THE CANADIAN PHYTOPATHOLOGICAL SOCIETY

LA SOCIÉTÉ CANADIENNE DE PHYTOPATHOLOGIE

2016 Annual Meeting of the Canadian Phytopathological Society

Delta Beauséjour

Moncton, New Brunswick, Canada

June 12-15, 2016

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Sunday, June 12

3PM – 5PM Introduction to Effectoromics workshop, D. Joly's group – Université de Moncton

4:59PM Tidal Bore Estimated time – Bore Park

5PM – 9PM Registration / Poster Set Up - Mezzanine

7PM – 10PM **Opening Reception (sponsored by McCain Foods)** - Shediac A/B Room

Monday, June 13

8AM – 5PM Registration / Poster Set Up - Mezzanine

8:15AM Welcome and Opening Addresses – Ballroom B

8:30AM – 12PM **Symposium 1: Genomics-based applications in plant pathology – Ballroom B (sponsored by Genome Atlantic)**

8:30AM [S1-1] **The Innate potato: from concept to commercialization.** *Nicolas Champouret, Simplot, Boise, ID, USA*

9:15AM [S1-2] **Genomic screens to identify next-generation MAMPs and their cognate pattern recognition receptors.** *Darrell Desveaux, University of Toronto, Toronto, ON*

10:00AM **Break (sponsored by FMC Canada) - Mezzanine**

10:30AM [S1-3] **Genomics applications for biosurveillance of forest diseases.** *Richard C. Hamelin, University of British Columbia, BC*

11:15AM [S1-4] **A new twist on antibiosis: Exposure to subinhibitory concentrations of antibiotics alters the transcriptome of plant pathogens.** *Martin Filion, Université de Moncton, NB*

12PM – 2PM **Lunch (sponsored by BASF) – Ballroom A**

2PM – 5:30PM **Contributed Paper Session 1 - Student Competition - Ballroom B (sponsored by Novozymes)**

2:00PM [O1-1] **The dynamics of biomass accumulation by Ptr ToxA and Ptr ToxB producing isolates of *Pyrenophora tritici-repentis* on wheat.** X. MA, R. ABOUKHADDOUR, S.F. HWANG, AND S.E. STRELKOV. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada; (S.F.H) Crop Diversification Centre North, Alberta Agriculture and Forestry, Edmonton, Canada, AB T5Y 6H3*

2:15PM [O1-2] **Durability of blackleg resistance genes in *B. napus* and the emergence of virulent isolates in *L. maculans*.** M.H. RASHID, S. LIBAN, X. ZHANG, P. PARKS, M.H. BORHAN, AND W.G.D. FERNANDO. *Department of Plant Science, University of Manitoba, Winnipeg, MB, R3T 2N2 Canada;* (M.H.B) Agriculture *and Agri-Food Canada, Saskatoon Research Station, SK, S7N 0X2, Canada*

2:30PM [O1-3] **Identification of *Ustilago maydis* RNA helicases and investigation of their function in the teliospore.** A.M. SETO, M.E. DONALDSON AND B.J. SAVILLE. *Environmental and Life Sciences Graduate Program, Trent University, 1600 West Bank Drive, Peterborough, ON, K9L 0G2, Canada; (M.E.D.,B.J.S.) Forensic Science Program, Trent University, 2140 East Bank Drive, DNA Building, Peterborough, ON, K9L 0G2, Canada*

2:45PM [O1-4] ***Pseudomonas fluorescens* LBUM636 controls potato late blight through phenazine-1-carboxylic acid production.** C. MORRISON, T ARSENEAULT, A. NOVINSCAK, AND M. FILION. *Université de Moncton, 18 Antonine-Maillet, Moncton, NB, Canada, E1A 3E9*

3:00PM [O1-5] **RNA-Seq analysis reveals transcriptome alteration in *Phytophthora infestans* by phenazine-1-carboxylic acid producing *Pseudomonas fluorescens* LBUM223.** R. ROQUIGNY, D.L. JOLY AND M. FILION. *Université de Moncton, 18 Antonine-Maillet, Moncton, NB, Canada, E1A 3E9*

3:15PM [O1-6] **Intra-host interactions of the pea root pathogens *Aphanomyces euteiches* and *Fusarium* spp.** T. WILLSEY, J. THOMAS and S. CHATTERTON. *University of Lethbridge, 4401 University Drive, Lethbridge, AB, T1K 3M4, Canada; (S.C) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403–1 Avenue South, Lethbridge, AB, T1J 4B1, Canada*

3:30PM **Break (sponsored by the PEI Potato Board) - Mezzanine**

4:00PM [O1-7] **Genetic diversity and colonization patterns of *Onnia tomentosa* in a plantation of black spruce (*Picea mariana*) in northwestern Ontario.** Z.R.W. HOEGY, D. MORRIS, D. REID, AND L.J. HUTCHISON. *Faculty of Natural Resources Management, Lakehead University, Thunder Bay, Ontario P7B 5E1; and (D.M., D.R.) Centre for Northern Forest Ecosystem Research (CNFER), 421 James Street S., Suite 103, Thunder Bay, Ontario P7E 2V6*

4:15PM [O1-8] **Epidemiology and management of stemphylium leaf blight on onion in the Holland Marsh, Ontario.** S.C. TAYVIAH, B.D. GOSSEN, AND M.R. MCDONALD. *Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada; (BDG) Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, Saskatoon, SK, Canada*

4:30PM [O1-9] **Management of plant-parasitic nematodes on carrots grown in organic (muck) soils in Ontario.** D. VAN DYK, K. JORDAN, AND M. R. MCDONALD. *Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph ON N1G 2W1, Canada*

4:45PM [O1-10] Open

5PM – 7PM **Poster Session (sponsored by Pro-Lab Diagnostics) – Mezzanine**

7:30PM **Evening Graduate Student Social (sponsored by Cargill) – Navigators Pub (191 Robinson Street) (Non-students – on your own)**

Tuesday, June 14

8:30AM – 12PM **Contributed Paper Session 2 – Molecular Diagnostics and Screening – Ballroom B**

8:30AM [O2-1] **Sequence-based identification of fungi from ginseng roots and soils.** D. ERRAMPALLI, C. NICOL, A. HALDAR, M. PARCEY, K.I. SCHNEIDER AND S. WESTERVELD. *Agriculture and Agri-Food Canada, 4902 Victoria Ave. N., Vineland Station, ON L0R 2E0 Canada. (SW) Ontario Ministry of Agriculture, Food and Rural Affairs, 1283 Blueline Road, Simcoe, Ontario, N3Y 4N5 Canada*

8:45AM [O2-2] **Transcriptomic insight into emerging wheat leaf rust races of Ontario.** K.M. MARSH, B.D. MCCALLUM, X. WANG, A. TENUTA AND B.J. SAVILLE. *(K.M.M., B.J.S.) Environmental & Life Sciences Graduate Program, Trent University, DNA Building, 2140 East Bank Dr, Peterborough, ON K9J 7B8, Canada; (B.D.M., X.W.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB R6M 1Y5 Canada; (A.T.) Ontario Ministry of Agriculture and Rural Affairs, Ridgetown Resource Center, Argronomy Building, Main St. E, Ridgetown, ON N0P 2C0, Canada; and (B.J.S.) Forensic Science Program, DNA Building, Trent University, 2140 East Bank Dr Peterborough, ON K9J 7B8, Canada*

9:00AM [O2-3] **Next-generation sequencing (NGS) using Ion Torrent technology for biosurveillance from spore and insect traps.** G.J. BILODEAU, É. TREMBLAY AND J.A. BERUBE. *Canadian Food Inspection Agency, Ottawa Plant Laboratory, Ottawa, ON, K2H 8P9, Canada; (J.A.B.) Natural Resources Canada, Laurentian Forestry Centre, Québec, QC, G1V 4C7, Canada*

9:15AM [O2-4] **Geographic atlas of mycotoxigenic fungi through metagenomic surveys of DNA barcodes using a novel taxonomic classification approach.** W. CHEN, C. VISAGIE, M. LIU, K. SEIFERT, T. GRAEFENHAN, S. HAMBLETON AND C. A. LEVESQUE. *Ottawa Research & Development Centre, Science & Technology Branch, Agriculture and Agri-Food Canada, 960 Carling Ave., Ottawa, ON, K1A 0C6, Canada*

9:30AM [O2-5] **Development and validation of high-resolution DNA melting (HRM)-based markers derived from Rysto-STS markers YES3-3A and YES3-3B for high-throughput marker-assisted selection of potatoes carrying Rysto.** X. NIE, D. SUTHERLAND, V. DICKISON, M. SINGH, A. MURPHY AND D. DE KOEYER. *Fredericton Research and Development Centre, Agriculture and Agri-Food Canada, 850 Lincoln Road, Fredericton, NB E3B 4Z7, Canada; (M.S.) Agricultural Certification Services, Fredericton, NB E3B 8B7, Canada; and (D.D.K) International Institute of Tropical Agriculture, PMB 5320, Oyo Road, Ibadan 200001, Oyo State, Nigeria*

9:45AM [O2-6] **Development and validation of diagnostic procedures based on the next generation sequencing technology for screening potato accessions imported to Canada.** H. XU, S. LI, D.L. HAMMILL, S. CODY AND J. NIE. *Canadian Food Inspection Agency, Charlottetown Laboratory, 93 Mt. Edward Rd., Charlottetown, PE, Canada, C1A 5T1*

10AM **Break (sponsored by Université de Moncton) - Mezzanine**

10:30AM – 12PM **Contributed Paper Session 3 – Host-Pathogen Interactions – Ballroom B**

10:30AM [O3-1] **Transcription factor Zfp1 and its role in *Ustilago maydis* pathogenesis.** H.Y.K. CHEUNG, M.E. DONALDSON, K.L. SPENCE AND B.J. SAVILLE. *(M.E.D., B.J.S) Environmental and Life Sciences Graduate Program, Trent University, Peterborough, ON, K9J 7B8, Canada; (K.L.S.) Department of Population Medicine, Ontario Veterinary College, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada*; *and (M.E.D, B.J.S) Forensic Science Program, Trent University, Peterborough, ON, K9J 7B8, Canada*

10:45AM [O3-2] **Degradome studies provide new insights into viroid pathogenicity.** C.R. ADKAR-PURUSHOTHAMA AND J.-P. PERREAULT. *RNA Group/Groupe ARN, Département de Biochimie, Faculté de médecine et des sciences de la santé, Pavillon de Recherche Appliquée au Cancer, Université de Sherbrooke, 3201 rue JeanMignault, Sherbrooke, Québec, J1E 4K8, Canada*

11:00AM [O3-3] **Update on Manitoba horticultural crops disease and insect pests in 2015.** V. BISHT. *Crop Industry Branch, Manitoba Agriculture, 65, 3rd Avenue NE, Carman, Manitoba. R0G 0J0*

11:15AM [O3-4] **Comprehensive assessment of grapevine virus diseases in British Columbia.** S. POOJARI, T. D. LOWERY, J. BOULÉ, N. DELURY, M. ROTT, A-M. SCHMIDT AND J. R. ÚRBEZ-TORRES. *Agriculture and Agri-Food Canada, Summerland Research and Development Centre, Summerland, BC V0H1Z0, Canada; and (M.R., A-M.S.) Canadian Food Inspection Agency, Centre for Plant Health, Sidney Laboratory, Sidney, BC V8L1H3, Canada*

11:30AM [O3-5] **Grapevine trunk diseases studies in British Columbia.** J.R. ÚRBEZ TORRES AND D. T. O'GORMAN. *Agriculture and Agri-Food Canada, Summerland Research and Development Centre, Summerland, BC V0H1Z0, Canada*

11:45AM [O3-6] **What are Plant Canada and Global Plant Council.** D. ERRAMPALLI. *Agriculture and Agri-Food Canada, 4902 Victoria Ave. N., Vineland Station, ON L0R 2E0 Canada*

12PM – 2PM **CPS Annual General Meeting and Lunch (sponsored by Syngenta) – Ballroom A**

2PM – 3:30PM **Contributed Paper Session 4- Pathology of Field and Horticultural Crops**

2:00PM [O4-1] **Temperature adaptation of *Puccinia striiformis* f. sp. *tritici*, cause of stripe rust of wheat.** V.A. TRAN AND H.R. KUTCHER. *Crop Development Centre/Department of Plant Science, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada*

2:15PM [O4-2] **Developing a wheat germplasm collection with diverse pathogen and pest resistance.** B.D. MCCALLUM, C.W. HIEBERT, T.G. FETCH, C.A. MCCARTNEY, M.A. HENRIQUEZ, H.S. RANDHAWA AND S.J. CLOUTIER. *(B.D.M., C.W.H, C.A.M, M.A.H) Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Unit 100, Morden, MB, R6M 1Y5, Canada; (T.G.F.) Brandon Research and Development Centre, Agriculture and Agri-Food Canada, Brandon, MB, R7A 5Y3, Canada; (H.S.R.) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada Canada, 5403 1st Avenue South, P.O. Box 3000, Lethbridge, AB, T1J 4B1, Canada; and (S.J.C) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, K.W. Neatby Building, 960 Carling Avenue, Ottawa, ON, K1A 0C6, Canada*

2:30PM [O4-3] **Re-emergence and rapid spread of the Goss's wilt disease pathogen of corn: possible scenarios.** J.T. TAMBONG, R. XU, A. SOLIMAN AND F. DAAYF. *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; and (F.D. & A.S.) Department of Plant Science, University of Manitoba, Winnipeg, Manitoba, Canada*

2:45PM [O4-4] **Diverse population of *Septoria linicola* causing pasmo disease in flax.** K.Y. RASHID**.** *Agriculture and Agri-Food Canada, Morden Research and Development Centre, 101 Route 100, Morden, Manitoba, Canada R6M 1Y5*

3:00PM [O4-5] **A detached fed-leaf bioassay to assess bacterial antagonists against *Phytophthora infestans* isolates.** P. AUDY, N. FORAN, S.M. BOYETCHKO AND V. GRAVEL. *Quebec Research and Development Centre, Agriculture and Agri-Food Canada, Quebec, QC, G1V 2J3, Canada; (N.F. and V.G.) Department of Plant Science, McGill University, Macdonald Campus, 21 111 Lakeshore Road, Sainte-Anne-de-Bellevue, QC H9X 3V9, Canada; (S.M.B) Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, Saskatoon, SK, S7N 0X2, Canada*

3:15PM [O4-6] **What's on my weed? Preliminary insights into the *Cannabis*-powdery mildew pathosystem.** D.L. JOLY, N. PÉPIN, F. SORMANY, A. ROY AND N. HACHÉ. *(D.L.J., N.P., F.S.) Université de Moncton, 18 avenue Antonine-Maillet, Moncton, NB E1A 3E9, Canada; (A.R., N.H.) OrganiGram Inc, Moncton, NB, Canada*

3:30PM **Break (sponsored by VWR) - Mezzanine**

4PM – 5:00PM **Contributed Paper Session 5 – Pathogen Propagules – Ballroom B**

4:00PM [O5-1] **A molecular method for determining the viability of *Synchytrium endobioticum*.** D.S. SMITH AND U. SINGH. *Canadian Food Inspection Agency, Charlottetown Laboratory, 93 Mount Edward Road, Charlottetown, PE C1B 1M2, Canada*

4:15PM [O5-2] **Estimation of viable resting spores of *Plasmodiophora brassicae* in a six-year crop rotation study using propidium monoazide-assisted PCR.** F. AL-DAOUD, J. ROBSON, D. PAGEAU, B. D. GOSSEN, J. A. DALTON AND M. R. MCDONALD. *Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada; (D.P.) Agriculture and Agri-Food Canada, 1468 St-Cyrille Street, Normandin, QC, G8M 4K3, Canada; and (B.D.G.) Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, 107 Science Place, Saskatoon, SK, S7N 0X2, Canada*

4:30PM [O5-3] **Oospore dose-response and spatial distribution of the pea root pathogen, *Aphanomyces euteiches*, in Saskatchewan soils.** S. CHATTERTON, A. ERICKSON AND S. BANNIZA. *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403–1 Ave. South, Lethbridge, AB T1J 4B1; (S.B.) Crop Development Centre, University of Saskatchewan, 51 Campus Dr., Saskatoon, SK S7N 5A8*

4:45PM [O5-4] **Thirty years of postharvest biological control research: the journey from simplicity to complexity.** *Michael Wisniewski, USDA-ARS, Appalachian Fruit Research Station, Kearneysville, WV, USA*

6:51PM Tidal Bore Estimated time – Bore Park

7PM – 11PM **CPS Banquet and Award Ceremony – Ballroom A**
(sponsored by Potatoes NB)

Wednesday, June 15

7:19AM Tidal Bore Estimated time – Bore Park

8AM – 12PM Poster take-down - Mezzanine

8:30AM – 12PM **Symposium 2: Biovigilance: a framework for effective pest management – Ballroom A**
(sponsored by Taylor & Francis)

8:30AM [S2-1] **Using biovigilance-based information for strategic and tactical disease management decisions.** *Odile Carisse, AAFC, Saint-Jean-sur-Richelieu, QC*

9:15AM [S2-2] **Using genomics approaches for rapid development of species-specific diagnostics for cucurbit downy mildew.** *Lina Quesada-Ocampo, North Carolina State University, Raleigh, NC, USA*

10AM **Break (sponsored by Western Grains Research Foundation) - Mezzanine**

10:30AM [S2-3] **The Biovigilante: Monitoring threats to plant health in an era of globalization and climate change.** *Kirk Broders, Colorado State University, Fort Collins, CO, USA*

10:30AM [S2-4] **How to get published?** *Alison Paskins, Taylor and Francis*

19:43PM Tidal Bore Estimated time – Bore Park

Poster session index (P1-P5 = Student Competition)

P1. **Expression analysis of three NADPH oxidase genes in germination and infection of wheat leaf rust.** M.Z. CHE, X.B. WANG, B.D. MCCALLUM, H.B. KHALIL, G. BAKKEREN AND B.J. SAVILLE. *(M.Z.C.; X.B.W.; B.D.M.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Unit 100, Morden, MB, R6M 1Y5, Canada; (M.Z.C.) Department of Plant Pathology, China Agricultural University, Beijing, 100193, People's Republic of China; (H.B.K. and G.B.) Summerland Research and Development Centre, Agriculture and Agri-Food Canada, Summerland, BC, V0H 1Z0, Canada; and (B.J.S.) Forensic Science Program Trent University, Peterborough, ON, K9J 7B8, Canada* **(Student Competition)**

P2. **Identification of *Albugo candida* causing white blister rust of *Wasabia japonica* in British Columbia.** J.L. MACDONALD AND Z.K. PUNJA. *Summerland Research and Development Centre, Agriculture and Agri-Food Canada, 4200 Highway 97, Summerland, British Columbia, V0H 1Z0, Canada; and (Z.K.P.) Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, British Columbia, V5A 1S6, Canada* **(Student Competition)**

P3. **Variation in boron tolerance and clubroot severity in *Brassica napus* and *B. rapa* lines in a field trial in 2015.** A. MCLEAN, B.D. GOSSEN AND M.R. MCDONALD. *Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON N1G 2W1, Canada; and (B.D.G.) Agriculture and Agri-Food Canada (AAFC), 107 Science Place, Saskatoon, SK S7N 0X2, Canada* **(Student Competition)**

P4. **Genes differentially expressed during pathogenesis by two *Plasmodiophora brassicae* pathotypes on canola (*Brassica napus*).** J. JIANG, R. FREDUA-AGYEMAN, S.F. HWANG, AND S.E. STRELKOV. *(J.J., S.E.S.) Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada; (R.F.A., S.F.H.) Crop Diversification Centre North, Alberta Agriculture and Forestry (AAF), Edmonton, AB T5Y 6H3, Canada* **(Student Competition)**

P5. **Identification of microsatellite markers linked to quantitative trait loci associated with partial resistance to Aphanomyces root rot in field pea**. L.F. WU, R. FREDUA-AGYEMAN, K.F. CHANG, R.L. CONNER, S.F. HWANG, D. FEINDEL, K.B. MCRAE AND S.E. STRELKOV. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, ABT6G 2P5, Canada (L.F.W., S.E.S.); Crop Diversification Centre North, Alberta Agriculture and Forestry (AAF), Edmonton, Canada, AB T5Y 6H3 (R.F.A., K.F.C., S.F.H.); Agriculture and Agri-Food Canada (AAFC), Morden Research and Development Centre, Morden, Manitoba, Canada R6M 1Y5 (R.L.C.); AAFC, Kentville Research and Development Centre, Kentville, NS B4N 1J5 (K.B.M.).* **(Student Competition)**

P6. **An assessment of the genetic basis for resistance to stem rust race TRTTF in Canadian hexaploid wheat cultivars.** C.W. HIEBERT, M.N. ROUSE, J. NIRMALA, C.A. MCCARTNEY, M.T. KASSA, AND T.G. FETCH. *(C.W.H and C.A.M.) Agriculture and Agri-Food Canada, Morden Research and Development Centre, 101 Route 100 Morden, Manitoba, Canada, R6M 1Y5;*

(M.N.R. and J.N.) United States Department of Agriculture-Agricultural Research Service (USDA-ARS) Cereal Disease Laboratory and University of Minnesota Department of Plant Pathology, 1551 Lindig Street, St. Paul, MN, USA; (M.T.K.) National Research Council, 110 Gymnasium Place, Saskatoon, SK, S7N 0W9, Canada; (T.G.F.) Agriculture and Agri-Food Canada, Brandon Research and Development Centre, Brandon, MB R7A 5Y3, Canada

P7. **Investigating the etiology of tree fruit decline in British Columbia.** J. R. ÚRBEZ-TORRES, J. BOULÉ AND D. T. O'GORMAN. *Agriculture and Agri-Food Canada, Summerland Research and Development Centre, Summerland, BC V0H1Z0, Canada*

P8. **Effect of maleic hydrazide on stem rust seedling infection type.** T. FETCH JR. *Brandon Research & Development Centre, Agriculture & Agri-Food Canada, 2701 Grand Valley Road, Brandon, MB, R7A 5Y3 Canada*

P9. **Nematology research at Agriculture and Agri-Food Canada: renewed emphasis on an old pest.** C. KORA, Q. YU, B. MIMEE AND T.A. FORGE. *Pest Management Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; (Q.Y.) Ottawa Research and Development Centre, Canadian National Collection of Nematodes, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; (B.M.) Saint-Jean-sur-Richelieu Research and Development Centre, Agriculture and Agri-Food Canada, 430 Gouin Blvd, St-Jean-sur-Richelieu, QC J3B 3E6, Canada; (T.A.F.) Summerland Research and Development Centre, Agriculture and Agri-Food Canada, 4200 Highway 97, Summerland, BC V0H 1Z0, Canada*

P10. **DNA-barcoding the Powdery Mildews - sampling herbarium specimens in the National Mycological Herbarium (DAOM).** S. HAMBLETON, Q. EGGERTSON, C.A. LEVESQUE, W. CHEN, T. BARASUBIYE, S.A. REDHEAD AND M.LIU. *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, K.W. Neatby Building, 960 Carling Avenue, Ottawa, ON Canada K1A 0C6*

P11. **Molecular mapping of common bunt resistance in a 'Vesper' X 'Lilian' population.** F. BOKORE, R. CUTHBERT, R.E. KNOX, C. POZNIAK, A. N'DIAYE, A. SHARPE, AND Y. RUAN. S*wift Current Research and Development Center, Agriculture and Agri-Food Canada, Swift Current, SK S9H 3X2, Canada; (C.P., A.N'D.) Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada; (A.S.) National Research Council of Canada, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada*

P12. **Spectral signatures of bio-polymer changes in the wheat cell-wall resulting from *Puccinia striiformis* f. sp. *tritici* infection in compatible and incompatible interaction on Yr10.** G.S. BRAR, R. LAHLALI, D. QUTOB, H.R. KUTCHER, AND C. KARUNAKARAN. *Crop Development Centre/Department of Plant Science, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada; (R.L., C.K.) Canadian Light Source-National Synchrotron Research Facility, 44 Innovation Blvd, Saskatoon, SK S7N 2V3, Canada; (D.Q.) Canadian National Research Council, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada*

P13. ***Fusarium* species complex infecting oat in Manitoba.** M. BANIK, M. BEYENE AND X. WANG. *Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB R6M 1Y5 Canada*

P14. **An investigation of fungal isolates associated with ginseng diseases.** A. MUNAWAR, A. F. SHI, S. WESTERVELD AND M. R. MCDONALD. *(A.M. & M.R.M.) Department of Plant Agriculture, Simcoe Research Station, University of Guelph, Simcoe, Ontario, N3Y 4N5, Canada*; *(A.F.S.) Ontario Ginseng Growers Association, Simcoe Research Station, Simcoe, Ontario, N3Y 4N5, Canada; and (S.W.) Ontario Ministry of Agriculture, Food and Rural Affairs, Simcoe, Ontario, N3Y 4N5, Canada*

P15. **Downy mildew and cone diseases of hop in Ontario in 2015**. A. MUNAWAR, A. F. SHI, M. FILOTAS, C. BAKKER AND M. R. MCDONALD. *(A.M., C.B and M.R.M) Department of Plant Agriculture, Simcoe Research Station, University of Guelph, Simcoe, Ontario, N3Y 4N5, Canada; (A.F.S.) Ontario Ginseng Growers Association, Simcoe Research Station, Simcoe, Ontario, N3Y 4N5, Canada; and (M.F.) Ontario Ministry of Agriculture, Food and Rural Affairs, Simcoe, Ontario, N3Y 4N5, Canada*

P16. **Genome analysis and pathogenicity of a new potential biothreat, *Pantoea allii*, to onion production in Canada.** S. HSIEH, R. XU, T. J. AVIS AND J.T. TAMBONG. *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; and (S.H. & T.J.A.) Department of Chemistry, Food Science and Nutrition Program, Carleton University, 1125 Colonel By Drive, Ottawa, ON, K1S 5B6, Canada*

P17. **Expression of late blight resistance in potato using a tobacco rattle virus vector system.** C.P. WIJEKOON AND L.M. KAWCHUK. *Agriculture and Agri-Food Canada, 5403, 1st Ave S, Lethbridge, AB, T1J 4B1, Canada*

P18. **Strawberry nursery stock as a source of virus inoculum and on-farm spread of strawberry viruses in New Brunswick, Canada.** M.T. TESFAENDRIAS, C. MAUND and R.J.A. TREMBLAY. *New Brunswick Department of Agriculture, Aquaculture and Fisheries, 850 Lincoln Road, Fredericton, NB E3B 4Z7, Canada*

P19. **Development of a botanical pesticide for the control of powdery mildew: the challenge of performing fungicide efficacy trial on obligate biotrophic fungi.** S. BEAUSEIGLE, P. H. ONTCHANGALT, A. BILLONG, S. KERNER, Y. RUDOLPH-BINETTE AND A. VIALLE. *(S.B.; P. H. O., A. B. and A.V.) Biopterre-Bioproducts development center, 1642 rue de la ferme, La Pocatière, QC G0R 1Z0, Canada, (S. K, Y. R.) iFact inc. 1117 rue Sainte-Catherine Ouest, suite 410, Montréal, QC H3B 1H9, Canada, and (Y R-B) Arbressence inc., 77 rue Omer Desserres, suite 6A, Blainville, QC J7C 5N3, Canada*

P20. ***Fusarium graminearum* chemotypes from infected winter wheat crops in Manitoba.** M.A. HENRIQUEZ, B.D. MCCALLUM, M.F. BELMONTE, C.A. MCCARTNEY, T. OUELLET, F.M. YOU, AND H. S. RANDHAWA. *(M.A.H, B.D.M., C.A.M., F.M.Y.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, Unit 101 Route 100, Morden, MB, R6M 1Y5, Canada; (M.F.B.)*

Department of Biological Sciences, University of Manitoba, 50 Sifton Road, Winnipeg, MB, R3T 2N2, Canada; (T.O.) 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

P21. **In-vitro molecular interaction between the helper component-proteinase of Potato virus Y and cuticle proteins of potato aphid.** R. HEPAT, S. BOQUEL AND X. NIE. *Fredericton Research and Development Centre, Agriculture and Agri-Food Canada, 850 Lincoln Road, Fredericton, NB E3B 4Z7, Canada; and (S.B.) SIPRE – Comité Nord, Rue des Champs Potez, 62217 Achicourt, France*

P22. **Advances in elucidating the mode of action of mineral oil on reduction of aphid-mediated PVY transmission.** S. BOQUEL, R. HEPAT, AND X. NIE. *Fredericton Research and Development Centre, Agriculture and Agri-Food Canada, 850 Lincoln Road, Fredericton, NB E3B 4Z7, Canada; and (S.B.) SIPRE – Comité Nord, Rue des Champs Potez, 62217 Achicourt, France*

P23. **DNA-barcoding the rusts - sampling herbarium specimens in the National Mycological Herbarium (DAOM).** S. HAMBLETON, Q. EGGERTSON, S. WILSON, S.A. REDHEAD AND C.A. LEVESQUE. *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, K.W. Neatby Building, 960 Carling Avenue, Ottawa, ON Canada K1A 0C6*

P24. **Re-classification of *Clavibacter michiganensis* subspecies into multiple new species.** X. LI, J. TAMBONG, X. YUAN, H. XU, AND S.H. DE BOER. *Canadian Food Inspection Agency (CFIA), Charlottetown Laboratory, 93 Mt. Edward Rd., Charlottetown, PE, Canada, C1A 5T1; and (J.T.) Agriculture and Agri-Food Canada (AAFC), 960 Carling Ave, Ottawa, Canada, K1A 0C6*

P25. **Management of apple scab in organic apple orchards.** D. ERRAMPALLI, A. HALDAR, C. JACKSON, A. ZWIEP, F. BETANCOURT, L. KRZYWDZINSKI, M. PARCEY, K. SCHNEIDER. *Agriculture and Agri-Food Canada, 4902 Victoria Ave. N., Vineland Station, ON L0R 2E0, Canada*

P26. **Effects of dazomet on clubroot and root rot of canola.** S.F. HWANG, H.U. AHMED, S.E. STRELKOV, Q. ZHOU, B.D. GOSSEN, M.R. MCDONALD, G. PENG AND G.D. TURNBULL. *Crop Diversification Centre North, Alberta Agriculture and Forestry, Edmonton, AB T5Y 6H3, Canada; (S.E.S.) Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada; (B.D.G & G.P) Agriculture and Agri-Food Canada (AAFC), Saskatoon, SK S7N 0X2, Canada; (M.R.M) Department of Plant Agriculture University of Guelph, Guelph, ON N1G 2W1, Canada*

P27. **Differential proliferation of *Plasmodiophora brassicae* in *Brassica napus* cultivars.** T. CAO, S.F. HWANG, I. FALAK, AND S.E. STRELKOV. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada; (S.F.H.) Alberta Agriculture and Forestry, Crop Diversification Centre North, 17507 Fort Road, Edmonton, AB T5Y 6H3, Canada; (I.F.) Pioneer Hi-Bred Production Ltd., 12111 Mississauga Road, Caledon, ON L7C 1X1, Canada*

P28. **Efficacy of two fumigants against clubroot (*Plasmodiophora brassicae*) in three field trials.** J. ROBSON, B.D. GOSSEN, F. AL-DAOUD AND M.R. MCDONALD. *Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada; (B.D.G.) Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, 107 Science Place, Saskatoon, SK, S7N 0X2, Canada*

P29. **Use of genotype-by-sequencing to characterize populations of *Plasmodiophora brassicae.*** M. D. HOLTZ, S.F. HWANG, J. ZANTINGE, AND S.E. STRELKOV. *Field Crop Development Centre, Alberta Agriculture and Forestry, 6000 C and E Trail, Lacombe, AB T4L 1W1, Canada. (S.F.H.) Alberta Agriculture and Forestry, Crop Diversification Centre North, 17507 Fort Road, Edmonton, AB T5Y 6H3, Canada. (S.E.S.) Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada*

P30. **Occurrence of soybean root rot and associated pathogens in western Canada.** K. F. CHANG, S. F. HWANG, H. U. Ahmed, Q. ZHOU, H. FU, S. E. STRELKOV, R. L. CONNER, D. L. MCLAREN, M. W. HARDING AND G. D. TURNBULL. *Crop Diversification Centre North, Alberta Agriculture and Forestry (AAF), Edmonton, AB T5Y 6H3, Canada; (S.E.S.) Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada; (M.W.H.) CDC South, AAF, Brooks, AB T1R 1E6, Canada; (R.L.C.) Agriculture and Agri-Food Canada (AAFC), Morden, MB R6M 1Y5, Canada; (D.L.M.) AAFC, Brandon, MB R7A 5Y3, Canada*

P31. **Slip-skin disorder on sweet cherry (*Prunus avium* L.).** D.T. O'GORMAN, G. HEALY, P. M. TOIVONEN AND J.R. ÚRBEZ-TORRES. *Agriculture and Agri-Food Canada, Summerland Research and Development Centre (SuRDC), 4200 Hwy. 97, Summerland British Columbia, V0H 1Z0*

P32. **Development of a grapevine trunk diseases macroarray.** D.T. O'GORMAN, J. FRASER, J. DICK AND J. R. ÚRBEZ-TORRES. *Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre (SuRDC), 4200 Hwy 97 Summerland British Columbia, V0H 1Z0*

P33. **Blackleg resistance by Rlm1 may be triggered by localized activation of salicylic acid and suppression of abscisic acid and auxin pathways.** C. ZHAI, X. LIU, T. SONG, F. YU AND G. PENG. *Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada*

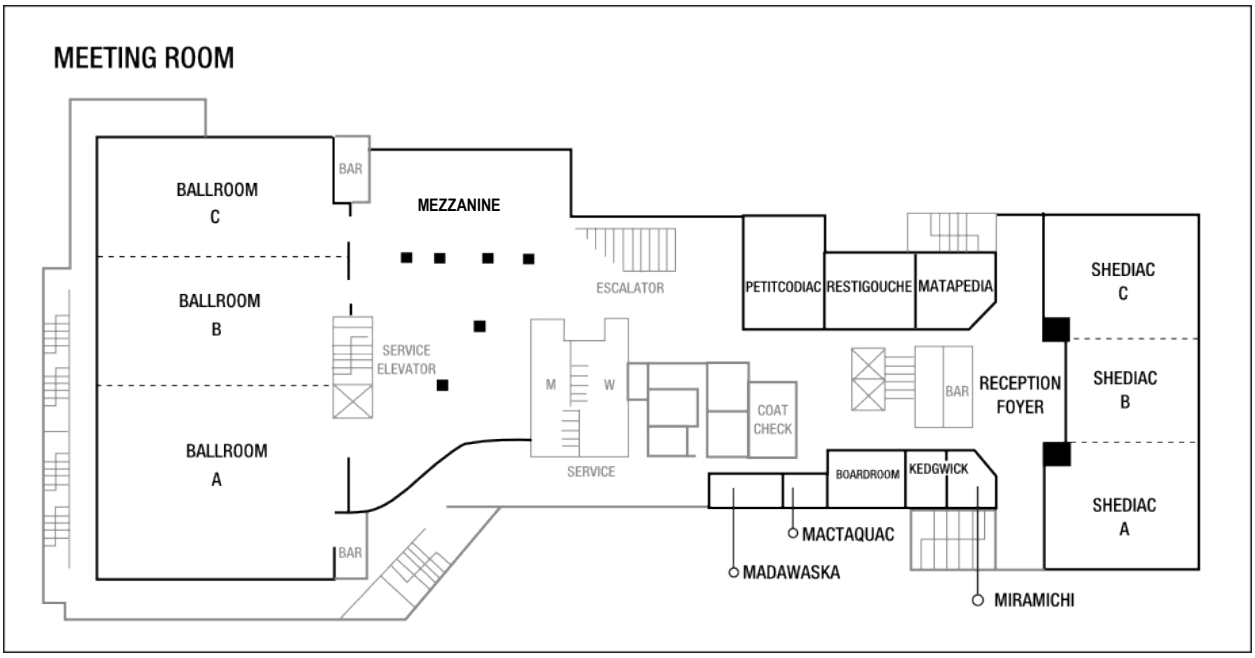
P34. **Non-race specific resistance to blackleg by Canadian canola cultivars shows delayed or reduced pathogen spread from infected cotyledons into petioles and stems.** W. M. SOOMRO, H. R. KUTCHER AND G. PENG. *Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada;* (*H.R.K*) *Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada*

P35. **Mining the microbiomes of crop wild progenitors for co-evolved beneficial microbes.** G. IRIARTE, I. HALE AND K. BRODERS. *(G.I.) Department of Molecular, Cellular and Biomedical Sciences, University of New Hampshire, Durham, NH 03824; (I.H.) Department of Biological*

Sciences, University of New Hampshire, Durham, NH 03824; and (G.I., K.B.) Department of Bioagricultural Sciences and Pest Management, Colorado State University, Fort Collins, CO 80523

P36. **Major shift in the virulence of sunflower rust races in Manitoba.** K.Y. RASHID. *Agriculture and Agri-Food Canada, Morden Research and Development Centre, Morden, Manitoba, R6M 1Y5*

P37. **Survival and productivity in an environment of multiple stressors: responses to drought in interior Douglas-fir (*Pseudotsuga menziesii* var. *glauca*) seedlings.** E.M. BECKER, M.G. CRUICKSHANK AND R.N. STURROCK. *Natural Resources Canada, Canadian Forest Service, Pacific Forestry Centre, 506 West Burnside Road, Victoria, BC V8Z 1M5, Canada*



Abstracts

Symposium 1: Genomics-based applications in plant pathology

[S1-1] **The Innate potato: from concept to commercialization.** N. CHAMPOURET. *Simplot, Boise, ID, USA*

Simplot Innate® technology permits the selective improvement of positive traits or minimization of negative traits of widely used, conventional potato varieties without incorporation of foreign genes. The Innate® platform of genetic modification also leverages the utilization of disease resistance traits from wild potato species. Resistance genes can be combined in various desirable permutations to keep at bay a particular pathogen population or to enhance the natural resistance of a variety. The technology effectively accelerates genetic improvement of conventional varieties faster than is currently possible using traditional breeding methods. The second generation of Innate® potatoes will have reduced blackspot bruise, reduced asparagine (which reduces the potential for the formation of acrylamide), cold storage capability and foliar late blight resistance against common North American strains. Therefore, Innate® potatoes are genetically engineered with traits appealing to potato growers, packers, processors, retailers and consumers.

[S1-2] **Genomic screens to identify next-generation MAMPs and their cognate pattern recognition receptors.** A. G. MOTT, S. THAKUR, E. SMAKOWSKA, P. W. WANG, Y. BELKHADIR, D. S. GUTTMAN AND D. DESVEAUX. *(A.G.M., S.T., D.S.G., D.D)* Department of Cell & Systems Biology, University of Toronto, 25 Willcocks St., Toronto, Ontario M5S 3B2, Canada; *(E.S., Y.B.)* Gregor Mendel Institute (GMI), Austrian Academy of Sciences, Vienna Biocenter (VBC), Dr Bohr Gasse 3, Vienna 1030, Austria; *(P.W.W., D.S.G., D.D.)* Centre for the Analysis of Genome Evolution & Function, University of Toronto, Toronto, Ontario, Canada

The front line of plant defence against pathogens depends on the action of extracellular leucine-rich repeat, receptor-like kinases (LRR-RLKs), which serve as Pattern Recognition Receptors (PRRs) to recognize essential and therefore evolutionarily conserved features of pathogens called Microbe-Associated Molecular Patterns (MAMPs). MAMP recognition by PRRs activates PRR-triggered immunity (PTI) which suppresses the growth of nearly all “non-host” microbes, as well as many potential pathogens. Next generation sequencing of *Pseudomonas syringae* pathovars has allowed the successful *in silico* prediction of MAMPs through the identification of positive selection signatures on proteins of the core genome. Although these “next-generation MAMPs” induce the hallmark responses of PTI, including virulence suppression, the PRRs that recognize them remain to be identified. I will present our latest genomic approaches to identify novel MAMPs and their cognate PRRs, as well as our efforts to translate resistance conferred by these genes into agricultural crops.

[S1-3] **Protecting Canada’s forests using next generation genomic biosurveillance.** R. C. HAMELIN. *The University of British Columbia, Vancouver, BC and Institut de Biologie Intégrative et des Systèmes, Université Laval, Québec*

The world’s forests face unprecedented threats from invasive insects and pathogens that can cause large irreversible damage to the environment. This threatens Canada’s capacity to provide long-term

fibre supply and ecosystem services that range from carbon storage, nutrient cycling, water and air purification, soil preservation and maintenance of wildlife habitat. The number of new introductions and interceptions of invasive alien forest pathogens is escalating at an alarming rate and the movement of goods and people is responsible for most of the documented incursions. The key to reduce the likelihood of invasive alien pathogens introductions is via vigilant biosurveillance combined with rapid and accurate detection. This leads to increased preparedness and early interventions that help prevent establishment. The TAIGA (Tree Aggressor Identification using Genomes Approaches) team has developed a pipeline to generate and analyse genome sequences and identify genome regions that are unique and can be translated into detection tools and regions that are highly variable and can be developed into monitoring tools. Real-time genome sequencing is promising to become part of routine diagnoses and could help predict disease outcome and model transmission risks to inform forest managers about prevention. Genome-wide population sequencing data will generate global databases that will provide accurate identification of forest enemies and reveal genomic patterns that can identify sources and novel variants and can inform outbreak management. This genomic biosurveillance pipeline has the potential to generate transformative changes to address the challenges of biosurveillance of invasive alien forest pathogens.

[S1-4] **A new twist on antibiosis: Exposure to sub-inhibitory concentrations of antibiotics alters the transcriptome of plant pathogens.** M. FILION. *Université de Moncton, 18 Antonine-Maillet, Moncton, NB, Canada, E1A 3E9*

Antibiotic-producing rhizobacteria show promise for use as successful biocontrol agents against many plant pathogens affecting agricultural crops. Antibiosis, or the capacity to control plant pathogens using antagonistic microorganisms that produce antibiotics, usually involves a significant reduction in the pathogen's population following exposure to lethal doses of antimicrobial compounds, leading to reduced disease pressure and symptoms. Although this classic definition of antibiosis has been shown to be the main biocontrol mechanism operating in many pathosystems, recent advances in transcriptomics depict an alternate mode of action for antibiosis. It is now increasing believed that under natural rhizosphere conditions, mostly sub-lethal doses of antibiotics are produced by rhizobacteria and therefore pathogen populations are not necessarily altered when exposed to such low doses of antibiotics. Instead, exposition to sub-lethal doses of antibiotics may lead to targeted effects on the expression of key genes involved in pathogenesis, leading to reduced disease symptoms. In this presentation, the impact of the phenazine-1-carboxylic acid producer *Pseudomonas fluorescens* LBUM223 on the transcriptome of the plant pathogen *Streptomyces scabies* causing common scab of potato will be presented to illustrate this new mode of action for antibiosis.

Contributed Paper Session 1 - Student Competition

[O1-1] **The dynamics of biomass accumulation by Ptr ToxA and Ptr ToxB producing isolates of *Pyrenophora tritici-repentis* on wheat.** X. MA, R. ABOUKHADDOUR, S.F. HWANG, AND S.E. STRELKOV. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada; (S.F.H) Crop Diversification Centre North, Alberta Agriculture and Forestry, Edmonton, Canada, AB T5Y 6H3*

The fungus *Pyrenophora tritici-repentis* causes tan spot of wheat. Fungal virulence is mediated by the production of several necrotrophic effectors that selectively induce foliar necrosis or chlorosis on sensitive host genotypes. These include the small proteins Ptr ToxA and Ptr ToxB, which cause necrosis and chlorosis, respectively, and are encoded by the *ToxA* and *ToxB* genes. While sensitivity to both proteins is widespread in Canadian wheat cultivars, Ptr ToxA producing isolates of the fungus are much more common than Ptr ToxB producers. In order to assess whether or not Ptr ToxA confers a greater competitive advantage to the fungus than Ptr ToxB, the accumulation of fungal biomass was compared following the inoculation of $ToxA^+$ and $ToxB^+$ isolates in various combinations onto a wheat genotype sensitive to both proteins. Fungal biomass was measured over a 5 day period by quantitative PCR analysis with *ToxA*, *ToxB* and chitin synthase gene-specific primers. When the isolates were inoculated individually, fungal biomass accumulation was significantly greater for the $ToxA^+$ vs. the $ToxB^+$ isolate. However, when the isolates were inoculated together, the amount of biomass of the $ToxA^+$ isolate decreased while that of the $ToxB^+$ isolate increased, although it remained lower than the $ToxA^+$ isolate. The results suggest that production of Ptr ToxA allows for greater accumulation of fungal biomass and/or host colonization by *P. tritici-repentis* than production of Ptr ToxB, and that colonization by the $ToxA^+$ isolate facilitated growth by the $ToxB^+$ isolate.

[O1-2] **Durability of blackleg resistance genes in *B. napus* and the emergence of virulent isolates in *L. maculans*.** M.H. RASHID, S. LIBAN, X. ZHANG, P. PARKS, M.H. BORHAN, AND W.G.D. FERNANDO. *Department of Plant Science, University of Manitoba, Winnipeg, MB, R3T 2N2 Canada;* (M.H.B) Agriculture *and Agri-Food Canada, Saskatoon Research Station, SK, S7N 0X2, Canada*

Canola (*Brassica napus*) interacts with a few major plant pathogens including *Leptosphaeria maculans* causing blackleg disease. A number of single dominant resistance (R)-genes have been identified in different *Brassica* species but a single R-gene may not offer durable resistance to the disease indicating the need of proper management of R-genes for the improvement of host resistance. A 4-year study was initiated to generate useful data to implement a canola cultivar rotation strategy based on an understanding of *R*-gene durability and the nature of emergence of virulent races. Five single *Rlm* (resistance against *L. maculans*) Topas near isogenic lines (NIL) were used in the study along with cultivar Topas as a control (no R-genes). Each plot was inoculated with 90% avirulence genes-carrying isolates for durability study and 100% avirulence genes-carrying isolates for emergence study, respectively. Each plot was set up for canola-wheat-canola over 2-years rotation. The pathogen isolates collected from either infected stubble or a 7-day Burkard spore trap were subjected to differential testing as well as PCR identification for the presence of avirulence genes. Disease incidence significantly varied among the NILs as well as between years in both the durability and emergence trials; however, similar trend of disease reduction was observed among the NILs in each year in both trials. The emergence trial revealed higher disease severity which is 71.42% of Topas control for *Rlm3* in 2014 and 38.46% of Topas control in 2015. The rest of the cultivars showed disease severity ≤ 28.57% of Topas control irrespective of trial and year. Differential phenotyping as well as PCR analysis of *L. maculans* isolates indicated that the *AvrLm3* gene frequency completely disappeared from the isolates of *Rlm3* stubble in durability trial of 2015 whereas it was ~37% in 2014 trial. On the other hand, *AvrLm3* gene frequency from the isolates of *Rlm3* stubble increased from 10 to 80% in emergence trial by the year 2015. The study will continue for four years to observe the likelihood and timeline for the breakdown of *R*-genes and the emergence of new races.

[O1-3] **Identification of *Ustilago maydis* RNA helicases and investigation of their function in the teliospore.** A.M. SETO, M.E. DONALDSON AND B.J. SAVILLE. *Environmental and Life Sciences Graduate Program, Trent University, 1600 West Bank Drive, Peterborough, ON, K9L 0G2, Canada; (M.E.D.,B.J.S.) Forensic Science Program, Trent University, 2140 East Bank Drive, DNA Building, Peterborough, ON, K9L 0G2, Canada*

Ustilago maydis D.C. Corda is dispersed as thick-walled dormant diploid teliospores, which germinate, complete meiosis, and initiate new rounds of infection. We hypothesize that the stored mRNAs in teliospores code for proteins important for germination and/or the subsequent developmental events. Some of these mRNAs are stabilized through the formation of double-stranded RNAs (dsRNAs). RNA-seq and gene ontology (GO) enrichment analyses were carried out to identify the patterns of transcript level change during germination and the functional categories of genes represented by the stored RNAs. RT-qPCR on RNA isolated from teliospores at distinct stages of germination will be used to confirm the patterns indicated by RNA-seq data. The presence of RNA helicases among the teliospore expressed genes suggested that unwinding dsRNAs was an early molecular event in germination. RNA helicases are widely conserved proteins involved in RNA strand annealing, RNA duplex unwinding, protein displacement from RNAs and other aspects of RNA function. Among the 46 RNA helicase we identified in *U. maydis*, four had expression patterns, revealed by RNA-seq, consistent with a role in teliospore germination. RT-PCR supported the expression pattern of an orthologue to *S. cerevisiae* RNA helicase, *ded1*. The creation of *ded1* deletion strains and functional analysis of this protein are underway. We will present the RNA-seq analyses of teliospore transcripts, and our initial investigation of RNA helicases in relation to a model of the molecular events of teliospore formation and germination.

[O1-4] ***Pseudomonas fluorescens* LBUM636 controls potato late blight through phenazine-1-carboxylic acid production.** C. MORRISON, T ARSENEAULT, A. NOVINSCAK, AND M. FILION. *Université de Moncton, 18 Antonine-Maillet, Moncton, NB, Canada, E1A 3E9*

Phytophthora infestans causes late blight of potato, one of the most devastating diseases affecting potato production. Alternative approaches for controlling late blight are being increasingly sought due to increasing environmental concerns and *P. infestans* resistance to chemical pesticides. Our research group has isolated a new strain of *Pseudomonas fluorescens* (LBUM636) of biocontrol interest due to its production of the antibiotic phenazine-1-carboxylic acid (PCA). Wild-type LBUM636 was shown to significantly inhibit the growth of *P. infestans* in *in vitro* confrontation assays while its isogenic mutant (*phzC*-; not producing PCA) barely altered the pathogen's growth. Wild-type LBUM636, but not the *phzC*-mutant, also completely repressed disease symptom development on tubers. Pot experiments in growth chambers revealed that wild-type LBUM636 can significantly reduce *P. infestans* populations in the rhizosphere and in the roots of potato plants, as well as reduce *in planta* disease symptoms due to PCA production. The expression of eight common plant defense-related genes (*ChtA*, *PR-1b*, *PR-2*, *PR-5*, *LOX*, *PIN2*, *PAL-2*, and *ERF3*) was quantified in tubers, roots and leaves by RT-qPCR and revealed that the biocontrol observed was not associated with the induction of a plant defense response by LBUM636.

Instead, a direct interaction between *P. infestans* and LBUM636 is required and PCA production appears to be a key factor for LBUM636's biocontrol ability.

[O1-5] **RNA-Seq analysis reveals transcriptome alteration in *Phytophthora infestans* by phenazine-1-carboxylic acid producing *Pseudomonas fluorescens* LBUM223.** R. ROQUIGNY, D.L. JOLY AND M. FILION. *Université de Moncton, 18 Antonine-Maillet, Moncton, NB, Canada, E1A 3E9*

Phytophthora infestans is responsible for late blight, one of the most important potato diseases. Phenazine-1-carboxylic acid (PCA)-producing *Pseudomonas fluorescens* LBUM223 isolated in our laboratory shows strong potential to control late blight. An *in vitro* confrontational assay was performed using *P. infestans* inoculated alone (control) or in the presence of wild-type LBUM223, its *phzC*- isogenic mutant not producing PCA, or synthetic PCA. Destructive sampling was performed at 6, 9 and 12 days and the transcriptome of *P. infestans* was analysed using RNA-sequencing. Both LBUM223 and synthetic PCA significantly repressed *P. infestans*' growth at all times, while the mutant barely altered the growth of the pathogen. Transcriptomic analysis showed that the non-producing PCA mutant did not significantly alter the transcriptome of *P. infestans* and yielded results similar to the control treatment. However, LBUM223 and synthetic PCA significantly altered *P. infestans* gene expression. Although time had a slight effect on the number of differentially expressed genes, LBUM223 and synthetic PCA yielded similar responses. The number of overexpressed *P. infestans* genes varied between 4% and 6% (LBUM223) and between 1% and 6% (synthetic PCA), while both treatments repressed the expression from 1% to 2% of genes. Gene ontology analyses revealed that PCA production by LBUM223 is altering the expression of key functional genes involved in various functions of interest.

[O1-6] **Intra-host interactions of the pea root rot pathogens *Aphanomyces euteiches* and *Fusarium* spp.** T. WILLSEY, J. THOMAS and S. CHATTERTON. *University of Lethbridge, 4401 University Drive, Lethbridge, AB, T1K 3M4, Canada; (S.C) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403–1 Avenue South, Lethbridge, AB, T1J 4B1, Canada*

Pea root rot complex (PRRC) describes a group of closely associated soil-borne fungi that cause root rot disease in field pea (*Pisum sativum* L.). The oomycete *Aphanomyces euteiches* Drech. and several *Fusarium* species are frequently the most prevalent and damaging microorganisms within this complex, and cause severe reductions in the quality and quantity of crop yield. Fungicidal application, crop rotation, and resistance breeding have been unsuccessful in managing either microorganism. Both pathogen groups have been studied extensively in isolation, but the effect of intra-host interactions on disease development remains largely unexplored. Therefore, interactions between *A. euteiches* and three *Fusarium* spp. were examined in greenhouse trials, in which *P. sativum* was exposed to root pathogens under controlled conditions. Results from three independent trials indicate an increase in disease symptoms in the presence of multiple pathogen species compared to inoculations with a single pathogen. Further trials have indicated that application of the fungicides fludioxonil and ethaboxam as

seed treatments may inhibit proliferation of *Fusarium* spp. and *A. euteiches,* respectively, but efficacy is influenced by initial inoculum concentration. Results from controlled seed treatment trials will be confirmed in field experiments conducted in 2016. Insight into the interactions between *A. euteiches* and *Fusarium* spp. is necessary to inform timely mitigation strategies aimed at controlling both pathogens simultaneously.

[O1-7] **Genetic diversity and colonization patterns of *Onnia tomentosa* in a plantation of black spruce (*Picea mariana*) in northwestern Ontario.** Z.R.W. HOEGY, D. MORRIS, D. REID, AND L.J. HUTCHISON. *Faculty of Natural Resources Management, Lakehead University, Thunder Bay, Ontario P7B 5E1; and (D.M., D.R.) Centre for Northern Forest Ecosystem Research (CNFER), 421 James Street S., Suite 103, Thunder Bay, Ontario P7E 2V6*

Onnia tomentosa (Fr.) Karst. is prevalent throughout North America, Europe, and Asia and is responsible for causing a significant root-rot disease of conifers commonly known as stand-opening disease. Although the disease infects both spruce and pine, it is more severe on the former. In the late summer of 2014, the spatial coordinates of 124 basidiomata were taken, and the basidiomata collected from a 50 year old black spruce plantation near Limestone Lake, north of Nipigon, Ontario that had undergone thinning treatments six years prior. The three thinning treatments were light thinning (25% tree removal), heavy thinning (45% tree removal), and control (no thinning occurred). There was also a clear cut treatment, however, no basidiomata of *O. tomentosa* were found. Using extracted DNA from each of the basidiomata, single strand conformational polymorphism polymerase chain reaction (SSCP-PCR) of two nuclear loci, and DNA sequencing of two mitochondrial loci were used to measure genetic diversity and consequently genet size in order to see if stand density had an effect on *O. tomentosa*'s colonization patterns. One hundred and sixteen genetically distinct individuals were found, suggesting that the majority of the basidiomata represented unique genets. Stand thinning does seem to negatively influence *O. tomentosa* colonization, however, it is inconclusive whether the light or heavy thinning treatments are better at countering the fungal pathogen.

[O1-8] **Epidemiology and management of stemphylium leaf blight on onion in the Holland Marsh, Ontario.** S.C. TAYVIAH, B.D. GOSSEN, AND M.R. MCDONALD. *Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada; (B.D.G.) Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, Saskatoon, SK, Canada*

Stemphylium leaf blight, caused by *Stemphylium vesicarium* Wallr Simmons (telemorph; *Pleospora allii* (Rabenh) Ces. & de Not.), is a new disease of onion in Ontario. It is presently managed with multiple applications of fungicide. To understand its epidemiology, air-borne spore concentrations were monitored continuously for 120 days in 2015 using a Burkard 7-day volumetric sampler. Hourly spore counts revealed a diurnal pattern, with 48% of ascospores and 73% of conidia captured between 0500–1200 hours. The highest concentrations of ascospores (54 ascospores m^{-3} air day^{-1}) were captured prior

to disease onset, but capture of conidia was highest (97 conidia m^{-3} air day^{-1}) during disease development. Spore concentrations increased dramatically 24–72 hours after precipitation. The first appearance of blight symptoms coincided with high conidia numbers, rainfall, and warm days (temp ≥ 18°C for ≥ 9 hr). Conidia appear to be important in the development of blight epidemics, but the role of ascospores is not yet clear. A foliar fungicide (fluopyram 12.5%, pyrimethanil 37.5%) was applied based on calendar spray timings, initiation of calendar application based on spore trapping, spray prediction models (BOTCAST threshold 1, TOMCAST DSV 15, and a model modified specifically for stemphylium leaf blight), and a non-sprayed control. TOMCAST prompted six sprays compared to 10 with the spore trapping treatment and eight applications with the other models. Early spray applications reduced foliar blight severity, but no treatment increased marketable yield. More effective fungicides and spray timings are required to provide effective management of stemphylium leaf blight.

[O1-9] **Management of plant-parasitic nematodes on carrots grown in organic (muck) soils in Ontario.** D. VAN DYK, K. JORDAN, AND M. R. MCDONALD. *Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph ON N1G 2W1, Canada*

Carrots (*Daucus carota* L., subsp. *sativus* (Hoffm) Arcang) can be particularly susceptible to plant-parasitic nematode damage, especially during taproot formation. In Ontario, two common nematode pests of carrot are the root-knot nematode (*Meloidogyne hapla* Chitwood) and carrot cyst nematode (*Heterodera carotae* Jones). Restrictions around fumigant use are increasing and many nematode control products are no longer available to vegetable growers, creating a need to identify effective non-fumigant nematicides. To evaluate some of these new products, field trials were conducted in the Holland Marsh, ON during 2014 and 2015 in fields with a history of nematode damage. A randomized complete block design with six replicates per treatment was used. The treatments were: PicPlus (chloropicrin 86%) at 78 kg/ha, Vapam (metam sodium 42%) at 275 L/ha, Nimitz (fluensulfone 15%) at 8.3 L/ha, PicPlus at 78 kg/ha + Vapam at 275 L/ha, PicPlus at 78 kg/ha + Nimitz at 8.3 L/ha, MustGrow (oriental mustard seed meal 100%) at 1680 kg.ha, Dazitol (capsaicin 0.42%, oleoresin of capsicum 3.7%) at 60 L/ha, AgriMek (abamectin 2%) at 20 L/ha, and an untreated check. Carrots, cv. Cellobunch (~65 seeds/m) were direct seeded on raised beds. Each experimental unit consisted of three rows, 66 cm apart and 13 m long. PicPlus, Vapam, Nimitz, and a combination of these products increased carrot yield and percent marketable carrots while reducing disease severity. The non-fumigant nematicide, Nimitz, reduced damage and increased yields comparable to the grower standard fumigants in 2014 but not in 2015 so further research is required.

Contributed Paper Session 2 – Molecular Diagnostics and Screening

[O2-1] **Sequence-based identification of fungi from ginseng roots and soils.** D. ERRAMPALLI, C. NICOL, A. HALDAR, M. PARCEY, K.I. SCHNEIDER AND S. WESTERVELD. *Agriculture and Agri-Food Canada, 4902*

Victoria Ave. N., Vineland Station, ON L0R 2E0 Canada. (SW) Ontario Ministry of Agriculture, Food and Rural Affairs, 1283 Blueline Road, Simcoe, Ontario, N3Y 4N5 Canada

Replant disease causes severe yield losses in ginseng. Detection and identification of pathogens are the first critical steps in developing disease control. The goal of this study was to determine whether sequence analysis of internal transcribed spacer region (ITS) can be used to detect and identify fungal pathogens in soils in which the ginseng was grown and symptomatic ginseng roots. Soils were collected from gardens (fields) with and without replant disease (control) in 2014. Ginseng roots with symptoms were collected from three ginseng gardens in Ontario. Fungi were isolated from soils and root samples on different selective media. Genomic DNA was extracted from each of the fungal isolates and the ITS region was amplified by PCR with ITS1 and ITS4 primers. The amplified DNA was sequenced and aligned against sequences in GenBank. Sequence based identification was carried out on 109 fungal isolates: a) *Fusarium oxysporum* (44%), *Fusarium solani* (14.8%), and *Cladosporium cladosporoides* (16.0%) *and Fusariun species* (13%) were from 55 isolates from the soils in which ginseng was cultivated, b) *Bionectria sp./ Clonostachys sp.* (27.3%), *Cylindrocarpon* (13.6%), and *Mortierella sp.*, (13.6%) were from 22 isolates from the soils around wild ginseng plants ,and c) *F. solani* (46%), *Epicoccum nigram* (12.5%), *Pseudallescheria boydii / Scedosporium minutisporum* (9.4%) were from 32 isolates from the symptomatic ginseng roots. This information is important for determining the complex that causes ginseng replant disease.

[O2-2] **Transcriptomic insight into emerging wheat leaf rust races of Ontario.** K.M. MARSH, B.D. MCCALLUM, X. WANG, A. TENUTA AND B.J. SAVILLE. *(K.M.M., B.J.S.) Environmental & Life Sciences Graduate Program, Trent University, DNA Building, 2140 East Bank Dr, Peterborough, ON K9J 7B8, Canada; (B.D.M., X.W.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB R6M 1Y5 Canada; (A.T.) Ontario Ministry of Agriculture and Rural Affairs, Ridgetown Resource Center, Argronomy Building, Main St. E, Ridgetown, ON N0P 2C0, Canada; and (B.J.S.) Forensic Science Program, DNA Building, Trent University, 2140 East Bank Dr Peterborough, ON K9J 7B8, Canada*

Puccinia triticina Eriks., wheat leaf rust fungus (WLR), is the most economically damaging rust pathogen on a global scale. The emergence of a WLR race in Ontario with a new virulence type enabled a study of the transcriptome changes occurring in the newly emerged race relative to its putative ancestors. This investigation utilized wheat near isogenic lines (NIL) carrying different WLR resistance genes, the isolated new WLR race, and other races thought to be its potential ancestors. Illumina paired-end RNA-seq was carried out on specific infections of wheat NILs with WLR races. Fungal transcripts were aligned to 15686 genes from the WLR reference sequence. The identification of potential effector genes whose expression level was altered in the new WLR race relative to presumed ancestors was completed using a conservative approach. The selection of altered candidate effectors included ascertaining which genes were 2-fold up or down regulated, identifying transcript ORFs containing secretion signals, and detecting SNPs which altered protein secondary structure. This process resulted in a list of 97 candidate effector-encoding genes. Of these, 7 unique genes were identified to have at least one nonsynonymous SNP

which altered the amino acid sequences and secondary structure of the resulting protein. If these gene alterations influence virulence, then we will have identified a basis for new WLR virulence types. Predicted orthologs to these candidate effector genes were found in *Ustilago maydis* (DC.) Corda, a model plant pathogen. Functional investigation of the *U. maydis* orthologs is currently underway.

[O2-3] **Next-generation sequencing (NGS) using Ion Torrent technology for biosurveillance from spore and insect traps.** G.J. BILODEAU, É. TREMBLAY AND J.A. BERUBE. *Canadian Food Inspection Agency, Ottawa Plant Laboratory, Ottawa, ON, K2H 8P9, Canada; (J.A.B.) Natural Resources Canada, Laurentian Forestry Centre, Québec, QC, G1V 4C7, Canada*

Plant pathogenic fungal spores spread by wind, rain and through vectors (insects) can cause the introduction of exotic diseases and are responsible for the devastation of various plant species. New technologies such as metagenomics are now an option for quicker detection by avoiding time-consuming culturing methods. As a proof of concept of biosurveillance using this new technology, DNA was extracted from spore trap filtrates and insect trap preservation liquids from collections from 2013-2015. DNA was sequenced on the Ion Torrent PGM™ platform using fusion primers designed to multiplex three genic regions (350-400bp amplicons from 2 ribosomal DNA region ITS1 (fungi and oomycetes) and the mitochondrial DNA region ATP9-NAD9 (*Phytophthora* sp.)). Bioinformatic analyses were also done to process the millions of sequences generated, which were then compared with species-specific qPCR testing for multiple specific targets. We compared the NGS contents to qPCR data obtained for the detection of forest pathogens species, which led us to find several closely related species to our targeted *Phytophthora* species and forest fungi. The method we developed allows us to identify potential sources of entry into Canada and to access sample abundance, biodiversity and phylogeny in order to accelerate the identification process of current risk associated with these exotic plant pathogen species.

[O2-4] **Geographic atlas of mycotoxigenic fungi through metagenomic surveys of DNA barcodes using a novel taxonomic classification approach.** W. CHEN, C. VISAGIE, M. LIU, K. SEIFERT, T. GRAEFENHAN, S. HAMBLETON AND C. A. LEVESQUE. *Ottawa Research & Development Centre, Science & Technology Branch, Agriculture and Agri-Food Canada, 960 Carling Ave., Ottawa, ON, K1A 0C6, Canada*

Mycotoxins are toxic secondary metabolites produced by species of fungal genera such as *Alternaria, Aspergillus*, *Claviceps*, *Fusarium* and *Penicillium*. Species of one genus often produce different biosynthetic groups of mycotoxins, which have adverse health effects on human and livestock. Some of these species are considered pathogens of agricultural/medical importance. For risk assessment and mycotoxin management, it is important to accurately identify these organisms. This is challenging for Metagenomic surveys using DNA barcodes. The internal transcribed spacer (ITS) of the rDNA region is the official fungal barcode, but often lacks sufficient discriminatory power at the species/subspecies ranks. Furthermore, existing algorithms for sequence classification are similarity- and composition-

based, which are imprecise for taxonomic profiling below the genus level and for accommodating the inherent error rate of various Next Generation Sequencing (NGS) platforms. Our three objectives were: 1) using clades-specific oligonucleotides to facilitate and improve species/subspecies-level interpretation of metabarcodes; 2) developing a living geographic atlas of mycotoxin producing fungi in Canada; 3) discovering known and putatively unknown species and provide critical information to taxonomists for species discovery and reference database development. A total of 45 million ITS1 and ITS2 454-pyro-tagged sequences from air/rain samples and commodity seed wash samples collected during 2009–2013 were compared with the curated UNITE fungal ITS database. Preliminary results showed that ITS1 and ITS2 recovered different numbers of putative species (Operational Taxonomic Unit, OTU) at 97% similarity cutoff, with ITS2 recovering almost double the OTUs for *Aspergillus*, *Penicillium* and *Claviceps*.

[O2-5] **Development and validation of high-resolution DNA melting (HRM)-based markers derived from Rysto-STS markers YES3-3A and YES3-3B for high-throughput marker-assisted selection of potatoes carrying Rysto.** X. NIE, D. SUTHERLAND, V. DICKISON, M. SINGH, A. MURPHY AND D. DE KOEYER. *Fredericton Research and Development Centre, Agriculture and Agri-Food Canada, 850 Lincoln Road, Fredericton, NB E3B 4Z7, Canada; (M.S.) Agricultural Certification Services, Fredericton, NB E3B 8B7, Canada; and (D.D.K) International Institute of Tropical Agriculture, PMB 5320, Oyo Road, Ibadan 200001, Oyo State, Nigeria*

Sequence analysis of the chromosome region harbouring the Ry_{sto} STS markers YES3-3A and YES3-3B in tetraploid potato cultivars 'Barbara' (*Rrrr*) and 'AC Chaleur' (*rrrr*) as well as 5 progeny selections revealed 3 sequence variants in 'Barbara' and the resistant (R) selections, and 2 variants in 'AC Chaleur' and susceptible (S) selections. Further analysis of the sequence variant ratio as well as *in-silico* PCR with YES3 primers indicates that a variant with a 21-nucleotide (nt) deletion is likely the chromosome copy harbouring the Ry_{sto}. Two primer pairs, one targeting the region containing the 21-nt deletion and the other targeting the region anchoring the YES3-3A reverse primer, were designed. As anticipated, pair one produced two visible fragments in 'Barbara'/R pool and one visible fragment in 'AC Chaleur'/S pool; pair two produced one visible fragment in all samples. When subjected to high-resolution DNA melting (HRM) analysis, two distinct melting profiles for R and S samples were observed. Analysis of 147 progenies of 'Barbara' x 'AC Chaleur' revealed 72 and 75 progenies with R and S melting profiles, respectively, which was100% consistent with YES3-3A and YES3-3B assays and phenotyping analysis. The results demonstrate the potential of HRM profiles as novel molecular markers for Ry_{sto}. The efficacy of the newly developed HRM markers for marker-assisted selection (MAS) was further validated with three populations involving 'Barbara' as the resistant parent. HRM markers offer rapid and accurate detection of potatoes carrying Ry_{sto} and can be used for high-throughput MAS in potato breeding to identify Ry_{sto}-conferred extreme resistance to *Potato virus Y*.

[O2-6] **Development and validation of diagnostic procedures based on the next generation sequencing technology for screening potato accessions imported to Canada.** H. XU, S. LI, DESMOND L. HAMMILL,

SHARA CODY AND JINGBAI NIE. *Canadian Food Inspection Agency, Charlottetown Laboratory, 93 Mt. Edward Rd., Charlottetown, PE, Canada, C1A 5T1*

Small quantities of *Solanum* spp. germplasm may be introduced into Canada, for vegetative propagation under the potato post-entry quarantine (PPEQ) program. Potato accessions entered into the PPEQ program are routinely propagated in vitro followed by multiplication in greenhouse followed by serial testing using biological, serological and molecular methods for detecting any possible potato pathogens. The entire process of PPEQ quarantine testing is costly and time consuming. In 2015, mini potato tubers (5 kg) illegally brought into Canada, were seized and entered in the PPEQ facility for quarantine testing. The mini tubers were grown out in the greenhouse and total RNA was extracted from leaf samples of 8 plants. The RNA was then used for cDNA library construction followed by next generation sequencing (NGS) analysis. Over 300 million reads were obtained from the paired-end sequencing in a MiSeq platform (Illumina) and used for de novo assembly using CLC Genomics Workbench. After filtration against the potato genome sequence, over 350 assembled contigs from these samples were blasted against all known sequences available in the NCBI database. A number of viruses including *Potato leafroll virus* , potato viruses M, S, X and Y and *Potato aucuba mosaic virus* were detected based on nucleotide identity (>90%). The NGS results were then validated by bioassay using 19 indicator species and RT-PCR using gene specific primers. NGS followed by molecular confirmation provides a new strategy that can significantly reduce the time (5 vs 55 weeks) and the cost for the quarantine testing. In addition, *Tomato chlorosis virus* and some others were also identified on the basis of nucleotide identity and genome structional analysis, and are subject to further confirmation.

Contributed Paper Session 3 – Host-Pathogen Interactions

[O3-1] **Transcription factor Zfp1 and its role in *Ustilago maydis* pathogenesis.** H.Y.K. CHEUNG, M.E. DONALDSON, K.L. SPENCE AND B.J. SAVILLE. *(M.E.D., B.J.S) Environmental and Life Sciences Graduate Program, Trent University, Peterborough, ON, K9J 7B8, Canada; (K.L.S.) Department of Population Medicine, Ontario Veterinary College, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada*; *and (M.E.D, B.J.S) Forensic Science Program, Trent University, Peterborough, ON, K9J 7B8, Canada*

The basidiomycete biotrophic plant pathogen, *Ustilago maydis*, alters the host (*Zea mays*) to favour fungal growth through the secretion of effectors. The function of effectors has been well studied, yet little is known about the control of their expression. We identified a *U. maydis* transcription factor linked to effector gene expression, zinc finger protein 1 (Zfp1). It contains a DNA binding Zn(II)2Cys6 binuclear cluster domain and is localized to the nucleus. Infection by Δ*zfp1* (solopathogen deletion) strains is reduced. Pathogenesis, when it occurred, produced little or no anthocyanin and arrested at the leaf tumour stage. Complementation with wild-type *zfp1* partially restored pathogenesis and fully complemented anthocyanin production. Putative Zfp1 target genes were identified by RNA-seq analysis. Of the 1870 genes with significantly altered transcript levels in Δ*zfp1* infections, 111 code for predicted effectors, with a majority of the altered effectors down-regulated relative to wild-type infections.

Analysis of the corn transcriptome in Δ*zfp1* infections relative to wild-type infections revealed increased photosynthesis gene transcript levels, consistent with the maintenance of C4 photosynthesis observed in uninfected corn, as well as decreased transcript levels of genes encoding hormone metabolism, secondary metabolism, and pathogenesis-related proteins. Microscopy investigation of Δ*zfp1 in planta* development showed minimal hyphal branching consistent with the host detecting and containing fungal growth. This plant response is consistent with a change in effector gene expression by *U. maydis* Δ*zfp1* strains. The combined analyses support a role for Zfp1 as a transcription factor involved in pathogenesis through the control of effector gene expression.

[O3-2] **Degradome studies provide new insights into viroid pathogenicity.** C.R. ADKAR-PURUSHOTHAMA AND J.-P. PERREAULT. *RNA Group/Groupe ARN, Département de Biochimie, Faculté de médecine et des sciences de la santé, Pavillon de Recherche Appliquée au Cancer, Université de Sherbrooke, 3201 rue JeanMignault, Sherbrooke, Québec, J1E 4K8, Canada*

Viroids are single stranded, non-coding RNA molecules that infect and cause diseases in several economically important plants. Though it is well established that the viroid derived small RNA (vd-sRNA) down-regulate endogenous mRNAs by RNA silencing mechanism, it is not known how exactly viroid infections can induce severe disease symptoms given the fact that a smaller number of vd-sRNA binding to the specific target mRNAs were recovered from the infected plants. Hence in the present study, the role of viroid derived small RNA in pathogenesis was studied using *in silico* and *in cellulo* experiments. More specifically, the genome of *potato spindle tuber viroid* was dissected *in silico* into 21-nucleotide fragments, which were then used to interrogate publicly available tomato transcriptome data sets using the WMD3 Web-based tool. The resulting putative target mRNA sequences with known functions were selected for further analysis. The effect of *potato spindle tuber viroid* on the putative target mRNA was analyzed by RT-qPCR. The accumulation of viroid derived small RNAs in the viroid infected plants were verified by high-throughput sequencing and, the cleavage of putative target mRNA by Parallel Analysis of RNA Ends (PARE). Mapping of PARE sequences against endogenous mRNAs and subsequent comparison with control revealed the extensive degradation of endogenous mRNAs in viroid infected plants. This implies the possible involvement of secondary products of viroid infection in disease severity.

[O3-3] **Update on Manitoba horticultural crops disease and insect pests in 2015.** V. BISHT. *Crop Industry Branch, Manitoba Agriculture, 65, 3rd Avenue NE, Carman, Manitoba, R0G 0J0*

Potato and horticultural crops are high value and high input crops with significant disease and insect pest risks. Along with weather, pests are main issues for Manitoba. In 2015, late blight appeared late in season, in September first week, but still led to some storages having rot issues, leading them to be processed early. Scattered disease appeared in the west, central and southern parts of the province. The late blight strain was identified as US #23. A couple of fields of tomato crop also had significant late blight on fruits. Verticillium wilt appears to be an endemic issue in some fields. A GF2 project has been

initiated to understand various factors involved in impacting the productivity in MB. European corn borer injury incidence was quite noticeable in some fields, where early infested plants had reduced tuber production. Preliminary results from a national PVY-strain distribution study suggest that from Manitoba overall PVY in fields was low (<1 % in most fields), but most PVY strains were necrotic (PVY ^{NTN} being predominant). Carrot forking caused by *Pythium* spp. was found in some fields. Onion neckrot disease was significantly lower than 2 years ago; and may be attributed to dry harvest time. None of the fungicides tested, gave consistent and effective control of neckrot. Cauliflower blackrot disease was a significant disease in a couple of fields. High incidence of blackleg and cabbage maggots on crucifer vegetables, including rutabaga was recorded. On raspberry, fireblight along with the Spotted Wing Drosophila (SWD) caused significant losses.

[O3-4] **Comprehensive assessment of grapevine virus diseases in British Columbia.** S. POOJARI, T. D. LOWERY, J. BOULÉ, N. DELURY, M. ROTT, A-M. SCHMIDT AND J. R. ÚRBEZ-TORRES. *Agriculture and Agri-Food Canada, Summerland Research and Development Centre, Summerland, BC V0H1Z0, Canada; and (M.R., A-M.S.) Canadian Food Inspection Agency, Centre for Plant Health, Sidney Laboratory, Sidney, BC V8L1H3, Canada*

Virus and virus-like diseases are considered one of the major constraints to the sustainability of the wine industry worldwide. British Columbia (BC), with over 10,000 acres of wine-grapes (*Vitis vinifera* L.), is the second largest grape-production region in Canada. To determine the current health status of established vineyards in BC, a comprehensive survey was conducted between 2013 and 2015 and the incidence of economic important virus diseases was recorded using ELISA and PCR/RT-PCR. Over 3,000 samples (including random-composite and single-targeted samples) representing the most prevalent white and red grape cultivars were tested for the presence of non-regulated grapevine viruses in BC. Diagnostic test results showed Grapevine leafroll to be the most widespread virus disease in BC. Among all Grapevine leafroll associated viruses (GLRaVs), GLRaV-3 was the most prevalent (23.9%) followed by GLRaV-2 (7.1%), GLRaV-1 (2.7%), and GLRaV-4 (2.7%). In addition, high incidence (29.2%) of *Grapevine fleck virus* was also detected. Results indicated a low incidence of Grapevine red blotch associated virus (1.6%), *Grapevine fanleaf virus* (0.5%), and Grapevine Pinot Gris virus (0.14%) and no positive samples were detected for *Arabis mosaic virus*. Molecular analyses also confirmed the presence of Grapevine leafroll insect vectors in BC vineyards, including the grape mealybug (*Pseudococcus maritimus*) and the European fruit lecanium Scale (*Parthenolecanium corni*). These results, along with information generated on the genetic diversity and spatial distribution patterns of major grapevine viruses in correlation with insect vector population dynamics will contribute to develop sustainable management practices for grapevine virus diseases in BC.

[O3-5] **Grapevine trunk diseases studies in British Columbia.** J.R. ÚRBEZ TORRES AND D. T. O'GORMAN. *Agriculture and Agri-Food Canada, Summerland Research and Development Centre, Summerland, BC V0H1Z0, Canada*

Grapevine trunk diseases (GTD), caused by a wide range of taxonomically unrelated fungi, are considered the primary biotic cause of grapevine decline and mortality worldwide and thus, one of the major threats to the industry's future economic sustainability. British Columbia (BC) grapevine industry is internationally recognized for its award winning wines and contributes over $2.1 billion into the Canadian economy. However, the presence of GTD in BC has long been overlooked. Accordingly, studies to determine the current status of GTD in BC started in 2010. Field surveys were conducted between 2010 and 2013 and over 200 vineyards were visited throughout all grape-growing regions of the Province. Surveys also included assesment of foliar symptomatology from over 60,000 vines and fungal isolations from over 500 symptomatic vines (young and mature). Field results revealed the presence of all GTD in BC, including black-foot and Petri disease in young vines, and Botryosphaeria dieback, esca, and Eutypa dieback in mature vines. Morphological characterization along with DNA analyses and multi-locus phylogenetic studies of the internal transcribed spacer region (ITS1-5.8S-ITS2) of the rDNA, and part of the ACTIN, β-tubulin, and translation elongation factor 1-α genes, allowed the identification of over 30 fungal pathogens from 15 different genera associated with GTD in BC. This study represents the first attempt to identify and characterized the GTD causal agents in BC and provides the foundation to further investigate the impact of these diseases with the aim to develop and implement effective management strategies.

[O3-6] **What are Plant Canada and Global Plant Council.** D. ERRAMPALLI. *Agriculture and Agri-Food Canada, 4902 Victoria Ave. N., Vineland Station, ON L0R 2E0 Canada*

Plant Canada Federation of Canadian Plant Science Societies is an independent, not-for-profit umbrella organization of seven Canadian plant science societies including Canadian Phytopathological Society, Canadian Botanical Association**,** Canadian Society of Plant Biologists, Canadian Weed Science Society**,** Canadian Society of Agronomy**,** Canadian Society for Horticultural Science**,** Canadian Association for Plant Biotechnology. Plant Canada seeks to being together all those in research, education and training in plant science and related discipline in Canada. The Global Plant Council is a coalition of national, regional and international societies representing plant, crop and agricultural and environmental sciences across the globe. The global plant council has 28 member societies from 6 continents. Plant Canada is the founding member of the Global Plant Council. Deena Errampalli, the president of Plant Canada will present goals and achievements of both these organizations.

Contributed Paper Session 4- Pathology of Field and Horticultural Crops

[O4-1] **Temperature adaptation of *Puccinia striiformis* f. sp. *tritici*, cause of stripe rust of wheat.** V.A. TRAN AND H.R. KUTCHER. *Crop Development Centre/Department of Plant Science, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada*

Stripe rust is a destructive disease of wheat, caused by *Puccinia striiformis* Westend. f. sp. *tritici* Eriks. (*Pst*). Stripe rust epidemics have occurred since 2000 in western Canada and have been suggested to be due to the adaptation of *Pst* to warmer temperatures. The present study aimed to determine if new isolates (post-2000) were better adapted than old isolates (pre-2000) to warmer temperature. In total, nine new and four old *Pst* isolates were examined *in vitro*, for urediniospore germination at 5, 10, 15 and 20°C, and on seedlings of four susceptible wheat cultivars for latent period and the area under the disease progress curve (AUDPC) at 10, 15 and 20°C. Spore germination of all *Pst* isolates was greater at 5, 10 and 15°C compared with 20°C. Latent period was consistently shorter at 15 and 20°C compared with 10°C. Percent germination of new and old isolates was not significantly different at 5, 10 and 15°C, but new isolates had a higher germination rate than old at 20°C. Latent period was observed to be similar for both new and old isolates at 10°C, but new isolates had a shorter latent period compared with old isolates at 15 and 20°C. New isolates had a greater AUDPC than old isolates at all temperatures. Our results indicate that post-2000 isolates have higher germination rates, shorter latent periods and greater AUDPC at 20°C than pre-2000 isolates.

[O4-2] **Developing a wheat germplasm collection with diverse pathogen and pest resistance.** B.D. MCCALLUM, C.W. HIEBERT, T.G. FETCH, C.A. MCCARTNEY, M.A. HENRIQUEZ, H.S. RANDHAWA AND S.J. CLOUTIER. *(B.D.M., C.W.H, C.A.M, M.A.H) Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Unit 100, Morden, MB, R6M 1Y5, Canada; (T.G.F.) Brandon Research and Development Centre, Agriculture and Agri-Food Canada, Brandon, MB, R7A 5Y3, Canada; (H.S.R.) Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada Canada, 5403 1st Avenue South, P.O. Box 3000, Lethbridge, AB, T1J 4B1, Canada; and (S.J.C) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, K.W. Neatby Building, 960 Carling Avenue, Ottawa, ON, K1A 0C6, Canada*

Drs. Peter Dyck and Eric Kerber requested bread wheat (*Triticum aestivum* L.) and durum wheat (*Triticum durum* Desf.) germplasm from genetic banks across the world during the 1970s and 1980s. These diverse collections were screened at the time for leaf rust (*Puccinia triticina* Eriks.) and stem rust (*Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. & E. Henn.) resistance. In 2014, we initiated a project to identify promising lines from this material for leaf rust resistance by growing 200 lines in a leaf rust nursery. Resistant lines were harvested and retested in 2015, along with a new group of 200 lines. One hundred forty six were found to have resistance to leaf rust in the field in 2014 and/or 2015. These lines will be tested in 2016 for resistance to leaf rust, stem rust, stripe rust (*Puccinia striiformis* Westend.), Fusarium head blight (*Fusarium graminearum* Schwabe), and orange wheat blossom midge (*Sitodiplosis mosellana* Gehin). A new group of 200 lines from the Kyoto wheat collection will be screened in 2016 for leaf rust resistance, and resistant lines will be added to the germplasm collection for screening with multiple pests in 2017. We plan to generate a large and diverse collection of wheat germplasm, characterized for resistance to major pests of wheat in Canada. This should be an excellent resource for the development of resistance in wheat breeding programs. The genetic basis for resistance will be determined for many of the lines with the best levels of resistance to multiple pathogens.

[O4-3] **Re-emergence and rapid spread of the Goss's wilt disease pathogen of corn: possible scenarios.** J.T. TAMBONG, R. XU, A. SOLIMAN AND F. DAAYF. *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; and (F.D. & A.S.) Department of Plant Science, University of Manitoba, Winnipeg, Manitoba, Canada*

Goss's wilt disease of corn is caused by the Gram-positive bacteria, *Clavibacter michiganensis* subsp. *nebraskensis* corrig. (Vidaver and Mandel 1974) Davis et al. 1984 (CMN). Yield losses as high as 50% have been reported during systemic xylem infections. First reported in 1969, in south central Nebraska, the disease was mainly confined in four Midwestern states in the USA. It became sporadic after partially resistant cultivars were identified and cultivated. Recently, the Goss's wilt disease has re-emerged and is spreading rapidly into major corn growing regions of USA and Canada. The re-emergence of CMN may be due to the use of corn hybrids selected solely based on high yield potential, without a robust disease-resistance/tolerance component. Secondly, it could be as a result of changes in weather systems such as wind patterns, rainfall, temperature and humidity. It could also be a phenomenon of host-pathogen coevolution. Bacterial pathogens such as CMN are constantly changing their genetic capacity to enhance their virulence and adaptation to their hosts. In this presentation, genome sequences of CMN strains collected in Manitoba (Canada) during the 2014 growing season will be compared to that of the type strain isolated over 40 years ago in Nebraska (USA). Pathogenicity of these strains will be compared in association with variations of their genome sequences, and the potential impact on Goss's wilt disease trends will be discussed.

[O4-4] **Diverse population of *Septoria linicola* causing pasmo disease in flax.** K.Y. RASHID. *Agriculture and Agri-Food Canada, Morden Research and Development Centre, 101 Route 100, Morden, Manitoba, Canada R6M 1Y5*

Pasmo caused by the fungus *Septoria linicola* (Speg.) Garassini (sexual state *Mycosphaerella linorum* Naumov. is a major disease affecting flax (*Linum usitatissimum* L.), and is prevalent in most flax growing areas worldwide. The incidence and severity of this disease have been on the rise in Canada causing major reductions in yield and quality of the seed and fibre. This research aimed at studying the virulence in the pathogen population in western Canada. Diseases specimens have been collected from Manitoba and Saskatchewan and 100s of single spore isolates established. Each of seven representative isolates was tested on a set of 94 flax genotypes from diverse origin. Each isolate was inoculated onto 20-days old seedlings of the 94 flax lines and incubated for 48 h under controlled growth cabinet conditions equipped with a misting system. The disease incidence, severity, and defoliation were recorded at 10, 20, and 30 days after inoculation. The data collected showed some similarities among the interactions of the 7 isolates on some of the 94 flax genotypes. The specific host-pathogen interactions were summarized into 42 virulence combinations indicating the complexity of the virulence genes in the pathogen and the matching resistance genes in the 94 flax genotypes. Gene-pyramiding of the major race-specific genes will provide improved flax genotypes with wider genetic base for resistance to the diverse pathogen population in the flax crops in western Canada.

[O4-5] **A detached fed-leaf bioassay to assess bacterial antagonists against *Phytophthora infestans* isolates.** P. AUDY, N. FORAN, S.M. BOYETCHKO AND V. GRAVEL. *Quebec Research and Development Centre, Agriculture and Agri-Food Canada, Quebec, QC, G1V 2J3, Canada; (N.F. and V.G.) Department of Plant Science, McGill University, Macdonald Campus, 21 111 Lakeshore Road, Sainte-Anne-de-Bellevue, QC H9X 3V9, Canada; (S.M.B) Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, Saskatoon, SK, S7N 0X2, Canada*

Late blight of potato (*Solanum tuberosum* L.) caused by *Phytophthora infestans* (Mont.) de Bary, is the most devastating disease affecting potato, accounting for over six billion US dollars worldwide each year due to production losses and prevention measures. Chemical fungicides are heavily used by potato producers to prevent and control the disease but public pressure has created a demand for environmentally friendly control products and a preference for pesticide-free foods are driving the exploration for biological control options. In this study, a detached fed-leaf bioassay was developed to assess the ability of some bacteria to control potato late blight under environmental conditions optimum for disease development. Forty-six bacterial strains were tested against a *P. infestans* US-8 isolate (A2 mating-type). Four treatments were used: pathogen alone, whole bacterial culture + pathogen, bacterial filtrate + pathogen and autoclaved bacteria culture + pathogen. The six leading bacterial agents were then evaluated for their abilities to impede *P. infestans* development (four A1 and A2 mating-type isolates) using the same detached fed-leaf assay. Data analysis revealed that the level of biocontrol differed greatly among the six bacterial strains. Results showed that bacterial antagonists could be an effective addition to current prevention methods against late blight and contribute to the reduction of synthetic fungicides in potato production.

[O4-6] **What's on my weed? Preliminary insights into the *Cannabis*-powdery mildew pathosystem.** D.L. JOLY, N. PÉPIN, F. SORMANY, A. ROY AND N. HACHÉ. *(D.L.J., N.P., F.S.) Université de Moncton, 18 avenue Antonine-Maillet, Moncton, NB E1A 3E9, Canada; (A.R., N.H.) OrganiGram Inc, Moncton, NB, Canada*

Despite its longstanding history of cultivation as a source of fiber, food and medicine, knowledge on *Cannabis* L. diseases and pests is lacking, mainly because marijuana represents the most commonly used illicit drug. In Canada, the current number of licensed producers of medical marijuana is limited, but the number of consumers has increased intensely, raising concerns about the capability to meet demand. A better understanding of diseases and pests affecting *Cannabis* thus offers tremendous opportunities for increasing production and reducing crop losses, and also securing a continuous access to medical marijuana. Among diseases affecting *Cannabis* grown for medical purposes, powdery mildew is a recurring issue, especially with the high humidity and lack of air movement found in indoor growth rooms, which provide the perfect conditions for the germination and proliferation of fungal pathogens. In order to gain insight into the identity of powdery mildew species affecting *Cannabis*, sequence comparisons have been made with isolates from hops (*Humulus lupulus* L., the closest relative of *Cannabis*) and well-known powdery mildews. On the host side, a genome-wide analysis of the *Mildew*

resistance Locus O (*MLO*) gene family has been conducted, and follow-up studies will investigate whether loss-of-function mutations in one or more of these candidate genes leads to powdery mildew resistance.

Contributed Paper Session 5 – Pathogen Propagules

[O5-1] **A molecular method for determining the viability of *Synchytrium endobioticum*.** D.S. SMITH AND U. SINGH. *Canadian Food Inspection Agency, Charlottetown Laboratory, 93 Mount Edward Road, Charlottetown, PE C1B 1M2, Canada*

Determining the viability of *Synchytrium endobioticum* (Schilb.) Percival in infested soil is a key component of potato wart disease management, and is necessary for achieving the long-term goal of eradicating this pathogen from Prince Edward Island. Towards this end, a molecular method for determining the viability of the potato wart pathogen, *S. endobioticum*, was developed. The test targeted two messenger RNA sequences in resting sporangia of *S. endobioticum* that were identified as highly expressed in a set of whole mRNA transcriptome data. One of the targets, Locus 852, had high homology to a ribosomal protein. The second target, Locus 166, could not be identified, but had weak homology to a nematode late embryogenesis abundant protein. Real-time reverse-transcriptase polymerase chain reaction assays were developed for these targets, and transcript-specific primers were designed to cross intron-exon borders in order to prevent amplification of DNA. Viability of *S. endobioticum* in sieved soil samples and in heat-treated spore preparations was determined using a sprout infection bioassay. Detection of the target mRNA transcripts was highly correlated with *S. endobioticum* viability for both soil and spore preparations. The molecular test was more sensitive and much more rapid than the sprout-infection bioassay for detecting viable *S. endobioticum.* This molecular method may be useful in screening soil samples for viable sporangia in infested fields, and aid in the evaluation of risk-mitigating strategies.

[O5-2] **Estimation of viable resting spores of *Plasmodiophora brassicae* in a six-year crop rotation study using propidium monoazide-assisted PCR.** F. AL-DAOUD, J. ROBSON, D. PAGEAU, B. D. GOSSEN, J. A. DALTON AND M. R. MCDONALD. *Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada; (D.P.) Agriculture and Agri-Food Canada, 1468 St-Cyrille Street, Normandin, QC, G8M 4K3, Canada; and (B.D.G.) Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, 107 Science Place, Saskatoon, SK, S7N 0X2, Canada*

Resting spores of *Plasmodiophora brassicae* Woronin, the causal agent of clubroot in canola (*Brassica napus* L.) and other brassica crops, can remain viable in soil for many years. Quantitative PCR (qPCR) is used to quantify soil-borne resting spores, but it amplifies DNA from both viable and non-viable spores. However, pre-treatment with propidium monoazide (PMA) can suppress amplification of DNA from non-

viable spores in subsequent qPCR (PMA-PCR). PMA penetrates non-viable cells, binds to the DNA when photo-activated, and prevents amplification. The objectives of this research were: 1) to develop a protocol for using PMA-PCR on soil samples, and 2) to compare qPCR and PMA-PCR analyses of soil samples from a six-year crop rotation field experiment at Normandin, Québec. A soil dilution technique, which involves simply mixing soil in water, retained up to 916-fold more spores than the standard sucrose solution-based techniques. This technique was used in conjunction with PMA-PCR to analyze the crop rotation soil samples. There were $2.0x10^6 \pm 1.3x10^6$ and $7.4x10^5 \pm 2.6x10^5$ spores g^{-1} soil at year zero as estimated by qPCR and PMA-PCR, respectively. QPCR showed a quadratic decrease in spores over time with an 83% reduction in spore numbers after two years. PMA-PCR demonstrated a linear decrease in viable spores, with a 73% reduction in viable spores after three years. The half-life of spores at this site was estimated at 1.2 years by qPCR and 2.9 years by PMA-PCR. PMA-PCR is a useful technique to quantify viable resting spores, and reduce the need for resource-intensive bioassays.

[O5-3] **Oospore dose-response and spatial distribution of the pea root pathogen, *Aphanomyces euteiches*, in Saskatchewan soils.** S. CHATTERTON, A. ERICKSON AND S. BANNIZA. *Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, 5403–1 Ave. South, Lethbridge, AB T1J 4B1; (S.B.) Crop Development Centre, University of Saskatchewan, 51 Campus Dr., Saskatoon, SK S7N 5A8*

Aphanomyces root rot, caused by *Aphanomyces euteiches* Drechs., was first detected in pea fields in Saskatchewan and Alberta in 2012 and 2013, respectively, and can cause significant crop loss in both provinces. In order to determine oospore dose-response relationships, soils were collected from brown, dark brown and black soil zones in Saskatchewan, and sterilized or used as is (raw). Oospores were added to soils to provide final concentrations from 0 - 2000 oospores/g soil, *A. euteiches* DNA quantified using real-time PCR (qPCR), and then used to grow pea plants for root rot assessments. The threshold level for disease in raw soils was 100 oospores/g soil in all soil types, which was also the limit of detection using qPCR. For black and brown soil types, the threshold level for disease was 750 oospores/g soil in sterilized soils, demonstrating that other soilborne microorganism increase disease risk. To determine spatial distribution of oospores in the field, soils were collected from 0-20, 20-40 and 40-60 cm depths at 11 sites from 3 pea fields in each of the 3 soil zones in Saskatchewan. Peas were grown in each soil sample and rated for root rot. Disease levels were highest in the top 0-20 cm layer, and decreased with increasing depth. Horizontal distribution of *A. euteiches* varied between fields. Real-time PCR analysis to quantify *A. euteiches* DNA levels in these soil samples is underway. Results will be used to develop sampling protocols and soil tests to determine root rot risk.

[O5-4] **Thirty Years of Postharvest Biological Control Research: The Journey from Simplicity to Complexity.** M. WISNIEWSKI. *USDA-ARS, Appalachian Fruit Research Station, Kearneysville, WV 25430*

Finding safe and effective alternatives to synthetic fungicides for reducing postharvest losses of harvested commodities has been a focus of much research over the past three decades. Identifying

alternatives that are widely accepted and commercially viable has, however, been a challenge. The search to identify alternative approaches to postharvest disease management must be viewed in relation to a complex regulatory environment, the need to address disease problems in a wide array of commodities and conditions, industry and consumer acceptance, and last but not least, commercial viability. In order for companies to invest in new technologies, they must be able to clearly see both the value of a product and the financial return on their investment. This presentation will attempt to highlight how the search for alternative postharvest disease management technologies has been a journey from simplicity to complexity. Plant pathologists developing alternative technologies have been slowly moving away from the "silver bullet" concept where a single intervention can be used to control a disease to viewing plant disease as a process where multiple interventions may be required at different points in the disease process. Over the past thirty years, alternatives have moved from the simple idea of applying high concentrations of biocontrol agents to a harvested commodity, to using a wide array of other alternatives, and integrating them together into a systems approach based on the multiple decrement or multiple hurdle concept. The ease of sequencing genomes and obtaining related genotypic, transcriptomic, proteomic, and metabolomics information is leading to the development of new commercial technologies where problems are solved "biologically."

Symposium 2: Biovigilance: a framework for effective pest management

[S2-1] **Using biovigilance-based information for strategic and tactical disease management decisions.**
O. CARISSE*, AAFC, Saint-Jean-sur-Richelieu, QC*

Biovigilance can be defined as the study of the unintentional effects of farming practices on pest populations and ecological services (biodiversity). Since the second half of the last century, farming and pest management practices have undergone considerable changes, which were driven by increasing mechanization, the intensive use of fertilizers and pesticides, and the genetic improvement of crops. These practices have exerted pressure on pest populations, which have adapted by, among other means, developing pesticide resistance and overcoming crop resistance. In addition, climate change and the movement of plant products between different areas or countries also influence the diversity of pest populations and their natural enemies. As a result, pest management decisions must take into account these changes in pest populations. Biovigilance-based information can be used for strategic (long-term) decisions about matters such as the type of production system, crop rotation, and host genetic selection for perennial crops. Similarly, knowledge on pathogen aggressiveness or fungicide resistance should be considered when making tactical (short-term) disease management decisions. During this presentation, we will discuss how biovigilance information can help with making both types of disease management decisions. The discovery of new *Plasmopara viticola* ff. sp. (*P. viticola* f. sp. *riparia*, *P. viticola* f. sp. *aestivalis*, and *P. viticola* f. sp. *vinifera*) and their significance will be used as a case study for strategic decisions. Fungicide resistance in *Botrytis* spp. populations will be used as a case study for tactical decisions. The ultimate objective of biovigilance-based disease management is to mitigate potential

threats before they become a huge problem. Typically, this approach to disease management is forward-looking and requires a long-term commitment for research.

[S2-2] **Using genomics approaches for rapid development of species-specific diagnostics for cucurbit downy mildew.** L. QUESADA-OCAMPO*, North Carolina State University, Raleigh, NC, USA*

Advances in Next Generation Sequencing (NGS) allow for rapid development of genomics resources needed to generate molecular diagnostics assays for infectious agents. NGS approaches are particularly helpful for organisms that cannot be cultured, such as the downy mildew pathogens, a group of biotrophic obligate oomycetes that infect crops of economic importance. Unlike most downy mildew pathogens that are highly host-specific, *Pseudoperonospora cubensis* causes disease on a broad range of crops belonging to the Cucurbitaceae. In this study, we identified candidate diagnostic markers for *P. cubensis* by comparing NGS data from a diverse panel of *P. cubensis* and *Pseudoperonospora humuli* isolates, two very closely related oomycete species. *P. cubensis* isolates from diverse hosts and geographical regions in the United States were selected for sequencing to ensure that candidates were conserved in *P. cubensis* isolates infecting different cucurbit hosts. Genomic regions unique to and conserved in *P. cubensis* isolates were identified through bioinformatics. These candidate regions were then validated using PCR against a larger collection of isolates from *P. cubensis*, *P. humuli*, and other oomycetes. Overall seven diagnostic markers were found to be specific to *P. cubensis.* These markers could be used for pathogen diagnostics on infected tissue, or adapted for monitoring airborne inoculum with real-time PCR and spore traps.

[S2-3] **The Biovigilante: Monitoring threats to plant health in an era of globalization and climate change.** K. BRODERS*, Colorado State University, Fort Collins, CO, USA*

The Anthropocene epoch is defined as the point when human activities started to have a significant global impact on Earth's ecosystems. Certainly the phenomenon of globalization and changes in global climate patterns have resulted in an upheaval of how we view disease ecology, epidemiology, plant-microbe coevolution and the plasticity of the disease triangle in both forested and agricultural ecosystems. In order to sustain our ecosystem services and feed an every-growing population we must adapt to this new reality as many of our pathogen nemeses have already done. The number of emerging pathogens has increased significantly over the course of the last two decades, and will likely continue to increase in the more globally interconnected future. I will provide four independent scenarios of plant pathogen emergence including: the introduction of an invasive forest pathogen; an endemic pine pathogen that has reached epidemic levels due to changes in regional climatic patterns; an endemic beetle vectored pathogen that has expanded it's host range due to climate change and anthropogenic forces; and the combination of an introduction of a new, better adapted race of a crop pathogen followed by a rapid range expansion. Finally, based on these four examples I will provide a perspective on preparing for new emerging forest and crop pathogens in the future through the development of

next-generation methods for monitoring emerging pathogens, as well as developing networks for rapidly communicating information regarding emerging pathogens.

POSTERS – STUDENTS

[P1] **Expression analysis of three NADPH oxidase genes in germination and infection of wheat leaf rust.** M.Z. CHE, X.B. WANG, B.D. MCCALLUM, H.B. KHALIL, G. BAKKEREN AND B.J. SAVILLE. *(M.Z.C.; X.B.W.; B.D.M.) Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Unit 100, Morden, MB, R6M 1Y5, Canada; (M.Z.C.) Department of Plant Pathology, China Agricultural University, Beijing, 100193, People's Republic of China; (H.B.K. and G.B.) Summerland Research and Development Centre, Agriculture and Agri-Food Canada, Summerland, BC, V0H 1Z0, Canada; and (B.J.S.) Forensic Science Program Trent University, Peterborough, ON, K9J 7B8, Canada*

Leaf rust (*Puccinia triticina* Eriks.) of wheat (*Triticum aestivum* L.) is a widespread disease that causes significant reductions in grain yield and quality. Urediniospore germination and the infection of wheat plants are critical steps in the establishment of the pathogen. Reactive oxygen species (ROS) often plays an important role during host and pathogen interaction. However, very little is known about the role of these molecules in the pathogenesis of *Pt*. In this study, we identified two NADPH oxidase genes (*PtnoxA* and *PtnoxB*) and a regulatory gene (*PtnoxR*) which were potentially involved in the production of ROS from EST and RNAseq databases of *Pt*. We analyzed the expression levels of three NADPH oxidase genes over time during spore germination and plant infection using RT-qPCR. Total RNA was extracted from urediniospore germ tubes at 6, 12 and 24 hours after incubation (hai), and from inoculated wheat leaf tissues (Thatcher, leaf rust susceptible line) at 24, 48, 96, 144 hours post-inoculation (hpi) and 8 days post-inoculation. During urediniospore germination, the expressions of *PtnoxA* and *PtnoxR* peaked at 24hai whereas the highest level of *PtnoxB* transcripts was found at 6 hai. In comparison, the expression of three transcripts all peaked at 24hpi during the infection on Thatcher and downregulated when *Pt* has successfully penetrated leaf-surface. This result indicates that *PtnoxA*, *PtnoxB and PtnoxR* are differentially regulated during urediniospore germination and plant infection. The production of ROS is important for the pathogenesis of *Pt* and needs to be carefully regulated during host plant infection.

[P2] **Identification of *Albugo candida* causing white blister rust of *Wasabia japonica* in British Columbia.** J.L. MACDONALD AND Z.K. PUNJA. *Summerland Research and Development Centre, Agriculture and Agri-Food Canada, 4200 Highway 97, Summerland, British Columbia, V0H 1Z0, Canada; and (Z.K.P.) Department of Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, British Columbia, V5A 1S6, Canada*

Commercial plantings of *Wasabia japonica* (Miq.) Matsu. are expanding in the Pacific Northwest, where it is utilized in the culinary market and in sushi restaurants. The high moisture environment required to cultivate the crop has led to an increasing incidence of disease and occurrence of a number of destructive root and foliar pathogens. In 2015, wasabi ('Daruma') grown in a research polyethylene house in Agassiz, BC showed symptoms of white blister rust, including severe blistering and sori development. Sporangiospores were collected from white blister leaf samples into a water suspension and were morphologically identified as either *Albugo candida* (Pers. Ex Lev) Kuntze or *A. wasabiae* Hara. Sporangiospores were collected from white rust infected *Capsella bursa-pastoris* (L.) Medik in close proximity to the crop, and were shown to be morphologically indistinct. Genomic DNA was extracted and PCR conducted using ITS1F-ITS4 fungal primers. Sequence comparison in GenBank showed both isolates were *A. candida*. Inoculations with sporangiospores collected from *W. japonica* could not confirm pathogenicity on either *W. japonica* or *C. bursa-pastoris*; however, inoculations on *W. japonica* with sporangiospores collected from *C. bursa-pastoris* resulted in small galls. Albugo white rust can be a major foliar disease of wasabi in parts of Asia, but fungicide applications can control it. In Canada and the U.S.A. there are no products currently registered for the control of white rust on wasabi, and the growing complex of diseases will continue to be a major obstacle for the industry.

[P3] **Variation in boron tolerance and clubroot severity in *Brassica napus* and *B. rapa* lines in a field trial in 2015.** A. MCLEAN, B.D. GOSSEN AND M.R. MCDONALD. *Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON N1G 2W1, Canada; and (B.D.G.) Agriculture and Agri-Food Canada (AAFC), 107 Science Place, Saskatoon, SK S7N 0X2, Canada*

In a previous study, boron (B) applied at 4 kg ha^{-1} reduced clubroot (*Plasmodiophora brassicae* Wor.) incidence and severity, but higher rates produced severe toxicity on canola (*Brassica napus* L.). Variability in B-tolerance and clubroot severity were assessed on lines of *B. napus* and *B. rapa* in a field trial on muck (~70% organic matter) soil infested with *P. brassicae* at the Muck Crops Research Station in Bradford, Ontario in 2015. Seedlings of 88 accessions were grown in a greenhouse for 3 weeks, then transplanted to the field. Boron (Solubor, 20.5% B) was applied at 8 kg B ha^{-1} in 1500 L ha^{-1} of water using a backpack CO_2 sprayer 3 days after transplanting. Boron was reapplied 5 days after the initial application because leaching by heavy rainfall had reduced the effective rate of applied B. Toxicity was assessed 5 days after the second boron application and categorized by degree of leaf cupping and marginal burning (0-3 scale). Plants were harvested 9 weeks after seeding. Clubroot severity was rated (0-3 scale) and phytotoxicity and clubroot severity indices were calculated for each line. The above-ground growth (fresh and dry weight) of selected B-susceptible and B-tolerant lines was assessed. There were differences in boron tolerance among accessions. The only difference in clubroot severity was observed in the selected subset of B-tolerant accessions, where application of B reduced clubroot severity and increased fresh weight. Also, the water content and fresh weight of B-treated and nontreated plants from the B-tolerant and B-susceptible subsets differed.

[P4] **Genes differentially expressed during pathogenesis by two *Plasmodiophora brassicae* pathotypes on canola (*Brassica napus*).** J. JIANG, R. FREDUA-AGYEMAN, S.F. HWANG, AND S.E. STRELKOV. *(J.J., S.E.S.) Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada; (R.F.A., S.F.H.) Crop Diversification Centre North, Alberta Agriculture and Forestry (AAF), Edmonton, AB T5Y 6H3, Canada* **(Student Competition)**

Gene expression studies offer a means of understanding pathogenesis of clubroot disease caused by *Plasmodiophora brassicae*. In this study, the commercial canola cultivar '45H29' was inoculated with two *P. brassicae* pathotypes 5x and 5 and the pathogen/plant biomass was determined 7, 14 and 21 days after inoculation (dai) by quantitative real-time PCR (qPCR). To identify genes differentially expressed during the infection process, 205 genes encoding signal peptides were screened on total RNA extracted from the 14 dai samples. It was observed that the P5x/plant biomass increased across the time course while the P5/plant biomass decreased. The biomass and phenotypic data confirmed that P5x was virulent on 45H29 while P5 was avirulent. The qPCR results showed that only one of the 205 genes was up-regulated in samples inoculated with P5x than P5 while 15 genes were up-regulated in samples inoculated with P5 than P5x. At 21 dai, 12 of the above 16 genes were differentially expressed in the two pathotypes with nine being expressed higher in P5x and three being higher in P5. On the other hand, none of the 16 genes showed significant ($\alpha = 0.05$) expression difference in the two pathotypes at 7 dai. Nine of the 16 genes were exclusively present in *P. brassicae* and may offer important information on the canola-*P. brassicae* interaction.

[P5] **Identification of microsatellite markers linked to quantitative trait loci associated with partial resistance to Aphanomyces root rot in field pea**. L.F. WU, R. FREDUA-AGYEMAN, K.F. CHANG, R.L. CONNER, S.F. HWANG, D. FEINDEL, K.B. MCRAE AND S.E. STRELKOV. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, ABT6G 2P5, Canada (L.F.W., S.E.S.); Crop Diversification Centre North, Alberta Agriculture and Forestry (AAF), Edmonton, Canada, AB T5Y 6H3 (R.F.A., K.F.C., S.F.H.); Agriculture and Agri-Food Canada (AAFC), Morden Research and Development Centre, Morden, Manitoba, Canada R6M 1Y5 (R.L.C.); AAFC, Kentville Research and Development Centre, Kentville, NS B4N 1J5 (K.B.M.)* **(Student Competition)**

The development of partial resistance to Aphanomyces root rot of pea, caused by *Aphanomyces euteiches*, is considered to be the most durable method to manage this destructive soil-borne disease. In pea, partial resistance to *A. euteiches*, has been reported to be controlled by multiple loci. In this study, two recombinant inbred lines (RILs) populations, obtained by single-seed descent from the crosses F_6: '00-2067' × 'Reward' and F_8: 'Carman' × 'Reward', respectively, were used to identify the QTLs associated with the partial resistance as well as to evaluate the effectiveness and stability of genetic loci controlling the disease. A greenhouse study demonstrated that the resistant cv. '00-2067' remained highly resistant to *A. euteiches*, relative to the susceptible cv. Reward, while the resistance in 'Carman' eroded as inoculum concentration increased. This indicated that '00-2067' contained at least one major QTL for resistance that 'Carman' did not have. A total of 160 microsatellite markers were tested for polymorphism in the three parental cultivars. Forty-eight and 51 polymorphic markers were detected in the parents of the two RIL populations, respectively. Nine SSR markers from four chromosomes showed association with resistance to *A. euteiches*. The marker AB-64 had a significant association ($P < 0.05$) with the field phenotype data of the first population. As part of ongoing research, more SSR markers will be screened to better map the QTLs. In addition phenotyping will be conducted under controlled conditions in order to confirm the field data.

[P6] **An assessment of the genetic basis for resistance to stem rust race TRTTF in Canadian hexaploid wheat cultivars.** C.W. HIEBERT, M.N. ROUSE, J. NIRMALA, C.A. MCCARTNEY, M.T. KASSA, AND T.G. FETCH. *(C.W.H and C.A.M.) Agriculture and Agri-Food Canada, Morden Research and Development Centre, 101 Route 100 Morden, Manitoba, Canada, R6M 1Y5; (M.N.R. and J.N.) United States*

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Stem rust, caused by *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. & E. Henn. (*Pgt*), is a serious disease of wheat (*Triticum aestivum* L.). Stem rust can be controlled by utilizing effective stem rust resistance (*Sr*) genes in wheat cultivars. Over the past decade a number of virulent races of *Pgt* have evolved in Africa and pose a threat to much of the global wheat producing areas. One such example is race TRTTF which was discovered in Yemen and is virulent to approximately half of the Canadian wheat cultivars tested. 'Harvest' was identified as a resistant cultivar. A doubled haploid (DH) population from the cross LMPG-6S/'Harvest' revealed a single gene for resistance to race TRTTF which was mapped to the terminal region of chromosome arm 6DS using DNA markers. Cultivars assayed with race TRTTF were genotyped with DNA markers close to the resistance on chromosome arm 6DS. Resistant cultivars either carried the same resistance on 6DS as 'Harvest' or were known carriers of *SrCad*, a gene known to confer resistance to the Ug99 group of *Pgt* races. A DH population from the cross RL6071/'Peace' was assayed with race TRTTF. This population was previously used to map *SrCad*. Resistance to race TRTTF and TTKSK (Ug99) co-segregated in the population. Thus, resistance to TRTTF in Canadian wheat cultivars is conferred by a gene on chromosome arm 6DS that is likely to be an allele of *Sr8* and by *SrCad*.

[P7] **Investigating the etiology of tree fruit decline in British Columbia.** J. R. ÚRBEZ-TORRES, J. BOULÉ AND D. T. O'GORMAN. *Agriculture and Agri-Food Canada, Summerland Research and Development Centre, Summerland, BC V0H1Z0, Canada*

Tree fruits in British Columbia (BC) include 15,000 acres of apples, apricots cherries, nectarines, peaches, pears, and plums, which generate an annual farm-gate value of approximately $80 million. Fruit tree decline and variation in vigour have been recognized as an important problem for the BC industry. Much of this decline is associated with symptoms ranging from root rots, cankers, dieback, or a failure to thrive. However, a general lack of knowledge exists regarding the range of organisms associated with these disease symptoms. Accordingly, a preliminary survey to assess and identify the diseases and causal agents affecting cherry and apple tree health in BC was conducted between 2011 and 2013. In total, over 200 diseased samples showing characteristic decline symptoms were collected from 66 blocks. The most prevalent symptoms observed were perennial cankers affecting the trunk and branches of declining trees but also root and crown rot was observed in some young orchards. Morphological characterization along with DNA analyses of the ITS1-5.8S-ITS2, β-tubulin and translation elongation factor 1-α partial gene regions, allowed the identification of 15 fungal pathogens belonging to 13 different genera. Pathogenicity studies showed species within the *Cytopsora* and *Leucostoma* genera in cherries and within the *Diplodia* and *Neonectria* in apples to be the most virulent causing perenial cankers in those hosts. Species within the *Ilyonectria* and *Fusarium* genera were the most prevalent fungi isolated from symptomatic roots. Results from this study will significantly contribute to the devlopment and implementation of effective management strategies against these pathogens in BC.

[P8] **Effect of maleic hydrazide on stem rust seedling infection type.** T. FETCH JR. *Brandon Research & Development Centre, Agriculture & Agri-Food Canada, 2701 Grand Valley Road, Brandon, MB, R7A 5Y3 Canada*

Stem rust of wheat (*Triticum aestivum*), caused by *Puccinia graminis* f. sp. *tritici*, has recently inflicted substantial yield losses worldwide due to new races that have arisen. Races are typically characterized by their reaction (infection type, IT) on the first leaf of single-gene differential lines. Rating the IT is often hampered by extensive growth of subsequent leaves, and IT can be affected by shading. Maleic hydrazide (MH) is a growth inhibitor used by rust pathologists to stunt leaf elongation, but the effect of MH on stem rust IT is unknown. Seeds of 20 single-gene differential lines were planted in root-trainers, and 10ml of MH (0, 100, 200, 300, 400, or 500 ppm) were applied at primary leaf tip emergence. Seedlings were inoculated 6d after MH application with race QCCJB. Seedling ITs were assessed 14d later, and first and second leaf lengths (four reps) were measured. The MH treatments did not significantly reduce the length of primary leaves (except Sr9d), but significantly reduced second leaf length, starting at 100 ppm for most lines. Treatment using MH generally increased pustule size and IT score, but did not greatly alter the IT response of genes Sr6, Sr9e, Sr30, Sr36, Sr38, or SrMcN. However, MH treatments substantially changed the IT from resistant to susceptible for genes Sr7b, Sr8a, Sr9a, Sr9b, Sr11, Sr24, and SrTmp, beginning at the 200 ppm concentration. Further work is needed to optimize the MH application level that will reduce the length of second leaves but not affect the IT response.

[P9] **Nematology research at Agriculture and Agri-Food Canada: renewed emphasis on an old pest.** C. KORA, Q. YU, B. MIMEE AND T.A. FORGE. *Pest Management Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; (Q.Y.) Ottawa Research and Development Centre, Canadian National Collection of Nematodes, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; (B.M.) Saint-Jean-sur-Richelieu Research and Development Centre, Agriculture and Agri-Food Canada, 430 Gouin Blvd, St-Jean-sur-Richelieu, QC J3B 3E6, Canada; (T.A.F.) Summerland Research and Development Centre, Agriculture and Agri-Food Canada, 4200 Highway 97, Summerland, BC V0H 1Z0, Canada*

Agriculture and Agri-Food Canada (AAFC) scientists, through their research and discoveries, have made remarkable contributions to the advancement of the science of plant nematology in Canada. From the early 1960s to the late 1980s numerous AAFC nematologists expanded our knowledge of the biology, management and impact of nematodes on important crops, particularly for plant parasitic nematode species of concern to Canadian agriculture. However, with the extensive use of broad spectrum fumigant nematicides through the 1990s and early 2000s, the problems associated with nematode damage seemed to decline, allowing growers to shift their attention to other pest issues of priority. With this shift, the applied nematology research within AAFC was also marked by a period of decline in activity and scope. However, changes in cropping systems, production practices, and regulations over the past fifteen years, are having an impact. The increase in production of crops susceptible to nematodes, several nematode outbreaks with large economic impact, as well as restrictions and phase outs to the use of fumigants which were found to have unacceptable environmental impacts, have led to renewed awareness of the importance of plant parasitic nematodes and the need for new effective non-fumigant nematode management practices. As a result, nematology research programs within AAFC have gained new strength and are once more the focus of expertise and capacity building. Besides providing an historic perspective, this poster highlights current AAFC nematology research and development activities which aim to deliver sustainable nematode management options for the agricultural sector.

[P10] **DNA-barcoding the Powdery Mildews - sampling herbarium specimens in the National Mycological Herbarium (DAOM).** S. HAMBLETON, Q. EGGERTSON, C.A. LEVESQUE, W. CHEN, T. BARASUBIYE, S.A. REDHEAD AND M.LIU. *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, K.W. Neatby Building, 960 Carling Avenue, Ottawa, ON Canada K1A 0C6*

The obligate plant pathogens known as Powdery Mildews (Erysiphales) comprise a morphologically diverse group of fungi producing conspicuous symptoms of white mycelium covering mainly leaves. These fungi infect a wide range of plants, causing premature leaf fall, hypertrophy and deformation, and consequently significant economic losses in agricultural, horticultural and viticulture industries. Since the description of the first powdery mildew by Linnaeus in 1753, a comprehensive system for species identification gradually developed based on various biological characters and more recently, incorporating molecular characters. Although using DNA sequences is an efficient and effective approach for diagnoses by regulatory departments and pest diagnostic agencies, considerable data gaps still exist for DNA-based identifications and species complexes remain unresolved. In a metagenomics study of environmental samples, only 3% OTUs matched to the genera *Podosphaera* and *Erysiphe* could be identified to species. To fill gaps in reference sequences, 305 historical specimens of 149 species in 15 genera from DAOM were sampled to amplify ITS region for the pathogens and *rbcL*a for the hosts, using published primers from various sources. The preliminary data set generated included 105 ITS sequences of 35 species and 63 partial *rbcL*a of 15 species. Based on analyses supplemented with data from GenBank, the identifications of 82 DAOM specimens were revised in light of the new phylogeny-based classifications. No primer set was found to be universally specific for all species sampled and some also amplified non-target fungal contaminants co-occurring on the specimens. Primer design and optimization is a priority for this fungal group.

[P11] **Molecular mapping of common bunt resistance in a 'Vesper' X 'Lilian' population.** F. BOKORE, R. CUTHBERT, R.E. KNOX, C. POZNIAK, A. N'DIAYE, A. SHARPE, AND Y. RUAN. S*wift Current Research and Development Center, Agriculture and Agri-Food Canada, Swift Current, SK S9H 3X2, Canada; (C.P., A.N'D.) Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada; (A.S.) National Research Council of Canada, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada*

Common bunt caused by *Tilletia tritici* (Bjerk.) Wint. and *T. laevis* Kühn is an economically important disease of wheat (*Triticum aestivum* L.) causing grain yield and quality losses. An effective way to control common bunt is the use of resistant varieties. The objective of this study was to identify and map quantitative trait loci (QTL) for common bunt resistance in the Canadian hard red spring wheat variety 'Lillian'. A population of 280 doubled haploid lines, from the cross 'Vesper'/'Lillian', and parents were inoculated with races L16 (*T. laevis*) and T19 (*T. tritici*). The lines were evaluated for common bunt incidence in the field near Swift Current, Canada in 2014 and 2015. The lines were genotyped with the Infinium iSelect 90K wheat assay and a set of 1975 informative single nucleotide polymorphisms were used for QTL analysis. The bunt incidence scores of the lines ranged from 0 to 45% in 2014 and 1 to 50% in 2015. The susceptible check cultivar 'Biggar' scored 37.5% incidence in 2014 and 50% in 2015. 'Lillian' was rated at 5% incidence for both 2014 and 2015, and 'Vesper' at 30% in 2014 and 25% in 2015. 'Lillian' contributed QTL for common bunt resistance on chromosomes 3D, 5A and 7A, and 'Vesper' on 1D. The QTL explained from 4.8 to 7.7% of the variation in disease incidence. The 5A QTL expressed in both years, whereas the other QTL were confined to one season. The QTL have potential in breeding for bunt resistance in wheat.

[P12] **Spectral signatures of bio-polymer changes in the wheat cell-wall resulting from *Puccinia striiformis* f. sp. *tritici* infection in compatible and incompatible interaction on Yr10.** G.S. BRAR, R. LAHLALI, D. QUTOB, H.R. KUTCHER, AND C. KARUNAKARAN. *Crop Development Centre/Department of Plant Science, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada; (R.L., C.K.) Canadian Light Source-National Synchrotron Research Facility, 44 Innovation Blvd, Saskatoon, SK S7N 2V3, Canada; (D.Q.) Canadian National Research Council, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada*

Wheat stripe rust, caused by *Puccinia striiformis* f. sp. *tritici*, is a serious issue in Canada. The biotrophic fungus produces urediospores contained within uredia between the veins of wheat leaves; it obtains nutrition from the host through haustoria. In a compatible interaction, the fungus damages the cell-wall in a susceptible cultivar, however in a resistant cultivar the incompatible interaction occurs as a result of hypersensitive cell death in the host. The purpose of this study was to understand the biomolecular changes in cell-wall compounds in each of the interactions. Two Avocet lines: one carrying *Yr10* and other susceptible (no resistance allele) were inoculated with two isolates (one virulent on both and the other virulent only on *Yr10*). Infected and freeze dried leaves collected at 1 and 15 days post inoculation were assessed by Fourier transform infrared (IR) spectroscopy to probe changes in cell wall components following infection of the pathogen. A difference in disease severity was observed between the two wheat lines and principal component analysis of the IR spectra associated with proteins, and phenolic and aromatic rings indicated substantial differences in the cell-wall components before and after pathogenic infection.

[P13] ***Fusarium* species complex infecting oat in Manitoba.** M. BANIK, M. BEYENE AND X. WANG. *Morden Research and Development Centre, Agriculture and Agri-Food Canada, 101 Route 100, Morden, MB R6M 1Y5 Canada*

Oat is one of the most important cereal crops in western Canada. This crop has become desirable for human consumptions due its high nutritional value. In recent years, Fusarium head blight (FHB) emerged to be one of the most serious diseases on oat, especially in the Canadian Prairies. Several *Fusarium* species can infect oat and produce different mycotoxins in contaminated grains which cause immunosuppression and various health issues when consumed by human and animals. Of special interest among these Fusarium mycotoxins are the trichothecenes (e.g., T-2 and HT-2 toxins produced by *F. sporotrichioides*), deoxynivalenol (DON, mainly produced by *F. graminearum* and *F. culmorum*) as well as beauvericin and enniatin (mainly produced by *F. poae*). In this study, we investigated *Fusarium* species infecting oat in Manitoba. Oat samples were collected from 36 commercial oat fields in 2015. Species identification was performed based on morphological characteristics and species-specific PCR. *Fusarium* biomass in contaminated grain was assessed by real time qPCR using primer sets specific to *F. poae*, *F. graminearum* and *F. sporotrichioides.* Our results indicates that *F. poae* was the most common *Fusarium* species infecting oat in Manitoba in 2015, followed by *F. graminearum* and *F. sporotrichioides*. Most oat samples are contaminated by multiple *Fusarium* species and pathogen biomass mostly originated from *F. poae*, hence, suggesting that the production and/or accumulation of diverse mycotoxins in oat should be taken into consideration due to the mixed Fusarium infection commonly present in field samples.

[P14] **An investigation of fungal isolates associated with ginseng diseases.** A. MUNAWAR, A. F. SHI, S. WESTERVELD AND M. R. MCDONALD. *(A.M. & M.R.M.) Department of Plant Agriculture, Simcoe*

Research Station, University of Guelph, Simcoe, Ontario, N3Y 4N5, Canada; *(A.F.S.) Ontario Ginseng Growers Association, Simcoe Research Station, Simcoe, Ontario, N3Y 4N5, Canada; and (S.W.) Ontario Ministry of Agriculture, Food and Rural Affairs, Simcoe, Ontario, N3Y 4N5, Canada*

Ginseng, which is grown for its medicinal value, is a valuable horticultural crop in Ontario. Due to the three to four year life of a ginseng garden, roots are affected by a number of soil-borne pathogens. Although major pathogens for ginseng have been characterized, many unknown diseases were observed in the field. Therefore, there is a need to do a baseline study to investigate causal agents of ginseng diseases which may lower its marketable yield. In fall 2015, three-year-old ginseng roots were harvested from ten commercial gardens. Roots with symptomatic rots were separated into individual disease categories including: *Cylindrocarpon* root rot (*C. destructans*), *Phytophthora* root rot (*P. cactorum*), root lesion nematode (*Pratylenchus penetrans*) and an unknown disease category. The symptoms in the unknown disease categories ranged from eroded flaccid roots, dry crater-like rot, yellow patches, brown sunken lesions, rusty roots and superficial veins or netting on the roots. Over 35 various morphotypes of fungi were isolated from this category. Some isolates were identified using morphological characterises including *Rhexocercosporidium panacis*, *Alternaria* spp, *Fusarium* spp, *Chaetomium* spp, *Thielavia* spp, *Curvularia* spp, *Epicoccum* sp, and *Phoma* spp. Species of *Penicillium*, *Eupenicillium* and *Eurotium* have also been found. Identification will be furture tested using molecular techniques. In order to understand whether any of the isolated fungi is pathogenic on ginseng, further experiments are being carried out. The final outcome of this study will help build better IPM strategies for Ontario ginseng.

[P15] **Downy mildew and cone diseases of hop in Ontario in 2015**. A. MUNAWAR, A. F. SHI, M. FILOTAS, C. BAKKER AND M. R. MCDONALD. *(A.M., C.B and M.R.M) Department of Plant Agriculture, Simcoe Research Station, University of Guelph, Simcoe, Ontario, N3Y 4N5, Canada; (A.F.S.) Ontario Ginseng Growers Association, Simcoe Research Station, Simcoe, Ontario, N3Y 4N5, Canada; and (M.F.) Ontario Ministry of Agriculture, Food and Rural Affairs, Simcoe, Ontario, N3Y 4N5, Canada*

Hops (*Humulus lupulus* L.) is a re-emerging crop in Ontario with an increasing demand for high quality cones by both industrial and craft beer brewers. However, downy mildew (DM, caused by *Pseudoperonospora humuli*) and cone diseases are affecting the quality of hops. This project is focused on evaluating the spread of hop downy mildew, its effects on crop quality and effects of cone diseases at harvest. In summer 2015, three commercial hop yards and one replicated hop cultivar trial at the Simcoe Research Station (SRS) in Ontario, Canada were scouted for hop diseases. Most of the plants in all three yards showed initial DM symptoms in the form of occasional basal spikes and foliar DM lesions, however the disease did not progress further and impact on yield remained low. *Alternaria* cone disorder was the most prevalent disease as it was found in seven of the nine hop cultivars grown at the SRS. Other than *Alternaria* spp*, Botrytis* spp was also isolated from cones of 'Sterling' and 'Chinook' at SRS. *Alternaria* was also found in most of the cone samples from the commercial hop yards. At the SRS, powdery mildew caused severe damage on 'Bertwell' cones, resulting in no marketable yield. Powdery mildew was not found in cones collected from commercial yards. In order to determine if *P. humuli* was present in hop rhizomes used for propagation, four rhizomes were collected from growers in 2015. The morphological and molecular analysis confirmed the presence of *P. humuli* in one of the rhizome.

[P16] **Genome analysis and pathogenicity of a new potential biothreat, *Pantoea allii*, to onion production in Canada.** S. HSIEH, R. XU, T. J. AVIS AND J.T. TAMBONG. *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6,*

Canada; and (S.H. & T.J.A.) Department of Chemistry, Food Science and Nutrition Program, Carleton University, 1125 Colonel By Drive, Ottawa, ON, K1S 5B6, Canada

Onion is a root vegetable that is commonly consumed all over the world. It is easily grown in different types of soil. In 2004, a new species of *Pantoea*, *Pantoea allii* Brady et al. 2011, isolated from onions in South Africa and USA, was found to cause pathogenic infections to onions. There is currently no evidence of the presence of *P. allii* in Canada. Given that onion is an important export/import crop, the introduction of this new pathogen into Canada could have severe economic consequences. Thus, it is important to proactively study this 'new' pathogen, especially at the genome level, to generate new knowledge that can be used to develop diagnostic tools. Illumina MiSeq sequencing technology was used to generate paired-end reads and *de novo* assemblies were performed using CLC Genomics Workbench and ABySS platforms. In addition, the pathogenicity of *P. allii* DOAB 206 on commercially available Canadian bulb and green onions was investigated. The genome data based on the number of contigs, N_{50} and total sum of nucleotides, concluded that ABySS is the better platform. The size of the draft genome is about 5.2 Mb with 4880 protein-encoding sequences. *In silico* DNA-DNA hybridization of the draft genome sequence of *P. allii* with the closest phylogenetic relative, *Pantoea ananatis* revealed a 35.7-36.5% similarity. Pathogenicity tests showed that this pathogen can infect Canadian bulb and green onions. Precautionary measures are required to prevent infected onion imports from introducing *P. allii* into Canada.

[P17] **Expression of late blight resistance in potato using a tobacco rattle virus vector system.** C.P. WIJEKOON AND L.M. KAWCHUK. *Agriculture and Agri-Food Canada, 5403, 1st Ave S, Lethbridge, AB, T1J 4B1, Canada*

Late blight, caused by the oomycete *Phytophthora infestans* (Mont.) de Bary, is a devastating disease in potato and tomato and causes yield and quality loss worldwide. Very few varieties of potato are commercially available with late blight resistance. However, it is not enough to fulfil the high demand of potato with disease resistance. Russet Burbank is one of the late blight susceptible high yielding commercially important varieties used for baking, mashing, and French fries. In this study, we have transiently expressed the wild type *Solanum bulbocastanum* late blight resistance gene (*SbRB*) in Russet Burbank potato plants using tobacco rattle virus (TRV) expression vector system. The *RB* gene was cloned into the pTRV2 gene expression vector and infiltrated into plants using *Agrobacterium tumefaciens*. After 3-4 weeks of infiltration, the late blight assay and the gene transcript level analysis was performed to confirm the *RB* gene expression and the late blight resistance. The TRV expression vector system can be used as a tool for gene editing studies in plants. Russet Burbank plants expressing *SbRB* showed late blight resistance to *P. infestans* US-8 genotype. Therefore, the late blight resistance can be introduced into high yielding potato varieties using expression vector systems to overcome the problems regarding the future demand of this food crop.

[P18] **Strawberry nursery stock as a source of virus inoculum and on-farm spread of strawberry viruses in New Brunswick, Canada.** M.T. TESFAENDRIAS, C. MAUND and R.J.A. TREMBLAY. *New Brunswick Department of Agriculture, Aquaculture and Fisheries, 850 Lincoln Road, Fredericton, NB E3B 4Z7, Canada*

Strawberry decline disease (SDD) is caused by a combination of two or more viruses infecting the strawberry (*Fragaria x ananassa* Duchesne) plant. The infection results in a reduction of yield and fruit quality. Strawberry viruses and the strawberry aphid, *Chaetosiphon fragaefolii* (Cockerell), which transmits these viruses, were detected in New Brunswick (NB) surveys conducted in 2013 and 2014. The most common viruses identified were the strawberry mild yellow edge virus (SMYEV) and the strawberry mottle virus (SMoV). In 2015, a survey was conducted to identify the source of SDD viruses in NB strawberry fields and to follow on-farm spread of these strawberry viruses. In order to determine if the introduction of infected nursery stock into strawberry fields was the source of virus, 100 to 120 nursery stock plants were collected from each of six strawberry farms before transplanting. Subsequent samples were also collected twice during the growing season from strawberry fields at the end of June or early July and at the end of August. Plant tissue samples were tested for presence of the five strawberry viruses (SMYEV, SMoV, strawberry vein banding virus (SVBV), strawberry crinkle virus (SCV) and strawberry pallidosis associated virus (SPaV)) using reverse transcription polymerase chain reaction. Results showed the presence of SMYEV in nursery stock from two farms and SPaV in nursery stock from one farm. The most common viruses identified in both field sampling periods were SMYEV and SMoV. Virus incidence was lower during the first sampling period compared to the second sampling period, indicating on-farm spread of strawberry viruses. On one farm, there was an increase in SMYEV incidence from 5 to 45%. Survey results were used to develop best management practices for SDD management in New Brunswick.

[P19] **Development of a botanical pesticide for the control of powdery mildew: the challenge of performing fungicide efficacy trial on obligate biotrophic fungi.** S. BEAUSEIGLE, P. H. ONTCHANGALT, A. BILLONG, S. KERNER, Y. RUDOLPH-BINETTE AND A. VIALLE. *(S.B.; P. H. O., A. B. and A.V.) Biopterre-Bioproducts development center, 1642 rue de la ferme, La Pocatière, QC G0R 1Z0, Canada, (S. K, Y. R.) iFact inc. 1117 rue Sainte-Catherine Ouest, suite 410, Montréal, QC H3B 1H9, Canada, and (Y R-B) Arbressence inc., 77 rue Omer Desserres, suite 6A, Blainville, QC J7C 5N3, Canada*
Powdery mildew fungi cause important economic losses on a wide range of ornamental and agricultural plants. Repetitive application of synthetic fungicides is currently the main practice for powdery mildew management in crops. However, there is a high potential for powdery mildew species to develop fungicide resistance. Botanical pesticides, such as plant extract based biopesticides, offer a good alternative to conventional chemical pesticides since they are less likely to have resistance issues because of their broad and non-specific modes of actions. The objective of this project is to perform fungicide efficacy trials against powdery mildew species using Northern white cedar (*Thuja occidentalis)* hydrosol formulations as botanical fungicide. In order to proceed to the homologation of the product, the first step is to determine the fungicide efficacy among the range of powdery mildew species *in vitro*. However, the fact that powdery mildews are obligate biotrophs, coupled with the fact that there are multiple pathogen/host combinations, make any *in vitro* tests challenging to realize. We have developed a specific strategy to perform pesticide efficacy trial on obligate biotrophic pathogens. First, we have narrowed down the number of pathogen/plant host combinations targeted in focusing on powdery mildew species occurring under controlled production systems such as greenhouse (vegetables) and growth chamber production (cannabis). Since there are a limited number of fungal strains available, a 'fungal strains harvest campaign' has been initiated throughout Canada. Lastly, we have developed a protocol to test the fungicide efficiency of obligate, biotrophic fungal species *in vitro*.

[P20] ***Fusarium graminearum* chemotypes from infected winter wheat crops in Manitoba.** M.A. HENRIQUEZ, B.D. MCCALLUM, M.F. BELMONTE, C.A. MCCARTNEY, T. OUELLET, F.M. YOU, AND H. S.

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Fusarium head blight (FHB), is mainly caused by various *Fusarium* spp. of which the most important is *Fusarium graminearum*. FHB is considered as the most serious disease affecting wheat (*Triticum aestivum* L.), causing significant yield losses worldwide. Yield loss results mainly by reduction in grain quality due to shriveled and/or discolored kernels, which are referred to as Fusarium-damaged kernels (FDK) and contamination of grain with the trichothecene mycotoxin deoxynivalenol (DON). *Fusarium graminearum* frequently produces one of three sets of trichothecene metabolites: (i) deoxynivalenol and 3-acetyldeoxynivalenol (3-ADON chemotype), (ii) deoxynivalenol and 15-acetyldeoxynivalenol (15-ADON chemotype), or (iii) nivalenol and its acetylated derivatives (NIV chemotype). The objective of this research was to create a culture collection of *F. graminearum* species from infected winter wheat and to identify the most prevalent chemotypes in Manitoba. Spikes collected in 2015 from commercial winter wheat crops were processed for pathogen isolation and identification in the laboratory. Ninety-two monosporic cultures of *Fusarium* isolates from 32 fields were sequenced using the nuclear ribosomal intergenic spacer (IGS) to confirm their species identity. A multiplex-PCR was used to identify chemotype-specific nucleotide variation among a panel of *F. graminearum* isolates and it showed that 46 isolates were of 3-ADON chemotype and 25 isolates were of 15-ADON chemotype. *Fusarium gramineraum* isolates from different geographical areas in Manitoba and representing different chemotypes will be tested in fall / winter 2016/17 for their pathogenicity on winter wheat varieties. The most aggressive *F. graminearum* isolate will be selected for further transcriptome studies.

[P21] **In-vitro molecular interaction between the helper component-proteinase of Potato virus Y and cuticle proteins of potato aphid.** R. HEPAT, S. BOQUEL AND X. NIE. *Fredericton Research and Development Centre, Agriculture and Agri-Food Canada, 850 Lincoln Road, Fredericton, NB E3B 4Z7, Canada; and (S.B.) SIPRE – Comité Nord, Rue des Champs Potez, 62217 Achicourt, France*

Potato virus Y (PVY) is transmitted by aphids in a non-persistent manner. Upon acquisition, the virus is retained within the stylets of aphids. When the viruliferous aphids probe on a plant shortly after the acquisition, the virus is released from the stylets into plant cells. For better management of PVY, a study was undertaken to identify aphid proteins that may be involved in the virus-vector interactions. Cuticle proteins (CuPs), which are a major component of the insect cuticle, were examined for *in-vitro* binding to the PVY helper component-proteinase (HC-Pro) and purified PVY virions. Proteins in 8 M urea extracts from *Macrosiphum euphorbiae* and *Myzus persicae* were separated by 12% SDS-PAGE, electroblotted onto membranes, and incubated with cuticular protein-specific antibody for detection/identification of CuPs. Several CuPs ranging from 17 KD to 70 KD were detected. To test whether the CuPs interact with HC-Pro and PVY virion, the blotted protein extracts were overlaid with HC-Pro alone or in combination with purified PVY virion, and then incubated with HC-Pro-specific or PVY-specific antibodies. In blots overlaid with HC-Pro and incubated with HC-Pro antibody, CuPs-like proteins were detected; and in blots overlaid with HC-Pro+PVY and incubated with PVY antibody, similar CuPs-like proteins were also detected. Nevertheless, no bands were detected by PVY antibody in blots overlaid with PVY alone or HC-

Pro alone. Together, these results demonstrate that HC-Pro acts as a bridge for PVY virion and aphid CuPs. Molecular identification of CuPs that interact with HC-Pro is underway.

[P22] **Advances in elucidating the mode of action of mineral oil on reduction of aphid-mediated PVY transmission.** S. BOQUEL, R. HEPAT, AND X. NIE. *Fredericton Research and Development Centre, Agriculture and Agri-Food Canada, 850 Lincoln Road, Fredericton, NB E3B 4Z7, Canada; and (S.B.) SIPRE – Comité Nord, Rue des Champs Potez, 62217 Achicourt, France*

Mineral oil (MO) has been used in the management of non-persistent virus and more specifically *Potato virus Y* (PVY) for a long time. MO has been commercially available to Canadian seed potato growers for a few years and yet, its mode of action remains unknown. Deciphering the mode of action of mineral oil will allow refinement of the current recommendations given to growers, increasing its reliability in managing PVY. The aim of this study was to test the efficacy of a single or five MO sprays on PVY acquisition and inoculation by aphids under field conditions. Results showed no significant reduction of PVY acquisition in the field. However, a 39% and 44% reduction of PVY transmission was observed 15 days post-inoculation (dpi) with plants treated with a single or five sprays of mineral oil, respectively. Quantitation of PVY amplicons based on band intensity revealed that amongst plants successfully infected with PVY, plants treated with MO harbor less PVY than untreated plants. The percentage of strong intensity bands was reduced after one and five sprays as well as the percentage of medium intensity bands after five sprays of MO. Mineral oil was not effective in reducing PVY acquisition but provided a good control of PVY transmission. These results suggest that mineral oil could have reduced (i) the number of viral particles inoculated by the aphid while probing the treated plant, (ii) virus replication and/or accumulation in inoculated leaves between inoculation and 15 dpi. Experiments are ongoing to answers these questions.

[P23] **DNA-barcoding the rusts - sampling herbarium specimens in the National Mycological Herbarium (DAOM).** S. HAMBLETON, Q. EGGERTSON, S. WILSON, S.A. REDHEAD AND C.A. LEVESQUE. *Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, K.W. Neatby Building, 960 Carling Avenue, Ottawa, ON Canada K1A 0C6*

Plant pathologists, diagnosticians and regulatory agencies rely on access to comprehensive, accurate, and curated reference DNA sequence databases. These data are essential for rapid and authoritative identifications of plant pathogens in field samples, commodity imports/exports and environmental samples as represented by DNA sequences derived from next-generation sequencing (NGS) techniques. Herbarium collections are the most easily accessible source of obligate fungal pathogens and their hosts, with specimens often dating back to the 1800s and representing a broad diversity of hosts and geographic provenance. A processing pipeline was developed to minimize destructive sampling of these irreplaceable collections while maximizing DNA yield and facilitating high throughput. DNA-barcoding techniques were applied to both pathogen and host, targeting the ITS2 and *rbcL*a gene regions respectively, for over 1200 specimens of rust fungi (Pucciniales/Uredinales) preserved in DAOM. For specimen selection, from the more than 38K available, we focused on species of quarantine concern as listed by various countries, those not yet represented in public sequence databases, those occurring on agricultural hosts, and alternate hosts for species with complex life cycles. Our success rate ranged from 51-72% (rusts, depending on genus) and 60% (hosts), and the oldest specimen successfully sequenced for both was collected in 1889. We now have consensus sequences representing 88% (23/26) of genera and 73% (242/330) of species sampled. The primary impacts will be to increase the number of publicly

available and authoritatively identified reference DNA barcodes and reduce the risk of misinterpreting DNA signatures of innocuous species with those of regulated species.

[P24] **Re-classification of *Clavibacter michiganensis* subspecies into multiple new species.** X. LI, J. TAMBONG, X. YUAN, H. XU, AND S.H. DE BOER. *Canadian Food Inspection Agency (CFIA), Charlottetown Laboratory, 93 Mt. Edward Rd., Charlottetown, PE, Canada, C1A 5T1; and (J.T.) Agriculture and Agri-Food Canada (AAFC), 960 Carling Ave, Ottawa, Canada, K1A 0C6*

The bacterial genus *Clavibacter* is monospecific consisting of only one species, *C. michiganensis,* subdivided into five subspecies, each with specificity for a single host crop. *C. michiganensis* subsp. *michiganensis* (Cmm) causes bacterial canker of tomato (*Solanum lycopersicum*), *C. m. sepedonicus* (Cms) causes bacterial ring rot of potato (*Solanum tuberosum*), *C. m. insidiosus* (Cmi) causes bacterial wilt of alfalfa (*Medicago sativa*), *C. m. nebraskensis* (Cmn) causes the Goss's bacterial wilt of maize (*Zea mays*), and *C. m. tesselarius* (Cmt) causes bacterial mosaic disease of wheat (*Triticum* spp.). The taxonomic position of the subspecies was evaluated using whole genome sequences of multiple strains of Cmm, Cms, Cmi, Cmn, and Cmt, including type strains. Genomes were decoded using either BacBio single molecule real-time sequencing (McGill University and Genome Quebec Innovation Centre, Montreal, QC) or paired-end Illumina HiSeq sequencing with True Seq version 3 chemistry (National Research Council Canada, Saskatoon, SK, Canada). The assembled sequences were annotated and compared with sequences of Cmm, Cmi and Cms, and other *Clavibacter* spp. deposited in GenBank. Average nucleotide identity (ANI) values ranged from 91-95% among subspecies while pair-wise comparison among strains of the same subspecies had ANI values of 99-100%. Based on ANI values, 16S rRNA sequences, multi-locus sequence typing of house-keeping genes, and phenotypic characteristics, the taxonomic position of the phytopathogenic clavibacter subspecies should be raised to species status within the genus *Clavibacter* as *C. michiganensis* sp. nov.*, C. sepedonicus* sp. nov.*, C. insidiosus* sp. nov.*, C. nebraskensis* sp. nov.*,* and *C. tessellarius* sp. nov.

[P25] **Management of apple scab in organic apple orchards.** D. ERRAMPALLI, A. HALDAR, C. JACKSON, A. ZWIEP, F. BETANCOURT, L. KRZYWDZINSKI, M. PARCEY, K. SCHNEIDER. *Agriculture and Agri-Food Canada, 4902 Victoria Ave. N., Vineland Station, ON L0R 2E0, Canada*

Apple scab caused by *Venturia inaequalis* occurs apple growing regions in the world, including Ontario, Canada and also causes economic losses. The conidia of *V. inaequalis* are spread to leaves and the developing fruit through rainfall and air. This study aims to examine the effect of organic fungicides against *V. inaequalis* in reducing the development of apple scab in 'McIntosh' and 'Empire' apples in the orchard. During the summers of 2014 and 2015, apples were sprayed with three organic fungicides, a water control and a chemical control (N-trichloromethylthio-4-cyclohexene-1,2-dicarboximide). The three organic fungicides used were Sulphur (Kumulus), a 0.25% *Reynoutria sachalinensis* (Regalia #1) and 0.25% pre bloom and 0.75% post bloom *R. sachalinensis* (Regalia#2). A disease rating scale was used to take observations of the presence of apple scab on 'McIntosh' leaves and fruits. Observations on apple scab disease were made over a period of three months in 2014 and in 2015 which showed a gradual increase in disease progression. Two way ANOVA tests were also performed to determine any statistical differences between and among all five treatments. Results indicated that the Sulphur

treatment was the most effective organic fungicide followed by *R. sachalinensis* in reducing apple scab disease in 'McIntosh' apple leaves and fruits.

[P26] **Effects of dazomet on clubroot and root rot of canola.** S.F. HWANG, H.U. AHMED, S.E. STRELKOV, Q. ZHOU, B.D. GOSSEN, M.R. MCDONALD, G. PENG AND G.D. TURNBULL. *Crop Diversification Centre North, Alberta Agriculture and Forestry, Edmonton, AB T5Y 6H3, Canada; (S.E.S.) Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada; (B.D.G & G.P) Agriculture and Agri-Food Canada (AAFC), Saskatoon, SK S7N 0X2, Canada; (M.R.M) Department of Plant Agriculture University of Guelph, Guelph, ON N1G 2W1, Canada*

Experiments were conducted to examine the effectiveness of dazomet (trade name Basamid) in preventing infection of canola (*Brassica napus*) by *Plasmodiophora brassicae.* Greenhouse studies showed that seedling emergence and plant height increased, and infection (both primary and secondary) and clubroot severity decreased with increasing rates of dazomet pre-treatment of *P. brassicae*-infested soil. Under field conditions, clubroot severity was reduced and seed yield increased with increasing dosage of dazomet. However, seedling emergence, root mass and seed yield were reduced, especially at 400-800 kg/ha. Dazomet also increased emergence, plant survival and plant biomass in *P.brassicae*-infested soils that were inoculated with the soil-borne pathogens *Fusarium avenaceum*, *Pythium ultimum* and *Rhizoctonia solani*. These results indicate that dazomet may be an effective tool for the management of both clubroot and seedling blight of canola.

[P27] **Differential proliferation of *Plasmodiophora brassicae* in *Brassica napus* cultivars.** T. CAO, S.F. HWANG, I. FALAK, AND S.E. STRELKOV. *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada; (S.F.H.) Alberta Agriculture and Forestry, Crop Diversification Centre North, 17507 Fort Road, Edmonton, AB T5Y 6H3, Canada; (I.F.) Pioneer Hi-Bred Production Ltd., 12111 Mississauga Road, Caledon, ON L7C 1X1, Canada*

Clubroot is a devastating disease of canola (*Brassica napus*) in Alberta, Canada, and effective management relies mainly on genetic resistance. In order to improve understanding of host resistance, the proliferation of *Plasmodiophora brassicae* (Pb) within the roots of susceptible (45H26) and resistant (P2008-6) canola genotypes was monitored by quantitative PCR (qPCR) and histological analyses. Roots were sampled 1-44 days post-inoculation (dpi) with a single-spore isolate representing Pb pathotype 3. The concentration of pathogen DNA was significantly greater in 45H26 (4.68-1668.57 µg/g) than in P2008-6 (2.91-538.60 µg/g) starting at 4 dpi and at most of the subsequent time-points examined. Root hair infections were observed from 4 to 7 dpi in both hosts. Zoosporangia were found on P2008-6 at 10 dpi, and plasmodia were visible on 45H26 and P2008-6 starting from 11 and 12 dpi, respectively. From 11 to 30 dpi, plasmodia dramatically increased in both host genotypes, with more plasmodia in 45H26 than in P2008-6. At 37 and 44 dpi, more resting spores were visible in 45H26 than in P2008-6. While the extent of pathogen proliferation and the speed of its development were greater in the susceptible vs. the resistant genotype, Pb was able to complete its life-cycle and produce resting spores on the resistant host. This suggests that resistant canola genotypes may contribute to the build-up of Pb inoculum in the soil, although not to the same extent as susceptible varieties.

[P28] **Efficacy of two fumigants against clubroot (*Plasmodiophora brassicae*) in three field trials.** J. ROBSON, B.D. GOSSEN, F. AL-DAOUD AND M.R. MCDONALD. *Department of Plant Agriculture, University of Guelph, 50 Stone Road East, Guelph, ON, N1G 2W1, Canada; (B.D.G.) Agriculture and Agri-Food Canada, Saskatoon Research and Development Centre, 107 Science Place, Saskatoon, SK, S7N 0X2, Canada*

Seed treatments, biocontrol agents and soil amendments do not provide effective management of *Plasmodiophora brassicae* Woronin (clubroot) on canola (*Brassica napus* L.) in Canada. Field trials were conducted in a naturally infested mineral soil and a high organic content (muck) soil site in Ontario to assess the efficacy of two soil fumigants, metam sodium (Vapam HL, Busan 1236) or chloropicrin (Pic Plus) at selected rates on clubroot. Efficacy was assessed in plant bioassays with a susceptible cultivar of Shanghai pak choi. Furthermore, propidium monoazide (PMA) assisted qPCR was used to quantify the viability of resting spores in the soil after treatment. Disease pressure at the mineral soil site in 2014 was very low; there were no clubroot symptoms in any treatment that received metam sodium or chloropicrin, and only 8% severity in the nontreated control. In trials in 2014 and 2015 at the muck soil site, chloropicrin reduced clubroot severity when applied at 128 kg a.i. ha^{-1} or higher. Metam sodium was only effective at 150 kg a.i. ha^{-1} or higher in one year (2015) at this site. However the lack of efficacy in 2014 may have been due to ineffective sealing of the metam sodium treatments within the soil after application. Unexpectedly, the fumigants did not have a consistent effect on resting spore viability assessed with PMA-PCR. We conclude that fumigants can reduce clubroot, but that efficacy depends on both rate of application and effectively sealing the fumigant in the soil after application.

[P29] **Use of genotype-by-sequencing to characterize populations of *Plasmodiophora brassicae.*** M. D. HOLTZ, S.F. HWANG, J. ZANTINGE, AND S.E. STRELKOV. *Field Crop Development Centre, Alberta Agriculture and Forestry, 6000 C and E Trail, Lacombe, AB T4L 1W1, Canada. (S.F.H.) Alberta Agriculture and Forestry, Crop Diversification Centre North, 17507 Fort Road, Edmonton, AB T5Y 6H3, Canada. (S.E.S.) Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada*

Plasmodiophora brassicae Woronin is an obligate and soil-borne parasite that causes clubroot disease in canola (*Brassica napus* L.) and other cruciferous crops. Recently, new aggressive populations of the pathogen, virulent on clubroot resistant canola cultivars, have been found in Alberta, Canada. In order to determine the relationship of members of these aggressive populations to other *P. brassicae* populations present in Canada, a genotyping-by-sequencing (GBS) method was employed. Twenty-one populations or single-spore isolates were analyzed. DNA was extracted from spores purified from infected roots and used for GBS. Over 10 million sequences were generated using the Ion Torrent PGM™ platform. After variant calling and filtering over 15 000 variable loci were retained for analysis. Phylogenetic tree and population structure analysis clearly identified and separated the new aggressive populations from other *P. brassicae* populations. Thirty-six percent of the loci were group-specific, with no shared alleles between the aggressive populations and the other samples. Of these group-specific alleles, over a third caused non-silent mutations. The sequence information produced should allow for the development of markers and assays for the detection of resistance-defeating *P. brassicae* populations.

[P30] **Occurrence of soybean root rot and associated pathogens in western Canada.** K. F. CHANG, S. F. HWANG, H. U. Ahmed, Q. ZHOU, H. FU, S. E. STRELKOV, R. L. CONNER, D. L. MCLAREN, M. W. HARDING AND G. D. TURNBULL. *Crop Diversification Centre North, Alberta Agriculture and Forestry (AAF), Edmonton, AB T5Y 6H3, Canada; (S.E.S.) Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada; (M.W.H.) CDC South, AAF, Brooks, AB T1R 1E6, Canada; (R.L.C.) Agriculture and Agri-Food Canada (AAFC), Morden, MB R6M 1Y5, Canada; (D.L.M.) AAFC, Brandon, MB R7A 5Y3, Canada*

Soybean (*Glycine max* (L.) Merr.) has great potential as an alternative crop in western Canada. Root rot is a common constraint to soybean production worldwide. Surveys in 2015 determined the incidence, severity and causal organisms of root rot of soybean in 41 crops across nine counties in southern Alberta. A total of 100 root samples were collected per field. Root rot occurred at all locations, with an average incidence of 78% and a range of 33 to 100%. The average disease severity was 1.3 and ranged from 0.4 to 2.6 on a scale of 0-4. Species of *Fusarium* were most commonly isolated, followed by *Pythium* spp. and then *Rhizoctonia solani*. A total of 94 soil samples were collected from Alberta and Manitoba and seeded with the oomycete-susceptible pea cultivar 'Midas'. Isolation from the infected roots on semi-selective media yielded 151 isolates with morphological characteristics of *Pythium* or *Phytophthora* species. In greenhouse assays, 85 of these isolates caused more than 50% reduction in seedling emergence. Twenty-one of these isolates were moderately virulent (50-69% emergence reduction), 26 were virulent (70-84% emergence reduction) and 38 isolates were highly virulent (85-100% emergence reduction). Most of the isolates caused severe disease on the host (ratings of 3.0-4.0), while 13 isolates caused more moderate symptoms (ratings of 2.1-2.9). Plant height decreased as disease severity increased. The identity of these isolates will be determined by examining their morphological and reproductive structures, along with the use of molecular diagnostic tools.

[P31] **Slip-skin disorder on sweet cherry (*Prunus avium* L.).** D.T. O`GORMAN, G. HEALY, P. M. TOIVONEN AND J.R. ÚRBEZ-TORRES. *Agriculture and Agri-Food Canada, Summerland Research and Development Centre (SuRDC), 4200 Hwy. 97, Summerland British Columbia, V0H 1Z0*

Cherry slip-skin is a problem affecting the health, quality and sale-ability of (primarily) late season sweet cherry (*Prunus avium L.*). Reports of this condition causing major problems for producers in the 2012 harvest came from both British Columbia (BC) and Washington State (WA), with some orchards continuing to experience the problem in 2013 to 2015. The condition is not easily visible until just after harvest and may not show up until after shipping. Following harvest, the shoulder of the cherry becomes noticeably soft and the skin disassociates from the inner tissue, which has become macerated. With time, while the rest of the cherry remains firm, the symptoms develop radially causing breakage of the skin. During shipping, the affected areas may dehydrate forming sunken craters on the fruit's surface. Presently, the exact cause of this condition is unknown, but preliminary investigations in both BC and WA suggest the involvement of one or more different yeast species. Our survey results indicate yeast populations are found to increase in number on the surface of developing fruit throughout the growing season, however yeast cannot always be isolated from symptomatic fruit. To help elucidate key factors involved in cherry slip-skin, several field trials were set up in 2015. The first was a spray trial, incorporating both the commercial fungicide propiconazole (0.125 ppm) and potassium metabisulfite (5000 ppm) at different spray intervals. The second trial, involved canopy management to increase the light penetration and alter the microenvironment of the fruiting zone. Preliminary results of both trials will be presented.

[P32] **Development of a grapevine trunk diseases macroarray.** D.T. O'GORMAN, J. FRASER, J. DICK AND J. R. ÚRBEZ-TORRES. *Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre (SuRDC), 4200 Hwy 97 Summerland British Columbia, V0H 1Z0*

Grapevine trunk diseases (GTD) are caused by a wide range of taxonomically unrelated fungal pathogens (approx. 80 different species). The GTD complex includes: black-foot and Petri disease, affecting young grapevines, collectively known as young vine decline (YVD); as well as Esca, and dieback (Eutypa, Botryosphaeria and Phomopsis), primarily found in mature vines. Grapevine trunk diseases are relatively new in British Columbia (BC). The situation parallels that in other grape-growing regions of the world. In order to evaluate the magnitude of GTD in BC, field surveys were conducted. Overall, 30 GTD species were identified in BC, with 95.8% of all vineyards surveyed showing symptomatic vines, with 7.8% and 10.2% expressing YVD and dieback, respectively. Because of the large numbers of GTD pathogens found locally and globally, an accurate and rapid detection method is needed to facilitate the development of effective disease management strategies. Therefore, we have designed a DNA macroarray, with probes targeting β-tubulin gene sequences specific for the detection of 61 taxa including 34 YVD pathogens. The macroarray was shown to be accurate and sensitive, detecting as little as 10^{-6} ng of pathogen DNA. Work is currently being conducted to expand the DNA macroarray to include species-specific probes selected from the β-tubulin and elongation factor 1-α genes. The array will detect an additional 20 different fungal pathogens responsible for Botryosphaeria dieback and Eutypa dieback in mature vines. Once complete, the macroarray will be a rapid and comprehensive tool available for vineyard and nursery GTD management.

[P33] **Blackleg resistance by Rlm1 may be triggered by localized activation of salicylic acid and suppression of abscisic acid and auxin pathways.** C. ZHAI, X. LIU, T. SONG, F. YU AND G. PENG. *Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada*

Host resistance plays a critical role in managing blackleg [*Leptosphaeria maculans* (Desmaz.) Ces. & de Not] on canola (*Brassica napus* L.), but the information on resistance mechanism is lacking. A transcriptome study was conducted by inoculating a double-haploid canola line carrying the resistance genes *Rlm1* and *Rlm3* with an avirulent (*AvrLm1*) or virulent (*AvrLm4-7*) isolate of *L. maculans*. RNA sequencing identified 70,709 genes in this line by mapping the result to a reference *B. napus* genome, among which 3,015 and 6,999 were differentially expressed genes (DEGs) in the local tissues of incompatible and compatible interactions, respectively. Gene ontology found many of them are related to plant-pathogen interaction or plant hormone signalling; many DEGs involved in salicylic acid (SA) pathways were significantly activated in the incompatible interaction relative to a water control, while those involved in abscisic acid (ABA) and auxin signaling were triggered exclusively in the compatible interaction. This result indicates that recognition of the avirulence gene by *Rlm1* triggers a localized increase in SA, which possibly limits the infection via suppression of ABA and auxin signaling pathways. When systemic responses were assessed, RNA sequencing identified far fewer DEGs in the non-inoculated cotyledon of plants where the other cotyledon had been inoculated earlier. Additionally, few genes involved in SA were activated in the non-inoculated cotyledons and those involved in the ABA pathway were not suppressed relative to the control. When challenging the non-inoculated cotyledons with the virulent *L. maculans* isolate, the prior inoculation of the other cotyledon with the avirulent isolate showed no effect on infection.

[P34] **Non-race specific resistance to blackleg by Canadian canola cultivars shows delayed or reduced pathogen spread from infected cotyledons into petioles and stems.** W. M. SOOMRO, H. R. KUTCHER AND G. PENG. *Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada;* (*H.R.K*) *Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada*

In western Canada, the majority of canola (*Brassica napus* L.) cultivars carry the resistance (*R*) gene *Rlm3*, *Rlm1* or both to blackleg [*Leptosphaeria maculans* (Desmaz.) Ces. & de Not.]. Since the corresponding avirulence (*Avr*) genes (*AvrLm3*, *AvrLm1*) are rare in the current pathogen population, these *R* genes are no longer effective. However, widespread and severe damage by blackleg is still uncommon, suggesting that additional resistance mechanisms are present in commercial canola cultivars (CCCs). Three CCCs carrying *Rlm1* and/or *Rlm3* were assessed with "Westar" (susceptible) against virulent *L. maculans* isolates carrying no *AvrLm1* or *AvrLm3*. The infection of cotyledons and spread of the pathogen into the stem via the petiole were evaluated using a 09 scale and fluorescence microscopy. Droplet digital PCR (ddPCR) was used to quantify the DNA of spreading pathogen in petiole and stem tissues. At 7 days post-inoculation (dpi), a virulent isolate of *L. maculans* carrying a green fluorescent protein gene showed more limited hyphal spread in inoculated CCC cotyledons than in Westar. At 14 dpi, all inoculated cotyledons showed infection symptoms, but the mean severity was 5–6 for CCCs and 8–9 on Westar. ddPCR results showed that the amount of *L. maculans* DNA was substantially lower in petioles and stems of inoculated CCCs relative to Westar. It appears that non-race specific resistance associated with the CCCs plays a role against blackleg by delaying or reducing the spread of fungal hyphae from infected cotyledons into stems, which is where the most severe impact on plant yield occurs.

[P35] **Mining the microbiomes of crop wild progenitors for co-evolved beneficial microbes.** G. IRIARTE, I. HALE AND K. BRODERS. *(G.I.) Department of Molecular, Cellular and Biomedical Sciences, University of New Hampshire, Durham, NH 03824; (I.H.) Department of Biological Sciences, University of New Hampshire, Durham, NH 03824; and (G.I., K.B.) Department of Bioagricultural Sciences and Pest Management, Colorado State University, Fort Collins, CO 80523*

Wild progenitors of crop plants are potentially valuable to modern plant improvement efforts not only as sources of "lost" genetic diversity but also, if grown *in situ*, as assays for beneficial co-evolved microbial associations lost during the processes of domestication and translocation from centers of origin. To explore this idea, we investigated genotypes belonging to the Mesoamerican pool of common bean (*Phaseolus vulgaris*) due to the fact that both wild and cultivated forms of *P. vulgaris* can still be found growing in central Mexico, the center of diversity and one of the centers of domestication of the species. Replicated common gardens of six wild accessions and six cultivated varieties were grown in five locations: three *in situ* among wild *Phaseolus* populations in central Mexican and two *ex situ* under agricultural conditions in the northeastern U.S. Bacterial and fungal communities of the soil, rhizosphere, and roots were characterized via metagenomic analyses of the 16S and ITS regions, respectively. Sample type (bulk soil vs. rhizosphere vs. root) was associated with significant variation in microbial diversity across locations. Of particular interest was the varying compositions of microbial communities between rhizosphere and root samples, as such differences indicate the root colonization of both bacteria and fungi through either active or passive means in all locations. Finally, we identified and cultured potentially novel microbial species that associated with cultivated beans grown *in situ* in Mexico but were not found on cultivated beans when grown in the U.S. These organisms represent targets for future inoculation studies.

[P36] **Major shift in the virulence of sunflower rust races in Manitoba.** K.Y. RASHID. *Agriculture and Agri-Food Canada, Morden Research and Development Centre, Morden, Manitoba, R6M 1Y5*

Puccinia helianthi Schwein is a worldwide pathogen causing rust disease in sunflower (*Helianthus annuus* L.) with major epidemics and great losses in seed yield and quality. Annual disease surveys of the sunflower crops in Manitoba revealed a wide range in rust incidence and severity from year to year. Local severe rust epidemics occurred in various regions in Manitoba in most years since 2002. Prior to 2009, such epidemics were caused by the predominant rust race-group 300 including the races 324, 326, 327 and 336. Clear shifts in the virulence pattern of the sunflower rust population have been observed after 2009 with the prevalence of the race-group 700 including the races 723, 736, 766, 776, and 777. The most virulent race 777 appeared in 23% of the 2009 isolates but was not detected in 2010 and 2011. However, race 777 appeared at 5% in the isolates collected in 2012-2013, and rose sharply to 74% of the collected isolates in 2015. Race 777 is virulent on all the nine sunflower rust differential genotypes used to identify sunflower rust races, and on most commercial sunflower hybrids grown in Manitoba.

[P37] **Survival and productivity in an environment of multiple stressors: responses to drought in interior Douglas-fir (*Pseudotsuga menziesii* var. *glauca*) seedlings.** E.M. BECKER, M.G. CRUICKSHANK AND R.N. STURROCK. *Natural Resources Canada, Canadian Forest Service, Pacific Forestry Centre, 506 West Burnside Road, Victoria, BC V8Z 1M5, Canada*

The interior Douglas fir (Fdi) variety, (*Pseudotsuga menziesii* Mirb. Franco var. *glauca*), is a dominant and highly-valued tree that grows more slowly and is better adapted to drought than the coastal variety of the species (var. *menzies*). These long-lived trees face selective pressures for both growth and stress tolerance and must be able to compete for resources and light as well as being able to withstand decades of exposure to multiple biotic and abiotic stressors. We are characterizing the survival and tolerance responses of Fdi families from four distinct seed breeding zones in B.C. to multiple stressors, including drought and fungal diseases. We are testing the hypothesis that growth and stress tolerance are linked, and obtaining insight into underlying mechanisms of responses to drought and diseases. Objectives of the present study were to analyze the survival of Fdi in an environment of drought, and to characterise the responses of Fdi grown in a water-limited environment, compared to in an ideal environment (=tolerance). In this study, trees from the driest breeding zones, SA and WKL, were those with the most growth in the driest water-limited treatment. Trees from these drier zones, however, had the highest risk of mortality by drought. This work provides a foundation for future genetic studies to associate phenotypic stress responses with their genetic components. The results of these experimental trials will increase our knowledge of conifer responses to multiple disease agents, and inform and guide specific breeding strategies for Douglas-fir trees.