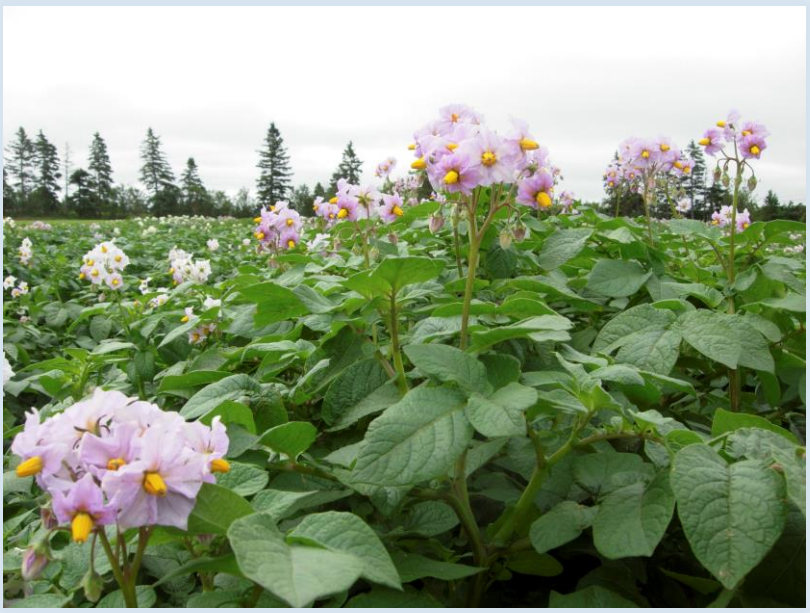
2023 NORTHEAST POTATO TECHNOLOGY FORUM

March 21-22, 2023



Conspectus

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NORTHEAST POTATO TECHNOLOGY FORUM - 2023

INTRODUCTION

The Northeast Potato Technology Forum is an annual event which brings together potato specialists from northeastern North America to discuss potato research and promote collaboration and information exchange. The Forum was held March 21-22, 2023 at the Radisson Kingswood Hotel in Fredericton, New Brunswick.

A total of 27 oral and seven poster scientific presentations were made as part of four sessions grouped by subject matter. Sessions dealing with pest management, pathogen detection and characterization, microbial dynamics, agronomy, and breeding were organized. The research represented by these presentations forms an important part of the ongoing development of the potato industry in the northeast region.

Many thanks to the session moderators, presenters, and all who participated in the Forum 2023. We would particularly like to thank Syngenta for sponsoring the reception and McCain Foods for publishing this book of abstracts. We would also like to thank all of the sponsors (see back cover) for their support.

Local Chair: Claudia Goyer

Local Organizing Committee: Jessica Vickruck, Khalil Al-Mughrabi, Mathuresh Singh, and Kyle Gardner

2023 NORTHEAST POTATO TECHNOLOGY FORUM
March 21 and 22, 2023

Tuesday, March 21, 2023

1:00 pm Welcome

Session 1: Agronomy
Moderator: Ryan Barrett

1:15 Exploring the benefits of fall cover cropping ahead of potato production
Ryan Barrett* and Morgan McNeil

1:30 Climate change impacts on the potato yield of Prince Edward Island
Toyin Adekanmbi* and Xander Wang

1:45 Using tile drain to enhance potato productivity and profitability in Prince Edward Island
Yefang Jiang*, Ana Kostic, Danielle Murnaghan, Judith Nyiraneza, and Jess Matheson

2:00 Soil, water and topography maps as a management tool to improve profitability and sustainability within the potato industry
Evan MacDonald*, Aitazaz Farooque

2:15-3:00 BREAK

Session 2: Pests and Pathogens
Moderator: Mathuresh Singh

3:00 Population Density of Potato Early Dying Pathogens and Their Potential Effect on Potato Yield in Prince Edward Island and New Brunswick
Dahu Chen[1], Louis-Pierre Comeau[1], Kamrun Nahar[1], Ryan Barrett[2], Sebastian Ibarra[3], Eileen Beaton[3], and Bernie Zebarth[1]

3:15 Pre-row closure treatment with BotaniGard 22WP (Beauvaria bassiana) as a potential practice to increase effectiveness in controlling Colorado potato beetle
Jess Vickruck*, Ian Scott, Pamela MacKinley, Jessica Stokes-Rees, Natasha Mosher-Gallant, Christine Noronha

3:30 Development and evaluation of simultaneous qPCR for quantifying Verticillium and Root Lesion Nematode in soil
Tyler MacKenzie*, Khalil Al-Mughrabi, Erika Naruzawa, Pat Toner, Dahu Chen, Mathuresh Singh

3:45 Clasnip: a web-based platform for the classification of closely-related bacterial and viral pathogens
Jiacheng Chuan*, Larry Hale, Wen Chen , and Xiang Li

4:00 Quantifying and Monitoring Silver Scurf Sporulation in Potato Storages: Adapting Spore Trapping Equipment from the Field to the Storage Environment
Kendra Thurston*, Stephen Moorehead, Colby Robertson, Kristine White, Michael Saleh, Yaima Arocha-Roset

4:15 Developing Bioinformatics Toolkits for the Identification and Detection of Plant Pathogens
Xiang (Sean) Li*, Jiacheng (Eric) Chuan and Wen Chen

4:30 Diversified Bacteria Causing Potato Blackleg and Soft Rot
Jianjun (Jay) Hao*

4:45 Closing remarks for Afternoon 1 session

Wednesday, March 22, 2023

7:00 am – 8:00 am BREAKFAST

8:15 am Welcome

Session 2 con't:

8:30 Bacterial and fungal communities associated with russeting and silver patch blemishes of potato tuber
Claudia Goyer* and Tracy Shinners-Carnelley

8:45 Benefits of a tripartite plant-mycorrhiza-Bacillus symbiosis in potato production
Martin Trépanier*, Mathieu Bouchard-Rochette, Jeremy Waugh and Marc Béland

Session 3: Soil Amendment and Nutrient Dynamics
Moderator: Jay Hao

9:00 High-Throughput Phenotyping of Potato Plants for Precision Nitrogen Management
Coralie Scissons*, Matthew Milne, Athyna Cambouris, Dion Durnford, Keshav Dahal

9:15 Comparison of two methods for delineating management zones for improved-nutrient management
David A. Ramirez Gonzalez*, Athyna N. Cambouris, Marc Duchemin, Sheldon Hann, Manphool S. Fageria, Yves Leclerc, Karem Chokmani

9:30 Delineated Management Zones via Soil Apparent Electrical Conductivity to Enhance Nitrogen Fertilization of Potato Production
Bilal Javed*, Athyna N. Cambouris, Noura Ziadi, Marc Duchemin, Antoine Karam

9:45-10:30 BREAK – Poster presentation

10:30 Measuring Effects of Slow Release Nitrogen on Yield, Economic Crop Value and Environmental Impacts on PEI Potatoes
Steve Watts*, and David Burton

10:45 Soil properties and nutrient cycling responses to willow chip application
Yvonne Uwituze*, Judith Nyiraneza, Yefang Jiang, Jacynthe Dessureault-Rompré, and Tandra D. Fraser

11:00 Molecular responses to nitrogen in potato leaves
Helen H. Tai*, Zhe Xie, José Héctor Galvez, Martin Lagüe, Bernie Zebarth, Mia T. Parenteau, Hong Gu, Athyna N. Cambouris, Jean Lafond, Alison Nelson, Judith Nyiraneza and Martina V. Strömvik

Session 4: Potato Traits and Breeding
Moderator: Kyle Gardner

11:15 Diploid potatoes: Too little not such little genetically and agronomically
Bourlaye Fofana*, David Main, Moshin Zaidi, Benoit Bizimungu

11:30 Development of a Flavorful Dihaploid Potato Germplasm; a Tool for Canadian Fresh Market Potato Breeding
Samuel Gagnon*, Cyntia Belzil, Ariane Poulin, Blandine Bulot, Louis Félix Nadeau, Jonathan Tremblay, Helen Tai, Charles Goulet

11:45 Exploring a New Method to Assess Tuber Skin Strength in the Field
Colby Robertson*, Stephen Moorehead, William Watts

12:00 -1:00 Lunch

1:00 Wild Potato Relatives for Breeding Colorado Potato Beetle Resistance
Hanna J. McCoy*, Sai Reddy Achakkagari, Cuijuan Zeng, Emily M. McCoy, Pamela MacKinley, Jess Vickruck, Martina V. Strömvik, Larry A. Calhoun and Helen H. Tai

1:15 Irrigation Effect on Yield, Skin Blemishes, Phellem Formation, and Total Phenolics of Red Potatoes
Manlin Jiang*, Tracy Shinners-Carnelley, Darin Gibson, Debbie Jones, Jyoti Joshi and Gefu Wang-Pruski

1:30 Development of a core collection of heirloom and heritage potato varieties for use in breeding, research and education
Benoît Bizimungu

1:45 Genomic prediction and association analysis in the Agriculture and Agri-Food Canada Potato Breeding Program
David De Koeyer*, Robyn Morgan, Erica Fava, Kyle Gardner, Benoit Bizimungu, and Helen H. Tai

2:00 Detecting historical selection in potato using genome-wide marker information
Kyle M. Gardner, Katheryn Douglass, Lana Nolan, Benoit Bizimungu, David De Koeyer, and Helen Tai

2:15 Closing remarks Day 2

Evaluating the effect of fall-seeded cover crops in the year before potato production on agronomic performance and environmental sustainability

Ryan Barrett and Morgan McNeil
Prince Edward Island Potato Board. 90 Hillstrom Ave, Charlottetown, PE C1E 2C6
ryan@peipotato.org

There is a growing body of research on the use of cover crops to reduce soil erosion and minimize over-winter nutrient losses in a variety of cropping systems. Most cover crop research in North America has been on traditional field crop rotation systems, not including vegetable crops such as potatoes. Conventional potato production practices in Prince Edward Island entails fall tillage in the year before potatoes are to be planted, often combined with termination of a forage crop. Historically, this termination and tillage has taken place in the late fall, leaving the ground without vegetation over-winter. Recently, many potato producers in Prince Edward Island are interested earlier forage termination and tillage (August/September) followed by planting of a fall cover crop which will self-terminate by spring.

As part of the Living Labs Atlantic initiative, our research team conducting on-farm trials from 2019 to 2022 in a total of 23 fields in Prince Edward Island. In each of these fields, one or more fall-seeded cover crops were planted along with a no cover control strip. Cover crops evaluated included barley, oats, spring wheat, oilseed radish, tillage radish, brown mustard, and mixtures of these species. The majority of cover crops were established following termination of a forage crop and subsequent tillage in August or September. Species selected by the producers were chosen in part because they will self-terminate over winter. Only one cover crop (spring barley) survived the winter due to mild winter weather and needed to be chemically terminated in the spring. Potatoes were then planted in these fields the following year.

Fields were analyzed for soil chemistry, soil health, soil nitrates at three depths, soil erosion potential (in a subset of fields), root lesion nematodes, *Verticillium*, compaction using a soil penetrometer, and potato yield and quality. Potatoes were graded either to the Cavendish Farms processing contract specifications or to Canada #1 fresh market grade, depending on the variety used.

No statistical differences were observed for soil nutrients, soil health metrics, root lesion nematodes, Verticillium, or compaction across the three years of the project. In the spring of 2022 (following increased sampling intensity) there was an increase in soil organic matter of 0.13% ($p = 0.057$) in favour of the cover cropped portion of the fields. There was 38-41% decrease in soil nitrates in the cover crop treatment compared with the no cover control ($p < 0.05$).

Across the three years of potato yield data, there was an average yield increase of 32 cwt/ac (11.2%) and $536/acre increase in crop value following a cover crop compared to the no cover control. Both were very highly significant at p values of 0.006 (marketable yield) and 0.005 (crop value). Comparisons of grain species cover crops (barley, oats, wheat) showed a greater increase in marketable yield (37 cwt/ac) than comparisons of brassica cover crops (radish, mustard) with no cover (19 cwt/ac). These levels of yield increase more than compensate for the cost of establishing fall cover crops. This will be a key factor in the knowledge transfer to producers on the value of cover crops, not just for long term factors such as erosion mitigation and soil health, but also in short term effects on subsequent crop yields.

Climate Change Impacts on the Potato Yields of Prince Edward Island

Toyin Adekanmbi & Xander Wang, Canadian Centre for Climate Change and Adaptation, UPEI

Potato is a significant staple crop in Canada, contributing to food security and the economy. PEI province produces a significant quantity of potato yields; meanwhile, in recent years, there have been fluctuations in the quantity and quality of potatoes in the province. In essence, it has become crucial for local farmers and decision-makers to understand how climate change will affect potato cultivation activities in PEI to strategize adaptation measures to the impacts of the changing climatic conditions on potato yield. In this study, the Decision Support System for Agrotechnology Transfer (DSSAT) potato model uses weather, soil, and management practices data to simulate future potato yields under the Coupled Model Intercomparison Project Phase 6 (CMIP6) climate scenarios (including SSP1-1.9, SSP1-2.6, SSP2-4.5, SSP3-7.0 and SSP5-8.5). The study considers the combined effect of temperature changes, changing precipitation patterns, and the concentration of carbon dioxide (CO_2) in the atmosphere. The results reveal a likely significant decline in the future potato yield in PEI under the current farming practices. Specifically, the potato yield in PEI will decline by 48%-60% in the 2070s and by 63%-80% in the 2090s under the high emission scenarios (i.e., SSP3-7.0 and SSP5-8.5). In addition, potato yield would reduce by 6% to 10%, even under low-emission scenarios (e.g., SSP1-1.9 and SSP1-2.6). Therefore, the study will enable us to develop effective coping measures, such as alternative farming practices and integrating irrigation plans, for the sustainability of potato cultivation in PEI.

Using tile drain to enhance potato productivity and profitability in Prince Edward Island

Yefang Jiang, Ana Kostic, Danielle Murnaghan, Judith Nyiraneza, and Jess Matheson

Agriculture and Agri-Food Canada, 440 University Ave., Charlottetown, PE C1A 4N6, Canada

Highly variable precipitation in the growing season (GS) presents a challenge for consistent potato production in Prince Edward Island (PEI), making water management increasingly important, especially under climate change. This study assessed the influence of tile drain on potato productivity and profitability in PEI. The provincial average marketable yield of Gold rush potato from 2000 to 2021 was conceptualized as the result of water supply management experiment, with growing season rainfall as water supply. Yield response to water supply followed a second order polynomial regression, with GS rainfall explaining 50% yield variation ($p=0.002$). Tuber yield increased with increasing GS precipitation in the 155–257 mm range (3/20 seasons), became relatively insensitive to GS precipitation in the 258–425 mm range (12/20 seasons), and decreased as GS precipitation increased from 426 to 479 mm (5/20 seasons).This equation predicted that the yield increase as a result of soil dewatering would fully offset the cost of tile drain installation ($2500/ha in 2018 Canadian dollars) after three wet seasons. The yields of three Gold rush potato crops in 10 seasons (under 3-yr rotation) from a 7.5-ha commercial field in Souris area indicated that the tuber yields were not significantly different between the tile drain and not tile drain field zones in 2014 and 2018 when GS rainfalls were normal, but the yields in the tile drain zones were 26% significantly higher than those in the not tile drain zones in 2021 when rainfall was more than the normal level. This yield trend was consistent with the provincial average yield data. The results from this study suggest that tile drain can increase tuber yield in a wet season and can be a good investment for enhancing potato production in this area.

Soil, water and topography maps as a management tool to improve profitability and sustainability within the potato industry

Evan MacDonald*, Aitazaz Farooque
University of Prince Edward Island, Charlottetown, Canada

Potatoes are an expensive crop to grow, requiring many inputs such as fertilizers, fungicides, pesticides and more to be profitable. Site specific management, known as Precision Agriculture (PA), has the potential to ensure optimal distribution of inputs across the field by identifying variability and then managing it. To properly manage inputs on a site-specific basis, it is important to understand the soil characteristics that drive fertilizer uptake and yield potential. To do this, Soil, Water and Topography Maps (SWAT MAPS) use electrical conductivity (EC) information about the soil in addition to accurate topographic modeling of the landscape. Soil EC gives an indication of differences in soil texture, water holding capacity, soil organic matter and more. Topography determines where water sheds, where it collects, and where erosion has occurred. These layers of information are fundamental for successful site-specific management of the potato crop and can assist in making decisions for fertilizer applications, seeding, irrigation, herbicide applications and more.

This project focuses on using SWAT MAPS to influence variable rate (VR) seeding of the potato crop. Today's planting technology can automatically adjust seed and fertilizer rates according to management zones within the field. VR seeding has the potential to increase profitability for the farmer by managing risk and lowering cost of production in poorer performing areas of a field, while taking advantage of areas of the field with greater soil potential. This study was carried out in six fields in Prince Edward Island, Canada in 2021 and 2022. Findings from this study indicate that VR seeding of potatoes can result in profitability increases of over $300 per acre. VR seeding and fertilization can also help to mitigate the environmental impacts of over application of fertilizers in areas of the field they are not likely to be taken up by the crop. This can help farmers in reducing greenhouse gas emissions and leads to more sustainable potato production.

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

Dahu Chen[1], Louis-Pierre Comeau[1], Kamrun Nahar[1], Ryan Barrett[2], And Sebastian Ibarra[3], Eileen Beaton[3], Bernie Zebarth[1]

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Potato early dying (PED) disease complex, primarily caused by *Verticillium dahliae* and the root lesion nematodes (RLNs, *Pratylenchus penetrans*), widely spreads in Canada and limits potato productivity. A study was conducted from 2019 to 2022 in Prince Edward Island (PEI) and New Brunswick (NB) with two objectives, 1) to assess population density of *Verticillium* spp and root lesion nematodes in potato fields in PEI and in NB, 2) to determine the effect of the pathogen population levels on PED severity (relative area under disease progress curve, or rAUDPC) and on potato tuber yield. 30 fields in the fall of 2019, 2020, and 2021 were surveyed. Eight fields representing low and high pathogen levels each year were selected to assess effect of pathogen population. *V. dahliae* was detected predominantly in 84% (range 0 to 770, median 76 pg g^{-1} of dry soil) and 89% (range 0 to 504, median 168 pg g^{-1} of dry soil) of the surveyed fields in NB and PEI, respectively, and *V. albo-atrum* was detected in 21% (range 0 to 191, median 0 pg g^{-1} of dry soil) and 8% (range 0 to 10, median 0 pg g^{-1} of dry soil) of the surveyed fields in NB and PEI, respectively. RLNs were detected in 99% (range 0 to 27488, median 1020 counts kg^{-1} of dry soil) and 98% (range 0 to 34445, median 5666 counts kg^{-1} of dry soil) of the surveyed fields in NB and PEI, respectively. The population levels of *V. dahliae* were positively significantly correlated with PED severity in PEI and NB in all trials, the RLN levels were not significantly increasing the PED severity in PEI and NB. The total tuber yield averaged across the fields with low pathogen levels was significantly higher than that of the fields with high pathogen levels in each trial in PEI and NB. The yield reduction in the fields with the high pathogen levels ranged from 11.4% to 21.3% compared to the fields with low pathogen levels in NB trials, and ranged from 15.7% to 20.3% in PEI trials. In NB, both *V. dahliae* and RLNs densities were significantly negatively correlated with the tuber yield in 2022, but were not in the 2020 and 2021 trials. In PEI trials, *V. dahliae* density was significantly negatively correlated with the tuber yield in the trials done in 2021, but not in 2020 and 2022, while the RLN density was significantly negatively correlated with the tuber yield in the trials done in 2020 and 2022. Results suggest that management practices that can suppress the population levels of *V. dahliae* and RLNs could improve potato productivity.

Pre-row closure treatment with BotaniGard 22WP (*Beauvaria bassiana*) as a potential practice to increase effectiveness in controlling Colorado potato beetle

Jess Vickruck[1], Ian Scott[2], Pamela MacKinley[1], Jessica Stokes-Rees[2], Natasha Mosher-Gallant[3], Christine Noronha[3]

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The Colorado potato beetle, *Leptinotarsa decemlineata*, is one of the most important pests in potato, causing millions of dollars of yield losses annually. Control of CPB is a constant challenge for producers, as this species can develop resistance to certain chemistries rapidly. In addition, changing regulations for permitted insecticides may limit the options available to producers in the future. Here we tested how the application of BotaniGard 22WP (*Beauvaria bassiana*) impacts the ability of Colorado potato beetle to complete development in potato crops. BotaniGard is comprised of *Beauvaria bassiana* strain GHA, a fungus and mycoinsecticide that is approved for use in the organic sector. We tested two different application times to see if it impacted the effectiveness of *B. bassiana* on CPB*:* a soil application four weeks after plant emergence, and a soil application immediately before canopy closure. We established small plots consisting of three rows by 5 plants. *B. bassiana* was applied to the hills and furrow on either side of the centre row at a rate of 2lbs/acre. The day following BotaniGard application 15 third instar CPB larvae were placed on each plant in the centre row. Larvae were placed on plants by reaching across the outside row so that we did not transfer *B. bassiana* throughout the field. Plots were then monitored every second day to count the number of beetles that were successful at completing development. Overall, the application of BotaniGard decreased the number of CBP that were able to complete development as compared to control plots, with some variation between sites. In New Brunswick we saw a 36% of beetles complete pupation in the plots treated with *B. bassiana* 4 weeks after plant emergence, as compared to 74% in the paired control plots. In the plots where the soil was sprayed just prior to canopy closure 23% of beetles completed development as compared to 53% in the paired control plot.

Development and evaluation of simultaneous qPCR for quantifying Verticillium and Root Lesion Nematode in soil

Tyler MacKenzie[1]*, Khalil Al-Mughrabi[2], Erika Naruzawa[3], Pat Toner[4], Dahu Chen[5], Mathuresh Singh[1]
[1]Agricultural Certification Services, Inc., 1030 Lincoln Rd., Fredericton, NB; [2]Potato Development Centre, 39 Barker Lane, Wicklow, NB; [3]Cavendish Farms, Victoria St E, Kensington, PEI; [4]NB Dept. of Agriculture Aquaculture and Fisheries, Fredericton, NB; [5]Fredericton Research & Development Centre AAFC, Fredericton, NB

Verticillium dahliae (fungus) and *Pratylenchus penetrans* (nematode) constitute the Potato Early Dying (PED) pathosystem that is a concern for the New Brunswick potato industry. They persist in soil for years, and work synergistically to reduced crop yield in potato. Traditionally, slow, labour intensive methods of soil preparation and microscopic counting could detect them; however, interest has been increasing for DNA-based tools to quantify their soil concentration. The Agricultural Certification Services Lab has developed real-time qPCR tools, and culturing techniques to grow *V. dahliae* and *P. penetrans* in the lab to validate our detection tools and pursue experimental inoculation trials in the greenhouse. Our qPCR system simultaneously quantifies both pathogens using species-specific molecular probes. They outperform existing PCR techniques and more traditional manual microscopic techniques. These tools were applied to greenhouse experiments to measure the pathogens' effects on potato growth and yield, and to track their growth over time. Potatoes (cv. Russet Burbank) were grown in steam-sterilized soil inoculated with *V. dahliae* and *P. penetrans* combinations. Plants grew normally for 60-80 days despite high combined pathogen levels, before wilting, slowing growth and becoming senescent weeks before control plants. Individually, *V. dahliae* and *P. penetrans* reduced tuber yield by 45-62% and 10-16%, together causing reductions of 62-67%. After inoculation, concentrations were confirmed by qPCR, and tracked over time. In steam-sterilized soil with growing potato plants, concentrations of *V. dahliae* and *P. penetrans* rose over time, though *P. penetrans* rose more than *V. dahliae*. We also tested pathogen growth in unsterilized soils from two sources in NB potato fields, both partially fumigated the previous year. The lasting effect of previous-year fumigation caused initial reduction in *V. dahliae*, lasting ~2 months, but recovering later in the season to match or exceed growth in the non-fumigated or steam-sterilized soils. Any effect of previous-year fumigation on *P. penetrans* was less clear, with fumigated and non-fumigated soil showing similar growth, but both lower than in steam-sterilized soil. Plant growth and yield were far better in natural field soils, especially those with previous-year fumigation from both widely separated sites with clear differences in soil quality other than fumigation. It is possible that the lasting effect of fumigation on the soil microbiome may have allowed better growth of the potato plants, as well as the initial depression but subsequent more rapid recovery of *V. dahliae*. In *P. penetrans*, it may be that any intact soil microbiome may cause slowed growth compared to the steam-sterilized soils. Our qPCR tools were also used to survey DNA of *V. dahliae* and *P. penetrans* in potato field soils submitted from across NB, showing a worrisome correlation in concentration of the two synergistic pathogens, and in some samples at levels shown to affect growth and tuber yield in our greenhouse experiments. Also, our sensitive, multiplex qPCR techniques were backed by simpler existing PCR methods, yet they departed substantially from traditional microscopic counting techniques. Future research directions should include correlation of crop yields and visible plant disease in fields with high levels of measured *V. dahliae* and *P. penetrans* DNA to field-validate the symptom thresholds determined in the greenhouse, and quantify microbiome differences in soil types and after fumigation to determine any connection to the growth of these pathogens.

Clasnip: a web-based platform for the classification of closely-related bacterial and viral pathogens.

Jiacheng Chuan*[1,2], Larry Hale[2], Wen Chen[3] , and Xiang Li[1]

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3. Agriculture and Agri-Food Canada, Ottawa Research and Development Centre, Ottawa, ON

The identification of pathological microorganisms using NGS and bioinformatics have developed rapidly, but practical applications for massive pathogen screening is expensive and time-consuming. In this study, we introduce Clasnip (www.clasnip.com), a fast, and reliable bioinformatics tool for the detection and classification of plant pathogens at interspecial and intraspeciel levels. Employing this classifier can facilitate quick disease containment and reduce costs in case of an outbreak or invasion of plant diseases. The input of Clasnip is not limited to single gene sequences obtained from Sanger sequencing, but also the assembled long sequences from next-generation sequencing data. As part of the results, Clasnip generates a classification summary table, showing sequence identity, SNP coverage, and probability of classification. Clasnip also outputs a multi-locus sequence typing table with SNPs details. Currently, Clasnip has curated databases for the classification of bacteria ring rot (*Clavibacter sepedonicus*), tomato canker (*C. michiganensis*), soft rot and blackleg (*Dickeya solani, D. dianthicola, Pectobacterium parmentieri, P. atrosepticum, P. brasiliense, P. wasabiae*), zebra chip ('*Candidatus* Liberibacter solanacearum', CLso), and potato virus Y (PVY) phylogroups. Users can also build custom databases of their interest. Databases of PVY, *Clavibacter, Dickeya* and *Pectobacterium* are built using whole genome sequences, and Clasnip reached a 100% accuracy for those databases. As for potato zebra chip pathogen CLso and associated Liberibacter, Clasnip can differentiate these close-related nonculturable pathogens on the basis of 1-2 SNPs on 16S, 16–23 integentic Spacer (IGS), and 50S ribosomal protein gene sequences, respectively. Based on the SNP statistics of CLso haplotypes, we proposed a novel standard for haplotyping CLso subgroups. To be classified as a new haplotype, the sequences should contain at least 2 SNPs in the combined region of 16S rDNA and 16–23s IGS (regions, and 2 SNPs in the 50s rplJ/rplL regions. In conclusion, Clasnip (www.clasnip.com) is a powerful bioinformatic tool for pathogen classification and identification.

Quantifying and Monitoring Silver Scurf Sporulation in Potato Storages: Adapting Spore Trapping Equipment from the Field to the Storage Environment

Kendra Thurston*[1], Stephen Moorehead[1], Colby Robertson[1], Kristine White[2], Michael Saleh[2], Yaima Arocha-Roset[3]
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[2]Spornado Inc, Toronto, ON, Canada
[3]Sporometrics Inc, Toronto, ON, Canada

Silver Scurf (*Helminthosporium solani)* is a progressive fungal potato disease that produces grey to light brown lesions with a shiny, silver appearance on the tuber surface. The lesions can vary in size but often coalesce to cover large portions of the tuber surface. These skin-deep lesions have a negative impact on tuber appearance and reduce product marketability in the fresh potato industry. While tuber infection begins primarily in the field, once in storage sporulation of diseased tuber lesions can lead to infection of clean tubers, particularly under aggressive ventilation schemes and high relative humidity conditions. In-season management tools exist to limit initial infection and post-harvest chemical applications can be made upon bin-filling to help suppress proliferation within storages. However, after door closure little can be done to control disease spread aside from managing storage conditions. As such, potato storage environments are monitored closely for optimal airflow and humidity to help minimize the spread of inoculum. The ability to quantify spore loads and track changing inoculum levels over time in the storage environment has been identified as a potential benefit to disease management. This would facilitate better-informed, timely management decisions that can reduce the spread of Silver Scurf between lots.

There is potential to use pre-existing equipment that is currently deployed for tracking Late Blight spores in-field during the growing season. *Helminthosporium solani*'s unique conidiophores allowed for a comparable disease evaluation program to be drawn up. Sporometrics Inc, in conjunction with Spornado Inc and The Little Potato Company, cultured several tubers infected with high levels of *Helminthosporium solani*, isolating inoculum to which potato storage spore samples can be compared via laboratory analysis. Spornado spore collection equipment units were mounted within commercial potato storages to evaluate Silver Scurf sporulation throughout both box and bulk storage buildings.

Preliminary data is being used to validate the potential of spore trapping technology within potato storage environments to improve Silver Scurf monitoring and aid in storage management. The change in total spore load over time will be assessed and data will be correlated with storage conditions, storage management practices, and commercial dockage for Silver Scurf at the packing facility as compared to samples taken at bin-filling. Objectives include modelling Silver Scurf sporulation patterns over time in different storage environments, determining the risk of spread to clean product, and improving the ability to respond and alter management decisions to reduce waste. Sample collection is on-going, with an interest to evaluate the required frequency of sample collection for tracking and forecasting purposes. Evaluation of whether a passive (free-standing) or active (fan-powered) collection device is needed for accurate sample collection is also on-going. Future work may include evaluation within washed product coolers in packing facilities to limit disease spread after product washing.

Developing Bioinformatics Toolkits for the Identification and Detection of Plant Pathogens.

Xiang (Sean) Li[1]*, Jiacheng (Eric) Chuan[1,2] and Wen Chen[3]

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In recent years, whole genome sequence (WGS) and bioinformatics analysis have gradually integrated into diagnostics and post-entry quarantine programs to prevent the introduction of invasive and regulated plant pathogens. (Rott, et al 2017). In general, WGS and NGS-based approaches for regulated bacterial and fungal pathogens are less efficient for direct application on regulated samples and commodities due to chromosome sizes.

To date, a few web-applications on whole-genome 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 direct applications for differentiation at interspecies and intraspecies levels of plant pathogens. For instance, both LINS and MiSI take days to process background analysis when dealing with bacterial genomes with 5 Mb, and funal genomes over 40 Mb. Both MiGA and GTDB are web-based servers requiring massive computation resources (CPU and RAM) for background computation. Their applications on diagnostic samples for regulatory decisions need to be tested and verified through cloud uploading and timely background analysis.

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 ring rot, zebra chip and soft rot of potato, as well as potato wart disease (Fig 1). 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*, *Dickeya solani*, *Pectobacterium parmentieri*, *P. atrosepticum*, and *Synchytrium endobioticum* (Fig 2). The Clasnip platform is a web-based platform to quickly classify pathogens and their close relatives based on SNPs and/or whole-genome sequences. It was developed to allow users with minimum bioinformatics background to compare SNPs with curated, high-quality reference databases. Clasnip can accurately identify CLso haplotypes based on specific genetic signatures in seconds, and is also available for identifying the bacterial ring rot pathogen from its close relatives of Clavibacter spp, differentiating different species of soft rot and blackleg bacteria, and different phylogroups of Potato Virus Y (PVY). The building of the customer database and the applications under the Clasnip platform will be detailed in a separate presentation by Eric (Jiacheng) Chuan.

Diversified Bacteria Causing Potato Blackleg and Soft Rot

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BSR is caused by several closely related bacterial species under the genera of *Dickeya* and *Pectobacterium* and is considered a seed-borne disease. Since the 2015 outbreak, potato blackleg and soft rot (BSR) has caused significant losses to potato production in the Northeastern region of the United States. DNA sequence analysis indicated that *Dickeya dianthicola* was highly isolated species in the outbreak, based on plant samples collected from potato fields. Whole genome analysis on 500 isolates collected during the epidemic period resulted in three genotypes, and genotype I was associated with the outbreak. The geographic distribution of the genotypes indicated that BSR might simultaneously originate from various locations. After the first year of epidemic, *Pectobacterium parmentieri* has been frequently detected and became a concern as it caused more damage in the storage. Multiple bacterial species had synergistic effects when they co-infected potatoes, causing much higher disease severity compared to that infected by one bacterial species. In most cases of field plant samples, more than one species of *Dickeya* and *Pectobacterium* were detected from a single lesion. Those bacteria included *D. polaris, D. dadantii, D. atroseptica, D. zeae, P. brasilliense,* and *P. versatile*. Noticeably, *P. versatile* has taken the top among all the species, and *D. aquatica* isolated from water (no host found) can cause severe BSR on potatoes. The pathogens do not survive well in soil. However, they may stay in the water for at least a year. Seed tubers carrying the pathogens may be decayed after planting and result in missed emergence. After planting, the pathogen starts to be active due to the increasing temperature and potato root exudates. The pathogen is spread from seed piece to seed piece by physical handling, cutting, and planting equipment.

Bacterial and Fungal Communities Associated with Russeting and Silver Patch of Potato Tuber

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Blemishes on potato skins including russeting and silver patch are problematic for selling potato tubers for the fresh market. Abiotic and biotic factors increase the presence of blemishes and induce plant stress response that leads to change in metabolic pathways resulting in changes in structural and chemical compounds in cells of potato tubers. However, how the bacterial and fungal communities associated with russeting and silver patch blemishes are affected is not known. The objective of this study was to evaluate the diversity of bacterial and fungal communities of Dark Red Norland tubers with silver patch or russeting blemishes using amplicon-next-generation sequencing. Potato peels were collected from 1) tubers without blemishes (control), 2) tubers with russeting, 3) healthy area of tubers with russeting, 4) tubers with silver patch and 5) healthy area of tubers with silver patch in 2019 and 2020. Most bacterial and fungal phyla had a change in their relative abundance between 2019 and 2020. The β-diversity of bacterial and fungal communities was different between years suggesting that the differences in environmental conditions and length of storage could influence these communities. The β-diversity of bacterial and fungal communities did not change among treatments in 2019 and 2020 except for a few differences among treatments in the β-diversity of fungal communities in 2020. The possibility that russeting and silver patch blemishes were caused by a biological factor was also evaluated by comparing operational taxonomic units (OTUs) present in blemishes to the healthy tuber (control). The criteria used to select the OTUs were 1) that the OTUs should be in high relative abundance in the blemishes, and 2) the OTUs should be the same in 2019 and 2020. This approach was used with lesions of common scab and using these criteria, the most abundant OTUs was classified as *Streptomyces*. Most of the very abundant OTUs in russeting and silver patch were also found in the control however, one bacterial and fungal OTU met these criteria. This study demonstrated that it was possible to use next-generation sequencing to identify OTUs that are repeatedly found in high abundance in blemishes compared to healthy potatoes. However, further investigation is required to determine if these species are simply favored by the change in plant cell metabolite composition structure associated with the blemishes or if they are the cause of the blemishes.

Benefits of a Tripartite Plant-Mycorrhiza-Bacillus Symbiosis in Potato Production

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Mycorrhizae are soil fungi that establish a symbiosis with plant roots. This combination allows better assimilation of water, phosphorus and other mineral elements, promoting better plant growth and better resistance to biotic and abiotic stresses. By exploring the soil, the intense network of hyphae of the mycorrhizal fungus also plays a major role in the physical and microbiological characteristics of soils. Indeed, the carbon exuded into the soil by the hyphae helps support the significant growth of bacterial communities and promotes soil aggregation.

For more than 25 years, mycorrhizal inoculants have been registered and marketed in Canada in agriculture. The objective of this project is to demonstrate whether inoculation with a mycorrhizal fungus can lead to a significant increase in yield for the producer. We also want to see if the addition of a biostimulant bacteria can lead to an additional increase in yield.

Since 2011, 1172 validation trials in real growing conditions have been carried out in Quebec, Ontario, New Brunswick, Prince Edward Island, Maine and France. The results indicate that the application of the mycorrhizal inoculant resulted in an increase in yield in 82.3% of cases. This significant yield increase averaged 9.8%, representing an average yield increase of 32.1 cwt/ac.

In 2021 and 2022, 6 experimental plots were implanted in Quebec, Ontario and Prince Edward Island. Three treatments were applied, namely an untreated control treatment, a treatment receiving a commercial mycorrhizal inoculant (AGTIV® REACH POTATO L) and a treatment receiving the same commercial inoculant supplemented with a biostimulating bacterium (*Bacillus inaquosorum*-PTB185). The results from the experimental plots demonstrate that inoculation with the mycorrhizal fungus brings an increase of 11 cwt/ac in yield, while simultaneous inoculation with the mycorrhizal fungus and a biostimulating bacterium results in nearly double the increase, i.e. a significant increase of yield in potato of 20 cwt/ac when compared to the control. The two microorganisms would therefore have additive or even synergistic effects on the improvement of the yield of marketable tubers.

The results obtained in real growing conditions demonstrate that it is profitable for a producer to apply mycorrhizal inoculants to his field. The use of biostimulant microorganisms in agriculture fits well with a sustainable agriculture perspective, by allowing better use of the water and nutrients present in the soil.

High-Throughput Phenotyping of Potato Plants for Precision Nitrogen Management

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Nitrogen plays a significant role in plant growth and is vital to optimal yields and tuber quality of potato crops. The importance of nutrient stewardship and reducing GHG emissions while maximizing yield potential aids growers both economically and environmentally. Currently, precision N applications are based on the petiole N content of the plant within the growing season. This method is tedious, time-consuming, costly, and not suited for large scale. In recent years, studies using hyperspectral data in agriculture have been promising. Utilizing hyperspectral reflectance data, as an indicator of plant N status within the growing season to make real-time decisions on fertilizer rates is an important step for precision N. Yet the limited application of high-throughput techniques to determine plant N content in field conditions constitutes major knowledge gaps among growers. The main objective of this study is to investigate how we can use leaf level spectral data collected in the field under different N fertilizer treatments and maturity stages to estimate plant N status. We conducted a field trial in summer 2022 in the experimental plots at Fredericton Research and Development Centre. Russet Burbank cut seeds were planted in a complete randomized block design, with 6 different hand applied nitrogen treatments (0, 47.5, 95, 142.5, 190 and 237.5 kg/ha) and 4 replicates totaling 24 plots (plus guard rows). Plants were monitored for leaf level hyperspectral reflectance, photosynthetic rate and chlorophyll *a* fluorescence at stolon initiation, tuber initiation and maturity stage. Leaf samples were collected immediately after measurements at all three stages to analyze total protein and chlorophyll content as well as N content. Preliminary results indicate a clear trend of increasing leaf N content with increasing nitrogen doses. We observed minimal differences in the rates of photosynthesis across the N treatments. Once additional data is received, all analyses will be performed to obtain more granular results that will help support the future findings of this study.

Comparison of two methods for delineating management zones for improved-nutrient management

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Management zones (MZs) is a precision agriculture approach that identifies within-field homogeneous regions with similar characteristics. The MZs are used to control the spatial variability of soil and crop properties. This can help to improve fertilization efficiency and increase yield, by reducing the excessive site-specific nutrient accumulation or loss that can lead to environmental and economic problems. The delimitation of the MZs is not a trivial process because of the complex relationships between topography, soil properties and nutrients. Many methods and tools for MZs delineation have been developed to address this problem. However, the integration of steps that require the adoption of specialized software, statistical analysis, data processing and lack of familiarity with spatial analysis limit the adoption of this practice. In this study, the main objective is to compare the efficiency of two algorithms currently used to delineate MZs using a combination of apparent soil electrical conductivity (ECa) measurements and topography: ISODATA procedure in ARCGIS software (ESRI) and Management Zone Analyst MZA (USDA, a freeware). Efficiency of the two algorithms was compared based on the following criterions: user facility, data process rapidity, similarity of the MZs and determination of the optimal number of MZs per field.
The fields studied in this project belong to the 23 fields of the McCain Farm of the Future, located in Florenceville (New Brunswick, Canada). In order to implement the fertilization management plan of the studied fields, an initial soil grid sampling of 50 m x 50 m was used (i.e. around 850 sampling points distributed in all the fields of the project) to measure soil texture, pH, total carbon and total nitrogen. Additionally, all soil macro- and micro-nutrients were extracted by Mehlich III extractant. Elevation and ECa (0-30 cm and 0-100 cm) were acquired in all the fields using a VERIS 3100. The fields B1 (9.29 ha) and H4 (10.77 ha) were used as an example in this presentation. At field B1, 2732 points were obtained from the VERIS and 38 samples (0 – 15 cm) were used for the analysis of soil properties. At field H4, 7481 points were obtained from the VERIS and 41 samples (0 – 15 cm) were used for the analysis of soil properties. MZs were delineated using elevation and soil ECa at two depths. Variance reduction and performance indices (Fuzzyness performance index, Normalized classification entropy) were used to identify the optimal number of management zones for the ISODATA and MZA methods respectively. Once the MZs were determined by the two methods, the soil samples in each MZ were used to calculate the descriptive statistics of the soil physicochemical characteristics.

Delineated Management Zones via Soil Apparent Electrical Conductivity to Enhance Nitrogen Fertilization of Potato Production

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Nitrogen (N) is the most important macronutrient which required by the potato plant to ensure proper growth and yield. Uneven N supply leads to poor quality production and causes groundwater pollution. The optimal response to N fertilizer application differ by within field spatial variability in terms of difference in soil properties such as soil type, nutrients availability and water supply. Hence, reduction of within field spatial variability through delineation of subfield regions with homogenous characteristics (management zones (MZs)) is helpful in wise utilization of N fertilizer. Herein, we hypothesize that use of soil apparent electrical conductivity (ECa) as a technique to delineate site specific management zones could be a viable approach for optimum N fertilizer application in pedoclimatic conditions of Prince Edward Island (PEI). Four fields located in two areas of PEI, Kensington and Souris were used to test this hypothesis. For the purpose on this communication only the experiment done at Kensington will be presented. Fields located at Kensington (OC 2020 & 2021) were treated with uniform and variable rate application (VRA) of N fertilizer and replicated four times. The experimental design was randomized complete block design. Initial sampling points (100-120) for both fields were selected to measure soil properties and this data was used for cross validation with MZs data. The ECa data was measured using VERIS 3100 soil sensor. Study results indicated that ECa data in combination with topography and yield monitor data was useful in the delineation of management zones for OC 2020 & 2021 fields. Similarly, variable N rate application exhibited more promising results than uniform application in terms of potato yield, production cost and N leaching. The findings suggest that delineated MZs and utilization of variable N rate application could be beneficial in potato production and to reduce N leaching.

Measuring Effects of Slow Release Nitrogen on Yield, Economic Crop Value and Environmental Impacts on PEI Potatoes

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Canadian agriculture is under pressure to reduce greenhouse gas emissions (GHG) associated with plant and animal agriculture by government, the marketplace and society in general at the present time. The potato crop due to it's relatively low nitrogen use efficiency status presents challenges across the country regardless of rainfed or irrigated systems. Field scale trials conducted in PEI 2019-2021 involved comparing current growers' standard practices (GSPs) for nitrogen application with two alternative treatments involving use of Super U^{TM} at two different rates. Results of the two main parameters under investigation - gross crop value and N_2O emissions will be discussed.

Soil properties and nutrient cycling responses to willow chip application

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Willow (*Salix viminalis* spp.) shrubs can be planted along riverbanks, on erodible and marginal farmland. Wood chips made from the woody biomass could improve the properties of light-textured soils with low organic matter content as alternative to being used for burning them for energy. Willow chips were applied at 0, 20, 40, and 60 metric tons ha^{-1} (fresh weight) as a soil amendment. Willow chip application increased soil aggregation, respiration, total C and N contents in whole soil, and plant-available K. Willow chip addition at rates of 40 and 60 Mg ha^{-1} induced mineral N immobilization and reduced barley grain yield and total N uptake. Our results suggest that shrub willow chips increased total organic C and immobilized N following their incorporation and can thus mitigate nitrate leaching after the potato harvest but can also depress yield of a cash crop in the following spring. The N immobilization by willow chips was short-lived and was not observed in the second spring. It would be recommended to seed a forage crop preferably a forage legume after willow chip incorporation. Willow chip incorporation is an effective means to increase soil carbon.

Molecular responses to nitrogen in potato leaves

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Nitrogen (N) supplementation in potato production is used to reach profitable yields and quality. Application of in excess of plant requirements can contribute to losses to ground and surface water and emissions of nitrous oxide, a potent greenhouse gas. High N rates can also negatively impact tuber quality and reduce profitability with increasing costs of fertilizer. The relationship between N supply and tuber production is complicated. The N Harvest Index (NHI) indicates the efficiency of conversion of N taken up by plants into tubers. Atlantic had a higher NHI compared to Russet Burbank in a field trial done at AAFC-Fredericton. Leaves were collected from these plants were used for gene expression analysis. Genes showing differential gene expression between 0 and 180 kg N/ha at time points before and after tuber bulking were compared between the two varieties. The results show that both varieties showed increased expression of a gene involved in N assimilation in photorespiration, amino acid mobilization, sulfur transport. Atlantic had decreased expression of gene for early tuberization. Russet Burbank had increased expression of genes involved in N remobilization. These results suggest differences in N responsive source-sink relations between Atlantic and Russet Burbank.

Diploid potatoes: Too little is not such little genetically and agronomically

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The higher proportion of the untapped potato genetic diversity remains within the diploid potatoes which, compared to the cultivated tetraploid potato (*Solanum tuberosum* L.), carry only two sets of each chromosome. As such, diploid potatoes have been regarded as little potatoes in many aspects, including morphological and genetic features, tuber size, and yield. However, have more attention and resources been deployed for diploid breeding as has been done for tetraploid breeding and selection? To provide some answers, a mutant diploid potato population was developed at the AAFC's Charlottetown Research and Development Centre. This collection is being characterized for genetic and agronomic traits. Here, we show that tuber size, yield potential, as well as agronomic traits such as resistance to biotic and abiotic stresses are not as little as generally thought. Based on the findings, we anticipate a bright and promising future for diploid potato in commercial production if more resources are deployed in it's cultivar development and agronomy.

Development of a Flavorful Dihaploid Potato Germplasm; a Tool for Canadian Fresh Market Potato Breeding

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Over the past decades, fresh potato consumption has steadily been decreasing in North America. Consumers are increasingly looking for more flavourful products and potato is often perceived, rightly or wrongly, as lacklustre. Because of its complex genetic, most potato breeding programs have not been able to efficiently target flavour. Potatoes are tetraploid, highly heterozygous, and suffer from male sterility and self-incompatibility. Those traits limit the use of genetic tools and make it difficult to predict the outcome of a cross between two parental lines. To facilitate the development of new potato lines, the scientific community is working on developing diploid potatoes from tetraploid cultivars. While the focus is predominantly on processing cultivars with high economic value, there is a clear need for new material oriented to the fresh table market. This reality is even more important in Quebec where fresh potatoes is the primary outlet for local growers. The main goal of the project was to develop a diploid germplasm from flavourful fresh market cultivars. Crosses between cultivars and inducer lines lead to a small percentage of dihaploid embryos retaining only the genetic material of the maternal gametes. In total, around 150 diploids were developed from 20 different parental lines covering various fresh potato types. Dihaploids were grown in greenhouses then transferred in a replicated field trial to assess their agronomic traits and their aroma profiles. Substantial differences were observed between dihaploids derived from the same parent and between each population. This germplasm will provide great resources for breeders to develop more flavourful cultivars and offer material for upcoming genomic studies.

Exploring a New Method to Assess Tuber Skin Strength in the Field

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Skin setting on potato (*Solanum tuberosum*) tubers is a well understood process, whereby the phelloderm, phellogen, and phellum are involved in producing a suberized periderm. This process occurs after natural senescence but is often induced prematurely in cultivated table potato production. Completing skin set on potatoes for the fresh market is important to reduce the likelihood of external defects, such as skinning, and to limit dehydration. One method of inducing skin set is to force senescence of the potato foliage via chemical means, effectively mimicking natural senescence and triggering the physiological pathways involved in skin set. In 2019, the European Union withdrew registration of herbicides containing the active ingredient diquat, which eliminated an option used to induce premature senescence. To investigate alternative options, such as the use of protoporphyrinogen oxidase (PPO) inhibitors, and their effect on skin set, a tool was developed with the goal of measuring skin shear strength in the field. The tool consists of a Sealey Torque Screwdriver (Model STS103) with a 15-millimeter diameter wooden dowel glued to the screwdriver bit. The flat surface of the wooden dowel is the contact point with the tuber. The flat surface of the wooden dowel is cleaned and sanded between measurements to keep a consistent surface. Knowing that a suberized periderm will have a higher shear strength than a non-suberized periderm, the tool measures the Newton-metres of force needed to shear the periderm free of the underlying tuber tissue. The resulting number provides an estimate of skin set in comparison to other tubers. This tool could be applied to trial novel herbicides for inducing skin set as well as assessing the skin set of novel potato varieties. This tool is more affordable than tabletop penetrometers but does not match their sensitivity. Further development will include addition of a compression spring in-line with the wooden dowel to buffer downward force applied to the tuber. Additional validation of the tool on Little Potato Company varieties will take place in the 2023 crop year. Paired comparisons between the thumb method of testing skin set, which is a current industry standard, and using the tool will provide further insight into the accuracy of the tool. Random locations in commercial fields will be selected for sampling of tubers after induced senescence. The thumb method's pass/fail result will be compared to the numerical result of the tool. Statistical analysis can be conducted on the resulting paired samples and correlation determined. Overall, the tool has potential for use in a field environment to quickly gauge skin set of a potato tuber.

Wild Potato Relatives for Breeding Colorado Potato Beetle Resistance

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The Colorado potato beetle (CPB) has become a global pest that primarily feeds on *Solanum* foliage, causing severe defoliation in potato. The beetle's adaptive resistance to insecticides has brought about increased interest in breeding for resistance in potato through intercrossing with wild relatives. *Solanum okadae*, a wild species native to Argentina and Bolivia, demonstrated natural deterrence towards CPB. Liquid Chromatography-Mass Spectrometry (LC-MS) metabolite profiling revealed differences in foliar metabolites between *S. okadae* and domesticated potato, *Solanum tuberosum* cv. Shepody. LC-MS profiles were consistent with the presence of cardiac glycosides in the foliar tissue of *S. okadae*, but not *S. tuberosum* cv. Shepody. This class of natural products have known insecticidal activity through inhibition of animal Na^+/K^+ ATPase. Foliar extracts from *S. okadae,* but not *S. tuberosum*, were found to inhibit CPB Na^+/K^+ ATPase, providing additional evidence for the presence of cardiac glycosides. Cardiac glycosides are rarely found in Solanaceae. This novel finding suggests a new mode of plant resistance against CPB that can be used in breeding.

Irrigation Effect on Yield, Skin Blemishes, Phellem Formation, and Total Phenolics of Red Potatoes

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Dark Red Norland is an important potato cultivar in the fresh market due to its attractive bright, red colour, and good yield. However, skin blemishes such as silver patch, surface cracking, and russeting can negatively influence the tuber skin quality and marketability. It is well known that potato is a drought-sensitive crop. This study was conducted to determine whether irrigation would affect Dark Red Norland's yield and skin quality. A three-year field trial was conducted by Peak of the Market in Manitoba, Canada. Plants were treated under irrigation conditions. The results show that irrigation increased the total yield by 20.6% and reduced the severity of surface cracking by 48.5%. Microscopy imaging analysis demonstrated that tubers from the rainfed trials formed higher numbers of suberized cell layers than those of the irrigated potatoes, with a difference of 0.360 to 0.652 layers in normal skins. Surface cracking and silver patch skins had more suberized cell layers than the normal skins, with ranges of 7.805 to 8.333 and 7.740 to 8.496 cell layers, respectively. A significantly higher amount of total polyphenols was found in the irrigated samples with a mean of 77.30 mg gallic acid equivalents (GAE)/100 g fresh weight (fw) than that of the rainfed samples (69.80 mg GAE/100 g fw). The outcome of this study provides a better understanding of the water regime effect causing these skin blemishes, which could potentially be used to establish strategies to improve tuber skin quality and minimize market loss.

Development of a core collection of heirloom and heritage potato varieties for use in breeding, research and education

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Genetic diversity preserved in crops genebanks such as the Canadian Potato Gene Resources (CPGR) in Fredericton, NB, plays a key role in food security by providing raw material for breeding new improved crop varieties. Genetic resources maintained at the CPGR include a collection of Canadian-bred varieties, breeding germplasm, disease resistant checks and heirloom varieties from Canada and other parts the world. The latter group exhibits a great diversity of skin and flesh colour combined with unusual tuber shapes, textures and flavours. These varieties have survived over 100 years and are reported to have unique culinary quality, adaptation traits or historical value. Enhanced phenotyping and next-generation genotyping technologies are being used to characterize and assemble a core collection of genetic diversity with minimum redundancy for use in breeding, research and education. Information generated will be useful for developing varieties that meet current and future demands of consumers and climate change.

Genomic Prediction and Association Analysis in the Agriculture and Agri-Food Canada Potato Breeding Program.

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Genomics-assisted breeding strategies have great potential to improve genetic gain in potato breeding programs. The AAFC potato breeding program has implemented several changes for measuring critical traits using quantitative approaches to improve data quality. These changes include digital image analysis and colorimeters for measuring key tuber traits. In parallel to improved phenotyping, DNA marker genotyping has been conducted using single markers linked to major disease resistance traits and genome-wide SNP markers. For this study, 1103 potato clones were genotyped using the SolCAP V4 SNP array through Neogen Canada. Filtering of the data resulted in 19,123 SNP marker genotypes. This marker data was combined with data collected between 2019 and 2022 for many traits evaluated in trials grown at breeding stations in New Brunswick and Alberta and in National trials across Canada. For each trial/trait combination, best linear unbiased estimators (BLUEs), variance-covariance matrices, and broad-sense heritabilities were calculated using mixed models in AS-REML/R. Multiple location analysis was completed to assess the proportion of variance attributed to additive, non-additive, and genotype x environment effects. Genome-wide association analysis (GWAS) was conducted to identify significant markers and determine the proportion of variance explained by the most significant marker effects. Best linear unbiased predictors (BLUPs) of breeding values were calculated for each clone/trait combination. The vast data sets generated provide valuable information for better understanding the genetics underlying key potato traits. Known marker-trait relationships were confirmed for several traits and new associations were identified. Breeding values were used to identify parents for crossing to generate the next cycle of breeding material for selection. Examples from the various analysis steps will be presented. Additional data will be added for new breeding clones each year and the prediction models will be improved each breeding cycle. This research has substantially changed AAFC's potato breeding program and will lead to better potato varieties for the Canadian industry.

Detecting historical selection in modern potato varieties using genome-wide marker information.

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Modern potato varieties are a result of two processes; the domestication process where wild species and/or landraces were adapted for cultivation, and the improvement process where early cultivated potato genotypes have been under intense selection by modern breeders for increased productivity and agronomics related to end use (e.g. processing vs. fresh market). Here we describe efforts to detect and characterize regions of the potato genome under putative selection during improvement by contrasting modern cultivars and breeding lines with a panel of heritage potato varieties that have been released (or described) before 1900. All potato clones were genotyped at ~40000 single nucleotide polymorphism markers through genotyping by sequencing, as part of a larger initiative to characterize the entire AAFC potato germplasm collection maintained in Fredericton NB. Using principal component analysis on the entire marker set we find low population structure among the modern and heritage clones, and between the processing clones and fresh market clones. Moreover, we also detect differences in linkage disequilibrium decay among the heritage clones and the modern clones, which may be indicative of increased opportunities for recombination in the modern group. Using a genome-wide scan for genome differentiation among each combination of market class and the heritage varieties, we identify the genomic regions exhibiting extreme differences in nucleotide diversity and F_{st} among the modern and heritage groups, and characterize these regions as unique to a market class, or shared among market classes. Gene ontology (GO) enrichment analysis was used across each extreme region in order to uncover any pattern of putative selection on particular gene functions.

Poster Presentations

Automatic Potato Calibration : Artificial Intelligence and Mobile App

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Making a good estimate of the characteristics of potato tuber yield after harvest is a tedious task that easily suffers from consistency and uniformity issues. We therefore designed an easy-to-use mobile application that uses artificial intelligence and computer vision to characterize a set of tubers simply from an image taken by a cell phone. The application makes it possible to consecutively process several photographs to obtain the characteristics (mass, length, width, calibers) of a representative sample as well as the associated statistical margins of error. The tuber recognition was implemented with a U-Net deep neural network with a total of 12 images subdivided in patches of 32 x 32 pixels. The final training set had 2400 patches and 20% were used for validation. The conversion of pixels to metric units for the measurements is done through the automatic detection by another U-Net neural network of 4 cm targets that are placed throughout the image. As for the weight estimation model, it is a multi-layer perceptron trained to infer weight from length and width for each variety. The algorithm was evaluated using a sample of 72 Mountain Gem tubers and 76 Burbank tubers. The measurements obtained by the neural network were compared to hand-measured data for those samples. The mean absolute error was under 4 mm for width and length of both varieties and the error for the total weight of each sample was under 2%. Even though the tests were conducted mainly with Mountain Gem Russet and Russet Burbank, the system would easily be generalizable to any variety that is similar in appearance. The results show promising performance and robustness to variations in the images such as a non-uniform background or unrelated color objects. This system therefore allows to quickly get an accurate estimation of the main characteristics that impact value for the buyer, which allows the producers to better plan their sales without the need for additional expensive equipment.

Projected Climate Change and Potato Varieties: Impact Analysis

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Potato (*Solanum tuberosum* L.) crop is one of the major food sources worldwide and is sensitive to changes in temperature and precipitation patterns. To mitigate the impact of climate change on potato production, it is crucial to study the impact of the changes on different potato varieties and identify varieties that are better adapted to changing climatic conditions. This project investigates the physiological and biochemical changes in 7 selected potato varieties (Alverstone, Columba, Dakota Russet, Highland Russet, Mountain Gem, Red Norland, and Russet Burbank). In the greenhouse experiment, plants were grown at 50% water-holding capacity (WHC) (drought stress treatment) and 100% WHC (control). In the growth chamber experiment, plants were grown at normal temperatures (based on the mean temperature in PEI from May to September) with 100% WHC (control) and 4^{o}C higher than normal temperature with 50% WHC (combination stresses treatment). The results from the greenhouse experiments showed that the varietal responses to stress were significantly different. Varieties Dakota Russet, Russet Burbank, and Red Norland showed a significant increase in greening compared to the other varieties. Dakota Russet is the only variety that showed a significantly higher specific gravity under drought conditions. Even though the number of tubers did not show a significant difference among the seven varieties, the total yield recorded for varieties Alverstone, Dakota Russet, and Mountain Gem were significantly lower than their counterparts under the 100% WHC condition. There was no significant difference in photosynthesis rate, transpiration rate, stomatal conductance, chlorophyll index and leaf area after the first treatment [tuber initiation stage, from 35-49 days after planting (DAP)], while after the second treatment (tuber bulking stage, from 63-77 DAP), the photosynthesis rate of varieties Alverstone, Dakota Russet, Russet Burbank, and Mountain Gem were reduced significantly. Varieties Dakota Russet, Russet Burbank, and Mountain Gem showed a significantly reduction in transpiration rate after the second treatment. Varieties Alverstone, Dakota Russet, and Red Norland showed a significant increase in chlorophyll index after the second drought treatment. From the growth chamber experiments, the results showed that plants that grew under both heat and drought stress germinated significantly faster. Varieties Alverstone, Dakota Russet, Russet Burbank, and Mountain showed a significant decrease in leaf area, while their photosynthesis rate, transpiration rate and water use efficiency were not significantly impacted. Varieties Alverstone, Russet Burbank, and Mountain showed a significant increase in chlorophyll index after the second treatment. The Dakota Russet, Russet Burbank, and Mountain Gem showed a significant reduction in tuber yield, but the specific gravity in all varieties did not show any significant difference among control groups and treatment groups. Future work will focus on the biochemical analysis of soluble sugar, soluble protein, glycoalkaloids, and proline.

Forecasting Greenhouse Gas Emissions from Potato Production Using Machine Learning and Artificial Intelligence Modelling

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Global climate is changing promptly and has become a significant environmental issue. The increased greenhouse gas (GHG) concentrations associated with anthropogenic activity is the primary cause of global warming. The most considerable GHGs are carbon dioxide (CO_2), methane (CH_4), and nitrous oxide (N_2O), which contribute 60%, 20%, and 10%, respectively, to global warming. Canada is among the top ten countries contributing to GHG emissions per capita. There are many sources responsible for contributing to emissions; however, agriculture is one of them and acts as a source and sink of GHGs emissions. The best management practices should be adopted to quantify and mitigate emissions. This study aims to quantify and predict GHG emissions during the growing season of the potato crop. The LICOR instruments will quantify the emission weekly according to experimental design. Different chamber techniques will be used to calibrate and validate the LICOR. This automatic chamber for soil gas flux provides high-quality data at high temporal resolution. To develop the denitrification and decomposition (DNDC) model, input parameters, including soil physical, chemical, and hydraulic properties, will be determined. Furthermore, climatic data and management practices (irrigation versus rainfed) will be utilized. The DNDC model, artificial intelligence (AI), and deep learning (DL) models will be calibrated and validated using the observed emission data during the potato growing season. Different scenario analyses using historical and future climatic data will be simulated for developing relationships of climatic parameters with emissions using DNDC, AI, and DL models. These state-of-the-art AI and DL techniques will help to predict emissions with minimal input parameters. These techniques can be upscaled to develop high-resolution emission maps at a regional scale.

The Future of Irrigation: Exploring the Potential of Variable Rate Systems using Internet of Things for Improved Water Productivity

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Climate change, extreme weather events, and irregular rainfall patterns have given rise to supplement irrigation needs in rainfed regions such as Prince Edward Island (PEI). This study aims to develop a variable rate irrigation (VRI) system to increase crop productivity in PEI. This project will develop, implement, and assess the VRI technology in water-stressed areas to optimize water resources with site-specific irrigation. In the first phase of this project, the Soil Water and Topographic (SWAT) based irrigation maps will be developed to assess water requirements spatially, with soil moisture probes using internet of things (IOT) and weather stations installed at experimental sites. . In the second phase, a central pivot irrigation system with variable rate controllers will be used to optimize water use efficiency based on moisture prescription maps. This study aims to integrate the SWAT map, soil moisture data, and weather station data into the SWAT program to prescribe irrigation maps. This project aimed to evaluate VRI technology's feasibility in ensuring sustainable irrigation in PEI. The outcome of this study ensured precision irrigation management by conserving water resources for future generations. The proposed methods and some initial investigation results will be presented at the conference.

A Cost-Effective Solution for Agricultural Crop Monitoring Using Generative Adversarial Networks and RGB Cameras

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Abstract

Vegetation indices (VI) are widely used in agriculture for crop growth monitoring, health, and yield potential. The VI provides valuable information to make informed decisions in crop management, fertilizer applications, irrigation scheduling and crop harvesting. This study used direct translation of RGB imagery in various useful VI, including normalized difference vegetation index (NDVI), enhanced vegetation index (EVI), transformed vegetation index (TVI), green index (GI) and simple ratio (SR). The generative adversarial networks (GAN) were trained on drone images captured with a RedEdge-MX sensor from five different potato fields in Prince Edward Island – Canada, during the growing season of 2020-2022. The images were captured throughout the growing season under vegetation (15-30 DAP: days after plantation), tuber formation (30-45 DAP), tuber bulking (75-110 DAP), and tuber maturation stages (>110 DAP). Five thousand pairwise images were generated for all the VI and used in the training and evaluation of GANs (80% training, 10% validation, and 10% testing). Two famous GANs, namely Pix2Pix and Pix2PixHD, were tested in comparison with various training and evaluation indicators. The results retrieved from training and evaluations of GANs were promising in translating RGB imagery into useful VI. After the training, the RGB images can be translated into VI without using a multispectral camera or infrared bands. This innovative protocol can also translate remote sensing imagery of large-scale agricultural fields into useful VI to extract information about plant health indicators. More detailed results will be presented at the conference.

Exploring Electrical Conductivity For Soil Compaction

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Soil compaction is a difficult issue to detect and goes unseen throughout many potato fields. With the increasing weight of agriculture machinery along with the repeated tilling of fields, this causes a decrease in soil quality and makes fields more susceptible to compaction. This can further lead to fields becoming waterlogged and eroded, resulting in a decrease in crop yield, which has a negative impact on farmers financially. The aim of my research is to use electromagnetic induction (EMI) to determine the relationship between the apparent electrical conductivity (ECa) in the rootzone depth (45 cm) of the potato crop and areas of compaction. The creation of within field management zones can help farmers conduct variable rate tillage to minimize soil disturbance, ultimately improving soil health, and crop yield.

Short Term Effects of Rotation Length and Plant Diversity in Potato Production Systems on Nitrogen Cycling Communities

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Potato production in the Atlantic region is characterized by two-to-three year rotations with low plant coverage and diversity, resulting in decreased soil quality and productivity. While improved potato production systems with greater diversity, soil coverage, and longer rotations could help mitigate these issues, unintended trade-offs such as increased nitrogen (N) loss through denitrification may occur. The objective of this study was to compare the effects of three improved potato production systems to the conventional potato-barley rotation on soil properties and the abundance of denitrifiers and nitrous oxide (N_2O) reducers. The field trial established in 2021 is a split-plot design with crop rotation as the main plot and the presence or absence of N fertilizer as the subplot, replicated four times. The crop rotations were: 1) potato-barley (P-B), 2) potato - multi-species mix (P-M), 3) corn-spring wheat under seeded with clover and timothy-potato (C-Wct-P), and 4) corn under seeded with ryegrass - spring wheat under seeded with alfalfa and timothy - potato (Cr-Wat-P). Soil samples were taken three times per growing season to measure soil properties (nitrate (NO_3^-), ammonium (NH_4^+), gravimetric water content (GWC), pH), and to quantify the functional nitrite reductase (*nirS*, *nirK*) and N_2O reductase (*nosZ* clade I, *nosZ* clade II) genes of denitrifiers and N_2O reducers. Permanganate oxidizable carbon (POX-C) was measured once per year in July. The fertilized soil of P-B and P-M had greater NO_3^- concentration compared to C-Wrc-P and Cr-Wat-P treatments in both years, while the remaining soil properties were unaffected by treatment. Averaged over time, the abundance of *nosZII* genes was greater under the fertilized P-B and P-M compared to both fertilized corn treatments in 2021, but in 2022 P-M had the highest, while P-B had the lowest abundances of *nirS* and *nosZII* compared to all treatments. The abundances of *nirK* and *nosZI* denitrifiers were unaffected by treatment in both years. Spearman's correlations revealed that all genes were positively correlated with pH, while *nirS*/*nosZII* and *nirK/nosZI* were negatively and positively correlated with GWC, respectively. Yearly variations in soil properties included a decrease in GWC, POX-C, NO_3^-, and NH_4^+ concentrations and an increase in pH between 2021 and 2022. Correspondingly, in 2021, *nirS* and *nosZII* genes were greater in abundance in fertilized soils of all treatments compared to the control plots averaged over time, while the reverse was observed for the abundance of *nosZI* denitrifiers. The opposite trends were seen in 2022. This suggested that the growth of *nirS*/*nosZII* and *nosZI* is favored in N-rich soils when GWC is lower or greater, respectively, suggesting the occupation of separate competitive niches under different environmental conditions. These results demonstrated that crop production systems can influence the abundance of denitrifiers and N_2O reducers, but there is a stronger effect of environmental conditions and fertilization regime. Further investigation is required to understand the possible links between the changes in the abundance of denitrifiers and N_2O reducers to N_2O emission


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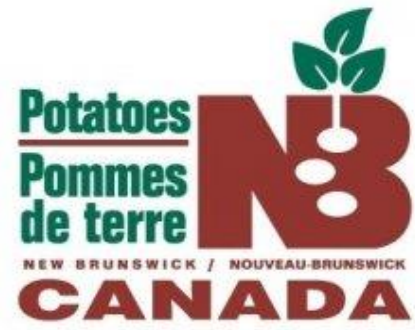
Fungal disease prevention detection program


Prince Edward Island
PEI
POTATOES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