

March 23-24, 2021



CONSPECTUS



NORTHEAST POTATO TECHNOLOGY FORUM - 2021

INTRODUCTION

The Northeast Potato Technology Forum is an annual event which together brings together potato specialists from northeastern North America to discuss potato research and promote collaboration and information exchange. The twenty-seventh annual Northeast Potato Technology Forum was held virtually on March 23-24, 2021 due to the COVID19 pandemic.

A total of 28 oral scientific presentations were grouped by subject matter into four sessions. Presentations consist of a wide range of topics including pest management, pathogen detection and characterization, host genetics and host/pathogen interactions, microbial dynamics, agronomy, nutrition and weed science. The research represented by these presentations forms an important part of the on-going development of the potato industry in the northeast region.

Many thanks to the session chairs, presenters and all who participated in the Forum 2021. We would like to thank our sponsors McCain Foods Ltd, AIR Fungal disease prevention program, Syngenta, Bayer, Corteva Agriscience, Potatoes New Brunswick, New Brunswick Department of Agriculture, Aquaculture and Fisheries and Agriculture and Agri-Food Canada.

Local Chair: Claudia Goyer

Local Organizing Committee: Claudia Goyer, Kyle Gardner, Jess Vickruck, Khalil Al-Mughrabi and Mathuresh Singh

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2021 NORTHEAST POTATO TECHNOLOGY FORUM

March 23 and 24, 2021

Tuesday, March 23, 2021

1:00 pm Welcome

Session 1: Agronomy

Moderator: Claudia Goyer (Agriculture and Agri-food Canada)

- 1:15 Potato Response to Struvite in Comparison with Conventional Phosphorus Fertilizer in Eastern Canada.
 Judith Nyiraneza*, Rim Benjannet, Lotfi Khiari, Athyna Cambouris, Keith Fuller, Sheldon Hann and Noura Ziadi
- 1:30 Examining the Effect of Fall-Seeded Cover Crops Before Potatoes on Soil Health and Marketable Yield of Potatoes
 Ryan Barrett* and Morgan McNeil
- 1:45 Long-Term Effects of Different Potato Cropping Systems on Soil and Crop Health and Productivity
 Robert P. Larkin
- 2:00 Screening of Potential Trap Crops for Management of Powdery Scab in Potato Production
 Mohammad Islam* Kamrun Nahar, Xianzhou Nie, Keenan Kavanaugh, Gefu Wang-Pruski, Mathuresh Singh, And Dahu Chen
- 2:15 Effect of Biofumigation and Fumigation on Population Density of Root-Lesion Nematodes, *Verticillium dahliae* and Potato Yield in New Brunswick
 Dahu Chen*, Louis-Pierre Comeau, Tom Dixon, Claudia Goyer, Kamrun Nahar, Mohammad Islam, Bernie Zebarth
- 2:30 BREAK

Session 2: Pathology

Moderator: Mathuresh Singh (Agricultural Certification Services)

 2:45 Extreme Resistance to Potato Virus A in Potato Cultivar Barbara is Independently Mediated by Ra and Rysto
 Wei Huang, Bihua Nie, Zhen Tu1, Chunyan Li, Agnes Murphy, Mathuresh Singh, Botao Song, Shu Zhang, Conghua Xie, *Xianzhou Nie

- **3:00** A new scheme for detecting viruses and viroids in the Potato Post Entry Quarantine program NGS screening followed by PCR confirmation **Huimin Xu* and Desmond L Hammill**
- 3:15 Update on PVY Control in New Brunswick and Recent Field Trials of Mineral Oil, Insecticidal and Biological Control Agents for PVY Management **Tyler MacKenzie*, Mathuresh Singh, Xianzhou Nie**
- **3:30** Development of sensitive and cost effective diagnostic procedures for detecting and identifying viral pathogens carried by true potato seeds (TPS). **Desmond Hammill* and Huimin Xu**
- 3:45 The Interspecies and Intraspecies Relationship among Liberibacter Spp. Xiang Li (Sean)*, Aiguo Zhou, Jingbai Nie, and Jiacheng Chuan (Eric)
- 4:00 Development of PCR-based diagnostic procedures for detecting eight viruses and one viroid in potato in vitro plantlets
 Shuchen Yan*, Patrick Quilty, Mathuresh Singh, Huimin Xu
- 4:15 Assessment of populations of *Phytophthora infestans* in Canada in 2019 changing tides. MacPhail, R.A.*, Burlakoti, R., Al-Mughrabi, K.I., Daayf, F., Bisht, V., Novinscak, A., Pawanpuneet, R., MacDonald, K., Gregory, D., Crane, B. and Peters, R.D.
- 4:30 Development of High-Resolution DNA Melting Analysis for Simultaneous Detection of Potato Mop-Top Virus and Its Vector, *Spongospora subterranea*, in Soil Xianzhou Nie*, Mathuresh Singh, Dahu Chen, Cassandra Gilchrist, Yasmine Soqrat1, Manisha Shukla, Alexa Creelman, Virginia Dickison, Bihua Nie, Jacques Lavoie, Vikram Bisht
- 4:45 The Transcriptomic Response of Tomato Plants to Potato Zebra Chip Disease Pathogens Jiacheng Chuan (Eric), Aiguo Zhou, Jingbai Nie, Larry Hale, and Xiang Li (Sean)*
- **5:00** Closing remarks for Afternoon 1 session

Wednesday, March 24, 2021

1:00 pm Welcome

Session 3: Soil Amendment and Nutrient Dynamics

Moderator: Kyle Gardner (Agriculture and Agri-food Canada)

- 1:15 The Effects of Chemical Fumigation and Biofumigation on CO₂, N₂O, and Denitrification Emission Rates, the Abundance of Soil Denitrifying Microorganisms, and the Soil Bacterial Diversity
 Louise Sennett*, David L. Burton, Claudia Goyer, and Bernie J. Zebarth
- 1:30 Compost Products Influence Soil Bacterial and Fungal Communities in a Potato Crop Production System Claudia Goyer*, Saraswoti Neupane, Bernie J. Zebarth, David L. Burton, Carolyn Wilson
- 1:45 Evaluation of Greenhouse Gas Emissions and Carbon Capture on New Brunswick Farms Leandro Passarini* and John Russell
- 2:00 Nitrate Leaching as affected by Nitrogen Fertilization in Irrigated Potato Production on Sandy Soils Chedzer-Clarc Clément*, Athyna N. Cambouris, Noura Ziadi, Bernie J. Zebarth, and Antoine Karam

Session 4: Potato Traits and Breeding

Moderator: Kyle Gardner (Agriculture and Agri-food Canada)

- 2:15 Revolutionizing Potato Variety Development for Climate Smart Agriculture Helen Tai*, David De Koeyer, Jonathan Neilson, Martina Strömvik, Kristine Naess, Charles Goulet, Joel van der Schaaf, Helga Miehle, Lukas Mueller, Noelle Anglin, Benoit Bizimungu, Kyle Gardner
- 2:30 Genomic Selection in Potato: Predicting Traits Using Genome-Wide Information Kyle M. Gardner*, Katheryn Douglass, Benoit Bizimungu, Helen Tai, and David De Koeyer
- 2:45 Break
- 3:00 AAFC Potato Breeding Modernization: Screening For Disease Resistance Using DNA Markers
 Robyn Morgan*, Erica Fava, Kyle Gardner, Xianzhou Nie, Helen Tai, David de Koeyer

- 3:15 Achieving More Crop per Drop through High-Throughput Screening of Drought Tolerant Potatoes
 Keshav Dahal* Taylor Gervais, Alexa Creelman, Anne Smith, Xiu-Qing Li, David De Koeyer and Benoit Bizimungu
- **3:30** Reputed Flavours in Heritage Potato Varieties-Implications for research **B. Bizimungu**
- 3:45 How much will periodic drought affects potato growth, yield and tuber quality? Sheng Li*, Yulia Kupriyanovich, Cameron Wagg, Sheldon Hann and Mohammad Islam

Session 5: Epidemiology and Pest Management

Moderator: Jess Vickruck (Agriculture and Agri-food Canada)

- 4:00 Canada-wide assessment of insecticide resistance in the Colorado Potato Beetle, Lepinotarsa decemlineata
 Jess Vickruck*, Ian Scott, Cam Donly, Sheldon Hann, Pamela MacKinley, Sophie Krolikowski, Pier J. Morin & Chandra Moffat
- 4:15 Alternation of Potato Foliar Sugar, Amino Acid, and Glycoalkaloid Concentrations Through Different Nitrogen Fertilization Practices
 Guoqi Wen*, Athyna Cambouris, Noura Ziadi, and Mohamed Khelifi
- 4:30 Population Density of Potato Early Dying Pathogens and Their Potential Effect on Potato Yield in Prince Edward Island and New Brunswick
 Dahu Chen*, Bernie Zebarth, Louis-Pierre Comeau, Kamrun Nahar, Ryan Barrett, And Sebastian Ibarra
- 4:45 Surveillance of Click Beetle (Coleoptera: Elateridae) Populations Across Prince Edward Island, Canada.
 Christine Noronha*, Lorraine Mackinnon, Sebastian Iberra and Carol Banks
- **5:00** Closing remarks for Afternoon 2 session

First Afternoon - Tuesday, March 23, 2021Session 1: Agronomy Abstracts 1:15-2:30 pm

Session 2: Pathology Abstracts 2:45-5:00 pm

Potato Response to Struvite in Comparison with Conventional Phosphorus Fertilizer in Eastern Canada

Judith Nyiraneza¹, Rim Benjannet^{1,2}, Lotfi Khiari², Athyna Cambouris³, Keith Fuller⁴, Sheldon Hann⁵ and Noura Ziadi³

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In acidic soils with high phosphorus (P) fixing capacity, higher P application than the crop requirements are common in high P demanding crops such as potato (Solanum tuberosum L.) which could lead to eutrophication. Recycled sources of P fertilizer such as struvite, can be efficient in meeting P crop demand while minimizing P losses. The objective of this three years (2016-2018) study conducted in four provinces over three years (12 sites in total) in Eastern Canada was to assess the impact of a partial substitution of triple superphosphate (TSP) with struvite on potato yield as well as on soil- and plant based P availability indices. Eight increasing P rates as TSP (0, 26, 52, 79, and 105 kg P ha⁻¹) and three treatments as a mixture of TSP and struvite (25, 50 and 75% struvite) at a rate of 79 kg P ha⁻¹ were applied. The effects of treatments were assessed on total (TY) and marketable yields (MY), P uptake (PU), apparent P recovery (APR), and on Mehlich-3 extracted P (P_{M3}), soil P adsorbed on anion exchange membranes (P_{AEMs}), and petiole P-PO₄ (P_{petiole}) measured at five sampling dates during the growing season. There was a response to P inputs at all sites with the control treatments showing lower potato yield at all sites. Overall potato yield, P_{petiole}, P_{M3} and P_{AEMs} were comparable between TSP at 100% and a its mixture with struvite to supply 79 P kg ha⁻¹ at 3 out of 4 sites with one exception at one site where mixing TSP with struvite at higher proportion was associated with lower value. Our results suggest that overall, the use of struvite could be a sustainable mean to address long-term globally P scarcity.

Examining the Effect of Fall-Seeded Cover Crops Before Potatoes on Soil Health and Marketable Yield of Potatoes

Ryan Barrett and Morgan McNeil

Prince Edward Island Potato Board

As part of the Atlantic Living Labs Initiative, six on-farm trials were established in 2019 with fall-seeded cover crops following primary tillage, in preparation for a potato crop to be planted in the spring of 2020. Establishment dates ranged from August 28th to October 2nd, 2019. A total of eight treatment crops were compared with a no cover crop control across the six fields: three treatments with a spring cereals (barley or oats), four treatments with a brassica crop (mustard, tillage radish, oilseed radish), and one treatment with an oats/mustard mixture.

Trial fields underwent composite soil sampling in the fall of 2019 (before or shortly after cover crop seeding) and in the spring of 2020 (before potatoes were planted). Tests conducted included soil chemical analysis and soil health tests from the PEI Analytical Lab, *Verticillium dahliae* (qPCR) analyzed by Agricultural Certification Services, root lesion nematodes (Baermann pan method) analyzed by the PEI Potato Quality Institute, and soil nitrogen supply analyzed by the Dalhousie Soil Health Lab. In addition, percentage of green cover was measured using the Canopeo smartphone app. A subset of fields was also measured for susceptibility to soil erosion using metal erosion splash pans. In the fall of 2020, a minimum of four 10-foot potato samples were obtained per treatment. These samples were graded by Cavendish Farms Central Grading and contract values were applied based on 2020 variety contracts based on late February 2020 delivery.

Across the six fields, there was no obvious trend for an increase in soil organic matter; however, it was not expected to observe a noticeable increase in organic matter in one year. Five of the eight comparisons of a cover crop treatment with no cover control showed a numerical increase in Active Carbon in the spring of 2020. This was the only soil health metric that appeared to show a noticeable difference after one year of study, though these comparisons are not statistically significant.

Differences for *Verticillium dahliae* and root lesion nematodes between treatment and control were quite variable and field dependent. No consistent trends were obvious from the first year of trial results but will continue to be observed in future years.

There was a wide range in observed percentage ground cover between fields, primarily related to planting date. Dry summer conditions in August 2019 followed by rains associated with Post Tropical Storm Dorian delayed cover crop establishment for some fields, limiting establishment for some crops.

A statistically significant increase in marketable yield of potatoes (p=0.10) was observed for three of the eight cover crop treatments when compared with the no cover crop control. Across all eight treatment/control comparisons, the average marketable yield increase was 24.2 cwt/acre and the increase in crop value was \$425 per acre. This project will continue for two more years.

Long-Term Effects of Different Potato Cropping Systems on Soil and Crop Health and Productivity

Robert P. Larkin

USDA-ARS New England Plant, Soil, and Water Lab, Orono, Maine 04469

Soil health is critical to agricultural productivity, sustainability, environmental quality, and ecosystem function, but may be readily degraded through intensive potato production. Soil and crop management practices beneficial to soil health, such as longer crop rotations, cover crops and green manures, organic amendments, and reduced tillage, may improve soil and crop health when incorporated into cropping systems. However, how to best incorporate various management practices into productive cropping systems has not yet been established. In addition, long-term trials are needed to adequately assess the full impacts and effects of these cropping systems on soil and crop health and productivity. In field trials originally established in 2004, three different 3-yr potato cropping systems focused on management goals of soil conservation (SC), soil improvement (SI), and disease suppression (DS) were evaluated and compared to a standard 2-yr rotation (SQ) and a non-rotation control (PP). Although some modifications have been made to the systems over the years, the core principles have remained, and the trials have now been in place for more than 15 years. Looking at results averaged over the last 4 years of the study (2015-2018), the SI system, which included a history of compost amendments, improved soil properties such as water-holding capacity, organic matter and other nutrient contents, aggregate stability, and CEC, relative to all other systems, as well as maintained higher tuber yields (by 26%) and higher microbial activity (by 44%) relative to the standard SQ system. The DS system, which included a disease-suppressive green manure rotation crop and fall cover crops, also has maintained improved yield (by 16%), higher OM content (by 15%), and increased microbial activity (by 23%) relative to SQ, as well as reducing soilborne diseases (black scurf and common scab) by 10-30%. The nonrotation PP system resulted in notable degradation of soil properties and yield over time whereas the standard SO system maintained soil and crop parameters at somewhat reduced levels. Soil microbial community characteristics, as represented by fatty acid ester methyl ester (FAME) profiles and preliminary molecular analyses of the soil microbiome, also showed distinct differences among the cropping systems. These results demonstrate that soil health management practices can be effectively incorporated into viable potato cropping systems that can improve soil properties and crop productivity, and may enhance longer-term agricultural sustainability and viability.

Screening of Potential Trap Crops for Management of Powdery Scab in Potato Production

Mohammad Islam¹, Kamrun Nahar², Xianzhou Nie², Keenan Kavanaugh³, Gefu Wang-Pruski³, Mathuresh Singh⁴, And Dahu Chen²

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 ⁴Agricultural Certification Services Inc. 1030 Lincoln Road, Fredericton, E3B 8B7

Potato powdery scab caused by Spongospora subterranea is a blemish tuber disease that can result in significant economic loss due to poor marketability of fresh tubers and rejection of potatoes in processing. The powdery scab lesions not only deteriorate tuber quality, but also serve as entry points for secondary infections, leading to tuber rot during storage. Powdery scab pathogen is also responsible for the transmission of potato mop-top virus (PMTV), which in turn causes significant suppression of plant growth and internal tuber necrosis. The life cycle of S. subterranea is complex, including asexual and sexual stages. The asexual zoospores are short-lived, whereas the sexual resting spores can survive in soil for up to 18 years. No effective management strategies are currently available to control this disease. Previously conducted chemical control trials in New Brunswick showed some potential but inconclusive results and thus led to further continuity of research. Besides chemical control, crop rotations also showed reduction in disease pressures, but the conventional crop rotation has limitations to effectively control powdery scab. A few studies showed that some plant roots could be infected by S. subterranea but no resting spores were formed after infection. These plants could be used as a trap crop to reduce the inoculum levels of S. subterranean in soil. However, an appropriate trap crop is not currently known. Screening to identify effective trap crops for New Brunswick cropping systems can provide an important component in the development of effective disease management strategies. Therefore, the two trials presented here were aimed at screening of plant species and their cultivated varieties as potential trap crops for controlling potato powdery scab in growth room conditions. The first study assessed the effects of pathogen inoculum exposure on infection. Germinated plants of different varieties of tomato, red clover, alfalfa, canola, rape and radish were screened at different time points for root infection caused by S. subterranea. Powdery scab inoculum was collected from infected potato tuber surfaces. Seedlings grown in Falcon tubes were inoculated at different time intervals: viz two-, nine-, sixteen- and twenty-three-days after germination. Following that, roots were screened for the presence of pathogen using light microscopy. It was found that roots of two varieties of alfalfa, one variety of each of canola, rape and tomato were potentially susceptible to infection. Delayed inoculum exposure appeared to significantly reduce the presence of pathogen inside the roots. The second study screened crop plants for the development of visible but abnormal root structures, such as root galls, caused by S. subterranea. Nine crops including ten varieties were grown for three months in pots containing S. subterranea infected soils. At maturity, all roots were collected and observed for abnormal root structures. It was found that one variety of rape and one variety of canola formed unusual root structures or galls. Further results will be presented.

Effect of Biofumigation and Fumigation on Population Density of Root-Lesion Nematodes, *Verticillium dahliae* and Potato Yield in New Brunswick

Dahu Chen¹, Louis-Pierre Comeau¹, Tom Dixon², Claudia Goyer¹, Kamrun Nahar¹, Mohammad Islam³, Bernie Zebarth¹

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Potato early dying disease complex (PED) is a major yield-limiting factor for potato production in New Brunswick, as well as in other provinces in Canada. PED is primarily caused by the fungal pathogen Verticillium dahliae, and PED severity is exacerbated by the root-lesion nematode, Pratylenchus penetrans. Management of PED is challenging, because no high resistance potato cultivars are available, both pathogens have a broad host range, the sclerotia of V. dahliae can survive in soil for many years and root-lesion nematodes can readily overwinter under Atlantic winter conditions. In New Brunswick, a two-year potato-cereal crop rotation is most common, but is not effective in controlling PED. Soil fumigation with either metam sodium or chloropicrin is commonly applied in the United States and some other countries with effectiveness in controlling PED, but it is not commonly practiced in New Brunswick. Chloropicrin was demonstrated to reduce visual PED severity and increase tuber yield in some observational field scale trials in New Brunswick, but its effect on pathogen population density and potato yield were not well studied. Concerns over potential negative effects of chemical fumigants on human health, environment, and soil health, as well as high cost of fumigation, have increased interest in alternative strategies to soil fumigation to manage PED. Biofumigation using high glucosinolate-containing mustard crops, as an optional to chemical fumigation, showed its potential in managing PED and other soil borne pests, but its effectiveness needs to be evaluated under New Brunswick potato production systems. In the present study, two trials were conducted to examine the potential of using 'Centennial Brown' brown mustard as a biofumigant crop to control PED in commercial fields with a history of PED in New Brunswick. Trial one (2017-2018) was conducted in a field which had never been previously fumigated and had greater pathogen pressure, whereas trial two (2019-2020) was conducted in a field with lower pathogen pressure which had previously been fumigated once in 2017. Three treatments were implemented in 2017 and 2019: 1) spring barley to represent conventional management, 2) spring barley plus fall Chloropicrin fumigation, and 3) two crops per year of brown mustard as biofumigation. Potatoes were grown in 2018 and 2020. Composite soil samples were taken to quantify the pathogen levels in the spring prior to planting rotation crops and potatoes, and in the fall after crop harvest. Chloropicrin significantly reduced the Verticillium density in the treated hills prior to planting potato, whereas biofumigation did not reduce the Verticillium density. Both biofumigation and Chloropicrin fumigation significantly reduced root-lesion nematodes in the two trials. In trial one, both biofumigation and fumigation significantly increased tuber yield compared with the control, but in the trial two, only the fumigation treatment increased the tuber yield. Results indicate that both Chloropicrin fumigation and mustard biofumigation have a potential to suppress the PED pathogens and increase the potato yield in fields with high PED pathogen pressure.

Extreme Resistance to Potato Virus A in Potato Cultivar Barbara is Independently Mediated by *Ra* and *Ry*_{sto}

Wei Huang¹, Bihua Nie^{1*}, Zhen Tu¹, Chunyan Li¹, Agnes Murphy², Mathuresh Singh³, Botao Song¹, Shu Zhang⁴, Conghua Xie¹, Xianzhou Nie²

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Potato virus A (PVA) and potato virus Y (PVY) are two of the most economically important viruses of potato worldwide. Host resistance offers the most effective means for the control and/or management of the viruses. In this study, 20 potato cultivars/breeding clones were screened for their resistance against PVA and PVY by mechanical and/or graft inoculation assay. Six cvs./clones, including Barbara, Jizhangshu 8, Longshu 7, Longshu 8, M6, and Solara, were found to be extremely resistant to both PVA and PVY; three cvs./clones (AC142, Eshu 3, and Shepody) were deemed to be extremely resistant to PVA but susceptible to PVY. To further reveal the inheritance of the extreme resistance (ER) against PVA, a tetraploid F₁ population of Barbara × F58050 and a tetraploid BC₁ population of BF145 (a PVA-resistant but PVYsusceptible progeny of Barbara × F58050) × F58050 were obtained and analyzed. Based on the phenotype of all progenies, two independent loci were found to control ER against PVA in Barbara: one confers ER to both PVA and PVY, and the other confers ER to PVA only. The deduced genotype of Barbara is *RyryryryRararara*.

A new scheme for detecting viruses and viroids in the Potato Post Entry Quarantine program – NGS screening followed by PCR confirmation

Huimin Xu* and Desmond L Hammill

Canadian Food Inspection Agency, Charlottetown Laboratory, 93 Mount Edward Road, Charlottetown, PE, Canada, C1A 5T1

The direct importation of tuber-producing species of *Solanum*, either as true seed or plant parts for vegetative propagation, is prohibited from all countries and some regions of the United States of America. But, small quantities of germplasm may be introduced into Canada as tissue culture microplants or tubers for propagation. Potato germplasm approved for entry under a Permit to Import must be subjected to a process of quarantine testing conducted at the Potato Post Entry Quarantine (PPEQ) facility of Canadian Food Inspection Agency, Charlottetown Laboratory (CL) in Charlottetown, Prince Edward Island. Methods employed presently for potato quarantine testing include Bioassay, Reverse polyacrylamide gel electrophoresis (R-PAGE), Real-time quantative polymerase chain reaction (qPCR), Reverse transcription PCR (RT-PCR) and visual inspection of plants grown from microplantlet for disease symptoms. Culture of microplantlet tissues on various media is performed for detecting bacteria and fungi. Grafting is occasionally performed using tomato and potato plants for confirming some non-mechanically transmissible pathogens. The next generation sequencing (NGS) technologies, since first published in 2009, have led to a revolution in virus discovery and exciting new possibilities for diagnosis of viruses and other organisms. The application of parallel sequencing approaches, and subsequent bioinformatic analysis for viral sequences, carries the promise of routine, generic detection of viruses and other pathogens alike. NGS technology can provide a rapid and sensitive methodology to reveal all pathogens present in one test sample. This feature makes NGS a perfect and powerful screening tool for plant quarantine testing. In recent years, efforts have been made in Charlottetown Laboratory to explore the potential applications of NGS technology as a sensitive, specific and cost-effective tool to reveal a wide range of viral and viroid pathogens in a test sample. Reliable procedures have been developed and optimized for the extraction of nucleic acids of high quality, construction of cDNA libraries, manipulation of raw NGS data and contig assembles. Millions of reads were generated in each NGS run without any prior knowledge of pathogen in the test sample and the sequence data obtained allowed a reliable detection of viral or viroid pathogens at low levels. The NGS procedures/workflows developed were validated using bioassay, pathogenicity and PCR amplification. Identification of host (potato) genome sequences was used as a reference to verify the NGS workflow. The new approach – NGS screening followed by PCR confirmation has been employed successfully in the CFIA PPEO program and detected common and quarantine viruses in over a dozen of potato accessions since 2018. The application of NGS can significantly reduce the time and cost for conducting quarantine testing.

Update on PVY Control in New Brunswick and Recent Field Trials of Mineral Oil, Insecticidal and Biological Control Agents for PVY Management

Tyler MacKenzie^{1*}, Mathuresh Singh¹, Xianzhou Nie²

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New Brunswick (NB) is an important regional producer of seed potatoes, mainly centered in the upper Saint John River valley alongside the large potato growing region of northeastern Maine, USA. Potato virus Y (PVY) is an important disease agent in this cross-border industry, that has been a major focus of management over the past decade. Since 2009, average post-harvest PVY in NB seed lots dropped from 11.8% to less than 1%, with a record low of 0.43% in 2016. A resurgence in 2017-18 doubled mean PVY level across NB, which has only slowly dropped to 0.55% by 2020. Statistical modeling shows that in recent years, PVY inoculum in seed and early-season aphid abundance are strong predictors of post-harvest PVY level, with April temperatures explaining much of the remaining variation - especially in the outbreak of 2017 following an unusually warm April. The ca. 20-fold reduction in average PVY in the industry occurred through an increasingly strict provincial post-harvest testing program, and evolving evidenced-based in-field management to reduce its spread on the farm. Another important development over the past decade is a substantial change in dominant strains of the virus. Since 2009, PVY strain dominance shifted from the traditionally common and easily recognized PVY^o strain, to the more visually cryptic and potentially more transmissible PVY^{N:O}, PVY^{N-Wi} and in particular PVY^{NTN} strains. Impact of these new dominant strains on the statistical relationships between post-harvest PVY, aphids and planted virus inoculum has become a focus of ongoing study.

ACS Inc (PotatoesNB) has also maintained an ongoing research project to determine best management practices for reducing PVY spread in the field. Since 2018, we have studied a range of alternative foliar sprays to interfere with aphid-vectored transmission of PVY in experimental trials at the Fredericton Research and Development Centre (AAFC). These sprays include a range of individual and combined mineral oil, chemical insecticide and biological treatments, and were compared to maximize PVY protection, while minimizing costs and environmental impact. This study confirmed the strong synergistic effect of combined oil and insecticide spray, and showed increased retention of insecticide residue on foliage when mixed with oil as a hypothesized explanation for the enhanced PVY protective effect. Another objective was to find similarly effective and low-cost alternatives for the widely used and effective lambda-cyhalothirn (i.e.: Silencer, Matador) insecticide, which came under PMRA review for possible banning in Canadian food crops. We have determined a promising low-cost alternative insecticide is deltamethrin (i.e.: Decis), which provided similar protection against PVY spread, no yield impact, consistent effect over several seasons and an agent most NB growers have experience with. A non-chemical, cost-competitive biological treatment (i.e.: LifeGardWG), which works by sensitizing the natural defense mechanisms of the plant, showed significant reduction in PVY spread - with and without supplemental insecticides - similar to or better than some of the conventional insecticide treatments. However, the biological-treated plots showed slightly lowered tuber yield. More general recommendations on spray program management, rogueing and volunteer and weed management will be discussed in concluding the presentation.

Development of sensitive and cost effective diagnostic procedures for detecting and identifying viral pathogens carried by true potato seeds (TPS).

Desmond Hammill* and Huimin Xu

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Over 50 viruses and 1 viroid have been known to infect potato plants naturally. Some of these viruses are considered to be extremely destructive and are regulated as quarantine pathogens. The Canadian Food Inspection Agency (CFIA) is responsible for the Seed Potato Certification Program and other policy directives to prevent the introduction and spread of diseases and regulated quarantine pests of potatoes in Canada. This includes the Potato Post-Entry Quarantine (PPEQ) program which tests microplants and mini-tubers for as many as 11 viruses and 1 viroid. The Seed Potato Certification Program is also responsible for nuclear stock certification. True potato seeds (TPS) can currently enter Canada without the need for quarantine testing if a phytosanitary certificate is provided based on the absence of disease in the country of origin. Recently, there has been an increased demand for the importation of TPS to Canada due to the fact that most known common potato pests cannot be transmitted by TPS which enables them to avoid guarantine testing. There are, however, 8 known non-common viruses (to Canada) and a viroid that can be transmitted by TPS. They are known as Alfalfa mosaic virus (AMV), Andean potato latent virus (APLV), Arracacha virus B (AVB), Potato virus T (PVT), Potato yellowing virus (PYV), Tobacco ringspot virus (TRSV), Tomato black ring virus (ToBRV), Tobacco streak virus (TSV), and Potato spindle tuber viroid (PSTVd). ELISA has been used to detect TPS-borne pathogens but has not been shown to be reliable. RT-PCR protocols have been established for some of these targets based on leaf samples - but not TPS. The CFIA is attempting to develop, validate, and implement molecular based diagnostic procedures for sensitive and reliable detection of TPS pathogens for surveillance testing upon arrival of imported TPS. The goals of this project is to identify extraction, amplification, and confirmation procedures using RT-PCR and RT-qPCR for detecting these pathogens to prevent their possible entry into Canada for the protection of Canadian seed potato production.

The Interspecies and Intraspecies Relationship among Liberibacter Spp.

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Zebra Chip (ZC) is a potato disease first discovered in Mexico, 1994. The disease caused severe economic impacts to the potato industries in USA, Mexico, New Zealand and other countries. The infected potato plants exhibit plant stunting, shortened internodes, yellowing and upward curling of leaves, pinkish discoloration, and growth of lateral shoots and aerial tubers, leading to plant wilting and sudden death. The infected potato tubers often display collapsed stolons, browning of vascular tissue concomitant with necrotic flecking of internal tuber tissues, which result in severe internal necrosis of potato tuber tissue that becomes dark blotches, stripes, or streaks after being processed into chips. The ZC pathogen was first identified as Candidatus Liberibacter solanacearum (CLso) by Lifting et al in 2008. Currently, there are six species as the members of the genus Liberibacter which mostly are plant pathogens transmitted by psyllids. 'Can.Liberibacter asiaticus, 'Can L. americanus' and 'Can. L. africanus' are causative agents of Huanglongbing disease (HLB), also known as citrus greening disease. The only cultivated species is *Liberibacter crescens* isolated from papaya growing in Puerto Rico. For CLso, haplotypes A and B (Nelson et al 2011) of CLso were revealed in USA as the pathogen of potato, tomato, pepper, eggplant and other Solanaceous plants, whereas haplotypes C and D was found to infect Apiaceous crops such as carrot, celery and leek in European countries. To date, eleven haplotypes of CLso have been identified around the world, including A, B, C, D, E, F, G, H, U, Cras1, and Cras2. Different haplotypes demonstrate variations in pathogenicity and virulence to distinct host plants. So far, CLso haplotype B is lethal to both potato and tomato plants, while haplotype A is lethal to potato but not to certain tomato varieties. So far, no resistant or tolerant varieties are discovered in potato, but some tomato landraces from Mexico demonstrated resistance or tolerance to CLso (Garzón-Tiznado et al. 2019). We believed that the virulence variations in tomato between haplotypes A and B may be potentially useful characteristics for developing stable resistance varieties of tomato and potato. Current haplotype system for intraspecies classification are based on the Multi-Locus Sequencing Typing (MLST) of 50S ribosomal protein (rplJ/rplL) gene, the 16S rDNA, and the 16S-23S intergenic spacer region sequences reflecting the geographic distribution and host specificity. There are eleven haplotypes of 'Ca. Liberibacter solanacearum' were described. Only haplotypes A and B, as well as a recentlydescribed haplotype F cause potato zebra chip disease and other disorders in solanaceous crops, and the biological characteristics of haplotype F were not clearly illustrated in comparison with haplotypes A and B.

Recent observations indicated that all potato varieties tested are susceptible to '*Can. Liberibacter solanacearum*' haplotypes A and B, and there were no resistance and tolerance potato varieties against potato zebra chip disease so far. However, study revealed that '*Ca. Liberibacter solanacearum*' haplotypes A and B displayed obvious variations in virulence on tomato plants. In general, CLso haplotype B causes tomato plant yellowing and plant decline leading to the plant death, while CLso haplotype A sometimes causes no obvious symptoms in some of the tomato varieties such as cv Moneymaker. Tomato plants (cvs Moneymaker and Roma) infected with CLs were maintained for up to five years with regular trimming off the flowering branches, while CLso haplotype A was consistently present in symptomless tomato plants. A recent observation (Garzón-Tiznado et al. 2020) indicated that some tomato landraces in Mexico may be considered resistant to CLso, resulting less symptom severity, relative lower CLsoB titers and longer incubation time relative to the other genetic traits. These resistant landraces are promising sources for developing resistance variety against CLso.

Development of PCR-based diagnostic procedures for detecting eight viruses and one viroid in potato *in vitro* plantlets

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The Canadian Food Inspection Agency implements the Nuclear Stock Certification Program to ensure the production of high-quality and disease-free seed potatoes. Currently, this program employs double and triple antibody sandwich enzyme-linked immunosorbent assays (DAS- or TAS-ELISA) and return-polyacrylamide gel electrophoresis (R-PAGE) for detecting the targeted viruses and Potato spindle tuber viroid (PSTVd), respectively. Pathogen-specific antibodies for ELISA are commercially available for detecting Potato virus M (PVM), Potato mop-top virus (PMTV), Potato latent virus (PotLV), Potato leafroll virus (PLRV), Potato virus Y (PVY), Potato virus S (PVS), Potato virus A (PVA), and Potato virus X (PVX). However, the aforementioned methods are highly labour-intensive and time-consuming procedures with low sensitivity that require large sample inputs for screening. Moreover, both methods are involved with extensive experimental procedures and only allow for the screening of one pathogen each time, which further prolongs and complicates the overall diagnosing process. In this study, multiplex PCR-based procedures were developed and validated to index the potato nuclear stock materials simultaneously in a qualitative way ("positive" or "negative"). Two mxRT-PCR (multiplex RT-PCR) and three mxRT-qPCR (multiplex real-time quantitative RT-PCR) procedures were developed for primary screening and confirmatory testing of all targeted pathogens under this program, respectively. As little as 1.0 µl of tissue sap from a microplant (in vitro plantlet) or 1.0 pg of total RNA extract was sufficient for reliable RT-PCR detection. Additionally, virus-specific RNA could be detected in RNA extracts with almost no non-specific amplification in the presence of other viral RNAs. The use of potato genome-specific primer set as an internal control provided a reference for assessing the quality of the RNA extracts and the amplification of the targeted RNAs. Furthermore, the genomes of virus and viroid isolates or strains used in this research were verified using the next-generation sequencing (NGS) technology to ensure the accuracy of the RT-PCR primers employed. All tests conducted using the mxRT-PCR and mxRT-qPCR procedures were validated using another diagnostic assay and known/unknown microplants.

Overall, the developed and validated standard multiplex PCR-based procedures in this study profoundly improved the sensitivity, specificity, efficiency, and feasibility with reductions in time and labour expenses for routine diagnostic testing of the nine targeted pathogens under the Nuclear Stock Certification Program compared to that of the currently employed ELISA and R-PAGE methods. Subsequently, the multiplex RCR-based procedures involved in this study are ready for implementation into the Nuclear Stock Certification Program.

Assessment of populations of *Phytophthora infestans* in Canada in 2019 – changing tides.

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Late blight, caused by *Phytophthora infestans*, is an important disease of both potatoes and tomatoes in Canada. In recent years, tomatoes in home gardens infected with the US-23 strain of the pathogen, have been important sources of inoculum for infection of adjacent commercial potato fields. A national study to determine the strains of *P. infestans* present in Canada, and some of their characteristics, is being conducted. In 2019, late blight was absent in much of Canada due to the warm, dry conditions, but some disease was found in potatoes and tomatoes in British Columbia (BC). In total, 89 isolates of P. infestans were obtained from 40 samples of potato and 49 samples of tomato in BC in 2019. Isolates were assessed for mating type, sensitivity to metalaxyl-m and allozyme banding pattern at the glucose-6-phosphate isomerase (GPI) locus. Most isolates were resistant to metalaxyl-m (19 highly-resistant; 65 moderatelyresistant), with only 5 isolates showing sensitivity. GPI assessments of selected isolates showed that isolates from tomato (42) banded as 100/100 (18 isolates) or 100/100/111 (24 isolates), whereas isolates from potato (37) banded as 100/100 (10 isolates), 100/111/122 (3 isolates), or 100/100/111 (24 isolates). Tests to determine the mating type of the 2019 isolates are on-going. Subsequent research will include further strain characterization using established molecular protocols as well as experiments on host preference and pathogenicity of the isolates.

Development of High Resolution DNA Melting Analysis for Simultaneous Detection of Potato Mop-Top Virus and Its Vector, *Spongospora subterranea*, in Soil Xianzhou Nie^{1*}, Mathuresh Singh², Dahu Chen¹, Cassandra Gilchrist^{1,3}, Yasmine Soqrat^{1,4}, Manisha Shukla¹, Alexa Creelman¹, Virginia Dickison¹, Bihua Nie^{1,5}, Jacques Lavoie⁶, Vikram Bisht⁷

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In this study, a set of duplex reverse transcription (RT)-PCR-mediated high resolution DNA melting (HRM) analyses for simultaneous detection of potato mop-virus (PMTV) and its protist vector, Spongospora subterranea f.sp. subterranea (Sss), was developed. The infestation of soil by PMTV was detected by using a tobacco-based baiting system. Total RNA extracted from the soil led to successful RT-PCR gel-electrophoresis detection of both PMTV and Sss. To facilitate more efficient detection, newly designed primer pairs for PMTV RNA species (i.e., RNA-Rep, -CP, and -TGB) were analyzed together with the existing Sss primers using real-time RT-PCR. The resulting amplicons exhibited melting profiles that could be readily differentiated. Under duplex RT-PCR format, all PMTV and Sss primer combinations led to successful detection of respective PMTV RNA species and Sss in the samples by high resolution DNA melting (HRM) analyses. When the duplex HRM assay was applied to soil samples collected from six fields at four different sites in New Brunswick, Canada, positive detection of PMTV and/or Sss was found in 63-100% samples collected from fields in which PMTV-infected tubers had been observed. In contrast, the samples from fields where neither PMTV- nor Sss-infected tubers had been observed resulted in negative detection by the assay. Bait tobacco bioassay for PMTV and Sss produced similar results. Between 63%-83% and 100% of the soil samples collected from PMTV-infested fields led to PMTV and Sss infections in the bait tobacco plants, respectively; whereas no PMTV or Sss infected plants were obtained from soil samples collected from PMTV/Sss-free fields.

The Transcriptomic Response of Tomato Plants to Potato Zebra Chip Disease Pathogens

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Zebra Chip is a potato disease first discovered in Mexico, 1994. It caused severe economic impacts to the potato industries. The pathogen Candidatus Liberibacter solanacearum (CLso) was first identified and described in New Zealand, 2008. It has been found that CLso can also infect Solanaceous and Apiaceous crops, such as tomato, carrot, pepper, eggplant, tamarillo, tobacco, celery and leek. Until now, eleven haplotypes of CLso have been identified around the world, including A, B, C, D, E, F, G, H, U, Cras1, and Cras2. Different haplotypes have variations in pathogenicity to distinct host plants. For example, CLso haplotype B is lethal to both potato and tomato, while haplotype A is lethal to potato but not to tomato. Although pathogenicity variation is observed, its mechanism is not well studied. In this study, we aim to discover the underlying mechanism of CLso pathogenicity by analyzing the transcriptomic response of tomato plants to CLso haplotypes A and B.Total DNA and RNA were extracted from ten tomato plants infected by CLso haplotype A, four tomato plants infected by haplotype B, and eleven healthy tomato plants. Haplotype was confirmed by PCR using C.li.po.F and O12c primer set followed by Sanger sequencing of the PCR amplicons. NGS sequencing Libraries were generated from total RNA using Illumina TruSeq Library Preparation Kit, and RNA-Seq data were then generated using Illumina MiSeq. Tomato SL4.0 genome data and ITAG4.1 annotation data were downloaded from Sol Genomics Network. Atria v0.1.0 was used to trim adapter sequences and low-quality reads. Salmon v0.12.0 was used for transcript quantification. DESeq2 was used to find differentially expressed genes (DEGs). Then, Gene Ontology (GO) and KEGG pathways were enriched using DEGs and visualized with ClusterProfiler. In total, 9913 transcripts have enough coverage. Among those, 138 genes are upregulated, and 331 genes are downregulated, comparing haplotype B to A. Healthy tomato plants and plants infected by haplotype A have similar expression levels, which is consistent with the fact that CLso haplotype A does not show obvious symptoms on tomato plants. GO enrichment analysis indicates that CLso haplotype B significantly affects hosts' carbohydrate metabolism, cell wall organization or biogenesis, and hydrolase activities. Starch accumulation is significantly affected in plants infected by pathogenic CLso. Specifically, genes related to photosynthesis were generally downregulated in tomato plants infected by CLso haplotype B. As the result, carbon fixation is compromised. Concurrently, enzymes catalyzing the biosynthesis of starch from glucose are also downregulated, while amylolysis genes are upregulated. The alternations indicate that carbohydrate consumption in affected plants is greater than accumulation. In potatoes, starch formation and accumulation affects tuber sizes, which directly influence potato yield and profit. Potato tubers infected by CLso caused the conversion of potato starch to water-soluble sugars, which develop discoloration along the vascular tissue, turning the chips to unsightly dark blotches, stripes, or streaks after cooking. Understanding the pathogenicity and virulence mechanism of CLso can enhance the disease control and create opportunity for breading resistant or tolerant varieties.

Second Afternoon – Wednesday, March 24, 2021

Session 3: Soil Amendment and Nutrient Dynamics 1:15-2:45 pm

Session 4: Potato Traits and Breeding 3:00-4:00 pm

Session 5: Epidemiology and Pest Management 4:00-5:00 pm

The Effects of Chemical Fumigation and Biofumigation on CO₂, N₂O, and Denitrification Emission Rates, the Abundance of Soil Denitrifying Microorganisms, and the Soil Bacterial Diversity

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Chemical fumigation and biofumigation are used to reduce soil-borne diseases; however, nontargeted microorganisms involved in essential soil processes, such as the soil nitrogen (N) cycle, may also be affected. This study compared biofumigation and chemical fumigation for their effects on 1) key soil N processes, 2) soil bacterial diversity, and 3) the abundance of key N-related microorganisms. Six treatments were examined: chemical fumigation with either chloropicrin, or metam sodium (MS), a combination of MS plus barley plant residues, biofumigation with mustard plant residues, barley plant residues, and an untreated control. Soil microcosms were incubated for 160 days under controlled conditions. The mustard residues did not inhibit soil nitrification, whereas chemical fumigation with MS (with and without barley) and chloropicrin inhibited soil nitrification for 16 and 64 days, respectively. Only treatments with organic carbon addition (mustard residues, barley residues, and MS+Barley) significantly increased CO₂, N₂O, and denitrification emission rates. Chemical fumigation with chloropicrin increased N₂O emission rates; however, it did not increase denitrification rates. Chemical fumigation with chloropicrin was the only treatment that significantly reduced nitrifier gene abundance compared to the control; however, chloropicrin, MS, and MS+Barley significantly decreased nitrifier gene abundance compared to the mustard residues. The mustard residues, MS, and MS+Barley did not significantly alter the abundance of denitrifying genes, whereas chloropicrin reduced the abundance of several denitrifying genes. The mustard residues significantly reduced the Shannon-Weaver, Chao1 richness, and Pielou's evenness diversity indices at early time-points, whereas chemical fumigation with chloropicrin reduced all three diversity indices at the end of the incubation. In contrast, MS and MS+Barley did not affect the diversity indices throughout the entire incubation. After 160 days, the bacterial beta-diversity of all the treatments was significantly different from the control, with chloropicrin exhibiting the greatest change in bacterial community composition. These results suggest that biofumigation with mustard residues have a greater effect on greenhouse gas emissions, whereas chemical fumigation, especially with chloropicrin, had a greater impact on nitrification, nitrifier and denitrifier gene abundance, and the bacterial community compared to biofumigation.

Compost Products Influence Soil Bacterial and Fungal Communities in a Potato Crop Production System

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The soil quality in potato fields of New Brunswick and Prince Edward Island is declining due to intensive production practices resulting in loss of soil organic matter (SOM). The addition of compost may be an effective means to rapidly increase SOM and soil quality, and may also influence soil microbial community diversity. This study compared three contrasting compost products with a no compost control on soil bacterial and fungal community diversity and soil physico-chemical properties. The composts consisted of municipal source separate waste compost (SSOC), forestry and poultry manure compost (FPMC) and forestry residues waste compost (FRC) with low, medium and high forestry wastes, respectively. The composts were applied at a rate of 45 Mg ha⁻¹ dry weight to field plots in October 2014, before the 2015 potato crop. Soil samples were collected in October 2014 (two weeks after compost application), May 2015, July 2015 and September 2015. The diversity of bacterial and fungal communities was determined using Illumina MiSeq Next-Generation sequencing targeting the V4 region of 16S rRNA gene and ribosomal internal transcribed spacer (ITS) region, respectively. Application of composts changed the soil physico-chemical properties including soil pH, total N and organic carbon pools. The wide differences in the composition of compost products resulted in different effects on the soil organic C pools. Application of the compost products to soil influenced the relative abundance of several bacterial phyla in soils including Acidobacteria, Proteobacteria and Verrucomicrobia but not the relative abundance of the fungal phyla. The β -diversity of bacterial and fungal communities was different among compost products. Similarly, the β -diversity of bacterial and fungal communities in soils was different among compost treatments and sampling dates. However, the β-diversity of bacterial communities from the compost-treated soils were becoming more similar to the control soils as time progress but no convergence of the β -diversity of fungal communities in compost-treated soils and the control soils was observed. Contrary to common belief, several bacterial and fungal species from the compost were still present in soils nearly a year after compost application to soil suggesting that these species succeeded in establishing in soil despite compost and soil being vastly different environments. The application of composts clearly changed the physico-chemical properties of soils which in turn influenced the bacterial and fungal communities. The effects on microbial communities were persistent, and could still be observed nearly a year after compost was applied.

Evaluation of Greenhouse Gas Emissions and Carbon Capture on New Brunswick Farms

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There is currently no tool being used by farmers or farmer groups to assess greenhouse gas emissions (GHG) and carbon capture on New Brunswick farms. Opportunities in the carbon market may be lost if farmers and farmer groups are not aware of their current emissions numbers and what they could be with changes in practices. Farms must be prepared for the future where GHG emissions data will be essential to marketing their product, and consumers will have information about the carbon footprint of the products they buy. We entered data from individual farms in a GHG calculator tool (Holos) and estimated the GHG emissions and carbon capture from three important New Brunswick agricultural commodities (potato, blueberry, and dairy products). The ultimate goal of this project is to, potentially, shortly, integrate a GHG emissions tool into the Environmental Farm Plan (EFP) program to help to tackle GHG emissions and climate change in New Brunswick. Five small and five large farms were selected for each commodity (four of each group located in the traditional production area, and one of them located in alternative provincial areas). Traditional potatoes production areas were Carleton, Victoria, and Madawaska counties; alternatives, Kent and Westmorland counties). For potatoes, we created 48 scenarios for each farm - three 3 yields (40000 - 45000 - 50000 kg/ha), 4 N levels (120 - 150 - 180 - 210 kg/ha), 4 P levels (60 - 110 - 160 - 210 kg/ha). For potatoes, for each scenario, the following output was obtained from Holos: direct N₂O (CO₂e) (kg), indirect N₂O (CO₂e) (kg), energy CO₂ (CO₂e) (kg), CO₂ (CO₂e) (kg), sub-total (CO₂e) (kg). From this data, it was calculated (CO₂e) / area (kg/ha) and $CO2 CO_2e$ / production (production = yield x area) (no unit). The main results for year 1 for potatoes indicated that farm localization (county) and farm size (small or large) have no impact on (CO₂e) / area and CO₂e / production. However, higher yields implied higher values of (CO₂e) / area and CO2e/ production. Also, increasing N and P levels increased values of (CO2e) / area and CO₂e / production, with a larger effect caused by N. In all scenarios, the carbon balance was positive; that is, crops emitted carbon to the atmosphere. The values of (CO₂e) / area varied from 1916 to 3254 kg/ha and the values of CO₂e / production varied from 0.05 to 0.07. For year 2 (hay mixed as a cover crop), the values of $(CO_{2}e)$ / area varied from -1572 to -1604 kg/ha and the values of CO₂e / production from -0.17 to -0.18. Therefore, the potatoes crop's carbon emission is partially compensated by the cover crop's carbon capture in year 2, significantly reducing the carbon balance of the potatoes/hay mixed cultures in a 2-year period.

Nitrate Leaching as affected by Nitrogen Fertilization in Irrigated Potato Production on Sandy Soils

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High N fertilizer amounts applied to potato (Solanum tuberosum L.) on coarse-textured soils often result in nitrate leaching during the growing season (NL) when they coincide with excess water. It was hypothesized that polymer-coated urea (PCU) significantly reduces NL compared to conventional soluble N fertilizers under irrigated potato production on sandy soils in Eastern Canada. This three-year (2010-2012) study compared a single application of PCU and split-applied soluble N fertilizers (ammonium nitrate, AN; ammonium sulfate, AS) at three N rates (120, 200 and 280 kg N ha-1) in addition to an unfertilized control, which were tested annually. Suction lysimeters were used in combination with a one-dimensional water mass balance model to quantify NL. Composite soil samples were collected at the 0-15, 15-30, 30-60, and 60-90 cm depths immediately after potato harvest in fall and again in the following spring to measure residual soil nitrate content in the 0-90 cm depth (RSN) and to estimate overwinter losses of soil nitrate. Fertilizer N application significantly increased NL and RSN. Regardless of the fertilizer N source, the results indicated that NL was primarily driven by precipitation. Application of PCU at planting increased NL in 2011 compared to AN and AS, which was attributed to a greater soil nitrate concentration under PCU combined with increased rainfall during the tuber bulking phase (60-90 d after planting). In 2012, NL was reduced by 29% with PCU and by 51% with AS compared to AN, which was attributed to reduced soil nitrate concentrations between planting and hilling when rainfall was high. At the equivalent N rates of 200 and 280 kg ha-1, application of PCU at planting resulted in significantly greater RSN than split-applied AN and AS in 2010 and 2011. Overwinter losses of soil nitrate were generally increased with increasing RSN. Overall, the results suggest that a single application of PCU is an effective strategy for reducing NL when there is significant rainfall between planting and hilling. They also suggest that reducing the fertilizer N rate is more important than the choice of N source in managing RSN.

Revolutionizing Potato Variety Development for Climate Smart Agriculture

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6 Tuberosum Technologies

7 Boyce Thompson Institute

8 International Potato Centre (CIP)

Potatoes are the fifth largest agriculture crop in Canada planted on approximately 362,000 acres and in every province. In 2019, potatoes contributed \$1.28 billion to Canada's farm cash receipts. Exports of Canadian potatoes and potato products were estimated at \$1.88 billion, up 5.2% from the previous crop year and 34.4% over the last five years. Maintaining the output of the potato production system in the face of climate change is a concern. Potato yields are impacted by global warming and there are threats of northward movement of new potato pests and pathogens into Canada. A more responsive and rapid potato breeding system is needed to develop varieties with resilience to changing climate. Additionally, variety improvement can foster reduction of greenhouse gas emissions in potato production and industrial processing. One target is reducing the 20 % loss of potatoes in the production system, which is largely low-quality rejects that do not meet market standards. The project will have a focus on tuber quality as a way to reduce wasted production and greenhouse gas emissions. The approach is to apply genomic prediction to selection and breeding. Genomic prediction involves using a training population to develop a prediction model. Dense genome-wide genotyping data along with trait data for all the individuals in the training population will be used for prediction model building. The model will then be used to predict traits in parental lines using just genotyping information early in the breeding scheme. The research project described is funded through AAFC and Genome Quebec and is structured around 5 inter-related activities that build genomic selection breeding schemes for potato:

• Activity 1: provides genome sequences and develops tools for genotyping included are activities that are part of the International Tetraploid Potato Pan-genome Sequencing Consortium, as well as genome sequencing of multiple diploid potato genomes. These combined efforts will provide improved resources to identify useful regions of the genome in parents of the potato breeding program.

• Activity 2: plays an essential role, propagating the germplasm needed for this research program. This activity has involved propagation of c. 1000 clones from the AAFC breeding and Canadian Potato Gene Resources collection. This will be reduced to c. 500 clones for the genomic prediction training population.

• Activity 3: develops methods for quantification of tuber quality and vine characteristics phenotyping. Commercial tuber optical graders and other imaging devices are being adapted for use to quantify tuber defects, shape, size and color. Other image-based methods for quantifying above ground plant phenology are also being developed. Development of high-throughput molecular analysis of plant stress and chemical analysis of flavor are also underway.

• Activity 4: integrates data for building genomic prediction models using a database tool, Potatobase. The genotyping data for each of the training population clones will be analyzed along with the phenotyping data for each of the clones.

• Activity 5: transfers genomic selection technology into potato breeding schemes. Methods for single marker and genome-wide genotyping early in the breeding schemes are under development.

Genomic Selection in Potato: Predicting Traits Using Genome-Wide Information

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Recent advances in high throughput genomics have made genomic selection a viable option in the breeding programs of many crop species. In contrast to traditional breeding methods, which rely on pedigrees and extensive trait evaluation in progenies, genomic selection uses a modest number of individuals that are extensively genotyped at thousands of genetic markers and evaluated for desirable traits in the field for several seasons. This "training population" of individuals is used to create a statistical model that can then predict a new individuals trait values based solely on its genetic marker genotype without ever growing the individual in the field. To investigate the utility of genomic selection in potato we conducted a proof of concept field trial involving 340 advanced potato lines, grown in 50 hill and 100 hill plots, which were (1) phenotyped for specific gravity, common scab coverage, tuber and flower colour, and maturity, and (2) genotyped at ~50000 single nucleotide polymorphism (SNP) markers via genotyping by sequencing. The set of SNP markers were first validated by using them to identify the known genetic loci controlling simple traits like tuber and flower colour using genome-wide association analysis, then used to construct genomic prediction models using several machine learning approaches. Genomic prediction accuracies for simple traits such as tuber colour were moderate (0.81) suggesting the dense SNP coverage captures most of the genetic variation in these traits. However, the mean prediction accuracies for specific gravity (0.40-0.45) and common scab coverage (0.38-0.40) were much lower, owing to more complex inheritance and greater environment effects on these traits. Here we discuss these results in the context of progeny selection based on prediction modelling, and we comment on the use of predicted breeding values (and marker genotypes) to choose pairs of parental lines for intercrossing.

AAFC Potato Breeding Modernization: Screening For Disease Resistance Using DNA Markers Robyn Morgan^{1*}, Erica Fava¹, Kyle Gardner¹, Xianzhou Nie¹, Helen Tai¹, David de Koeyer¹

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Over the past two years, in order to better support the potato industry, the Agriculture and Agri-Food Canada Potato Breeding Program has undertaken to improve and modernize the breeding pipeline. As part of this effort we are developing methods to implement Marker-Assisted-Selection (MAS) at early generations to identify selections with beneficial traits by using traitassociated SNP markers. The first steps to implement this workflow are to identify and test SNP markers that will work well in tetraploid potato germplasm and to screen our potential parental lines for markers for traits of interest. For developing SNP markers, we investigated two different marker platforms: RhAMP (Integrated DNA Technologies) and KASPTM (LGC, Biosearch TechnologiesTM) and four different SNP markers: RyADG (PVY), RySTO (PVY), Rx1 (PVX) and TG689-1P (Golden Nematode). Both marker platforms are for end-point genotyping although fluorescent changes can also be visualized during the amplification cycles with RhAMP. RhAMP uses a two-enzyme system coupled with RNA-DNA hybrid primers. KASPTM is a unique form of competitive allele-specific forward primers which then have unique tail sequences for fluorescent probe binding. Our results indicate that both RhAMP and KASPTM are capable of working with tetraploid DNA and, for some probes, are capable of differentiating between the five genotype calls that may be present in a tetraploid accession. However, due to differences in the marker technologies and how the SNP markers are designed, one platform may work better for a given marker than the other. Therefore, it may be beneficial to not concentrate all efforts on just a single platform. To date, we have completed screening of our potential parental accessions (1303 accessions) with these four markers. For some of these accessions we also have resistance results for the corresponding disease from pathology disease screens. For those accessions, the false positive rate of the markers is between 0 - 7%. The false negative rate cannot be determine as we are not screening all potential disease resistant genes for the given traits. In conclusion, we have optimized the initial markers we are testing and completed screening of our potential parental germplasm with four trait-linked markers. Further work will include the development of SNP markers for additional traits and the implementation of MAS by screening selections at the 2^{nd} or 3^{rd} field generation.

Achieving More Crop per Drop through High-Throughput Screening of Drought Tolerant Potatoes

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Drought poses a major challenge to potato yield and quality worldwide. Climate change is predicted to further aggravate this challenge by intensifying potato crop exposure to increased drought severity and frequency. Hence, there is an urgent need to adapt our potato production systems by developing drought tolerant cultivars that are appropriately engineered for the changing environment. This can be approached through the identification of drought-related physiological, biochemical and molecular traits and their deployment in new potato cultivars. However, our capacity to assess a large number of genotypes is constrained by the limited availability of high-throughput tools and technologies. The application of leaf and canopy level hyperspectral reflectance is a promising high-throughput field phenotyping tool for agricultural research. The reflectance data can be used to develop spectral indices to rapidly and efficiently screen germplasm under field conditions. Thus, the main objective of this work is to study the potential use of hyperspectral reflectance as a high throughput phenotyping tool to identify drought-related physiological, biochemical and morphological traits. We are currently evaluating 60 diverse potato genotypes subjected to drought stress. Our preliminary results revealed a wide difference across potato genotypes in their ability to tolerate drought stress, which was in turn associated with their capacity to maintain tuber yield, rates of photosynthesis, water use efficiency, leaf water content, leaf pigments, leaf protein and dry matter content. We will discuss whether these variations in drought-related characteristics are mirrored by differential spectral reflectance patterns across the potato genotypes.

Reputed Flavours in Heritage Potato Varieties-Implications for research

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Potato is the leading vegetable crop in Canada and an important food crop worldwide where it is expected to play an increasing role to address global food and nutrition security. In today's global food markets, there are many drivers for food choice, including the taste and perception of flavour, which are reported to greatly influence purchasing decisions. Adding these traits to new varieties has the potential to increase the consumption of fresh table potatoes and contribute to a healthy nutrition. Some of the heritage potatoes conserved in the Canadian Potato Genetic Resources (CPGR) genebank have survived for 100 years or more, and are believed have culinary traits which were valued by the people who maintained them for generations. These unique varieties along with the genetic diversity maintained in germplasm collections are valuable for understanding consumer preference and constitute a foundation for breeding potato varieties with improved productivity, nutritional quality and appeal to consumers.

How much will periodic drought affects potato growth, yield and tuber quality?

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Due to climate change, farmers in the northeast region of North America are facing increasing challenges of periodic drought. However, there is a lack of quantitative information on the effects of periodic drought on potato plant growth, yield and tuber quality. In this study, we conducted two pot experiments to test the effects of: 1) fixed length of short period (two weeks) of drought applied at four different potato growth stages (sprouting, vegetative, tuberization and bulking stage) and 2) the length of short period of drought during two critical potato growth stages (vegetative and tuberization stage), respectively, on potato vegetative development and tuber yield and quality. The results show that short period of drought overall had negative impacts on potato vegetative and tuberization stage. For these two growing stages, the negative impacts increases continuously with the length of the drought period. Although the impact of water deficit at the sprouting stage was minor, it was broad and long-lasting. These results confirm the benefits of supplemental irrigation. They further suggest that when the availability of water for irrigation is limited, using water strategically during the period when potato needs water the most can maximize the benefits of supplemental irrigation.

Canada-wide assessment of insecticide resistance in the Colorado Potato Beetle, *Lepinotarsa decemlineata*

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The Colorado potato beetle, Leptinotarsa decemlineata, is a common pest of potato crops in Canada, causing persistent and potentially devastating damage. Control of this insect in commercial fields relies heavily on systemic and foliar insecticides, predominantly neonicotinoids and spinosyns. However, CPB are notorious for rapidly developing insecticide resistance, which may be regionally specific. To better understand patterns of insecticide resistance in CPB across Canada we obtained live adults from five provinces where potato production is high. Along with each colony, producers completed a survey which indicated previous insecticide use over the last five years. In the lab, second instar larvae were tested with feeding assays for insecticide resistance on six commonly used insecticides: two neonicotinoids, two spinosyns and two anthrilic diamides. Thirty-one colonies were screened in 2019 and sixteen colonies were screened in 2020. In 2019 only 10% (3/31 colonies screened) were susceptible to all six insecticides tested. Forty-two percent (13/31 colonies) showed resistance to at least one insecticide tested. Regional patterns of resistance by province were evident in some cases. Further data will be collected during the summer of 2021 and combined with data from 2017-2020 to develop a mapping tool that growers can access to help make informed decisions when choosing chemistries to control CPB in their fields.

Alternation of Potato Foliar Sugar, Amino Acid, and Glycoalkaloid Concentrations Through Different Nitrogen Fertilization Practices

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A considerable number of potato pests, such as Colorado potato beetle, Leptinotarsa decemlineata (Say) and aphid, Macrosiphum euphorbiae (Thomas) are mainly feeding on potato leaves to maintain their general growth and development. Therefore, the potato foliar nutrients play an important role and altering the nutrient composition may impact the defoliated pest behaviors. A greenhouse experiment (cv. Russet Burbank and Goldrush) and 4-yr field trials (cv. Russet Burbank) were conducted to investigate the responses of potato foliar sugar, amino acid, and glycoalkaloid concentrations to different nitrogen (N) practices in Quebec, Canada. Twenty leaves were randomly collected from each experimental unit at different potato growing stages for nutrient analysis. In the greenhouse experiment, Goldrush potato leaves had higher concentrations of sugars and glycoalkaloids compared to Russet Burbank. Sugar and amino acid concentrations quadratically increased with increasing N rates. Under field conditions, sugar levels quadratically decreased while amino acid concentrations significantly increased with increasing N rates. The responses of foliar glycoalkaloid contents to N fertilizer application were closely sensitive to the N sources and external stresses, such as pest infection. Based on these findings, an integrated N management strategy may be critical to alter the potato defoliate pests feeding behaviors. Further studies are still required to evaluate the responses of specific pest activities to different N regimes.

Population Density of Potato Early Dying Pathogens and Their Potential Effect on Potato Yield in Prince Edward Island and New Brunswick

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Potato early dying (PED) disease complex, declining soil health and drought are the main potato yield limiting factors in Eastern Canada. The primary organisms causing PED are fungal pathogens (Verticillium spp.) and the root lesion nematodes (Pratylenchus penetrans). Dry weather conditions can further increase the disease severity. PED has been endemic in New Brunswick (NB) and Prince Edward Island (PEI), but in recent years has increasingly been identified as a major issue for potato production in response to changes in climate and agricultural practices. Before the 1990s, Pratylenchus penetrans and P. crenatus were the prevalent root lesion nematodes and V. albo-atrum was the dominant Verticillium species in NB and PEI. Knowledge of current population density of the PED pathogens is crucial for designing strategies to manage the PED. A survey of the population density of the Verticillium spp. and root lesion nematodes (Pratylenchus spp.) was conducted in commercial potato fields in NB and PEI from 2017 to 2020. Composite soil samples were collected from 20-30 commercial fields grown to rotation crops each year in NB and PEI to quantify the root lesion nematodes using a modified Baermann pan method and Verticillium spp using specie specific quantitative PCR. Selected soil physical properties (%N, %C and C:N ratio) were also determined. Based on the pathogen densities in the surveyed fields, eight fields representing a range of low to high densities were selected in NB and PEI, respectively, to determine the relationships among pathogen density, disease severity, soil properties and potato yields. Preliminary results showed that Verticillium spp. and root lesion nematodes were present in all surveyed fields in PEI and NB. Verticillium dahliae was the dominant species in all fields, and V. albo-atrum was only detected in some fields at a low level in NB and in PEI. No significant correlation between pathogen density and PED severity was detected, which could be attributable to environmental conditions that favor disease development above certain level of pathogen density. The PED severity was significantly negatively correlated with the potato yield, and the soil %N and %C was significantly positively correlated with the potato yield.

Surveillance Of Click Beetle (Coleoptera: Elateridae) Populations Across Prince Edward Island, Canada.

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Increasing wireworm populations are a major threat to the potato industry worldwide. Feeding damage, holes made in tubers by wireworms, can result in serious losses for potato producers. Click beetles, the adults of wireworms, are responsible for dispersal and spread of the species. In PEI, three European species, A. suptator, A. obscurus and A. lineatus are found with A. sputator being the dominant species damaging the potato crop. Increasing wireworm population in infested areas and the discovery of wireworms in previously non-infected fields prompted a province wide survey in 2009 and every 3 year thereafter. Pheromone traps, one per field (no. of fields 60(2009) 85(2012, 2016, and 2019)) were placed in the same fields across the island each trapping year. Results showed in 2009 higher number of beetles/trap in queens county with none to very low numbers in the western and eastern regions of the province, by 2012 a six fold increase in population and spread into all regions of the province was detected. A. sputator was the dominant species in all regions. In 2016, a further increase in population was noted. Survey results in 2019 showed a significant decrease in the population in every region. A few growers started using wireworms suppressive crops in rotation between the potato crop year in 2013. Over the years, the number of farms using wireworm suppressive crops increased resulting in the widespread use of these crops across the province by 2019. The decrease in click beetle numbers in 2019 could be attributed to the widespread use of this strategy. Surveillance will continue in 2022 to track the click beetle population and movement within the province.

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