CANADIAN PHYTOPATHOLOGY SOCIETY

ATLANTIC REGION HYBRID MEETING - 2023

Fredericton Research and Development Centre, AAFC, 95 Innovation Rd, Fredericton, E3B 4Z7, New Brunswick, November 23, 2023

Canadian Phytopathological Society
Atlantic Region Hybrid Meeting

November 23, 2023

Fredericton Research and Development Centre,
850 Lincoln Road, Fredericton, NB and virtually via MS Teams

Welcome to Fredericton (and to those joining virtually) to the 2023 Canadian Phytopathological Society (CPS) Atlantic Region Meeting. It is our pleasure to host this year's CPS regional meeting, and we are looking forward to a stimulating afternoon of scientific discussion and fellowship.

There are 7 oral presentations on various topics in phytopathology scheduled for the afternoon. A dinner will take place at 6:30 pm at Isaac's Way Restaurant, 649 Queen St, Fredericton, NB following the meeting.

Many thanks to all who are attending the meeting. After several years of absence due to the Covid-19 pandemic, we trust we will be able to get together on a regular basis in future, and on that note, plans are developing to host the 2024 meetings in Kentville, NS.

This booklet contains abstracts of the oral presentations in the order that they were presented. All abstracts will subsequently be published in an upcoming edition of the Canadian Journal of Plant Pathology. The research work represented by these papers forms an important part of the on-going development of phytopathological research in Atlantic Canada.

Rick Peters
Atlantic Region Rep, CPS
Dahu Chen
Local Host, AAFC Fredericton

Canadian Phytopathological Society - Atlantic Region Hybrid Meeting 2023
Scientific Program

Thursday, November 23, 2023
Conference Room, Fredericton Research and Development Centre

13:00-13:10 Introduction/Welcome:

Dr. Rick D. Peters, CPS representative – Atlantic region
Bonnie Robertson, Acting Associate Director, Research, Development and Technology, Fredericton Research and Development Centre, Fredericton, NB

Session A: Host-pathogen interaction and pathogen population dynamics

Moderator: Dahu Chen

13:10- 13:30 Genetic characterization of extreme resistance (ER) against potato virus A in potato cultivar Barbara and mapping one of the *R* genes conferring this EA.

W. HUANG, Z. TU, R. CHEN, C. LI, J. ZHENG, J. DONG, A. MURPHY, M. SINGH, K.M. GARDNER, J. LI, H. MA, B. SONG, B. NIE AND X. NIE*

13:30-13:50 Population structure of the late blight pathogen *Phytophthora infestans* on potato and tomato in Canada. (Student presentation for competition)

S.O. BABARINDE*, K.I. AL-MUGHRABI, R.D. PETERS, R.R. BURLAKOTI, A. NOVINSCAK, S. SAPKOTA AND B. PRITHIVIRAJ.

13:50-14:10 Correlation of soil properties, rotation crops, fall green cover crops with PED pathogen population densities in New Brunswick and Prince Edward Island.

DAHU CHEN*, LOUIS-PIERRE COMEAU, KAMRUN NAHAR, RYAN BARRETT, BENJAMIN MIMEE, TANYA ARSENAULT, SEBASTIAN IBARRA, EILEEN BEATON, BERNIE ZEBARTH.

14:10-14:50 Nutrition break and interaction

Session B: Pathogen detection and biopesticide discovery

Moderator: Khalil Al-Mughrabi

14:50-15:10 Development and application of simultaneous qPCR for Verticillium and Root Lesion Nematode in greenhouse and field studies.

TYLER MACKENZIE*, KHALIL AL-MUGHRABI, DAHU CHEN, MATHURESH SINGH

15:10-15:30 Current Trends in Detection and Identification of Plant Pathogenic Bacteria (Virtual presentation)

XIANG (SEAN) LI*, JIACHENG (ERIC) CHUAN, QIFAN (EVELYN) YANG, JINGBAI NIE, PHILLIP MAXWELL, AND WEN CHEN

15:30- 15:50 Battling Fusarium spp. with iChip: A Novel Approach to Biopesticide Discovery. (Student virtual presentation for competition)

L. K. GAUTHIER, C. W. KIRBY, A. FOSTER, B. WAGNER

15:50-16:10 Application of fungal endophytes isolated from apple (*Malus domestica*) trees for apple replant disease management (Virtual presentation)

S. ALI, M. ROY and A. WALKER

16:10- 16:30 Wrap-up

18:30 Dinner and Award Presentations (Isaac's Way Restaurant, 649 Queen St, Fredericton, NB E3B 1C3)

Note to presenters: Please ensure that your presentation is given to the audio/visual coordinator at least 1 hour prior to the start of the session for the in-person presentations.

Session A: Host-pathogen interaction and pathogen population dynamics

13:10- 13:30

Genetic characterization of extreme resistance (ER) against potato virus A in potato cultivar Barbara and mapping one of the *R* genes conferring this EA.

W. HUANG, Z. TU, R. CHEN, C. LI, J. ZHENG, J. DONG, A. MURPHY, M. SINGH, K.M. GARDNER, J. LI, H. MA, B. SONG, B. NIE AND X. NIE. *Key Laboratory of Horticultural Plant Biology, Huazhong Agricultural University, Wuhan 430070, China; (A.M, K.M.G., X.N.) Fredericton Research And Development Centre, Agriculture And Agri-Food Canada, 95 Innovation Road, Fredericton, New Brunswick E3B 4Z7, Canada; (M.S.) Agricultural Certification Services, Fredericton, New Brunswick E3B 8B7, Canada*

Potato virus A (PVA) is one of the major viruses affecting potato worldwide, and can cause serious disease symptoms and yield losses. Several cultivars including Barbara and Shepody have been identified possessing extreme resistance (EA) against PVA. Segregation analysis of a population of Barbara × F58050 suggests the involvement of two genes, likely Ry_{sto} and R_a, in controlling the EA in Barbara. Further analysis of a backcross population of a PVA-resistant but PVY-susceptible progeny (i.e., BF145) of "Barbara × F58050" × F58050 revealed a single copy of *Ra* conferring ER to PVA in Barbara and its progeny BF145. The deduced genotypes of Barbara and BF145 are *RyryryryRarara*ra and *Rarara*ra, respectively. Using a combination of next-generation sequencing and bulked-segregant analysis of the BC population, we mapped this *Ra* to the third homologus chromosome of chromosome 4. The *Ra* was delimited by the Indel markers M8-123 and M10-8 within a genetic interval of 4.09 cM, corresponding to a 1.38 Mb genomic region in the potato DM reference genome. The indel marker M10-8, which showed >98% agreement with the phenotyping results in the *Ry*-free segregating BC population, was also assessed for its correlation with PVA resistance in 43 potato cultivars/breeding clones. The results obtained above are of importance in further *Ra* cloning and the marker-assisted selection for PVA resistance.

Session A: Host-pathogen interaction and pathogen population dynamics

13:30-13:50

Population structure of the late blight pathogen *Phytophthora infestans* on potato and tomato in Canada.

S.O. BABARINDE, K.I. AL-MUGHRABI, R.D. PETERS, R.R. BURLAKOTI, A. NOVINSCAK, S. SAPKOTA AND B. PRITHIVIRAJ. *Department of Plant, Food and Environmental Sciences, Faculty of Agriculture, Dalhousie University, Truro, NS, B2N 5E3, Canada; (K.A.-M.) New Brunswick Department of Agriculture, Aquaculture and Fisheries, 39 Barker Lane, Wicklow, NB, E7L 3S4, Canada; (R.D.P) Charlottetown Research and Development Centre, Agriculture and Agri-Food Canada, 440 University Avenue, Charlottetown, PE, C1A 4N6, Canada and (R.R.B, A.N., S.S.) Agassiz Research and Development Centre, Agriculture and Agri-Food Canada, 6947 Hwy 7, Agassiz, BC, V0M 1A0, Canada*

Late blight caused by the oomycete *Phytophthora infestans* (Mont.) de Bary has been an annual disease issue for both potato and tomato crops in Canada in recent years. Increased disease incidence and severity have coincided with changes in the genetic composition of *P. infestans* populations in Canada, the USA, and worldwide. Pathogen isolates collected from potato and tomato across multiple years (2019-2022) from western Canada were characterized as either the US11 (A1 metalaxyl-insensitive), US17 (A1; metalaxyl-insensitive), or US8 (A2; metalaxyl-resistant) genotypes or 25 new recombinants. Isolates originating from eastern Canada were either US23 (A1; metalaxyl-sensitive) or recombinant (A1; metalaxyl-sensitive). A sharp dichotomy in late blight incidence, prevalence, and genetic composition between eastern and western Canada and the continued dominance of US23 in eastern Canada was observed. High genetic diversity was observed among *P. infestans* isolates originating from western Canada as indicated by the number of multilocus genotypes and the emergence of 25 recombinants. Close monitoring of *P. infestans* population composition in western Canada is expedient considering the increased potential of sexual recombination in this region as evidenced by the number of outbreaks each year, highly resistant isolates to metalaxyl-m, the emergence of recombinants, and detection of various genotypes. This could pose late blight management challenges.

A: Host-pathogen interaction and pathogen population dynamics

13:50-14:10

Correlation of soil properties, rotation crops, fall green cover crops with PED pathogen population densities in New Brunswick and Prince Edward Island.

D. CHEN, L.-P. COMEAU, K. NAHAR, R. BARRETT, B. MIMEE, T. ARSENAULT, S. IBARRA, E. BEATON, B. ZEBARTH. *(D.C., L-P. C., K.N, B.Z.) Fredericton Research and Development Centre, Agriculture and Agri-food Canada, 850, Lincoln Rd, Fredericton, NB E3B 4Z7; (R.B., E.B.) Prince Edward Island Potato Board, 90 Hillstrom Ave, Charlottetown, PE C1E 2C6; (B.M.) Saint-Jean-sur-Richelieu Research and Development Centre, Agriculture and Agri-food Canada, Saint-Jean-sur-Richelieu, QC J3B 7B5; (T.A.) 343 Université Avenue PO Box 5030 Moncton, NB E1C 9B6 Canada; (S.I.) Prince Edward Island Department of Agriculture and Land, PO Box 2000, Charlottetown, PE C1A 7N8.*

Potato early dying, primarily caused by *Verticillium dahliae* and root lesion nematodes (RLNs), widely spreads in Canada and limits potato productivity. A total of 112 and 126 fields grown with rotation crops were surveyed in the fall between 2017 and 2021 in NB and PEI to assess population density of *Verticillium* spp, and RLN, soil properties, and to determine the correlation of soil properties, green cover crops and rotation crops with the pathogen population density. *V. dahliae* was detected in over 90% of the fields in NB and PEI, and *V. albo-atrum* was sporadically detected at low level in both provinces. *Pratylenchus penetrans* was detected in 36 and 38% of the fields, accounting for 8 and 11% of RLN population in NB and PEI, respectively. *P. crenatus* was detected in all fields, accounting for 92 and 89% of RLN population in NB and PEI, respectively. PEI soil and NB soil were similar in soil pH, NH4-N, P and K, but differed in soil texture, carbon and nitrogen content, macro- and micro-nutrients, and cation exchange capacity. RLN population density did not correlated with any soil property parameters in NB, but was significantly correlated with %N, %C, total organic N, P, K and CEC in PEI. *V. dahliae* population density was significantly correlated with different soil parameters in NB and PEI, except the K which was significantly positively correlated in both provinces. Results imply that the effect of soil properties on pathogen population densities may be soil-type dependent and influenced by other environmental conditions and agricultural operations.

Session B: Pathogen detection and disease management

14:50-15:10

Development and application of simultaneous qPCR for Verticillium and Root Lesion Nematode in greenhouse and field studies

T. MACKENZIE*, K. AL-MUGHRABI, D. CHEN, M. SINGH *(T.M., M.S.) Agricultural Certification Services, Inc., 1030 Lincoln Rd., Fredericton, NB; (K.A.) Potato Development Centre, 39 Barker Lane, Wicklow, NB; (D.C.)Fredericton Research & Development Centre AAFC, Fredericton, NB*

Verticillium dahliae (Kleb., 1913) and *Pratylenchus penetrans* (Cobb, 1917) are soil-borne pathogens known to cause Potato Early Dying (PED) syndrome. Our new qPCR system simultaneously quantifies both, using DNA, rather than labour intensive microscopic counting. qPCR was applied in greenhouse and field to measure pathogens' effects on potato growth and yield. Greenhouse-grown potatoes (cv. Russet Burbank) were inoculated with *V. dahliae* and *P. penetrans* in sterile soil and fresh soils from fumigated and non-fumigated fields. Tuber yields were reduced, but more so by *V. dahliae* and combined *V. dahliae* and *P. penetrans*. The lasting effect of previous-year fumigation caused initial reduction in *V. dahliae* in the pots, but it later matched or exceeded growth in the non-fumigated or steam-sterilized soils; this effect was less clear with *P. penetrans*. Plant growth and tuber yield were better in post-fumigated field soil despite artificial inoculation with *V. dahliae* and *P. penetrans*, and far better than in sterilized soil. Soil microbiome changes may be implicated in this, and is subject of current study. Initial results of applying our qPCR tools in the field in the 2023 crop season show tuber yields were negatively correlated with pathogen levels in soil between widely different fields. Multiple samples from within a highly-variable field showed significant correlation of qPCR and traditional nematode microscopic counts. Correlation was poor across multiple fields and from different diagnostic labs, however, which may indicate lesser specificity of the microscopic counts, and this is currently subject to ongoing testing to resolve this difference.

Session B: Pathogen detection and disease management

15:10-15:30

Current trends in detection and identification of plant pathogenic bacteria.

X. LI, J. CHUAN, Q. YANG, J. NIE, P. MAXWELL AND W. CHEN. (X.L., J.C., Q. Y., J., N., P.M.) *Canadian Food Inspection Agency, Charlottetown Laboratory, 93 Mount Edward Road, Charlottetown, PE, Canada; (W. C.) Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, 960 Carling Ave, Ottawa ON, Canada*

NGS and WGS-based bioinformatics analyses has become a spotlight, gradually integrating into diagnostic and post-entry quarantine programs to prevent the introduction of invasive and regulated plant pathogens. In general, NGS and associated bioinformatics approaches for plant pathogenic bacteria and fungi are less efficient for direct applications on regulated samples and commodities due to huge chromosome sizes. A few web-applications on WGS based taxonomy, including Life Identification Numbers (LINS), Microbial Species Identifier (MiSI), Microbial Genomes Atlas (MiGA) and Genome Taxonomy Database (GTDB) are available for general biodiversity investigation and microbial identification using genome sequence data. However, none of these online systems are efficient in time and computing resources for differentiating plant pathogens at interspecies and intraspecies levels. At the Charlottetown Laboratory, the PolyChrome (PC) system and the Clasnip platform (www.clasnip.com) were developed for the early detection and identification of bacterial and fungal pathogens. The PolyChrome system, is comprised of two command-line pipelines (PCC and PCD), an integrated state-of-the-art bioinformatics software and a high-quality genomic reference database. The analysis system allows for timely and accurate detection and identification of high-risk pathogens at the species/subspecies levels, such as *Clavibacter sepedonicus, Ralstonia solanacearum,* and *Synchetrium endobioticum*. The Clasnip platform is a web-based platform to classify pathogens and their close relatives based on SNPs using PCR amplicon or whole-genome sequences. It was developed to allow users with minimum bioinformatics background to compare SNPs with curated, high-quality reference databases. Clasnip is available for identifying bacterial ring rot and brown rot pathogens of potato.

Session B: Pathogen detection and disease management

15:30- 15:50

Battling Fusarium spp. with iChip: A Novel Approach to Biopesticide Discovery.

L. K. GAUTHIER, C. W. KIRBY, A. FOSTER, B. WAGNER. *(L.G., C.W.K., A.F.) Charlottetown Research and Development Center, Agriculture and Agri-Food Canada (AAFC)*, *440 University Ave, Charlottetown, PE, C1A 4N6;* and *(L.G., C.W.K, B.W.) Department of Chemistry*, *University of Prince Edward Island, 550 University Ave, Charlottetown, PE, C1A 4P3.*

An ichip culturing device was used to isolate novel biopesticidal microorganisms from high disease pressure soil. Culturing environmental organisms using an ichip has been shown to increase the recovery rates of novel microorganisms by providing a period of domestication in-situ before culturing in traditional laboratory conditions. We hypothesize that microorganisms able to survive in heavy disease pressure soil exhibit mechanisms that inhibit the growth of the pathogen, making them promising biopesticide candidates. Using soil taken from the artificially inoculated *Fusarium* nursery at the AAFC Harrington Experimental Farm in PEI, bacteria were isolated using an ichip, identified by total genome sequencing and comparison to known species by Tetra correlations, and subsequently subjected to competition assays against *Fusarium gr*. Results from this work exploring a *Fusarium* nursery as an untapped source of novel biopesticides using an ichip will be discussed.

Session B: Pathogen detection and biopesticide discovery

15:50-16:10 Ali's presentation (virtual presentation)

Application of fungal endophytes isolated from apple (*Malus domestica*) trees for apple replant disease management

S. ALI, M. ROY and A. WALKER *(S.A., M. R.) Kentville Research and Development Centre, Agriculture and Agri-food Canada, 32 Main Street, Kentville, NS B4N 1J5;* (M. *R., A. W.) Department of Biology, Acadia University, 33 Westwood Avenue, Wolfville, NS, B4P 2R6*

Apple Replant Disease (ARD) refers to the poor growth of young apple trees (*Malus domestica*), replanted on an old orchard site that was previously used to cultivate apple or related plant species. Additionally, ARD reduces fruit yield and delays fruit bearing that causes economic losses to the growers. The restriction and deregistration of some chemical fumigants, the conventional way to address ARD in the past, has created a demand for environmentally friendly alternative treatments. We have explored fungal endophytes from healthy, mature apple roots as potential biocontrol agents to manage ARD. Forty-eight fungal endophytes were isolated from apple root and tested in dual culture assays for inhibitory properties against ARD causing pathogens such as *Pythium ultimum* and *Rhizoctonia solani*. Several endophytes were able to inhibit pathogens growth to some extent and different types of endophyte-pathogen interactions were observed. From the results of these assays, five biocontrol candidates were selected for further investigation, including two *Trichoderma* species, a *Talaromyces* sp., a *Mortierella* sp. and a *Gongronella* sp. Culture filtrate from these isolates demonstrated a range of inhibition against four ARD causing pathogens, with *Mortierella* NS-01 inhibiting all four pathogens to the greatest extent. In trials with micropropagated apple rootstocks, inoculation of *Talaromyces* NS-01 and *Mortierella* NS-01 in combination resulted in greater apple rootstock height compared to controls, indicating potential growth promoting effects. The five biocontrol candidates were also tested for phosphate solubilization ability, fungicide tolerance, optimal growth temperature and range of inhibitory potential against diverse microbes.

Appendix

Participants of CPS Atlantic Region Hybrid Meeting 2023

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