of the most economically important diseases of canola (*Brassica napus* L.) in Canada. Management for the disease has focused on pathogen race monitoring, extension of crop rotation, and use of resistant (R) cultivars. R cultivars have been deployed since the1990s, which helped to minimize the disease impact by using major-gene and race-nonspecific resistance. Recently, an increase in blackleg incidence and

severity has been observed on the prairies, even on R-rated cultivars. The recommendation for canola producers finding increased blackleg was to select a different cultivar, which could be a gamble; it may or may not be effective since the new cultivar may carry the same set of resistance gene(s). The Canadian canola industry has decided to adopt a new resistance labelling scheme to identify the major resistance genes deployed in canola cultivars. If substantial increases in blackleg are seen with one cultivar, producers will be recommended to switch to a cultivar with an alternative major-gene resistance group to target the dominant *L. maculans* races within their fields. A new diagnostic test has also been developed for producers to identify *L. maculans* races and select cultivars carrying effective resistance genes. The adoption of major-gene resistance groups and the *L. maculans* race diagnostics test will provide producers with new tools to help manage and mitigate blackleg on their farms.

Contributed session 5: Genetics and resistance II (Student competition)

CS5-1. The Cross-Kingdom Biosynthesis and Signaling of Cytokinins during the Formation of Tumors in the *Ustilago maydis-Zea mays* Pathosystem. I. O. ALIMI, R. J. N. EMERY and B. J. SAVILLE.*Environmental and Life Sciences Graduate Program, Trent University, 1600 West Bank Drive, Peterborough, ON K9J 0G2, Canada; (R.J.N.E.) Biology Department, Trent University, 1600 West Bank Drive, Peterborough, ON K9J 0G2, Canada; and (B.J.S.) Forensic Science Program, Trent University, 1600 West Bank Drive, Peterborough, ON, K9J 0G2, Canada.*

Cytokinins are plant hormones that stimulate cell growth and cell division. During the *Ustilago maydis* infection of *Zea mays,* the levels of cytokinins rise dramatically and are thought to be integral to tumor growth. Since both organisms can produce cytokinins, we determined the timing of cytokinin production and the expression of biosynthetic and response regulator genes in both organisms during pathogenesis in order to determine the biosynthetic origins of cytokinin and the biological responses of each organism to these cytokinins. Primers were designed for species and gene specific amplification allowing us to use reverse transcription PCR to detect and estimate levels of transcripts at different stages of infection and in the organisms grown independently. We also identified and determined the levels of cytokinin present at the different stages of infection. The results indicate that both organisms contribute to biosynthesis of cytokinins and that both respond to cytokinin production. The alteration in timing of cytokinin production, and the expression of response regulators during infection with a *U. maydis* strain that does not produce cytokinins, suggests a model that involves early synthesis of cytokinins by the fungus. This production may stimulate increased pathosystem production of cytokinins and enable response to the cytokinins at specific stages in pathogenesis. We hypothesize that response to cytokinins is a component of the signaling that stimulates changes in cell growth and cell division in both the host and the pathogen. Progress on experimental results that support this model of interaction will be presented.

CS5-2. QTL mapping of PI 494182, a new source of resistance to soybean cyst nematode.
V. T. ST-AMOUR, F. BELZILE, B. MIMEE AND L. S. O'DONOUGHUE. *Département de phytologie and Institut de Biologie Intégrative et des Systèmes, Université Laval, 1030 avenue de la Médecine, Québec, QC, G1V 0A6, Canada; (L.O.) Le Centre de recherche sur les grains (CÉROM), 740 chemin Trudeau, Saint-Mathieu-de-Beloeil, QC, J3G 0E2, Canada ; (B.M) Saint-Jean-sur-Richelieu Research and Development Centre, Agriculture and Agri-Food Canada, 430 Gouin Boulevard, Saint-Jean-sur-Richelieu, QC, J3B 3E6, Canada.*

Soybean cyst nematode (SCN), *Heterodera glycines*, is the most devastating pest of soybean (*Glycine max*) globally. Plant resistance is the most durable and yield-efficient strategy to fight this pathogen. Currently, the parental line PI 88788 is widely used and nearly the sole source of resistance against SCN in commercialized cultivars. Unfortunately, field reports show that this source of resistance is being overcome in many areas. With the goal of diversifying the sources of resistance to SCN, we studied PI 494182. This soybean introduction from Japan has previously shown good resistance to HG-type 2.5.7, the most prevalent virulent type of SCN in North America. Using Genotyping by Sequencing (GBS) on a RIL population of 150 lines (PI 494182 x Costaud), we produced a genetic map that allowed us to identify QTLs associated with resistance to SCN. We report five QTLs that were previously identified in different resistant lines, such as Peking and Hartwig. The higher resolution conferred by GBS has allowed the accurate positioning of these QTLs on the physical map. Furthermore, re-sequencing data will provide additional information to identify candidate genes putatively involved in resistance to SCN in PI 494182. Overall, this work will give breeders new tools, genetic markers, to diversify sources of resistance against SCN.

CS5-3. Effects of over-expressing the Mgv1 mitogen-activated protein kinase in *Fusarium graminearum*.
D. GONZÁLEZ-PEÑA FUNDORA, A. ERANTHODI, R.K. GOYAL, R.G. SUBRAMANIAM, C. RAMPITSCH, N. THAKOR AND N. A. FOROUD. *(D.G.F., A.E, R.K.G., N.A.F.) Agriculture and Agri-Food Canada (AAFC)-Lethbridge, 5403 1st Avenue South, Lethbridge AB T1J 4B1, Canada; (D.G.F., N.T.) University of Lethbridge, Department of Chemistry and Biochemistry, 4401 University Dr W, Lethbridge, AB T1K 6T5, Canada; (A.E.) University of Lethbridge, Department of Biological Sciences, 4401 University Drive West, Lethbridge, AB T1K 6T5, Canada; (R.G.S.) AAFC-Ottawa. 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; and (C.R.) AAFC-Morden, 101 Route 100, Morden, MB R6M 1Y5, Canada.*

Mitogen-activated-protein kinase (MAPK) cascades are involved in signal transduction processes in the cell, through sequential phosphorylation. MAPK kinase kinases phosphorylate MAPK kinases,

which in turn phosphorylate MAPKs. In *Fusarium graminearum*, one of the causal agents of Fusarium head blight disease of cereals, three MAPK pathways have been identified. Among these, the Mgv1 (MAP kinase for growth and virulence 1) pathway is part of the Bck1-Mkk2-Mgv1 kinase cascade, and previous reports have shown that deletion of *MGV1* affects female fertility, mycelial growth, mycotoxin accumulation, and virulence (possibly due to reduced fitness). Despite the significance of research focused on these pathways, little is known about the downstream components of the Mgv1 cascade. With the aim of identifying Mgv1 targets, *F. graminearum* strains over-expressing *MGV1* under a constitutive promoter were generated by *Agrobacterium*-mediated transformation of the wild type (WT) strain, GZ3639. The colony pattern and mycelial growth of the transformants on potato dextrose agar were similar to the WT, even in the presence of chemicals affecting cell wall integrity, such as congo red and calcofluor white. Quantitative RT-PCR analysis showed a higher relative gene expression for *MGV1* in the transformants compared to WT, but not for *RLM1*, a known downstream target of Mgv1. The down-regulation of *TRI5*, a key gene involved in trichothecene biosynthesis, may explain the low levels of the mycotoxin deoxynivalenol detected in the transformant compared with the WT. The active form of Mgv1 will be used in future proteomics studies to identify and further characterize the downstream signaling pathway.

CS5-4. Deoxynivalenol-3-Glucoside content of two-row barley infected with *Fusarium graminearum* measured by ultra-performance liquid chromatography - tandem mass spectrometry. J. R. TUCKER, A. BADEA, R. BLAGDEN, K. PLESKACH, S. A. TITTLEMIER AND W. G. D. FERNANDO. *Agriculture and Agri-Food Canada, Brandon Research and Development Centre, 2701 Grand Valley Road, P.O. Box 1000A, R.R. 3, Brandon, MB R7A 5Y3, Canada; (R.B, K.P., S.A.T.) Grain Research Laboratory, Canadian Grain Commission, 303 Main St., Winnipeg, MB R3C 3G8; and (J.R.T., W.G.D.F) Department of Plant Science, 222 Agriculture Building, University of Manitoba, Winnipeg, MB, R3T 2N2, Canada.*

Fusarium graminearum Schwabe produces a range of secondary metabolites such as mycotoxins, which can be associated with pathogenicity. Deoxynivalenol (DON) is a common mycotoxin associated with infected barley grains. This mycotoxin is known to inhibit protein synthesis in Eukaryotes through ribosomal interference, thereby limiting resistance response of the host. A common host defence mechanism is induction of detoxification genes that code for enzymes which facilitate conjugation of mycotoxins to alternate molecules. While these conjugated mycotoxins demonstrate reduced toxicity *in planta*, such forms represent a risk to industry as they can be transformed back to toxic state under processing. Strict guidelines for maximum limits have been set by malting and brewing and livestock feed industries, and grains are monitored. However, bound-

mycotoxins are not detected by standard analytical procedures and are typically not an assayed target. A study was conducted at Brandon, MB in 2016 and 2017 to evaluate mycotoxin profile of 16 barley genotypes that differed in there resistance response to fusarium head blight and DON production. Plots were artificially inoculated with conidia suspension using a mixture of isolates and grown under irrigation to promote disease. Plots were split-harvested at soft-dough and ripe stage followed by desiccation in a high capacity drier. The soft dough samples were divided into rachis and seed components. A panel of 13 mycotoxins were assessed on all samples via UPLC-MS/MS, which included targets: DON, 3ADON, 15ADON, ZEA and DON-3-Glucoside. Results from mycotoxin analyses will be discussed in reference to level barley host resistance.

CS5-5. Mutations in the *os-1* gene of *Microdochium nivale* (*mnos-1*) confer resistance to the dicarboximide fungicide iprodione. R. GOURLIE AND T. HSIANG. *University of Guelph, School of Environmental Sciences, Guelph, ON, N1G 2W1, Canada.*

Microdochium nivale (Fr.) Samuels & I.C. Hallett causes Microdochium patch and pink snow mould on turfgrasses in cool-wet climates. Isolates of *M. nivale* from coastal British Columbia were found to have decreased sensitivity to iprodione, a dicarboximide fungicide, relative to isolates collected in Ontario. Genomic DNA of five isolates with decreased sensitivity to iprodione (EC_{50} 10.4 to 191 µg mL^{-1}) and eight iprodione-sensitive isolates (EC_{50} 1.4 to 5.6 µg mL^{-1}) were sent for sequencing on the Illumina HiSeq platform at Genome Quebec, Montreal. Raw reads were assembled using SOAPdenovo (1.05) and Abyss (1.3.6). Gene sequences previously reported to be associated with resistance to dicarboximides were obtained from GenBank, and *M. nivale* genomes were queried for homologous sequences. A point mutation (A3503G) in *os-1* homologs (*mnos-1)*, which encodes for an osmosensing histidine kinase, was found in two of five insensitive isolates, while two other insensitive isolates had a 32 bp deletion (Δ430-462) in *mnos-1*. The isolates with a deletion also had three point mutations in *mnos-4* (G49A, T182C, C396T). The fifth insensitive isolate had point mutations and deletions in the 5’ region of *skn7* (*dic2*). Sensitive isolates had none of these mutations. These results suggest that mutations in *mnos-1* can lead to dicarboximide insensitivity in *M. nivale*, and that mutations in *mnos-4* and *skn7* are potential candidates for further dicarboximide insensitivity. This is the first work which identifies mutations which could cause dicarboximide resistance in this species.

CS5-6. Identification of QTLs associated with horizontal resistance against *Phytophthora sojae* in early maturing soybeans. M. DE RONNE, A. LEBRETON, C. LABBÉ, J. LAUR, A. RASOOLIZADEH, C. DUSSAULT-BENOIT, D. GOVARE-MONROE, F. BELZILE, L. O'DONOGHUE, R.R. BÉLANGER. *Envirotron, Université Laval, 2480 Boulevard Hochelaga, Québec, QC G1V 0A*
(F.B.) Pavillon Charles-Eugène-Marchand, 1030 Rue de la Médecine, Québec, QC G1V 0A6
(L. O.) CEROM, 740 Chemin Trudeau, Saint-Mathieu-de-Beloeil, QC, J3G 0E2, Canada.

Although the deployment of resistance genes that confer complete immunity against *Phytophthora sojae* is currently the most attractive means to reduce soybean losses, the constant evolution of new avirulence genes lead to a breakdown in resistance. A complementary approach is to rely on horizontal resistance, or partial resistance, that is not dependent on a gene-for-gene interaction. The objective of this study is to identify QTLs associated with horizontal resistance against *P. sojae*, in a soybean recombinant inbred line (RIL) population that has been obtained from one early maturing line adapted to Canadian conditions, and one line showing high levels of horizontal resistance both in field observations and greenhouse testing. For phenotyping purposes, we relied on a new hydroponic bioassay that reproduces the natural infection process of the pathosystem soybean – *P. sojae* and allows a reproducible evaluation of horizontal resistance among the RILs. In parallel, genotyping-by sequencing (GBS) was performed on all RILs and the resulting reads (~1M/line) were used for SNP calling and construction of a genetic map. The combination of these two innovative approaches led to the identification of new QTLs involved in horizontal resistance of soybean, which will help breeders to develop new varieties adapted for Canadian conditions with a higher durable resistance against *P. sojae*.

Contributed session 6 Epidemiology II

CS6-1. Introducing an odd pathogen of coriander: *Heterosphaeria.* C. L. ARMSTRONG-CHO and S. BANNIZA. *Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada.*

Renewed research on blossom blight of coriander in Saskatchewan has led to identification of a pathogen implicated in the majority of disease outbreaks observed from 2015-2017. This fungal organism is very slow-growing, difficult to recover using conventional plating, and easily overlooked due to its lack of distinct structures when grown on various agar-based media. A tentative identification was reached using sequence information of the ITS and TUB regions in consultation with taxonomists, placing this fungus in the Leotiomycetes, close to *Heterosphaeria patella* (Tode) Grev. Macroconidia have been successfully induced to form on wheat straw, and efforts to induce teleomorph formation are underway in order to better assess the taxonomic position of this organism. The sensitivity of this pathogen to strobilurin fungicides was investigated as well as its ability to infect other Apiaceae crop flowers. Primers for molecular detection of the pathogen in plant and seed samples will be used to assess seed to seedling transmission. Germplasm collections of coriander were screened in 2017 for their reaction to *Heterosphaeria* infection in the hopes of finding a source of disease resistance.

CS6-2. Inoculum threshold and quantification of *Aphanomyces euteiches*, causal agent of root rot of peas. S. CHATTERTON, S. BANNIZA, R. BOWNESS, AND M.W. HARDING. *Agriculture and Agri-Food Canada, Lethbridge Research Centre, 5403 1st Ave S, Lethbridge, AB T1J 4B1, Canada; (S.B.) Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada; (R.B.) Alberta Agriculture and Forestry (AAF), Lacombe Research Centre, 6000 C & E Trail, Lacombe, AB T4L 1W1, Canada; and (M.W.H.) Crop Diversification Centre South, AAF, 301 Horticultural Station Road East, Brooks, AB T1R 1E6, Canada.*

In Canada, 1.5 million hectares of field pea are grown annually across the prairies, under diverse soil zones and environments (semi-arid to parkland). Aphanomyces root rot, caused by the oomycete *Aphanomyces euteiches*, has emerged as a major disease over the past 5 years and causes substantial yield losses. Oospore levels required to cause disease across diverse soil types were evaluated in greenhouse trials. Field soil, collected from multiple locations across Alberta and Saskatchewan with no history of pulse production, was inoculated with oospores at concentrations ranging from 0 to 1,000 per gram of soil. Disease response of pea differed based on soil physical properties, such as clay content

and water-holding capacity, and presence of other soilborne pathogens (particularly *Fusarium* spp.). In the presence of *Fusarium* spp., approximately 100 oospores per gram of soil were required to cause moderate root rot across all soil types. In the absence of *Fusarium* spp. (autoclaved soil treatments), the threshold dose was 750 oospores/ g soil in soils with high sand or organic matter content, but remained at 100 oospores/g soil in high clay soils. Oospore concentrations in infested field soils were also quantified using greenhouse bioassays and quantitative PCR and most fields had oospore concentrations well above threshold levels. This represents the first step towards developing a decision support system based on quantifying soilborne oospore inoculum levels.

CS6-3. Modelling and mapping the suitability of Canada's climate for an insect-vectored, exotic blue-stain fungal pathogen, *Endoconidiophora polonica*. K. R. Sambaraju, R. Saint-Amant, C. Côté, and B. Filion. *Natural Resources Canada, Canadian Forest Service, Laurentian Forestry Centre, 1055 du P.E.P.S., P.O. Box 10380, Stn. Sainte-Foy, Québec, QC G1V 4C7, Canada*.

Dramatic increases in the numbers of non-indigenous pest invasions have been observed globally over the past decades owing to increased global trade. At risk in forest ecosystems are "naïve" trees that are susceptible to damage as they may lack defense mechanisms to counter harmful invasives. Introductions of non-native forest insects and pathogens can cause catastrophic tree declines endangering ecological balance and causing serious economic losses. In case of an accidental invasion or when a risk of introduction exists, it is critical to understand the climatic suitability of susceptible forests in order to develop proactive plans for pest detection and spread assessment. In this work, we assessed the suitability of Canada's climate for an exotic blue-stain fungal pathogen, *Endoconidiophora polonica* (Siemaszko) Z.W. de Beer, T.A. Duong & M.J. Wingf., that is vectored by the European spruce bark beetle, *Ips typographus* L. We collected occurrence data of *E. polonica* from several sources including online databases, journal articles, and culture collections. We then generated twenty two bioclimatic variables that summarized the tolerances of the pathogen in its native habitat. Two different modeling approaches were used to develop climatic suitability indices that were used to create maps for the pathogen for Eurasia under the current climate. We compared the outputs from the two models with a random model to select the "best" model for mapping Canada's climatic suitability. Mapping suggests that current climatic conditions are conducive for the establishment of the pathogen in Canada, and forests further north will become favorable in the future.

CS6-4. Distribution of viable resting spores of *Plasmodiophora brassicae* in infested fields. F. AL-DAOUD, B.D. GOSSEN, AND M.R. MCDONALD. *Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1, Canada; (B.D.G.) Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, Saskatoon, SK, S7N 0X2, Canada.*

Resting spores of *Plasmodiophora brassicae* Woronin, the causal agent of clubroot of Brassicaceae crops, can survive in soil for many years. The objectives of this study were to assess the vertical distribution of viable spores in newly-infested and heavily-infested fields in Alberta, Canada, and the horizontal distribution of viable spores in a hot spot in one infested field. Soil cores (1-3 cores per site, 2-3 sites per field) were collected at 7.5 cm increments from 0-45 cm depth from three fields. Also, samples (5 per site) to 15 cm depth were collected from 15 sites within a 0.5 ha section of a hot spot in one field. Spores were quantified using qPCR and propidium monoazide-assisted qPCR (PMA-PCR). PMA inhibits amplification of DNA of non-viable cells in qPCR. High variability in the vertical and horizontal distribution of spores was observed in each field. In general, spores were detected at greater depths in heavily-infested fields (10^3-10^5 spores g^{-1} soil at 30-45 cm deep) as compared to the newly-infested field (10^5 spores g^{-1} soil, only in 0-7.5 cm sample). Most of the spores found in the heavily-infested field were viable. The horizontal distribution of viable spores was highest in the middle of the hot spot (10^5-10^6 spores g^{-1} soil) and declined rapidly towards the outer sampling sites (10^3-10^4 spores g^{-1} soil). This supports previous reports on the high site to site variability of spore concentration within a field, and that resting spores move downward in the soil profile over time.

CS6-5. Genomic profiling of Sudden Oak Death (SOD) populations. G. J. BILODEAU, R. HEINZELMANN, N. FEAU, A. DALE and R.C. HAMELIN. *(G.J.B.) Canadian Food Inspection Agency (CFIA), 3851 Fallowfield Road, Ottawa, ON, K2H 8P9, Canada; (R.H.;N.F.;A.D.) University of British Columbia (UBC), 2424 Main Mall, Vancouver, BC, V6T 1Z3, Canada; (R.C.H.) UBC and Universite Laval, 1030, avenue de la Médecine, Quebec, QC, G1V 0A6, Canada.*

Phytophthora ramorum is the causal agent of sudden oak death (SOD) and sudden larch death in the Western United States and the United Kingdom, respectively, as well as ramorum blight on several woody ornamental plants. Prior to 2009, three genetically divergent clonal lineages of this pathogen were known (EU1, NA1, and NA2), each named according to the continent where it was first detected. In 2009, a fourth lineage (EU2) was discovered in the United Kingdom. Several different markers have been developed for genotyping *P. ramorum* including ASO-PCR (Allele-specific oligonucleotide-PCR), microsatellites, and TaqMan assays; however, SNP markers can be used to gain a better understanding of inter- and intra-lineage genetic diversity and population structure. By targeting

multiple SNPs and SNPs unique to geographic populations, we can also gain a better understanding of migration patterns. One of the objectives of the BioSAFE (BioSurveillance of Alien Forest Enemies) project is to study the genomic epidemiology of SOD populations. We aim to sequence the genomes of approximately 500 *P. ramorum* individuals covering the entire Canadian outbreak, as well as some of the US and European outbreaks, across several years and nurseries in order to track the Canadian SOD outbreak, uncover migration patterns, and identify sources and pathways.

CS6-6. Identification and Characterization of Verticillium isolates from *Brassica* crops in Manitoba, Canada. Z. Zou, V. Bisht, and W.G. D. Fernando. *Department of Plant Science, University of Manitoba, Winnipeg MB, R3T 2N2, Canada; (V. B.)Primary Agriculture Branch, Manitoba Agriculture, Carman MB, R0G 0J0, Canada.*

Verticillium stem striping of canola (*Brassica napus* L.), caused by *Verticillium longisporum*, was first reported in Manitoba in 2014. In this study, *Brassica* crops including canola, Mustard (*B. juncea*), and Radish (*Raphanus sativus*) with wilt symptoms were collected and pathogen isolated. Isolates from canola and radish were characterized to *V. longisporum*, which produced longer conidia (7.92-12.00 µm) than conidia of *V. dahliae* (4.32-7.04 µm). Isolates derived from mustard were characterized to *V. dahliae*. Molecular diagnostics with primers 18S rDNA, 5.8S rDNA, mating type were used to confirm the identification of verticillium isolates. PCR-RFLP of mitochondrial small subunit rDNA and cytochrome b gene were also employed to distinguish *V. longisporum* isolates to *V. dahliae*. Subtypes of *V. longisporum* isolates indicated that isolates from canola and radish are in A1/D1 group. *V. longisporum* was inoculated on to canola cultivar 'Westar', which caused stem striping, stunting, shorter plant height ($p<0.05$), significant yield loss including total seed weight and 1000 seed weight ($p<0.05$), lower oil content ($p<0.05$), and a higher glucosinolate content.

Contributed session 7: Disease management II

CS7-1. Selection of antagonistic bacteria from pea root and rhizosphere to manage aphanomyces root rot. Z. HOSSAIN, L.D. BAINARD and Y. GAN. *Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, 1 Airport Road East, Swift Current, SK, S9H 3X2, Canada.*

Aphanomyces root rot caused by *Aphanomyces euteiches* Drechs is a serious disease of pulse crops worldwide and is becoming a major constraint to pea (*Pisum sativum* L.) and lentil (*Lens culinaris* Medik) production in Canada. Seed treatments are not effective, and resistance is limited, and use of crop rotation to minimize the disease pressure has a limited scope. The current project was designed to identify endemic bacteria that were antagonistic toward *A. euteiches*. Rhizosphere and root samples were collected from diseased and healthy pea plants from nine locations across southern Saskatchewan. Approximately 6000 rhizosphere and endophytic bacterial colonies were isolated on various media (Luria Bertani, Potato Dextrose, Pseudomonas, and Tryptic Soy agar). Bioassays were conducted with 410 selected bacteria *in vitro* to evaluate their antagonistic potential toward *A. euteiches*. Thirty five isolates were identified based on their ability to completely inhibit growth of *A. euteiches*. These isolates were then tested in a replicated greenhouse study and nine were selected for field evaluations. Each of these selected antagonistic bacteria suppressed the pathogen, such that treated plants were as healthy as the control plants. Also, a gene expression study was conducted to investigate the disease mechanism and formulate a disease management strategy. Initial results showed stronger expression of several pathogenesis-related genes in pathogen-inoculated plant leaves compared to the healthy control. Similar study on lentil is in progress. Management of Aphanomyces root rot using antagonistic bacteria may provide a disease control strategy insuring a sustainable pulse production system on the Canadian prairie.

CS7-2. Plant growth promotion by bacterial consortia. L. EMAD, P. BEAUREGARD AND C. BEAULIEU. *Centre SÈVE, Département de biologie, Faculté des sciences, Université de Sherbrooke, Sherbrooke, QC J1K 2R1, Canada*.

Plant growth promoting rhizobacteria (PGPR) can be used as active ingredients of biofertilizers as they promote plant growth by different mechanisms such as auxin production. However, individual PGPR strains sometimes show inconsistent results under field conditions while bacterial consortia of PGPR have been shown to provide more consistency. The aim of this project was to establish PGPR consortia from actinobacteria and *Bacillus* isolates. Members of these collections were screened for auxin production. The capacity of the highest auxin producing strains to promote plant growth was tested on

Lemna minor which was used as a model plant as it is characterised by a rapid growth in addition to its importance as animal fodder. Respectively, 73% and 11% of the selected auxin producing actinobacteria and *Bacillus* isolates promoted the growth of *L. minor*. The compatibility between the selected strains was determined by using double agar overlay technique. It was not possible to form bacterial consortia containing more than three strains due to antagonism between strains. A total of sixteen consortia were tested and nine promoted *L. minor* growth. No synergy between consortia members was observed when these consortia were applied to the plant growth medium since the ability of a combination of compatible isolates to promote *L. minor* growth was found to be equal or lower than the ability of the single strains composing the consortia**.** Preliminary data indicated that the selected consortia could also promote the growth of lettuce seedlings indicating that *L. minor* is an interesting model to screen PGPR.

CS7-3. The elusive *Puccinia tritici-duri* – pathology, taxonomy and relationship to *Puccinia recondita*. S. HAMBLETON AND M. LIU. *Ottawa Research and Development Centre (ORDC), Agriculture and Agri-Food Canada, 960 Carling Ave. Ottawa ON K1A 0C6, Canada.*

Common usage of the name *Puccinia triticina* Erikss. specifically for the fungus causing leaf rust of wheat is relatively recent in its taxonomic history. Described in 1899, subsequent names were as a forma specialis, variety or subspecies of *P. dispersa* Erikss. & Henning, *P. rubigo-vera* (DC.) G. Winter, *P. perplexans* Plowr. or *P. persistens* Plowr., until it was included as one of 52 synonyms in the *P. recondita* Roberge ex Desm. complex in 1971. By the 1980s in North America, the concept of a species restricted to wheat as its primary host was clearly articulated and accepted, with alternate hosts in the Ranunculaceae and clear morphological differences of the spores and sori. Another leaf rust species on wheat, *Puccinia tritici-duri*, was described by Viennot-Bourgin in 1941. It infects durum wheat but is thought to be restricted to Morroco, Spain and Portugal and to alternate hosts in the Boraginaceae. Tracking down information about the species was not straightforward. The name was not listed on-line in the fungal nomenclature databases, the original description was published in a difficult-to-locate journal, and references to this species were not always by name but rather implied. A review of published pathogenicity studies and phylogenetic analyses of brown leaf rust fungi suggests that *Puccinia tritici-duri* is closely related to *Puccinia recondita sensu stricto* and as such is one member of a lineage restricted to alternate hosts in the Boraginaceae. Analyses of DNA data for authentic specimens are needed to test this hypothesis and anchor the name taxonomically.

CS7-4. Practical solutions for managing clubroot (*Plasmodiophora brassicae*) on canola in western Canada. DAN ORCHARD, BRUCE D. GOSSEN, MARY RUTH MACDONALD, AND STEPHEN E. STRELKOV. *Canola Council of Canada, 400-167 Lombard Avenue, Winnipeg, MB R3B 0T6, Canada; (BDG) Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada; (MRM) Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada; and (SES) Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada.*

Since it was first identified on canola (*Brassica napus* L.) in Alberta in 2003, the spread of clubroot caused by *Plasmodiophora brassicae* (Woronin) has been relentless, with about 3,000 infested fields confirmed as of 2017. Genetic resistance has been the main approach used for managing clubroot since the commercial release of resistant cultivars in 2009, but numerous pathotypes able to overcome the existing resistance have recently been identified at sites across the region. In the long term, management of clubroot will require adoption of management practices beyond simple major-gene resistance. Research indicates that strategies such as raising soil pH with lime, mapping infestations and recognizing hot-spots, rotating to non-host crops, seeding a densely rooted grass crop, knocking soil off of equipment, and other tactics can also be employed to reduce the spread of clubroot and the concentration of resting spores in soil. Deploying the results of this research in a practical combination with genetic resistance on fields and farms should result in more effective clubroot management and slower spread of the pathogen compared with reliance on major gene resistance alone. Potentially effective strategies include: i) grassing and/or liming field entrances, hot-spots and low or wet areas, ii) reducing tillage, iii) minimizing field traffic, iv) creating new exits far removed from entrances, and v) dedicating a sanitation zone to reduce the spread of resting spores. These approaches are being recommended in current extension efforts, and several options are also being assessed in replicated research studies.

CS7-5. Évaluation de la détection moléculaire et de l'observation visuelle pour établir le seuil de nuisibilité de la tache argentée et de la dartrose sur les semences de pommes de terre. J. D'ASTOUS-PAGÉ[a], S. MORISETTE[b], A. GAGNON[c] ET R. HOGUE[a]. (JDP, RH) *Institut de recherche et de développement en agroenvironnement, 2700 rue Einstein, Québec, Qc G1P 3W8, Canada; (SM) Groupe Pousse-Vert, 301-49 rue de l'Église, Saint-Arsène, Qc G0L 2K0, Canada; (AG) Progest2001, 6833 route Marie-Victorin, Sainte-Croix, Qc, G0S 2H0, Canada.*

La tache argentée (*Helminthosporium solani Durieu & Mont.;* Hs) et la dartrose (*Colletotrichum coccodes (Wallr.) S.J. Hughes*; Cc) sont deux maladies reconnues pour causer des anomalies de coloration de l'épiderme des tubercules et réduire la valeur de la récolte. En se basant sur l'observation des taches et la présence de microsclérotes, il est difficile de faire la distinction entre les deux maladies et d'en prédire le développement à l'entreposage. Les symptômes sont parfois visibles à la récolte mais c'est à l'entreposage qu'ils se développent. Comme les traitements au champ et en entrepôt sont limités, la prévention des sources d'inoculum demeure la méthode la plus économiquement efficace à ce jour. Nous avons développé une approche moléculaire de détection de Hs ou de Cc sur les pelures des tubercules prélevés avant la mise en entrepôt de la récolte. Cette détection sensible et économiquement efficiente a permis d'élaborer les bases d'un modèle prévisionnel des dommages de Hs et Cc sur les tubercules en entrepôt. Nos résultats suggèrent que les seuils de nuisibilité de Hs et Cc devraient être adaptés selon le niveau de sensibilité du cultivar. Il a aussi été observé que Hs et le Cc sont détectés par qPCR sur les pelures de tubercules d'apparence saine et sans symptôme, même après plusieurs mois d'entreposage. La compétition entre les deux pathogènes sur le même tubercule est peu connu et pourrait masquer des symptômes. Ainsi, nous proposons une nouvelle approche d'observation et de détection combinée de Hs et Cc.

CS7-6. Resistance characterization of potato *Fusarium* dry rot. *D. CHEN[1], H. H. TAI[1], K. GARDNER[1], B. BIZIMUNGU[1], SYLVIA SOUCY[1], AND R. PETERS[2]. [1.] Fredericton Research and Development Centre, Agriculture and Agri-Food Canada, 850 Lincoln Road, Fredericton, New Brunswick, E3B 4Z7, Canada[2.] Charlottetown Research and Development Centre, Agriculture and Agri-Food Canada, 440 University Avenue, Charlottetown, PEI, C1A 4N6, Canada*.

Potato *Fusarium* dry rot (FDR) is one of the most important storage diseases in potatoes. Annual losses to FDR were estimated from 6 to 25%, and occasionally up to 60%. Multiple *Fusarium* species can cause FDR with different aggressiveness. Fungicide application is commonly used to control *Fusarium* diseases, however fungicide resistance has been developed in some *Fusarium* spp. Use of host resistance is the most effective and environmentally sound approach to manage diseases. However,

resistance to FDR in potatoes is not well understood. In the present study, six advanced potato breeding lines and standard variety Jemseg or Russet Burbank were inoculated with three *Fusarium* species, *F. sambucinum*, *F. oxysporum* and *F. coeruleum* to screen lines with resistance to the FDR, using two inoculated methods. The inoculated tubers were incubated at 13ºC and 95% humidity in first 48 hrs after inoculation, and then were kept at 13ºC and 65% for 6 weeks at dark before disease assessment. Two lines, F14034 and F14028 were resistant or highly tolerant to the infection of *F. sambucinum*, the most aggressive species, compared to the susceptible variety Jemseg. The *F. sambucinum* was used to investigate the gene differential expression using transcriptome profiling approach to identify host and pathogen genes involved in initial infection responses. The *Fusarium*-infected tuber samples from the six lines and Jemseg were taken at 0, 4, 10, 24 and 48 hrs after inoculation with a 7mm diameter punch. The RNA samples were extracted from the tuber samples for transcriptome profiling.

CS7-7. Control of pathogens of *Triticum aestivum* using endophytic fungal isolates. A. ABAYA AND T. HSIANG. *Environmental Sciences, Bovey 3224, University of Guelph, 50 Stone Rd E, Guelph, ON N1G 2W1, Canada*".

More than 100 endophytic fungi were collected from root and leaf tissues of field grown winter wheat ‘AC Morley’ and ‘25R34’ and spring wheat ‘Sumai’ and ‘Scotia’ which are all considered to be moderately resistant to Fusarium head blight. The plants were collected from Ariss, Ontario in June 2016. These fungal strains were screened using dual culture plates for antagonism against three wheat pathogens Fusarium graminearum, Waitea circinata and Microdochium majus. Out of 101 strains, 38 were found to be antagonistic showing distinct inhibition zones with at least one of the three wheat pathogens. These antagonistic strains were then tested for pathogenicity on wheat leaves in lab tests, and 16 showed no pathogenicity. Among these non-pathogenic strains, three were selected and identified by internal transcribed spacer-polymerase chain reaction (ITS-PCR) as Valsa friesii, Simplicillium lamellicola and Cladorrhinum flexuosum. These three were then tested for their ability to inhibit disease in growth room tests along with a positive control, Clonostachys rosea ACM941. When agar plug inocula were applied to 21-day-old wheat leaves (four-leaf stage) at 3 days prior to inoculation with agar plugs of Fusarium graminearum, S. lamellicola and ACM941 significantly reduced disease severity. The three wheat endophytes and ACM941 were effective against W. circinata for disease reduction, but only ACM941 was effective against M. majus. Simplicillium lamellicola is a promising biocontrol agent against *F. graminearum* and *W. circinata*.

POSTERS/AFFICHES.

P1. Novel techniques for screening Cercospora leaf spot resistant fenugreek (*Trigonella foenum-graecum* L) genotypes. U. SUBEDI, S.N. ACHARYA, S. CHATTERTON, J. THOMAS, R. BARENDREGT, AND D. FRIEBEL. *Department of Biological Sciences, University of Lethbridge, 4401 University Dr W, Lethbridge, AB T1K 6T5, Canada and Lethbridge Research and Development Center, Agriculture and Agri-Food Canada, 5403 1 Ave S, Lethbridge, AB T1J 4P4, Canada; (S.N.A., S.C. and D.F.) Lethbridge Research and Development Center, Agriculture and Agri-Food Canada, 5403 1 Ave S, Lethbridge, AB T1J 4P4, Canada and (R.B) Department of Geography, University of Lethbridge, 4401 University Dr W, Lethbridge, AB, T1K 6T5, Canada.*

Cercospora leaf spot (CLS) caused by *Cercospora traversiana* is an important phyto-pathological problem of fenugreek (*Trigonella foenum graecum* L), a multiuse legume crop. Field screenings for resistant plants although accurate and effective, demand significant time and a sizable workforce to accomplish the goal. Also, weather conditions in the field may not always be favourable for uniform disease spread which eventually may lead to failure of the overall experiment. Whole plant assay (WPA) and detached leaf assay (DLA) with artificial inoculation not only help in scaling up the number of plants screened but also reduce the space, time and the amount of inoculum needed for the experiment. The results in our experiment indicated that both WPA and DLA methods could be used reliably to differentiate the resistant and susceptible genotypes of fenugreek. In addition, the correlation coefficient ($r = 0.784$, $p<0.01$) derived from the mean disease score from each genotype, between WPA and DLA showed that they can be used interchangeably while screening fenugreek for CLS. The DLA was found to be temperature sensitive for development of CLS symptoms and wounded leaves developed symptoms faster than un-wounded leaves. These indoor methods can be used for development of CLS resistant fenugreek cultivar in areas where disease development is difficult under field condition.

P2. Identification of rutabaga accessions resistant to new and old pathotypes of *Plasmodiophora brassicae* from Alberta. Z. YU, R. FREDUA-AGYEMAN, S.F. HWANG AND S.E. STRELKOV, *Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB T6G2P5, Canada; and (R. F.-A., S.F.H.) Alberta Agriculture and Forestry, 17507 Fort Road NW, Edmonton, AB, T5Y6H3, Canada.*

Clubroot, caused by *Plasmodiophora brassicae* Wor., is a devastating yield-limiting disease of *Brassica* crops worldwide. The identification of new pathotypes of *P. brassicae* that can cause disease

on clubroot-resistant canola (*Brassica napus* L.) cultivars in Canada has necessitated a search for new resistance sources to be used in breeding. Sixty rutabaga (*B. napus* spp. *napobrassica*) accessions were evaluated for resistance to 10 field- or single-spore isolates representing several of the 'new' and 'old' pathotypes. The new pathotypes included three field isolates classified as pathotype 5X and one field isolate each of pathotypes 5L and 5I. The old pathotypes included one single-spore isolate of each of pathotypes 2F, 3H 5I, 6M and 8N. One accession FGRA107 was resistant (index of disease ≤ 30%) to all 10 isolates while two accessions FGRA037 and FGRA044 were each resistant to nine and moderately resistant (30% < index of disease ≤ 50%) to one isolate. In addition, 58-68% of the rutabaga accessions were resistant to pathotypes 5L, 5I and one isolate of 5X. In contrast, only 5-10% of the rutabaga accessions were resistant to the old pathotypes. The observation that the rutabaga accessions showed significantly ($P < 0.05$) higher resistance to isolates representing the new vs. old pathotypes suggests that clubroot resistance to the new and old pathotypes may be under different genetic control.

P3. Rapid detection of *Leptosphaeria maculans* avirulence gene *AvrLm4-7* conferring the avirulence/virulence specificity on *Brassica napus* using a tetra-primer ARMS-PCR.

Z. Zou, F. Liu, and W.G. D. Fernando. *Department of Plant Science, University of Manitoba, Winnipeg, MB, R3T 2N2, Canada.*

Leptosphaeria maculans is the causal agent of blackleg disease in canola (*Brassica napus*), resulting in significant yield loss in canola fields worldwide. AvrLm4-7 is an avirulence effector gene in *L. maculans*, and a single nucleotide mutation at codon 358 is responsible for the absence of the *AvrLm4* allele. A tetra-primer amplification refractory mutation system-PCR assay (ARMS-PCR) was developed to rapidly differentiate the *AvrLm4AvrLm7* and *avrLm4AvrLm7* genes of L. maculans isolates, which differ by a single point mutation. By this approach, we were able to amplify distinct PCR products to infer the gene of the tested isolates. These results were also confirmed through phenotyping, using the cotyledon inoculation test and two canola genotypes with the corresponding resistance genes. The tetra-primer ARMS-PCR assay developed in this study is a simple, rapid, and useful protocol to identify the *AvrLm4-7* alleles in *L. maculans* isolates. This assay has potential applications in the selection of resistant canola cultivars as part of broader antifungal strategies.

P4. Common bean genotypes selected in field for partial resistance to white mold. T. J PAULA JÚNIOR, R. F. VIEIRA, AND J. E. S. CARNEIRO. *EPAMIG, CP 216, 36570-000 Viçosa (MG), Brazil; (JESC) Department of Plant Sciences, Universidade Federal de Viçosa, 36570-000 Viçosa (MG), Brazil.* *Financial support by CNPq and FAPEMIG.*

Genetic resistance can help farmers to manage white mold (WM) caused by *Sclerotinia sclerotiorum*. We evaluated the performance in field of 20 common bean genotypes screened for reaction to WM in trials conducted between 2008 and 2016. These genotypes included elite lines and recommended control cultivars. Two irrigated trials were conducted in the 2017 fall-winter season in areas with history of WM in Viçosa and Oratórios. Ten lines and the cultivars Ouro Branco and Vereda were selected in field trials for partial resistance to WM; the cultivars Pérola and Estilo for moderate resistance; and the cultivars Ouro Negro, Majestoso and Ouro Vermelho for susceptibility to WM. The international genotypes A195, G122 and Cornell 605, with partial resistance to WM, were also included for comparison. A randomized complete block design with four replications was used. Plots were two 3 m-long rows, spaced 0.50 m apart. WM pressure was moderate in Viçosa and moderate/high in Oratórios. The lines CNFC 10432 and CNFP 11990 were in the group of the genotypes with the highest yield in both sites. These lines and the genotypes A195 and G122 generally were in the group with lower white mold severity. The cultivars Ouro Negro, Ouro Vermelho and Majestoso as well as the line CNFC MG11-08 were the genotypes most susceptible to WM. The carioca bean line CNFC 10432 and the black line CNFP 11990 confirm the good performance they have had since 2012 in areas with a history of WM.

P5. Genetic analysis of ergot resistance in a Canada Western Red Spring Wheat population. S. BERRAIES, H. L. CAMPBELL, R. E. KNOX, R. D. CUTHBERT, Y. RUAN, V. BHADAURIA, B. MEYER, S. KUMAR AND R. M. DEPAUW. *Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, 1 Airport Road, Swift Current, SK S9H 3X2; (S.K.) Department of Genetics and Plant Breeding, Chaudhary Charan Singh University, Meerut, Uttar Pradesh, India; (R.M.D) Advancing Wheat Technology, 870 Field Drive, Swift Current, SK, S9H 4N5, Canada.*

The fungal pathogen *Claviceps purpurea* (Fr.) Tul. infects wheat ovaries during flowering causing ergot disease. The disease is significant because toxic alkaloids present in ergot sclerotia are harmful to the circulatory system and neurotransmission of both humans and animals when infested grain is consumed. Few sources of resistance to *C. purpurea* have been reported in wheat and no specific resistance genes have been identified. We grew in the field near Swift Current, Canada over multiple years a doubled haploid hard red spring wheat population of 774 lines from a cross of Carberry by AC

Cadillac and evaluated natural ergot infection. Genotyping was done with the Infinium II iSelect 90K wheat assay and 6806 single nucleotide polymorphisms were mapped. Composite interval mapping detected seven quantitative trait loci (QTL) were detected. Carberry contributed resistance alleles for QTL on chromosomes 2B, 5A, and 6A while QTL on chromosomes 2A, 3D2, 6B, and 7B were contributed by AC Cadillac. The expression of the 2B, 5A, and 6B QTL was more stable as they were detected in more than one environment. Among the seven QTL, the 7B QTL explained the least phenotypic variation of 1.3%, while the QTL on chromosome 6B accounted for the most phenotypic variation at 4.4%. This information will be valuable in marker assisted breeding for ergot resistance in hexaploid wheat.

P6. A stable quantitative trait locus conditioning leaf rust (*Puccinia triticina*) resistance on chromosome 2D of the wheat cultivar 'Stettler'. F. E. BOKORE, R. D. CUTHBERT, R. E. KNOX, B. D. MCCALLUM, C. HIEBERT, A. N'DIAYE, R. DEPAUW, C. MCCARTNEY, C. J. POZNIAK, Y. RUAN, C. MUNRO, H. L. CAMPBELL AND B. MEYER. *Swift Current Research and Development Centre, Agriculture and Agri-Food Canada, 1 Airport Road Box 1030, Swift Current, SK, Canada, S9H 3X2; (B.D.M., C.H., C.M.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Unit 100, Morden, MB, Canada, R6M 1Y5; (A.N., C.J.P.) Department of Plant Sciences and Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK, Canada, S7N 5A8; (R.D.) Advancing Wheat Technology, 870 Field Drive, Swift Current, Saskatchewan, Canada, S9H 4N5; (C.M.) Plant and Food Research Canterbury Agriculture and Science Centre, Gerald St, Lincoln 7608, New Zealand.*

'Stettler' is moderately susceptible to prevalent races of leaf rust (*Puccinia triticina* Erikss.) but expresses uncharacterized resistance. The objective of this study was to investigate the genetic basis of resistance to leaf rust in 'Stettler'. A doubled haploid population of 218 lines was developed from a cross of 'Stettler' with the heritage cultivar 'Red Fife'. The population was evaluated for leaf rust reaction in four field nursery environments in Canada near Swift Current, SK in 2014 and 2015, Morden MB in 2015 and New Zealand near Lincoln in 2014. Genotyping was performed using the 90K Infinium iSelect assay and linkage maps were constructed by JoinMap using 1548 non-redundant markers. Quantitative trait locus (QTL) analysis was performed in MapQTL6. 'Stettler' generally exhibited lower leaf rust infection than 'Red Fife' and most DH lines. A stable QTL conditioning leaf rust resistance was identified from 'Stettler' on chromosome 2DS. QTL confined to single environments were also contributed by 'Stettler' on chromosome 6B and 'Red Fife' on chromosomes 7A and 7B. Although SNP markers associated with the QTL on 2DS are in the proximity of SSR markers that co-segregate with *Lr22*, based on pedigree and level of gene expression, the 'Stettler' locus is more likely *Lr2a* than *Lr22*, but could be another unique gene. With the genetic markers reported here, the potential exists for the stacking of the 2D minor resistance gene with other genes.

P7. Quantitative trait loci associated with pasmo resistance in flax. F. M. You[1], L. He[1,2], K. Y. Rashid[3], Z. Yao[3], P. Li[3], J. Xiao[2], X. Wang[2], and S. Cloutier[1]. *[1]Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa, ON, Canada; [2]State Key Lab of Crop Genetics and Germplasm Enhancement, Nanjing Agricultural University, Nanjing, China; [3]Morden Research and Development Centre, Agriculture and Agri-Food Canada, Morden, MB, Canada.*

Pasmo is one of the most prevalent and widespread diseases limiting flax production. To improve genetic resistance to this disease, we phenotyped 370 accessions of the flax core collection in the field for pasmo resistance (PR) from 2012 to 2015 in Morden, MB, Canada. Genome-wide association study (GWAS) analyses using 258,873 SNPs were performed using ten different statistical models including the traditional single-locus and the most recent multi-loci methods. A total of 355 unique quantitative trait nucleotides (QTNs) with significant effects, corresponding to 296 potential quantitative trait loci (QTL), were identified from the four individual year's datasets. Different QTNs were obtained from the various methods and datasets, indicative of the complementation between analytical methods and/or genotype x environment interaction of the QTL effects. From these putative QTL, 47 were stable across all four years, had relatively large effects (>5%), and explained 22-46% of the total variation for PR. Of these, 40 span resistance gene analogs. The number of positive-effect QTL (NPQTL) in accessions was significantly correlated to PR, indicative of their additive effects. NPQTL was also significantly associated with morphotype where most of the positive-effect QTL for PR were present in the fiber type accessions, thus making this germplasm an important source for PR improvement of linseed. The identified QTL can be used as molecular markers for germplasm evaluation, and parent and offspring selection in flax PR molecular breeding.

P8. Genetic mapping of leaf rust resistance genes *LrCen* and *LrMar*. B. McCALLLUM, M.Z. CHE, M. BOYCE, C.W. HIEBERT, A.L. BRULE-BABEL; C.A. McCARTNEY, AND Z.J. ZHANG. (B.M., C.W.H., C.A.M.) *Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Unit 100, Morden, MB, R6M 1Y5;* (M.Z.C., Z.J.Z.) *Department of Plant Pathology, China Agricultural University, Beijing, 100193, People's Republic of China;* (M.B.) *Global Edible Oil Solutions - Specialties, Cargill Ltd. Canada, 701 Central Ave. Aberdeen, SK, Canada, S0K 0A0; and* (A.L.B.-B.) *Department of Plant Science, University of Manitoba, Winnipeg, MB, R3T 2N2, Canada.*

A group of *Puccinia triticina* Eriks. isolates with similar virulence phenotypes, represented by TDBG, predominated in the annual Canadian virulence surveys from 2004 to the present. These had an unusual mesothetic infection type on most plants within the Thatcher-*Lr1* line, RL6003, which was due to a previously undetected second resistance gene in this line, temporarily named *LrCen*. *LrCen* was mapped to chromosome arm 7AL, 1.1 cM from the closest marker, cfa2240. RL6071, a rust susceptible

Marquis derivative, was also found to carry a phenotypically similar resistance gene effective only against this same group of virulence phenotypes. However, this gene from RL6071 was mapped on 7BL at 1.8 cM from marker barc182 in a doubled haploid population from the cross RL6071/KU168-2, and was temporarily named *LrMar*. These genes are widely distributed in Canadian wheat, are effective against the same small number of virulence phenotypes, and map to similar locations on homeologous chromosomes.

P9. Field testing of alfalfa populations carrying root-rot resistance and freezing tolerance.

P. AUDY, S. ROCHER AND A. CLAESSENS. *Quebec Research and Development Centre, Agriculture and Agri-Food Canada, Québec, QC G1V 2J3, Canada.*

Two important traits affecting productivity in alfalfa under cold climate conditions are root-rot disease resistance and freezing tolerance. In the last few years, Castonguay's group in Quebec has improved several alfalfa backgrounds for their tolerance to freezing (TF populations) using recurrent selections under controlled conditions (Castonguay et al., 2009). In the present study, we have used two alfalfa cultivars, Apica and Caribou that has previously gone through three cycles of recurrent selection for freezing tolerance (TF3-derived populations). We proceeded with three additional cycles of selection for resistance to Phytophthora root rot (PRR) caused by Phytophthora medicaginis. PRR is one of the major causes of decline of established alfalfa in North America. At each cycle of selection, 1500 genotypes of these two PRR-sensitive backgrounds were screened using a blend of four PRR isolates coming from diverse locations in Canada. PRR-resistant cultivar Amerigraze and PRR-sensitive cultivar Saranac seedlings were used as controls. The one hundred (100) most PRR-tolerant genotypes of each background were selected and intercrossed to generate seeds for the next cycle of selection (eg; APRR1 for Apica TF3 after one cycle of selection, CPRR1 for Caribou TF3 after one cycle of selection, etc...). We assessed these alfalfa populations (for Apica; ATF3, APRR1, APRR2, APPR3; for Caribou; CTF3, CPRR1, CPRR2, CPRR3, and controls; Amerigraze, Saranac) for their yield performance under clay-rich field conditions for two years (third year now) in plots near Quebec City. A 3-summer cut schedule was used. Phytophthora medicaginis is a naturally occurring pathogen in the chosen field and therefore, the test plot was not further inoculated. Aphanomyces euteiches was also present in the soil but to a less extent. Alfalfa populations with improved PRR-resistance were significantly more productive than the original TF3-Apica and TF3-Caribou populations (improved tolerance to freezing). The notable yield increase was mostly due to the fact a lot more alfalfa plants survived in the PRR-improved populations whereas no significance yield difference between the surviving plants was found for all treatments.

P10. Evaluation of different oak leaf extracts for the control of bacterial leaf spot of lettuce. V. TREMBLAY, V. TOUSSAINT AND R. J. TWEDDELL. *Département de phytologie, Université Laval, Québec, QC, G1V 0A6, Canada; and (V.T.) Agriculture and Agri-Food Canada, 430 boulevard Gouin, Saint-Jean-sur-Richelieu, QC J3B 3E6, Canada.*

Oak (*Quercus* spp.) leaf extracts were reported in several studies to have antimicrobial properties. Such properties could be exploited for the control of bacterial diseases affecting horticultural crops for which very few antibacterial chemicals are available. As part of ongoing research aimed to develop new strategies to control bacterial leaf spot (*Xanthomonas campestris* (Pammel) Dowson pv. *vitians*) of lettuce (*Lactuca sativa* L.), the objectives of the study were (1) to test different red oak (*Quercus rubra* L.) leaf extracts (aqueous, ethanol:water, acetone:water) for their antibacterial activity against *X. campestris* pv. *vitians* and (2) to evaluate their efficacy to control bacterial leaf spot of lettuce. Antibacterial activity of the extracts was determined using standard procedures. Efficacy of the extracts to control bacterial leaf spot was tested on lettuce plants grown in greenhouse. With a minimum bactericidal concentration of 12.5 mg mL^{-1}, ethanol extracts (40:60 and 20:80, ethanol:water) showed the strongest antibacterial activity. Foliar application of aqueous, ethanol (80:20, 60:40, and 40:60), and acetone (50:50 and 20:80, acetone:water) extracts allowed a marked reduction in disease severity when the disease pressure was low to moderate. Moreover, addition of sodium bicarbonate (0.2 M) was shown to increase the efficacy of ethanol extracts (80:20 and 60:40) to control the disease. In conclusion, oak leaf extracts show potential for controlling bacterial leaf spot of lettuce and could eventually find application to control bacterial diseases affecting horticultural crops.

P11. Evaluation of antagonistic activity of *Bacillus pumilus* and *Bacillus subtilis against Botrytis cinerea.* M. BOUCHARD-ROCHETTE, T. T. A. NGUYEN, R. NAASZ, H. ANTOUN AND R. J. TWEDDELL. *Département de phytologie, Université Laval, Québec, QC, G1V 0A6, Canada; (T.T.A.N., H.A.) Département des sols et de génie agroalimentaire, Université Laval, Québec, QC G1V 0A6, Canada; and (R.N.) Premier Tech, 1 avenue Premier, Rivière-du-Loup, QC G5R 6C1, Canada.*

Gray mold, caused by the fungus *Botrytis cinerea* Pers., is one of the most damaging diseases affecting horticultural crops. *Bacillus pumilus* Meyer and Gottheil strain PTB 180 and *Bacillus subtilis* (Ehrenberg) Cohn strain PTB 185 have shown antifungal activity against several soilborne fungal pathogens. This study aims to investigate *in vitro* the antagonistic activity of PTB 180, PTB 185, and a mix (1:1) of both strains against *B. cinerea*. The antagonistic activity of PTB 180 and PTB 185 was evaluated on agar (using a double layer technique) and on tomato (*Solanum lycopersicum* L.)/cucumber (*Cucumis sativus* L.) leaf discs placed in petri plates. Both strains were shown on agar to inhibit *B.*

cinerea mycelial growth by more than 90% and spore germination by more than 50%. When applied (1×10^7 colony forming units mL^{-1}; 1 mL) prior to *B. cinerea* inoculation (1×10^6 propagules mL^{-1}, 100 µL) PTB 180, PTB 185, and a mix (1:1) of both strains inhibited significantly mycelial growth of the fungus on tomato/cucumber leaf discs as compared to the control. In conclusion, PTB 180 and PTB 185 showed strong antagonistic activity against *B. cinerea,* suggesting that they could eventually find application as biocontrol agents against gray mold. Greenhouse tests will be conducted to evaluate their efficiency in controlling the disease on tomato/cucumber plants.

P12. *Bacillus pumilus* and *Bacillus subtilis* for the biocontrol of soilborne diseases of greenhouse cucumber. E. DEMEULE, T. T. A. NGUYEN, R. NAASZ, H. ANTOUN AND R. J. TWEDDELL. *Département de phytologie, Université Laval, Québec, QC G1V 0A6, Canada; (T.T.A.N., H.A.) Département des sols et de génie agroalimentaire, Université Laval, Québec, QC G1V 0A6, Canada; and (R.N.) Premier Tech, 1 avenue Premier, Rivière-du-Loup, QC G5R 6C1, Canada.*

Soilborne diseases cause important economic losses in greenhouse cucumber (*Cucumis sativus* L.) production. Chemical fungicides are widely used to control these diseases. However, concerns about their negative effects (development of resistance, residues in food, occupational exposure, environmental impacts) have motivated the development of new alternatives such as biocontrol agents. As part of ongoing research on the biocontrol capability of *Bacillus pumilus* Meyer and Gottheil strain PTB180 and *Bacillus subtilis* (Ehrenberg) Cohn strain PTB185, we investigated their antagonistic activity against *Rhizoctonia solani* J.G. Kühn, *Pythium ultimum* Trow, *Sclerotinia sclerotiorum* (Lib.) de Bary, *Phytophthora capsici* Leonian, and *Fusarium oxysporum* Schltdl. on agar using a double layer technique. Greenhouse experiments were subsequently conducted to determine the efficacy of the strains to control collar and root rot on cucumber plants inoculated with *R. solani*. Results showed that both PTB180 and PTB185 strongly inhibited mycelial growth of *R. solani, P. ultimum, S. sclerotiorum, P. capsici*, and *F. oxysporum* on agar. PTB180, PTB185, and a mix (1:1) of both strains reduced significantly the severity of collar and root rot caused by *R. solani* on cucumber plants grown in greenhouse. This study suggests that strains PTB180 and PTB185 could eventually represent a sustainable alternative to the use of chemical fungicides for the control of soilborne pathogens affecting greenhouse cucumber production.

P13. Integrated management of grey mold on greenhouse tomato: efficacy of biological control. O. CARISSE, T. ARSENEAULT AND G. MARCHAND. (O.C., T.A.) *Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu Research and Development Centre, 430 Gouin Boulevard, Saint-Jean-sur-Richelieu, QC J3B 3E6, Canada; and (G.M.) Agriculture and Agri-Food Canada, Harrow Research and Development Centre, 2585 County Road 20, Harrow, ON N0R 1G0, Canada.*

Table tomato (*Lycopersicon esculentum* Mill.) is the leading greenhouse vegetable crop in Canada. Grey mold (*Botrytis cinerea*) is endemic and can result in high yield losses due to stem wound infections, which may cause the death of an entire plant. In greenhouse tomato production, de-leafing of plants is necessary to manage vegetative/reproductive balance. However, this practice can result in *B. cinerea* spores being shaken from lesions, becoming airborne, and settling onto the fresh stem wounds. Considering the high level of fungicide resistance in *B. cinerea* populations, biological control should play a key role in integrated grey mold management. The objective of this study was to evaluate the efficacy of Botector, a bio-fungicide containing two strains of *Aureobasidium pullulans* (de Bary) Arnaud, a yeast-like fungus. Results from this study Results from competition experiments confirmed the ability of Botector to establish itself in stem lesions in the presence or absence of *B. cinerea*. Efficacy of Botector was significantly higher when it was applied prior to *B. cinerea* inoculation, and efficacy increased with increasing time between sprays of Botector and *B. cinerea* with 87.6%, 92.4%, and 99.0% reduction of symptoms for intervals of 1, 6, and 24 h, respectively. However, when Botector was applied after inoculation with *B. cinerea*, efficacy was reduced and decreased with increasing time between sprays of Botector and *B. cinerea*, with efficacies of 75.3%, 69.5%, and 29.8% for intervals of 1, 6, and 24 h, respectively. Results from these experiments suggest that Botector should be used as a preventative, pre-infection treatment.

P14. Date palm-*Fusarium oxysporum albedinis* interaction: enhancement of defense responses with different non-pathogenic microorganisms. M. El HASSNI, A. EL HADRAMI, F. DAAYF, A. DIHAZI AND K. NAAMANI. *Laboratoire de Biotechnologie et Développement Durable des Ressources Naturelles, Faculté Polydisciplinaire, Mghila BP. 592, Université Sultan Moulay Slimane Beni Mellal 23000, Maroc; (A. E.) OMEX Agriculture Inc. 290 Agri Park Road, Oak Bluff, MB R4G 0A5, Canada; (F. D) Department of Plant Science, 222 Agriculture Building, University of Manitoba, Winnipeg, MB, Canada R3T 2N2; (A. D) and (K. N) Laboratorie de Protection et Valorisation des Ressources Végétales, Faculté des Sciences **Semlalia**, Université Cadi Ayyad Avenue My Abdellah BP 2390, Marrakech 40 000 Maroc.*

The Bayoud, caused by *Fusarium oxysporum* f. sp. *albedinis* (Foa), is the most devastating disease of date palm (*Phoenix dactylifera* L.) in Morocco and southwest of Algeria. Since no effective treatments are currently available, biological control and the enhancement of plant defense responses provide an

alternative for disease management strategy. The first part of this work consisted of eliciting defense reactions in roots with a hypo-aggressive isolate of *Fusarium oxysporum* (AHD). Pre-treatment of the seedlings with AHD enhanced faster enzymatic activities (PPO and POX) to reach levels as high as those obtained in response to the inoculation with the aggressive isolate ZAG in both the susceptible (JHL) and resistant (BSTN) cultivar. Inoculation with AHD also induced a rapid increase in caffeoylshikimic acids and an accumulation of non-constitutive hydoxycinnamic acid derivatives and chiefly a sinapic derivative known as I2. In the second part, four bacteria *Bacillus pumilus* W1, *Bacillus cereus* X16, *Rahnella aquatilis* W2 and not yet identified S1 were selected among 21 microorganisms exhibiting a high inhibition toward mycelia growth of Foa (70-77%) and its sporulation (80-95%). These antagonists in addition to *Bacillus subtilis* B1 and *Pseudomonas* Sp. P1 have presented the potential in the induction and synthesis of non-constitutive hydoxycinnamic derivatives in the roots of the inoculated seedlings. The level of their accumulation varied based on the antagonist and the time of incubation. Results are discussed in the perspective of implementing a control strategy that relies on the use of biocontrol agents to trigger defenses responses against bayoud.

P15. Genome analysis of *Pseudomonas sp.* strain S1Bt23, a potent fungal antagonist, reveals the presence of phenazine and pyrrolnitrin gene clusters. S. F. PINTO, H. BALASUNDARAM, R. XU AND J. T. TAMBONG. *Ottawa Research and Development Research Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, Ontario, K1A 0C6, Canada.*

Species of the genus *Pseudomonas* have been proven to be environmentally significant e.g. as phytopathogens, biological control agents, and xenobiotic degraders. Certain species such as *Pseudomonas chlororaphis* are able to synthesize metabolites implicated in bioprotection of crops against fungal pathogens. We demonstrated that strain S1Bt23 inhibited, *in vitro,* in dual cultures, the growth of *Rhizoctonia solani, Fusarium graminearum, Alternaria solani, Pythium ultimum* and *Pythium arrhenomanes.* The objectives of this study were (1) to determine the taxonomic position of the strain using a polyphasic approach and (2) to analyze the genome of strain S1Bt23 for antifungal gene clusters. 16S rRNA sequence analyses suggested that strain S1Bt23 was affiliated with the genus *Pseudomonas*. Multi-locus sequence analyses (MLSA) using *rec*A, *gyr*B, *rpo*B and *rpo*D clustered strain S1Bt23 uniquely within the subspecies of *P. chlororaphis*. The genome of S1Bt23 was sequenced and genome-based DNA-DNA hybridization (dDDH) and MuMmer-based average nucleotide identity (ANIm) performed with four putative *P. chlororaphis* subspecies. Based on dDDH, ANIm and proteome data, we conclude that strain S1Bt23 is an authentic novel subspecies within the species *P. chlororaphis.* In-depth genome analysis of strain S1Bt23 identified the presence of phenazine and pyrrolnitrin gene clusters known to produce antifungal metabolites. Work is now focused on

determining whether these gene clusters are involved in the potent antifungal properties of strain S1Bt23.

P16. Evaluation of different crop residues for the control of bacterial leaf spot of lettuce. V. TREMBLAY, A. BELLEY, V. TOUSSAINT AND R. J. TWEDDELL. *Département de phytologie, Université Laval, Québec, QC G1V 0A6, Canada; and (V.T.) Agriculture and Agri-Food Canada, 430 boulevard Gouin, Saint-Jean-sur-Richelieu, QC J3B 3E6, Canada.*

Over the past decades, numerous studies have reported that many plant extracts show toxicity against fungi and bacteria. The exploitation of the bactericidal properties of plant extracts represents an interesting approach that could find application for the control of bacterial diseases affecting lettuce (*Lactuca sativa* L.), namely bacterial leaf spot (BLS; *Xanthomonas campestris* (Pammel) Dowson pv. *vitians*). The objectives of the study were (1) to test different extracts produced from crop residues for their antibacterial activity against *X. campestris* pv. *vitians* and (2) to test their efficacy to control BLS. Determination of antibacterial activity of the extracts was carried out using standard procedures. Efficacy of the extracts to control BLS was determined on lettuce plants grown in greenhouse. Aqueous extracts of radish (*Raphanus sativus* L.) leaf and cranberry (*Vaccinium macrocarpon* Ait.), and ethanol:water (80:20) extract of kale (*Brassica oleracea* var. *sabellica* L.) with respective minimum bactericidal concentrations (MBC) of 12.5, 50, and 50 mg mL^{-1} showed the strongest antibacterial activities. Aqueous extracts of broccoli (*Brassica oleracea* L. var. *italica* Plenck), canola (*Brassica napus* L.), kale, radish, and rocket (*Eruca sativa* Mill.) showed MBC higher than 100 mg mL^{-1}. When applied on lettuce plants inoculated with *X. campestris* pv. *vitians*, aqueous, ethanol:water (80:20, 60:40, and 20:80), and acetone:water (40:60 and 20:80) extracts of kale allowed a marked reduction of BLS severity that was observed only under low to moderate disease pressure.

P17. Survival of *Bacillus pumilus* and *Bacillus subtilis* on the phyllosphere of greenhouse tomato and cucumber. M. BOUCHARD-ROCHETTE, T. T. A. NGUYEN, R. NAASZ, H. ANTOUN AND R. J. TWEDDELL. *Département de phytologie, Université Laval, Québec, QC G1V 0A6, Canada; (T.T.A.N., H.A.) Département des sols et de génie agroalimentaire, Université Laval, Québec, QC G1V 0A6, Canada; and (R.N.) Premier Tech, 1 avenue Premier, Rivière-du-Loup, QC G5R 6C1, Canada.*

Bacillus pumilus Meyer and Gottheil strain PTB 180 and *Bacillus subtilis* (Ehrenberg) Cohn strain PTB 185 showed *in vitro* antagonistic activity against *Botrytis cinerea* Pers., suggesting that these bacteria could show antagonistic activity against the pathogen *in plantae*. As part of ongoing research on the

biocontrol capability of strains PTB 180 and PTB 185 against gray mold (*B. cinerea*), the objective of the study was to evaluate their survival, when applied alone and in combination, on tomato (*Solanum lycopersicum* L.) and cucumber (*Cucumis sativus* L.) plants. Tomato and cucumber plants, aged 4 and 2 weeks respectively, were sprayed until runoff with a suspension (1×10^7 colony forming units (CFU) mL^{-1}) of either strain PTB 180, strain PTB 185 or a mix (1:1) of both strains and were then grown in greenhouse for 21 days. Three leaves of each tomato/cucumber plant were collected after 0 (1 hour after the plants were sprayed) 7, 14, and 21 days. Leaves were shredded, placed in sterile water, and mixed thoroughly. The suspensions were submitted to serial dilutions, heated (55°C, 15 minutes), and plated on nutrient agar. After an incubation period of 24 hours at 37°C, the number of CFU was determined. Populations of both strains of *Bacillus* estimated at about 1×10^7 CFU g^{-1} of fresh leaf (0 day) remained as high as 5×10^6 CFU g^{-1} of fresh leaf 21 days following their application on tomato and cucumber plants. In addition, when applied as a mix (1:1), ratio of each bacterial population remained unchanged.

P18. *In vitro* antagonism of biocontrol agents against fungal diseases affecting hemp and marijuana. C. BALTHAZAR, M. FILION AND D. L. JOLY. *Université de Moncton, 18 avenue Antonine-Maillet, Moncton, NB E1A 3E9, Canada.*

Cannabis sativa L. is a herbaceous plant grown worldwide for its narcotic and medicinal uses (marijuana) or as a source of food and fiber (hemp). Following the legislative changes to legalize recreational marijuana in Canada later this year, a renewed interest for this crop now raises concerns about potential recrudescence of its associated diseases and pests. Of particular interest are pathogenic fungi, due to the magnitude of their impact on *C. sativa*. Our goal is to develop and characterize wide-spectrum biological agents that would help control six fungi that have been isolated from hemp or marijuana: *Botrytis cinerea* Pers. causing grey mold, *Sclerotinia sclerotiorum* (Lib.) de Bary causing hemp canker, *Fusarium* sp. causing wilt, root rot and damping-off, *Alternaria alternata* (Fr.) Keissl. causing brown blight, *Nigrospora* sp. potentially causing leaf spot and *Phoma glomerata* (Corda) Wollenw. & Hochapfel causing brown leaf spot and stem canker. Our biological agents are soil-borne beneficial bacteria screened from 184 strains of *Pseudomonas* spp. and *Bacillus* spp. Confrontational assays were set up *in vitro* and revealed great biocontrol potential for at least 2 strains of *Pseudomonas* spp. and 3 of *Bacillus* spp. Whole genome sequencing and transcriptomic studies are currently underway, along with a validation of the reduction of symptoms *in planta.* Biological control could be a viable alternative to the use of chemical fungicides, the use of which is controversial in *Cannabis* production. Moreover, a better understanding of the molecular interactions between the host plant, the

pathogenic fungi and the beneficial bacterium could offer new insights to control emerging threats against this crop.

P19. Does inoculation with the biocontrol agent *Pseudomonas fluorescens* LBUM223 impact the rhizosphere and geocaulosphere microbiomes of potato? R. ROQUIGNY, A. NOVINSCAK, M. FILION AND D. L. JOLY. *Université de Moncton, 18 avenue Antonine-Maillet, Moncton, NB E1A 3E9, Canada.*

The phenazine-1-carboxylic acid (PCA)-producing *Pseudomonas fluorescens* Migula strain LBUM223 shows biocontrol capacity by reducing symptoms of the causal agent of common scab of potato, *Streptomyces scabies* (Thaxter) Waksman & Henrici. The aim of this study is to better characterize the impact of inoculating a specific biocontrol agent under natural field conditions on the microbiomes of the rhizosphere and the geocaulosphere of potato plants using Next-Generation sequencing. Single or biweekly applications of LBUM223 were performed up to 11 weeks after planting (in addition to non-inoculated plants). Rhizosphere and geocaulosphere (when potato tubers were produced) soils were sampled every two weeks. Following soil DNA extractions, 16S rRNA gene amplification and sequencing were performed using the Illumina MiSeq technology. The QIIME pipeline was used for data analyses. Results were generated from 45 rhizosphere and 27 geocaulosphere samples, for which 63,502 and 44,469 different operational taxonomical units were observed. Diversity comparisons were performed between both datasets. To our knowledge, this is the first time that the geocaulosphere microbiome is characterized and compared to the rhizosphere. Eleven phyla accounted for 95% of the diversity, with Actinobacteria, Proteobacteria, Chloroflexi and Acidobacteria being the most important ones. Overall, the results obtained suggest that *Pseudomonas fluorescens* LBUM223 does not significantly interfere with the autochthonous rhizosphere or geocaulosphere microbiomes, providing first insights on its non-target safety in the field.

P20. Preliminary Results of the 2017 Manitoba Soybean Cyst Nematode Survey. N. GHAVAMI*, M. TENUTA., AND D. LANGE. *Department of Soil Science, University of Manitoba, Winnipeg, MB, Canada, R3T 2N2; (D.L.) Manitoba Department of Agriculture, Altona, MB, R0G 0B0, Canada.*

Soybean Cyst Nematode (SCN), *Heterodera glycines*, is one of the most devastating disease/pest organisms of soybean worldwide. The nematode is expected to soon be present in Manitoba as the pest is in every major soybean growing region of the world, including Ontario and Quebec in Canada, and North Dakota and Minnesota that border Manitoba. Early detection of SCN before it establishes in

Manitoba is critical to limit yield losses. Therefore, the objective of this on-going study is to survey soybean fields in Manitoba for the presence of SCN. The project continues from surveys conducted from 2012 to 2015 that did not find the nematode. In the current study, 30 commercial soybean fields in Manitoba near the U.S. border with history of soybean and edible bean cultivation were sampled. Each field was sectioned into areas prone for the establishment of SCN, including; headlands, entrances, in-field drainage courses, depressions and remaining field. A total of 90 composite soil samples were obtained for about 3 samples for analysis per field. A modified Fenwick elutriator (soil washing unit) based on the USDA soil cyst extractor was used to recover nematode cysts. Cysts were extracted from debris obtained from the elutriator by using ethanol flotation. Overall, 17 of the composite samples from 12 fields had nematode cysts. One to a few cysts were recovered from each of these 17 composite samples. In total, 42 cysts were recovered and most of the cysts were round and not lemon-shaped as expected of SCN, the cysts also were intact for morphological and molecular examination. Cyst identification based on morphology and genetic structure is on-going and will be presented. We hope to address the question, "is Manitoba still free of the soybean cyst nematode?"

P21. Development of multiplex protocols to detect grapevine wood diseases. C. PROVOST, K. OZAKI, C. GUERTIN AND E. DEZIEL. *Centre de recherche agroalimentaire de Mirabel. 9850 rue Belle-rivière, Mirabel. Québec, J7N 2X8, Canada; (K.O, C.G, E.D.) INRS – Institut Armand-Frappier, 531 boulevard des Prairies, Laval, Québec, H7V 1B7, Canada.*

Grapevine wood diseases are considered very damaging to the sustainability of viticultural heritage in all major wine regions of the world. Several fungi are responsible for these diseases and attack the perennial organs of the vine, which causes plant death in a short or medium term. Grapevine wood diseases can affect young plantations such as aging vineyards where the risk related to the presence of these diseases is growing in vineyards across the province of Quebec. The main objective of this project is therefore to develop laboratory methods to rapidly detect ten pathogenic fungi associated with five grapevine wood diseases that are, or are expected to become, prevalent in Canada. The diseases targeted in the project are Esca, Black foot, Black dead arm, *Eutypa* dieback, and Dead-arm disease. To achieve this goal, we chose an approach that uses multiplex real-time PCR, in which TaqMan® hybridization probes can target and bind to different genomic markers of the pathogenic agents. Four multiplex systems were developed, one for each disease, and are ready to use with field samples. For example, the first duplex system, targeting the internal transcribed spacer 1 (ITS1) region of the studied pathogens, can detect DNA from *Phaemoniella chlamydospora* and *Phaoacremonium aleophilum*, which are two fungal species that cause Esca. The benefits of this project will enable the various

stakeholders in the vineyard to have access to accurate, reliable and rapid diagnostic methods, which will have a positive impact on the overall health of Quebec's vineyards.

P22. Physiologic races of *Puccinia coronata* var *avenae* f. sp. *avenae* in Canada during 2010 to 2017. J. Menzies, A. Xue, C. Azar. *Morden Research and Development Centre, Agriculture and Agri-Food Canada, Unit 101 Route 100, Morden, MB R6M 1Y5, Canada; (A.X.) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; (C.A.) Crop Production Research Farm, La Coop fédérée, Saint-Hyacinthe, QC J2T 5J4, Canada.*

Crown rust of oat, caused by *Puccinia coronata* Corda var *avenae* f. sp. *avenae* (Urban & Marková, 1993) (*Pca*), is a problematic disease of oat. Breeding for resistant varieties has been an important method of controlling this disease. Since *Pca* is highly genetically variable, a thorough knowledge of the races in the pathogen population is necessary to identify effective genes for resistance for breeding and gene deployment. This study's objective was to determine the frequency of virulence genes present in *Pca* isolates collected from oat plants in Canada during 2010 to 2017. Single pustule isolates from infected leaves were inoculated onto a standard set of 16 differential isolines (*Pc28*, *Pc39*, *Pc40*, *Pc45*, *Pc46*, *Pc48*, *Pc50*, *Pc51*, *Pc52*, *Pc54*, *Pc56*, *Pc58*, *Pc59*, *Pc62*, *Pc64*, *Pc68*) and 8 additional isolines (*Pc91*, *Pc94*, *Pc96*, *Pc97*, *Pc98*, *Pc101*, *Pc103-1*, *Pc104*) at the seedling stage. Virulence frequencies varied between eastern Canada (Ontario and Quebec) and western Canada (Manitoba and Saskatchewan). Virulence to *Pc38* and *Pc68* was observed at frequencies of >50% in Canada. *Pc94* was the most effective resistance gene in western Canada, with virulence frequencies to *Pc94* of <2%. Virulence to *Pc98* and *Pc101* was not observed in eastern Canada. The most dramatic increase in virulence was to *Pc91* in western Canada with frequencies that increased from 0% in 2010 and 2011 to 80% in 2016.

P23. Towards improved recovery efficiency and identification accuracy of cereal rust fungal pathogens in environmental samples. W. CHEN, S. HAMBLETON, H-Y ZHANG, K. CHUENG, Mei-Lan de Graaf, Q. EGGERTSON, G. BAKKEREN. *(W.C., S.H. H-Y.Z, K.C) Ottawa Research and Development (R&D) Centre, Agriculture and Agri-Food Canada (AAFC), 960 Carling Ave., Ottawa, ON, K1A 0C6, Canada; (K-Y.Z) Inner Mongolia Agricultural University, 306 Zhaowuda Rd, Hohhot, Inner Mongolia, China, 010000; (M-L.deG, G.B) Summerland R&D Centre, AAFC, 4200 Highway 97, Summerland, BC, V0H 1Z0, Canada.*

The rust fungus family Pucciniaceae includes devastating pathogens to cereal crops which produce airborne spores disseminated by wind and storms, generating a source of inocula to nearby and distant host plants. The abundance and dispersal pathways of the inocula can be monitored by analyzing DNA from spore collectors using metabarcoding approaches, providing early warning of potential disease epidemics. From 2007 - 2011 (n=344) and 2015 - 2016 (n=117), air/rain-borne spore samples were collected by a network of equipment in agricultural fields across Canada. ITS DNA barcodes, obtained using universal primers ITS5/ITS4 to amplify both internal transcribed spacers (ITS1 and ITS2) and 454-pyrosequencing technology in 2007-2011, recovered only 17 Pucciniaceae Operational Taxonomic Units (OTUs) (0.2% richness, 0.38% total abundance). Using rust-enhanced primers targeting ITS2 (Rust2inv/ ITS4var) and the Illumina MiSeq platform in 2015-2016, 1594 Pucciniaceae OTUs (10.5% richness, 7.65% total abundance) were recovered and they showed spatial-temporal distribution patterns in Canada's air. The identity of these metabarcodes were evaluated utilizing signature oligonucleotides designed from a curated in-house reference database using the automated oligonucleotide design pipeline (AODP). Our results show that the universal primer set, commonly used for fungal DNA barcoding studies, did not recover the near-complete diversity of rusts from environmental DNAs, partially due to low primer efficiency and the challenge in sequencing the ITS1 region for this group. Considering the severe economic loss related to cereal rust epidemics, improved recovery efficiency and identification accuracy of the causal agents are essential knowledge for establishing a reliable pest management protocol.

P24. A molecular evaluation of collections (2005-2016) of *Plasmodiophora brassicae* from Alberta for the presence of pathogen populations able to overcome clubroot resistance. M.D. HOLTZ, S.F. HWANG, V.P. MANOLII AND S.E. STRELKOV. *Field Crop Development Centre, Alberta Agriculture and Forestry, 5030-50 Street, Lacombe, AB T4L 1W8, Canada; (S.F.H.) Alberta Agriculture and Forestry, Crop Diversification Centre North, 17507 Fort Road, Edmonton, AB, T5Y 6H3; and (V.P.M., S.E.S.) University of Alberta, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, T6G 2P5, Canada.*

Plasmodiophora brassicae Woronin, the cause of clubroot, was first identified as a disease of canola (*Brassica napus* L.) in central Alberta in 2003 and has since spread to more than 30 counties in the province. Clubroot resistant (CR) canola cultivars became available in 2009 and now represent the most important clubroot-management tool. Highly virulent *P. brassicae* strains able to overcome this resistance, however, have been confirmed in more than 100 fields in Alberta, with the first of these strains identified in Westlock County in 2013. Initial genetic analysis of these Westlock strains indicated that they belonged to a population that was distinct from other *P. brassicae* strains. Using SYBR green and TaqMan-based quantitative PCR assays developed to distinguish members of the pathogen population virulent on CR canola from the more common population, samples of *P. brassicae* collected in Alberta from 2005-2016 were examined to determine the historical occurrence and distribution of these virulent strains. Two hundred and nineteen root-gall samples were examined, of which 10 samples were identified as being infected with members of the *P. brassicae* population virulent on CR canola. These samples were found in Flagstaff County starting in 2008, Westlock County starting in 2009, the County of Vermillion River in 2011, and Red Deer County in 2014. Although relatively uncommon, members of this population were relatively widespread, occurring at locations 170 km apart prior to the release of CR canola. This widespread distribution may have helped hasten the loss of resistance in the CR canola varieties.

P25. Evans blue staining is a rapid and accurate method for evaluating inactivation of *Plasmodiophora brassicae* resting spores by chemical disinfectants. M. W. HARDING, T. B. HILL, G. C. DANIELS, S. E. STRELKOV, S. F. HWANG AND J. FENG. *Alberta Agriculture and Forestry, Crop Diversification Centre South, 301 Horticultural Station Road East, Brooks, Alberta T1R 1E6; (S.E.) University of Alberta, Agriculture Food and Nutritional Sciences, 410 Agriculture-Forestry Centre, Edmonton, Alberta T6G 2P5; (S.F.H., J.F.) Alberta Agriculture and Forestry, Crop Diversification Centre North, 17507 Fort Road NW, Edmonton, Alberta, T5Y 6H3, Canada.*

Clubroot is an important disease on canola caused by the protist *Plasmodiophora brassicae* Woronin. Over the past 15 years, it has spread rapidly across much of central and northern Alberta and was more recently confirmed in Saskatchewan and Manitoba. It is widely accepted that the rapid spread in Alberta has been due in large part to movement of infested soil on farm or construction equipment. Equipment sanitization is the recommended practice for preventing unintentional spread of infested soil to new fields. The thick-walled resting spores produced by *P. brassicae* are very capable of surviving harsh physical and chemical treatments, therefore it is important to know which disinfectants, if any, can quickly and effectively inactivate resting spores. Evans blue, a vital stain that can discriminate viable from non-viable resting spores, was used to evaluate ten chemical disinfectants for their efficacies versus resting spores. Repeated experiments, comparing bioassay results with spore staining, indicated that Evans blue staining was a reliable and rapid method to evaluate efficacies of most disinfectants tested. Only two of the disinfectants tested, sodium hypochlorite and ethanol, were capable of achieving greater than 95% inactivation of resting spores.

P26. Survey of clubroot (*Plasmodiophora brassicae*) pathotypes in canola and Brassica vegetable fields in Ontario in 2017. F. AL-DAOUD, M. MORAN, T.J. CRANMER, M.J. CELETTI, B.D. GOSSEN, A. TENUTA, AND M.R. MCDONALD. *Department of Plant Agriculture, University of Guelph, Guelph, ON, N1G 2W1, Canada; (M.M.) Ontario Ministry of Agriculture, Food, and Rural Affairs, Stratford, ON N5A 6S5, Canada;* (*T.J.C., M.J.C., A.T.*) *Ontario Ministry of Agriculture, Food, and Rural Affairs, Guelph, ON N1G 4Y2*; *(B.D.G.) Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, Saskatoon, SK, S7N 0X2, Canada.*

Plasmodiophora brassicae Woronin is the causal agent of clubroot, a major disease affecting several economically important members of the family Brassicaceae. Clubroot is endemic on Brassica vegetables in many regions of Ontario, and in 2016 it was reported for the first time on canola in the province. The pathotype of *P. brassicae* was assessed from six canola fields and seven vegetable fields in Ontario in 2017. The inoculum from clubbed roots was increased on a susceptible host (Shanghai

pak choy cv. 'Mei Qing Choi', *Brassica rapa* var. *chinensis*) grown under controlled conditions (25/20 ºC day/night, 60% relative humidity, 18 hrs photoperiod). The resulting clubs were harvested at 6 weeks post inoculation (wpi) and used to inoculate cultivars that comprise Williams' differential set. Four replicates were used with 5-6 plants per experimental unit. Plants were rated for clubroot symptoms using a 0-3 scale at 5 wpi, and a disease severity index (DSI) was calculated. A host was resistant if DSI + 95% confidence interval < 50%; otherwise it was susceptible. Samples from four canola fields were pathotype 2, one was pathotype 5, and one was pathotype 8. Samples from five vegetable fields were pathotype 6, one was pathotype 5, and one is being determined. Therefore, the most common pathotype in canola fields is pathotype 2 and in vegetable fields it is pathotype 6. This is similar to survey results from 1969 where pathotype 6 was found on cabbage and cauliflower and pathotype 2 was identified from a field of clubroot-infected rutabagas.

P27. First report of verticillium wilt of faba bean (*Vicia faba*) caused by *Verticillium dahliae* in western Canada. K.F. Chang, S.F. Hwang, H. Fu, H.U. Ahmed, Q.X. Zhou, H.T. Yu, A.J. Ho, G.D. Turnbull, and S.E. Strelkov. *Alberta Agriculture and Forestry, Crop Diversification Centre North, 17507 Fort Road, Edmonton, AB T5Y 6H3, Canada; (H.T.Y.) Institute of Food Crops, Yunnan Academy of Agricultural Science, Kunming, Yunnan, 650205 China; and (A.J.H., S.E.S.) University of Alberta, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada.*

Faba bean (*Vicia faba* L.) with tannin-free seed has potential for use as food, feed and aquaculture in the Canadian prairies. However, the crop is susceptible to vascular wilts caused by soil-borne pathogens. In a disease survey of faba bean conducted in 2017, plants with wilt symptoms were observed near Namao, Alberta. Symptomatic plants were collected, and their infected stem tissues were surface-sterilized and plated onto potato dextrose agar (PDA) medium. Five isolates which developed colony morphology similar to that of *Veriticillium* species were purified by hyphal tip culture and single-spore isolation. On PDA, the colonies were dark with compact mycelium embedded with numerous microsclerotia and conidial masses 14 days after plating. The isolates formed conidiophores with 4 - 5 verticillate phialides. The conidia were hyaline, elliptical, aseptate, with a mean length of 3.34 µm, and range of 2.56 - 5.14 µm. The mean width was 1.94 µm with a range of 1.31 - 2.56 µm. The isolates produced irregular to elliptical microsclerotia of various sizes. The DNA sequence of seven isolates, obtained with a primer set (ITS5/4), revealed 99% similarity with *Verticillium dahliae* Kleb. sequences available in GenBank, confirming the identity of the isolates. Inoculation of one of the isolates onto the faba bean cultivars 'Earlibird' and 'Snowbird' resulted in typical symptoms and signs of verticillium wilt. The pathogen was re-isolated from all parts of the infected plants. This is the first report of natural infection of faba bean by *V. dahliae* in western Canada.

P28. First report of clubroot (*Plasmodiophora brassicae*) on canola in the Peace Region, Alberta. S.F. HWANG, H.U. AHMED, Q.X. ZHOU, V.P. MANOLII, G.D. TURNBULL, R. FREDUA-AGYEMAN, S. KAUS AND S.E. STRELKOV. *Alberta Agriculture and Forestry, 17507 Fort Road NW, Edmonton, AB T5Y 6H3, Canada; (V.P.M., S.E.S.) Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB T6G 2P5, Canada; and (S.K.) Big Lakes County, 5305-56 Street, High Prairie, AB T0G 1E0, Canada.*

Clubroot of canola (*Brassica napus* L.), caused by *Plasmodiophora brassicae* Wor., has spread to more than 2,700 fields in Alberta since it was first identified in 2003. The disease, however, had not been reported in the Peace Region of northwest Alberta until 2017, when 46 cases of clubroot were identified in the Municipal District of Big Lakes. Surveys of the infested crops found a clubroot incidence of <10% in 40 fields and >10% in the other six. Individual plants were rated for clubroot severity on a 0-3 scale. In most (32) fields, clubroot symptoms were mild, with all affected plants rated as a 1, although severely infected plants (with a rating of 3) also were found in 10 fields. Rotation histories were obtained for 20 of the affected fields, which indicated that canola had been grown either back-to-back or in alternating years in at least 63% of the cases. A PCR-based quantitative analysis with primers developed for pathotype 5X, which is able to overcome clubroot resistance in canola, found it (or similar strains) was present in 88% of the fields tested, but at a very low frequency (0.5%) relative to the old pathotype 3H. Phenotypic evaluation for pathotype classification on the Canadian Clubroot Differential (CCD) Set revealed that of 17 *P. brassicae* populations tested from Big Lakes, 11 were pathotype 3H, two each were pathotype 8N and pathotype 5I, and two appeared to have novel virulence patterns which require further investigation. The identification of pathotype 5X at a very low frequency suggests the potential for shifts in the virulence of the *P. brassicae* populations in Big Lakes, particularly if clubroot resistant canola is grown in short rotations in the region.

P29. Assessing incidence of eastern filbert blight in Ontario hazelnuts A. MUNAWAR, C. BAKKER, M. FILOTAS, AND K. S. JORDAN. *(A.M., C.B and K.S.J.) Department of Plant Agriculture, Simcoe Research Station, University of Guelph, Simcoe, Ontario, N3Y 4N5, Canada and (M.F.) Ontario Ministry of Agriculture, Food and Rural Affairs, Simcoe, Ontario, N3Y 4N5, Canada.*

Eastern filbert blight (EFB), caused by the fungus *Anisogramma anomala* (Peck) E. Müller, is the main disease affecting hazelnut trees in eastern North America. This pathogen is an obligate, biotrophic parasite and is known to attack only species of the genus *Corylus* L. To support increased production of this crop in Ontario, there is a need to better understand the overall incidence and severity of this disease in commercial orchards in the province, and how that varies among cultivars, ages of orchards and management practices. It is also important to determine the incidence of latent infection in asymptomatic trees as symptom development usually takes place 1-1.5 years after the initial infection.

Six hazelnut orchards in Ontario were scouted for visible symptoms of EFB infection from February-March 2018. The incidence of EFB varied from orchard to orchard and ranged from less than 1% to 12 %. The young trees in orchard 1-3 had severe cankers although the number of symptomatic trees was small. The cultivars 'Yamhill' and 'Jefferson' were also found infected although these cultivars are reported to be resistant in Oregan. The latent infection was assessed in the twigs of twenty-five asymptomatic trees from orchards 1-4 using polymerase chain reaction method. Orchard 1 had the highest percentage of latent infection (64 %) followed by orchard 3 (44 %) and orchard 4 (20%). Orchard 2 had the lowest infection (4%). The trees that tested positive for latent infection have been marked and will be monitored for symptom development in fall 2018.

P30. Assessment of genetic variation in new strains of *Plasmodiophora brassicae* in Alberta by ITS sequence analysis. Q. ZHOU, S. F. HWANG, H. FU, R. FREDUA-AGYEMAN, V.P. MANOLII, AND S. E. STRELKOV. *Alberta Agriculture and Forestry, Crop Diversification Centre North, 17507 Fort Road, Edmonton, AB, T5Y 6H3, Canada; and (V.P.M., S.E.S.) University of Alberta, Department of Agricultural, Food and Nutritional Science, Edmonton, AB, T6G 2P5, Canada.*

Clubroot of crucifers, caused by *Plasmodiophora brassicae* Wor., is an important soilborne disease of canola (*Brassica napus* L.) in Alberta, Canada. The disease is managed mainly by growing clubroot-resistant cultivars in the field. However, new strains of *P. brassicae* capable of overcoming this resistance were identified from more than 60 fields in Alberta between 2013 and 2016, suggesting shifts in the virulence of the pathogen populations. Evaluation of the virulence phenotypes of selected *P. brassicae* populations on the hosts of the Canadian Clubroot Differential Set revealed the occurrence of pathotypes A-P and X, but information on genetic variation is lacking. Such information is important for assessing diversity in pathogen populations and understanding the relationship between pathotypes. In the present study, the 18S and internal transcribed spacer (18S-ITS) regions of *P. brassicae* populations representing a total of 62 fields were amplified with a pathogen-specific forward primer RP2F and a universal reverse primer ITS4. The resultant amplicons were cloned and sequenced, and genetic variation was analyzed by the neighbour-joining and bootstrap methods. The results of this analysis will be presented.

P31. Plant pathogenic fungi in bentonite-amended sandy soil under corn monoculture in Northern China. H-Y ZHANG, J. H. LIU, W. CHEN. *(W.C., H-Y.Z) Ottawa Research and Development (R&D) Centre, Agriculture and Agri-Food Canada (AAFC), 960 Carling Ave., Ottawa, ON, K1A 0C6, Canada; (H.Y.Z, J.H.L) Inner Mongolia Agricultural University, 306 Zhaowuda Rd, Hohhot, Inner Mongolia, 010000, China.*

Sandy soils of aerolian origin are light-textured, alkaline, with poor water and nutrient retention and prone to compaction. The economic loss associated with sandification was estimated at 54 million RMB/year in China, with Horqin Sandy Land (a farming-pastoral ecotone in Northern China) being most severely affected. Over 70% arable lands in Horqin are under continuous corn production, often constrained by water deficits. Our long-term experiments on corn monocultural plots showed the addition of natural bentonite improved the aggregate stability, water content and enzymatic activities of sandy soil and maize production. The dynamics of the soil mycobiota, especially soil-borne fungal plant pathogens, in response to bentonite amendment was investigated using the fungal internal transcribed spacer 1 (ITS1) metabarcodes. The results showed that Ascomycota abundance was twice that of Basidiomycota in corn fields, while the most abundant fungal genera included *Guehomyces*, *Alternaria*, *Mortierella*, *Cladosporium* and *Exophiala*. The pathogenic mycobiota (annotated by FUNGuild) was dominated by *Alternaria* (5.8%), *Cladosporium* (4.24%) and *Fusarium* (3.57%) in abundance. Fungal plant pathogens in bentonite-amended soils had higher diversity and prevalence and differed significantly in composition from those in non-amended soils. Further analyses revealed the key soil properties and bacterial OTUs that may enhance the soil fungistatic potential. Notwithstanding bentonite-amendment improves the overall performance of sandy soils in corn production, however the increased diversity and abundance of fungal pathogens, possibly due to increased nutrient levels, requires pest management attention.

P32. Évaluation des besoins en phytoprotection des cultures ornementales en serres. N. ROULLÉ, A. BÉLANGER, B. CHAMPAGNE, M.A. LAPLANTE et M.É. TOUSIGNANT, *Institut Québécois du développement en horticulture ornementale du Québec,3230 rue Sicotte, E-307, St-Hyacinthe, QC J2S 2M2, Canada.*

Au Québec, les cultures ornementales en serres représentent près de 136 millions de dollars de vente par an. Ce sont des productions qui incluent plus de 300 espèces de plantes et plus de 50 ennemis des cultures. Mandaté par le MAPAQ depuis 2016 pour réaliser la surveillance phytosanitaire dans les cultures ornementales du Québec, l'IQDHO a entrepris de réaliser une évaluation des besoins en phytoprotection du secteur des serres. L'objectif de cette évaluation était tout d'abord de mieux orienter les efforts de l'IQDHO en termes de choix de projets de recherche, de thèmes de formation et de sujets

de publications techniques. L'objectif était également de mieux communiquer les besoins du secteur aux différents intervenants provinciaux et fédéraux. Tout au long de la démarche, les treize conseillers et conseillères des cultures ornementales en serres du Réseau d'avertissements phytosanitaires du Québec (RAP) ont été consultés. La démarche s'est déroulée en 4 étapes : 1-Établissement de la liste des 13 ennemis des cultures les plus problématiques ; 2-Pour ces ennemis, évaluation des pertes économiques, de l'utilisation en pesticides et de la disponibilité en méthode de contrôle ; 3-Évaluation des besoins en projets de recherche, en formations et en demandes d'homologation de pesticides ; 4-Proposition de projets de recherche et de thèmes de formation. Cette consultation des conseillers et conseillères a permis d'établir un portrait des principales problématiques du secteur. Ce portrait sera un guide pour viser une réduction significative des impacts des ravageurs et des maladies, ainsi qu'une réduction de l'usage des pesticides.

P33. Évaluation des besoins en phytoprotection des cultures ornementales en pépinières

N. ROULLÉ, A. BÉLANGER, M.A. LAPLANTE et M.É. TOUSIGNANT, *Institut Québécois du développement en horticulture ornementale du Québec,3230 rue Sicotte, E-307, St-Hyacinthe, QC J2S 2M2, Canada.*

Au Québec, les cultures ornementales en pépinière représentent 65 millions de dollars de vente par an. Ce sont des productions qui incluent plus de 1000 espèces de plantes et plus de 200 ennemis des cultures. Mandaté par le MAPAQ depuis 2016 pour réaliser la surveillance phytosanitaire dans les cultures ornementales du Québec, l'IQDHO a entrepris de réaliser une évaluation des besoins en phytoprotection du secteur des pépinières. L'objectif de cette évaluation était tout d'abord de mieux orienter les efforts de l'IQDHO en termes de choix de projets de recherche, de thèmes de formation et de sujets de publications techniques. L'objectif était également de mieux communiquer les besoins du secteur aux différents intervenants provinciaux et fédéraux. Tout au long de la démarche, les cinq conseillers et conseillères du Réseau d'avertissements phytosanitaires du Québec des productions de pépinière ont été consultés. La démarche s'est déroulée en 4 étapes : 1-Établissement de la liste des 12 ennemis des cultures les plus problématiques ; 2-Pour ces ennemis, évaluation des pertes économiques, de l'utilisation en pesticides et de la disponibilité en méthode de contrôle ; 3-Évaluation des besoins en projets de recherche, en formations et en demandes d'homologation de pesticides ; 4-Proposition de projets de recherche et de thèmes de formation. La consultation des conseillers et conseillères en pépinière a permis d'établir un portrait des principales problématiques du secteur. Ce portrait sera un guide pour viser une réduction significative des impacts des ravageurs et des maladies en pépinières, ainsi qu'une réduction de l'usage des pesticides.

P34. Population dynamics of fungal pathogens on wheat heads in Alberta in 2015 and 2016. M. W. HARDING, G. C. DANIELS, T. GRÄFENHAN, T. K. TURKINGTON AND J. FENG.
Alberta Agriculture and Forestry, Crop Diversification Centre South, 301 Horticultural Station Road East, Brooks, Alberta T1R 1E6, Canada; (T.G.) Canadian Grain Commission, Grain Research Laboratory, 196 Innovation Drive, Richardson Centre, Winnipeg, Manitoba R3T 6C5; (T.K.T.) Agriculture and Agri-Food Canada, Lacombe Research and Development Centre, 6000 C and E Trail, Lacombe, Alberta T4L 1W1; (J.F.) Alberta Agriculture and Forestry, Crop Diversification Centre North, 17507 Fort Road NW, Edmonton, Alberta, T5Y 6H3, Canada.

Fusarium head blight, caused by *Gibberella zea* (Schwein.) Petch (syn. *Fusarium graminearum*), is a serious disease in cereals that reduces yield, grade and market acceptance. A comprehensive survey for the prevalence, incidence and distribution of wheat head pathogens was conducted in Alberta in 2015 and 2016. Over 800 wheat fields were sampled each year and grain analyzed for the presence of head blight pathogens such as *F. graminearum*, and other fungi commonly associated with cereal spikes. Dry conditions were reported in 2015 for much of Alberta during the heading and flowering stages of cereal crops, whereas 2016 was relatively wet during these stages for much of the Province. The environmental conditions, along with other factors, caused shifts in fungal populations on wheat heads. For example, the incidences of *Fusarium spp.* and *Phaeosphaeria nodorum* (E. Mull.) Hedjar., (1969) were significantly higher in 2016 when compared to those of 2015. Interestingly, the incidences of *Alternaria spp.* were significantly lower in 2016 compared to 2015 and those of *Pyrenophora spp.* were relatively unaffected.

P35. Assessment of transmission pathways for the presence of the cucumber downy mildew pathogen, *Pseudoperonospora cubensis* . A. MUNAWAR, C. BAKKER, CARA MCCREARY, AND K. S. JORDAN. *(A.M., C.B and K.S.J.) Department of Plant Agriculture, Simcoe Research Station, University of Guelph, Simcoe, Ontario, N3Y 4N5, Canada and (C.M.) Ontario Ministry of Agriculture, Food and Rural Affairs, Harrow Research Station, Harrow, Ontario, N0R 1G0, Canada.*

Pseudoperonospora cubensis (Berkeley & Curtis) Rostovtsev, is responsible for one of the most important foliar diseases of cucumber, namely downy mildew (DM). Symptoms include yellow angular lesions on the leaf surface and production of sporangia on the underside of the leaf. Control of DM depends on an intensive fungicide program which is not always feasible due to high cost of fungicides and evolution of resistant pathogen populations. The current project is focused on investigating cucumber seeds and fruit and alternative DM hosts as inoculum sources in a Canadian environment. In year 1-2 of the study, 295 fruit collected from infected cucumber fields were tested microscopically and none were found infected. Approximately, three-thousand cucumber seeds were grown for 4-weeks

in a greenhouse under ideal conditions for DM symptom development. Leaves of 108 plants developed yellow lesions similar to DM but did not show sporulation. However, a polymerase chain reaction (PCR) showed all tested symptomatic leaf samples were positive for ribosomal internal transcribed spacer DNA of *Pseudoperonospora*. PCR analysis on individual seeds, harvested from fruit of severely infected cucumber plants showed 96% of them positive for *Pseudoperonospora*. Four cucurbits namely, golden-creeper, bitter-melon, wild and bur cucumber were tested as alternative hosts using a detached leaf inoculation method. All wild cucurbits developed DM symptoms 3-5 days after inoculation and showed sporangial production. The last year of this study will generate data to confirm cucumber fruit and seeds, and alternative hosts as possible inoculum sources for DM and provide recommendations for disease management.

P36. Impact of blackleg (*Leptosphaeria maculans*) on canola yield. Y. WANG, S.-F. HWANG AND S.E. STRELKOV. *Department of Agricultural, Food and Nutritional Sciences, University of Alberta, Edmonton, AB T6G2P5, Canada; and (S.F.H.) Alberta Agriculture and Forestry, 17507 Fort Road NW, Edmonton, AB T5Y6H3, Canada.*

Blackleg, caused by *Leptosphaeria maculans* (Desm.) Ces & de Not., is one of the most devastating diseases of canola (*Brassica napus* L.) worldwide. Yield losses as high as 30-50% have been reported in susceptible cultivars, and total crop failure can occur in severe epidemics. In Canada, blackleg is managed mainly by the cultivation of resistant or moderately resistant canola hybrids. Field experiments were conducted in 2017 to determine the relationship between blackleg severity and yield in two moderately resistant hybrids '73-15RR' and '1950RR'. Blackleg disease severity gradients were generated by the application of different levels of *L. maculans* inoculum. The experiment was designed as a split plot and disease severity (on a 0-5 scale), pod number per plant and seed yield per plant were recorded at crop maturity. Regression analysis showed that pod number and seed yield had non-linear relationships with blackleg severity, and these relationships were best explained by second degree quadratic equations. Plants with a blackleg severity of 0 had a slightly lower seed yield than plants with a severity of 1 for both canola hybrids. Yield decreased by 15.6-100%, however, in plants with disease severities of 3-5 compared with plants with disease severities of 0-2. These results suggest that even in moderately resistant hybrid canola cultivars, seed yield per plant decreases as a result of *L. maculans* infection. Thus, alternative disease management strategies are required to mitigate yield losses due to blackleg. The experiment will be repeated in 2018 to confirm the results.

P37. Chocolate spot disease risk periods in faba beans in Alberta and Saskatchewan. S. KAUR, R. BOWNESS, S. BANNIZA AND S. CHATTERTON. *(S.K., S.C) Lethbridge Research Centre, Agriculture and Agri-Food Canada, 5403-1 Ave. South, P.O. Box 3000 Alberta, T1J 4P4, Canada; (R.B) Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, 6000 C and E Trail, Lacombe, Alberta T4L 1W1, Canada; (S.B) Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada.*

Chocolate spot (CS), caused by *Botrytis fabae* Sard., is one of the most important diseases of faba bean (*Vicia faba* L.) affecting its productivity in Alberta and Saskatchewan. Cool, wet, and humid weather conditions favour sporulation and secondary infection, but information of CS disease risk periods and inoculum release under prairie conditions is lacking. Therefore, this study was conducted to determine the duration of inoculum discharge and infectious periods under field conditions by using 3-week-old faba bean plants (cv. 'Malik' (tannin) and 'Snowdrop' (zero tannin) as spore traps. A total of sixteen trap periods from mid-June to mid-August were assessed in 2017. Five plants of each cultivar were placed within the canopy for a period of four days at each trap period at locations in Lethbridge and Lacombe, AB and Saskatoon, Melfort and Scott, SK. After the exposure period, plants were incubated in the greenhouse and CS severity was rated after 14 days. Data analysis showed significant effects of location and trap period on CS severity. However, the effect of cultivar on CS severity was not always significant. Infectious periods occurred earlier than expected (mid-June) at the Lethbridge sites, but was later (late July- August) at all other locations in AB and SK. High temperatures were negatively correlated with disease severity across all locations, whereas the significance of correlations between severity and precipitation or humidity were not consistent across locations. Experiments will be conducted for two more cropping season to assess the disease risk period, and model infectious periods to weather parameters.

P38. Incidence and management of hop downy mildew in Ontario in 2016 and 2017 . A. Munawar, M. Filotas, C. Bakker, M. R. McDonald AND K. S. Jordan. *(A.M., C.B., M. R. M. and K.S.J.) Department of Plant Agriculture, Simcoe Research Station, University of Guelph, Simcoe, Ontario, N3Y 4N5, Canada and (M.F.) Ontario Ministry of Agriculture, Food and Rural Affairs, Simcoe, Ontario, N3Y 4N5, Canada.*

Hop downy mildew (HDM), caused by *Pseudoperonospora humuli*, is one of the most devastating diseases of hops. The pathogen can overwinter in dormant buds or rhizomes causing a persistent systemic infection and subsequent infection of bines and cones. Due to the systemic nature of the infection, applying fungicides with systemic activity in the plant is an important management tool. The only systemic fungicide registered for hops in Canada is metalaxyl but resistance of *P. humuli* against this fungicide is unknown in Ontario. This project is designed to determine the incidence of HDM in

Ontario commercial hop yards and to evaluate the resistance of the pathogen to metalaxyl. In 2016 and 2017, the incidence of HDM varied among cultivars and was greatly affected by weather conditions. Eighty-four rhizomes were screened for systemic presence of *P. humuli* through polymerase chain reaction (PCR) using primers designed for ribosomal internal transcribed spacer DNA of the fungus. Approximately 30% of the 84 rhizomes showed systemic infection in PCR and percentage of infection varied from yard to yard. In preliminary work on resistant populations of *P. humuli*, eight downy mildew infected spikes from a conventional hop yard and one spike from an organic hop yard was tested for metalaxyl sensitivity. All spikes from the conventional yard were found resistant to metalaxyl at 50 and 100 ug/ml, whereas the spike from the organic yard was sensitive to the fungicide at both tested concentrations. Future work will focus on testing *P. humuli* populations from more hop yards.

P39. Age-related susceptibility of grapevine leaves and berries to infection by Elsinoe ampelina.
O. CARISSE, A., LEVASSEUR AND C. PROVOST. (OC) *Agriculture and Agri-Food Canada, Research Centre, 430 Gouin Blvd., Saint-Jean-sur-Richelieu, QC, Canada, J3B 3E6;* (CP) *Centre de recherche agroalimentaire de Mirabel, 9850 rue Belle-Rivière, Mirabel, Qc, J7N 2X8, Canada.*

Anthracnose, caused by *Elsinoe ampelina* Shear, is an important disease of grapevine. In recent years, there have been regular outbreaks in Eastern Canada on grape cultivars that are gaining in popularity. Young leaves and berries are reported to be highly susceptible to *E. ampelina*, but the time of onset and young leaves susceptibility among cultivar variation in ontogenic resistance have remained undefined. Age-related susceptibility was studied under greenhouse conditions by inoculating 1- to 19-day old grape leaves of the cultivars 'Vidal', 'Marquette' and 'Vandal-Cliche'. Similarly, flowers/berries were inoculated under field conditions on ten occasions from flower formation until berries at approximately 8°Brix. For all cultivars, there was a significant effect of leaf and flower/berry age on anthracnose severity. Susceptibility was highest on one-day old leaves and diminished as the leaves aged to reach 20%, 10% and 5% of the maximum susceptibility on 4-, 6-, and 8-day old leaves. The influence of leaf age on anthracnose severity was described with an exponential decay model (R^2=0.98). Susceptibility was highest at the early stage of flower formation and diminished to reach 50%, 40-20%, and 5% at the stage flowers separating (stage 17), fruit set (stage 27), and 4-6 mm berries (stage 29), respectively. These results suggest that the risks of anthracnose are high from bud-break to fruit set, and on newly emerged leaves either early in the season or following pruning. More knowledge on anthracnose epidemiology is needed, but these results could be used to improve timing of fungicide applications and of pruning activities.

P40. Virulence of *Puccinia striiformis f. sp. tritici* in Western Canada. E. AMUNDSEN, K. GHANBARNIA and R. ABOUKHADDOUR. *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB T1J 4B1, Canada.*

The virulence of 35 different isolates of *Puccinia striiformis f. sp. tritici* was tested on eighteen near-isogenic wheat lines in the Avocet background. These isolates are part of a collection obtained mainly from western Canada during 2015, 2016 and 2017. The seedlings were inoculated with a spore/talc mixture (ratio 1:20) and infection types (ITs), on the second leaf, were recorded 18–21 days after inoculation based on a scale of 0–9. In total, 21 different virulence patterns were observed. Near-isogenic wheat lines with resistance genes *Yr1*, *Yr 5*, *Yr15* and *Yr76* remain effective against all tested isolates, and the line harboring *YrSp* was defeated twice. Lines possessing *Yr6*, *Yr7*, *Yr8* and *Yr9* genes, were defeated by most tested isolates maybe due to worldwide use of these genes in commercial cultivars. This study represents results on a small subset of collected isolates, but it shows wide spectrum virulence in tested isolates and high variability in the yellow rust pathogen populations in Canada.

P41. Sensitivity *of Monilinia vaccinii-corymbosi* to propiconazole from wild blueberry fields
D.C. PERCIVAL, L. GUO, S. JOSE, A. SCHILDER, B. PRITHVIRAJ AND A.R. OLSON.
Department of Plant, Food & Environmental Sciences, Dalhousie University Agriculture Campus, Truro, Nova Scotia, Canada B2N 5E3; (A.S.) Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, Michigan, USA.

Monilinia blight, caused by *Monilinia vaccinii-corymbosi* (Reade) (*M.vc*) Honey, is one of the most devastating fungal diseases of wild blueberry. Chemical control of Monilinia blight is necessary to achieve high yield and quality berries in the absence of adequate host plant resistance. Propiconazole, the most effective fungicide against Monilinia blight has been used throughout the wild blueberry industry for the past 20 years. However, long-term use may lead to the development of resistance among fungal populations. Given the extensive usage of propiconazole, the occurrence of fungicide resistance in *M.vc* population was examined in 2011, 2012 and 2013 from five commercial fields in Nova Scotia. The effective concentration (EC_{50}) of fungicide were determined for 102 single spore isolates (isolated from mummy berries and Monilinia blighted shoots) and compared with the baseline EC_{50} value of isolates from unmanaged and conventionally managed fields in Maine, US. All isolates, regardless of collection date, were sensitive (ranged from 0.007 to 0.036 $\mu g \cdot mL^{-1}$) with an average of 0.015 $\mu g \cdot mL^{-1}$. The value was not significantly different from the mean propiconazole EC_{50} value of baseline isolate (0.016 $\mu g \cdot mL^{-1}$), but was lower than the mean propiconazole EC_{50} value of isolates (0.021 $\mu g \cdot mL^{-1}$) from conventionally managed fields in Maine. Although variation in sensitivity was

observed within and among isolates from different locations, it can be concluded that, *M.vc* isolates from Nova Scotia have not developed reduced sensitivity to propiconazole. Furthermore, the results from this study can serve as a benchmark for assessing any future decline in sensitivity to propiconazole.

P42. Preliminary sensitivity assessment of *Botrytis cinerea* isolates to four fungicides from wild blueberry fields. ABBEY[A], J. A, PERCIVAL[A], D., ASIEDU[A], S. K., PRITHIVIRAJ[A], B. AND SCHILDER[B], A. [a]*Department of Plant, Food, and Environmental Sciences, Dalhousie University, Faculty of Agriculture, 50 Pictou Road, P.O. Box 550, Truro, NS B2N 5E3, Canada;* [b]*Department of Plant, Soil and Microbial Sciences, Michigan State University, Center for Integrated Plant Systems 578 Wilson, Rm. 105 CIPS East Lansing, MI 48824, USA.*

Botrytis cinerea is a high risk pathogen capable of developing resistance to various groups of fungicides. Fifteen single-spore isolates of *B. cinerea* were collected from commercial wild blueberry fields in Nova Scotia. Eight baseline isolates were also collected to evaluate resistance development. The isolates were evaluated for their sensitivity to cyprodinil, fludioxonil, boscalid and penthiopyrad, using mycelium growth assay. The EC_{50} values for the 15 isolates ranged from 0.04 - 10.03, 0.0047 - 0.0073, 0.47 - 9.25 and 0.15 -1.88 for cyprodinil, fludioxonil, boscalid and penthiopyrad, respectively. Results from this study revealed the potential existence of cyprodinil and boscalid-resistant strains at frequencies of 100 and 73.3%, respectively. Compared to the baseline isolates, reduced sensitivity to penthiopyrad was found in two isolates, whereas eleven isolates exhibited reduced sensitivity to cyprodinil and boscalid, respectively. No isolate with reduced sensitivity to fludioxonil were detected. Significant cross-resistance existed between the SDHI fungicides boscalid and penthiopyrad ($r = 0.671$, $p = 0.006$). A negative linear correlation was observed between fludioxonil and boscalid ($r = -0.583$, $p = 0.023$). Though some isolates had reduced sensitivity to more than one fungicide, no cross-resistance were detected in the remaining fungicide pairs. This study reveals a possible shift of *B. cinerea* isolates towards resistance development to cyprodinil and boscalid. It also suggests a prompt occurrence of *B. cinerea* populations resistant to penthiopyrad unless suitable resistant management strategies are employed to curb future resistance challenges.

P43. Efficacy of registered fungicides to control cucurbit downy mildew isolates from Québec and Ontario. G. MARCHAND, C.L. TRUEMAN, M. L. FALL, O. CARISSE. *(G.M.) Agriculture and Agri-Food Canada, Harrow Research and Development Centre, 2585 County Road 20, Harrow, ON N0R 1G0, Canada; (C.T.) University of Guelph, 50 Stone Road E., Guelph, ON N1G 2W1, Canada; and (M.L., O.C.) Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu Research and Development Centre, 430 Gouin Boulevard, Saint-Jean-sur-Richelieu, QC J3B 3E6, Canada.*

Cucurbit downy mildew (*Pseudoperonospora cubensis* (Berk. & Curt.) Rost.) is an important disease issue for the field production of pickling cucumbers (*Cucumis sativus* L.), and also for cucumbers grown in the field and greenhouse, as well as other field cucurbits. Tolerance for the presence of the pathogen in pickling cucumbers is exceptionally low, as even a very low incidence will interfere with the fermentation process. Growers manage the pathogen with fixed interval spray programs, since genetic resistance has largely been overcome by the pathogen since the mid 2000s. Low efficacy or resistance to some single-site fungicides (strobilurins, fluopicolide) registered in Canada has previously been reported. This study was initiated with the objective of evaluating the efficacy of currently registered single-site fungicides under controlled conditions. Isolates were collected from commercial cucumber production sites (fields and greenhouses) in Québec and Ontario. Testing was performed on cucumber seedlings in growth chambers at the St-Jean-sur Richelieu and Harrow Research and Development Centres. Initial results from the first year of the project showed low efficacy for strobilurin (pyraclostrobin, fenamidone) fungicides. Mandipropamid also showed low efficacy in one series of testing, but this has not been replicated and will have to be validated in year two of the project. Fluopicolide, propamocarb, cyazofamid and oxathiapiprolin provided the expected level of control. Dimethomorph was also mostly efficacious. These initial results will be validated by testing more isolates during the second year of this project.

P44. First report of Radish (daikon) showing *Verticillium longisporum* infection in Manitoba, Canada. V. BISHT, M. PRADHAN, C. CAVERS, D. FERNANDO, T. BARASUBIYE. *Manitoba Agriculture, 65-3rd Ave NE, Carman, MB R0G 0J0, (M.P.) Crop Diagnostic Centre, MB Agriculture, 545 University Crescent, Winnipeg, MB R3T 5S6, (CC) Agriculture & Agri-Food Canada, 370 River Road, Portage La Prairie, MB, R1N 3V6, (DF) Plant Sciences, University of Manitoba, Rm 205 FAFS, 66 Dafoe Road, Winnipeg, MB R3T 2N2, (TB) Science & Technology Branch, Agriculture & Agri-Food Canada, 960 Carling Ave, KW Neatby Building, Ottawa, ON K1A 0C6.*

Verticillium wilt (renamed Verticillium stripe) disease was identified for the first time in 2014 from Manitoba, Canada on canola (*Brassica napus*). Since the first discovery, survey of crops and soils has confirmed the presence of the pathogen in several provinces in Canada. In 2015, in a Portage La Prairie

field, there was a high incidence of Verticillium stripe disease in a blackleg susceptible canola variety, but not in a blackleg resistant variety, suggesting interaction between the two pathogens. In 2016, in this infested field, various crucifer crops (broccoli, canola, cauliflower, daikon radish, mustard, rutabaga,) were planted in small plots to test the host reaction to Verticillium. Daikon radish, *Raphanus raphanistrum* subsp. *sativus*, showed external stem discoloration and internal vascular tissue blackening in stem and root. The incidence appeared to be high, over 50%. In 2017, daikon radish was planted again on the farm, in an adjoining field. Survey of the field showed >50% plants with internal vascular blackening. Isolation of the pathogen indicated Verticillium species. Based on DNA sequence of *ITS* barcode and partial sequence of *Actin* gene the strain isolated was identified as *Verticillium longisporum* Hybrid (A1 x D1). This appears to be the first report of *Verticillium longisporum* infecting radish in Manitoba, Canada.