2025 NORTHEAST POTATO TECHNOLOGY FORUM

March 13-14, 2025

Conspectus

NORTHEAST POTATO TECHNOLOGY FORUM - 2025

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 13-14, 2025 at the Delta Hotel Fredericton, New Brunswick.

A total of 32 oral and three poster scientific presentations were made as part of four sessions grouped by subject matter. Sessions dealing with pest and pathogen detection and management, agronomy, potato traits and breeding, and nutrient dynamics 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 2025. We would particularly like to thank Syngenta for sponsoring the reception. We would also like to thank all of the sponsors for their support.

Local Chair: Claudia Goyer

Local Organizing Committee: Jess Vickruck, Khalil Al-Mughrabi, Tyler MacKenzie, Kyle Gardner, and Sean Whitney

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2025 NORTHEAST POTATO TECHNOLOGY FORUM
March 13 and 14, 2025

Thursday, March 13, 2025

1:00 pm Welcome

Session 1: Soil Amendments and Nutrient Dynamics
Moderator: Ryan Barrett

1:15 Yefeng Jiang**: Impact of Cover Cropping on Nitrate Leaching from Potato Rotations**

1:30 Charles Karemangingo**: Predicting Plant-Available Nitrogen From Mineralization**

1:45 Takudzwa Nawu**: Labile Soil Health Indicators Response to Fertilizer N Management Strategies: Insights From On-Farm Trials in New Brunswick**

2:00 Li Sheng: **Developing a Field Evaluation of Soil Health (FESH) tool for New Brunswick**

2:15 Shu Zhang**: Carbon Flux Estimation for Potato Production: A Literature-Based Study**

2:30 Serban Danielescu**: Past and future climate change impacts on potato cropping: yield, nitrate leaching and nitrous oxide emissions**

2:45-3:15 BREAK

Session 2: Potato Traits and Breeding
Moderator: Kyle Gardner

3:15 Benoit Bizimungu: **Canadian Potato Genebank Update: Conservation and Use of Potato Genetic Resources**

3:30 Linqi Cai**: Identification of Gene Markers for Potato Drought Tolerance Prediction**

3:45 Keshav Dahal**: Effects of Elevated CO_2 on Photosynthetic Performance, Water Use Efficiency and Potato Yield**

4:00 Bourlaye Fofana**: Common Scab On The Genetic Grid Of Diploid Potatoes**

4:15 Robyn Morgan**: Examination and Genetic Analysis of a Novel Yellow-Green Leaf Mutant of Potato**

4:30 Helen Tai: **True potato seed – what was old is new again**

4:45 Jonathan Neilson: **Post harvest tuber phenotyping using large data and artificial intelligence.**

5:00 Yanxue Zhao**: Spray-Induced Gene Silencing (SIGS) as a Potential Tool to Control Wireworms (Agriotes spp.) in Potatoes**

5:15 Kyle Gardner**: The Colour and the Shape: genomewide association analysis of tuber colour and shape variability in a genetically diverse population of potato varieties.**

5:30 Closing Remarks Day 1

5:35 Syngenta Reception – Delta Hotel Suite

Friday, March 14, 2025

8:00 am **Welcome**

Session 3: Pest and Pathogen Dynamics
Moderator: Jianjun (Jay) Hao

8:15 Ryan Barrett**: Examining the Use of Minuet® Biopesticide for Control of Common Scab in Processing Potato Varieties**

8:30 Dahu Chen**: Impacts Of Primary Non-inversion Shallow Tillage And Moldboard Plowing On The Potato Early Dying Disease Complex In Prince Edward Island, Canada**

8:45 Jianjun Hao**: Evolving Dynamics: Shifting of Bacterial Species in the Potato Blackleg and Soft Rot Disease Complex over a Decade in the Northeastern U.S.**

9:00 Shuanglong Huang**: Biological Control Mechanisms and Their Role in Managing Potato Diseases: Insights into Pathogen Lifestyle**

9:15 Avneet Kaur: **Harnessing Machine Learning and Deep Learning for Potato Disease Identification: A Climate-Resilient Approach to Sustainable Agriculture**

9:30 Tyler MacKenzie**: Quantifying Rates of Resistance to Common Pyrethroid and Neonicotinoid Insecticides in New Brunswick Aphid Populations**

9:45 Shayli Morris**: Effects Of Successive Soil Fumigation With Metam Sodium On Verticillium Wilt Of Potato**

10:00-10:30 BREAK – Poster session

10:30 Charanpreet Singh**: A Robotic Solution for Automating the Rouging Process in PVY-Affected Potato Fields**

10:45 Jiacheng Chuan**: Exploring the Potential of Metagenomic Approaches for the Detection and Confirmation of *Clavibacter sepedonicus*.**

11:00 Claudia Goyer**: Managing Potato Common Scab with the synthetic auxin 2,4-D and the biopesticide Minuet**

11:15 Sneha Surya Narayana Murthy**: DNA-Based Profiling of Microbial Diversity in Four Streams of Agricultural Landscape in Atlantic Canada**

Session 4: Agronomy
Moderator: Tyler MacKenzie

11:30 Ikechukwu Agomoh**: The Impact Of Diversifying Potato Crop Production Systems With Perennial Multispecies On Soil Health And Greenhouse Gas Emissions**

12:00 -1:00 Lunch

1:00 Monica Everett**: Dacom the New Brunswick Experience**

1:15 Felix LaRoche-Johnston**: Improving Potato Production: How do Bacterial and Mycorrhizal Inoculants Work for You?**

1:30 Chukwuemeka Eneh**: An Improved Meteorological Drought Forecast Model Leveraging SPEI Time Series Decomposition For Atlantic Canada**

1:45 Saad Cheema**: Machine Learning-Driven Precision Irrigation: A Novel Approach to Optimizing Potato Crop Coefficient (Kc) for Enhanced Water Use Efficiency**

2:00 Closing Remarks Day 2

Impact of Cover Cropping on Nitrate Leaching from Potato Rotations

Y. Jiang*, J. Nyiraneza, T. Fraser, C. Noronha, A. Kostic, D. Murnaghan and J. Matheson
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Excessive nitrate leaching from intensive potato production has been linked to groundwater contamination and eutrophication in downstream surface waters. This study evaluated the effectiveness of two cover cropping practices in reducing nitrate leaching from the barley–red clover–potato rotation commonly used in Prince Edward Island, Canada. A field experiment was conducted from 2018 to 2023 at the Harrington Research Farm, Agriculture and Agri-Food Canada, on sandy loam soil. The rotation included red clover in 2018, Russet Burbank potatoes in 2019 and 2022, and barley in 2023. Three treatments were tested in a completely randomized design with three replicates each. Treatment 1 (control) incorporated red clover into the soil with a moldboard plow in early November, representing conventional management practices. Treatment 2 terminated red clover in mid-August using glyphosate and disking, followed by buckwheat cover crop planting. Treatment 3 planted fall rye cover crops after potato harvest in 2019 and 2022. Each 0.5-hectare plot was equipped with three 10-cm diameter perforated tile drains installed at an 85-cm depth, connected to a PVC main line for monitoring nitrate leaching. Daily tile drainage samples were collected using ISCO auto-samplers, and nitrate concentrations were analyzed with a Lachat QuikChem 8500 flow injection analysis system. LEACH-N was used to estimate daily soil drainage, and nitrate leaching mass was calculated by multiplying daily drainage volume by nitrate concentration. Cumulative nitrate leaching from cover crop planting to termination or harvest was used to assess treatment effects. A total of 9,299 tile drainage samples were analyzed during the study. The buckwheat cover crop in 2018 significantly reduced nitrate leaching by 24% compared to conventional management (buckwheat cover crop could not be implemented in 2021 under the COVID-19 restrictions). The fall rye cover crops in 2019 and 2022 reduced nitrate leaching by 28% and 10%, respectively, though these reductions were not statistically significant, likely due to limited replication. Both cover cropping practices also improved marketable potato yields, though the increases were not statistically significant. These findings highlight the potential of cover cropping practices to mitigate nitrate leaching while maintaining potato productivity, offering a promising approach for sustainable agricultural management in intensive potato rotations.

Predicting Plant-Available Nitrogen From Mineralization

Charles Karemangingo[1*], Tommy Dixon[1], Jean-Mars Jean-François[2], and Cedric MacLeod[3]

[1] New Brunswick Department of Agriculture, Aquaculture, and Fisheries, Fredericton
[2] New Brunswick Soil and Crop Improvement Association, North-West Region
3 Living Lab Project, AAFC, New Brunswick.

Cover crops introduced in many crop rotation systems can mineralize and supply appreciable amounts of nutrients, particularly nitrogen, to subsequent crops. In that perspective, this study was initiated in 2024 to assess soil nitrates (NO_3-N), soil carbon: nitrogen ratio (C:N ratio), and soil electrical conductivity (EC) as indicators of mineralization and predictors of plant N availability and uptake. The project was implemented in three fields located in the Woodstock area and in three more fields located in the Grand Falls area. Cover crops mainly consisted of mixes of Daikon radish and legumes (green peas and horse beans) in Grand Falls and peas /oats in Woodstock. They were incorporated with the 2023 fall tillage. Moderately late or late potato varieties were planted mid-May 2024. Mineralization was estimated as the differential nitrogen mass balance as the sum of the amounts of NO_3-N in the soil and N accumulations in the shoots and leaves at specific periods of the plant growth or N accumulations in the potato tubers at harvest time and discounting the amounts of fertilizer applied at planting. Preliminary results indicated maximum NO_3-N amounts in both 0-15cm and 0-30cm soil depths around 30 days after planting and fertilizer application. Soil EC highly correlated with soil NO_3-N throughout the season (r= 0.93 and 0.90 in 0-15cm and 0-30cm soil depth, respectively). Maximum N accumulations in potato shoots and leaves were obtained in mid-July. They varied from 153.9kg N ha^{-1} for moderately late maturing varieties to 194.1kg N ha^{-1} for late maturing ones. During that same period, nitrates in the 0-30cm soil depth varied from 20.8 to 86.7mg NO_3-N /kg. At harvest, positive net nitrogen mass balances, excluding unknown amounts associated with N losses, N immobilizations, and other mineral forms of N in the 0-30cm soil depth, varied from 85.8 kg N /ha to 306.6kg N /ha with an average amount of 171.0kg N /ha. Over the growing season, these amounts of nitrogen are considered to only represent partial net mineralization.

Labile Soil Health Indicators Response to Fertilizer N Management Strategies: Insights From On-Farm Trials in New Brunswick

Takudzwa Nawu*[1, 2], Ikechukwu Agomoh[1,2], Francis Zvomuya[1], Louis-Pierre Comeau[2], Claudia Goyer[2], Cameron Wagg[2], Sheldon Hann[2], Judith Nyiraneza[3], and Cedric MacLeod[4]

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[2]*Agriculture and Agri-Food Canada, Fredericton Research & Development Centre, Fredericton, New Brunswick, Canada*
[3]*Agriculture and Agri-Food Canada, Charlottetown Research & Development Centre, Charlottetown, Prince Edward Island, Canada*
[4]*Agriculture Alliance of New Brunswick*

Nitrogen (N) fertilizer is essential for optimal crop yield and quality, resulting in enhanced aboveground and belowground biomass that gradually contribute to soil organic matter. Strategies like optimizing the timing and rate of N fertilizer application can enhance plant N use efficiency and N cycling, which improves the quality and quantity of labile C and N indicators of soil health. This on-farm research investigated the effects of N fertilizer timing and the use of urease and nitrification inhibitors on labile soil health indicators during the growing season in annual cropping systems in New Brunswick, Canada. We conducted a 2-year study at three farm sites under corn-soybean, potato-soybean and oat-potatoes crop rotations. Each farm site had four treatment strips, including the recommended fertilizer N rate applied at planting with no inhibitor (NI-F_{100}), the recommended N rate applied with inhibitors at planting (I-F_{100}), split-applied fertilizer N (60% applied at planting and 40% as post planting N) with inhibitors (I-$F_{SPLIT100}$), and split application of N fertilizer at 85% of recommended rate with both inhibitors (I-$F_{SPLIT85}$). Soil samples were collected from the 0 – 15 cm layer in July each year. Labile soil health indicators which include potentially mineralizable N (PMN), soil respiration (24-h CO_2-C), permanganate-oxidizable carbon (POXC), water extractable organic carbon (WEOC), and water extractable organic N (WEON) were measured. Preliminary results showed that POXC was not significantly affected by fertilizer N treatment. Split application of N fertilizer with inhibitor treatments (I-$F_{SPLIT100}$ and I-$F_{SPLIT85}$) significantly enhanced PMN by 19% and 22.6%, and 24-h CO_2-C by 32% and 36.3%, respectively, compared to NI-F_{100}. This suggests that optimizing the timing and application rates of N fertilizers can enhance N use efficiency, which promotes plant root growth, increases rhizodeposition, and subsequently stimulates microbial activity, resulting in improved labile C and N pools. Additional data will be collected in the 2025 field season and will assist farmers make informed decisions regarding fertilizer N management strategies that will improve and maintain soil health and boost crop productivity thereby supporting sustainable crop production in New Brunswick's annual cropping systems.

Developing a Field Evaluation of Soil Health (FESH) tool for New Brunswick

Sheng Li[1,], Fangzhou Zheng[1], Yulia Kupriyanovich[1], Sheldon Hann[1]*

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Soil health is vital for agricultural production. Unfortunately, soil health has been steadily declining in New Brunswick (NB), posing great threat to the sustainability of agriculture. There is a growing attention on soil health from researchers and professionals to producers and general public. However, improving soil health requires the ability to evaluate the status of soil health. Existing evaluation methods rely heavily on lab analyses thus are expensive and difficult, not suitable for farmers to use. To meet this challenge, a grass-roots level Field Evaluation of Soil Health (FESH) tool was developed to take the advantage of citizen science. The FESH tool includes a set of Soil Health Indicators (SHIs) reflecting the physical, chemical and biological health of the soil. For each SHI, easy-to-use field methods were tested and adapted to conditions in NB. A Standard Operation Procedure(SOP) was developed for each SHI to facilitate its adoption by professionals and farmers. The outcome was an evaluation framework with a set of SHIs that can be scored with simple field methods. Meanwhile, a reference database and maps were established to provide the SHI scores a context for comparison at different locations in NB. The first version of the reference database and maps were developed from existing soil databases and maps. When the FESH tool is used, the results will provide fresh input data for the reference database and maps so that they will be constantly updated. The tool will provide famers the ability to track soil health change over time and to compare their fields to other fields in the region. The scores of individual SHIs can be used to guide management practices to targeted SHIs with low scores. The overall patterns of SHI scores in the province and their changes over time can provide useful information for policy making in order to enhance the sustainability of agriculture in NB.

Carbon Flux Estimation for Potato Production: A Literature-Based Study

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Objective: This study aims to estimate the carbon flux associated with potato production and seeks to identify the key components contributing to this flux and explore potential mitigation strategies.

Methods: Two calculation methods are employed to estimate the carbon flux of potato production. The first method considers potato production from a stage perspective, utilizing field-scale studies for the cultivation stage and Life Cycle Assessment (LCA) studies for the post-harvest handling stage. The second method examines potato production from a component perspective, identifying which elements act as emitters and which serve as sequestrators. While data for emitters is available, this approach has the limitation of only considering CO_2 sequestration and neglecting CH_4 sequestration in the soil, even though the amount of CH_4 sequestration is much smaller than that of CO_2 sequestration by potato plants and emissions from operations.

Results: The first method indicates that potato production serves as a net carbon sink, with a negative carbon flux of -382.430 kg CO_2 eq ha^{-1} $season^{-1}$ or -259.218 kg CO_2 eq t^{-1} $season^{-1}$. The second method evaluates three scenarios: Scenario 1, characterized by high inputs and emissions with minimal sequestration, identifies potato production as a carbon source, with a carbon flux of 151.598 kg CO_2 eq ha^{-1} $season^{-1}$. In contrast, Scenarios 2 and 3, which involve reduced inputs with enhanced sequestration and an optimized growing phase with high emissions from other phases, are classified as carbon sinks, with carbon fluxes of -39123.830 and -20046.673 kg CO_2 eq ha^{-1} $season^{-1}$, respectively. In addition, all potato production operations contribute to carbon emissions, with fertilization being a primary source, averaging 1066.911 kg CO_2 eq ha^{-1} $season^{-1}$.

Conclusions: The study indicates that potato production can function as both a carbon sink and a carbon source, depending on management practices and conditions. The growing phase has the most significant impact on the overall carbon flux of potato production, as it is during this period that the highest levels of carbon sequestration and emissions occur. To enhance carbon sequestration and reduce greenhouse gas emissions, it is essential to optimize farming practices, including fertilization, irrigation, tillage methods, and cultivar selection. Additionally, further research through controlled experiments is recommended to deepen the understanding of the relationships between various farming factors and carbon flux, ultimately supporting more sustainable potato production practices.

Past and future climate change impacts on potato cropping: yield, nitrate leaching and nitrous oxide emissions

Serban Danielescu*[1,2], Alex Cannon[3], Shrestha Rajesh[3], Roland Kroebel[4], Ikechukwu Agomoh[2], Judith Nyiraneza[5]
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[5]Agriculture and Agri-Food Canada - Charlottetown

The demand for production of potato is expected to continue to increase in the future; however climate change can impact both its growth and its environmental footprint. In this study, we focused on the dynamics of crop yield, nitrate (NO_3) leaching and nitrous oxide (N_2O) emissions associated with potato-barley-red clover (PBC) rotation in a temperate humid climate in Price Edward Island, Canada for past (i.e.; 1950-1995), reference (i.e.; 1995-2014) and future (i.e.; 2015-2100) periods. The impacts of climate change on the PBC rotation have been simulated using The Root Zone Water Quality Model (RZWQM) and showed that past climate changes had a muted impact, while future changes had mixed impacts. Thus, potato tuber yield is projected to be minimally impacted (i.e.; -1.72 to 5.03% change compared to the reference period), barley yield will be negatively (i.e.; -1.91 to -23.9 %) and red clover biomass will be positively (i.e.; 6.26 to 10.0%) impacted towards the end of the 21st century, while nitrogen use efficiency at the rotation level will decrease only by ~3.6% for the same period. NO_3 leaching is projected to increase by 23.5% and N_2O emissions by 32.9% at the rotation level for the same period. In some cases, significant seasonal changes in the dynamics and magnitude of these processes were observed. The potential impacts identified suggest that substantial efforts should be undertaken for developing adaptation strategies for maintaining agricultural production and minimizing environmental losses associated with this rotation, and with potato cropping systems in general.

Canadian Potato Genebank Update: Conservation and Use of Potato Genetic Resources

Benoît Bizimungu

Agriculture and Agri-Food Canada, Fredericton Research and Development Centre

The Canadian Potato Gene Resources (CPGR) collection is Canada’s potato genebank located at the Fredericton Research and Development Centre in Fredericton, New Brunswick, Canada. It has the mandate to preserve and make available potato genetic resources of special importance selected to support the development of improved cultivars and to contribute to genetic diversity. The collection is available to Canadian and international researchers and breeders under the terms of the International Treaty of Plant Genetic Resources for Food and Agriculture (ITPGRFA) of the United Nations’ Food and Agriculture Organisation (FAO). We present an update on new plant germplasm acquisition efforts targeted at filling gaps in the current collection, including Canadian-bred cultivars and elite germplasm, as well new accessions with beneficial traits to help solve current or potential production problems. Genebank material has successfully been used by breeders and researchers to identify favourable characteristics and parental lines to hybridize to develop potato cultivars better adapted to the Canadian growing conditions, potato processors and consumers’ demands. Future progress in potato breeding to meet nutritional needs as well as changing climate and production systems will depend on continued efforts to effectively safeguard and access diverse germplasm. We are in the process of making the inventory of CPGR collection available on-line through the Canadian national genebank information system – GRIN-Global-CA (https://pgrc-rpc.agr.gc.ca/gringlobal/search) homepage on the internet.

Identification of Gene Markers for Potato Drought Tolerance Prediction

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Drought stress poses a threat to potato production globally, which resulted in reduced yields from approximately 23.43 million hundredweight (cwt) in 2022 to 23.04 million cwt in 2023 in Prince Edward Island (PEI). Potato (*Solanum tuberosum* L.) is the world's fourth most important crop that also represent Canada's most valuable vegetable crop, while PEI contributes to around 24% of Canada's potato production. This study aims to identify gene markers to predict potato varieties that would have better drought tolerance capacity. Eighteen potential gene markers were selected from published literature and categorized into 4 functional groups: transcription factors, hormone regulation genes, enzyme-coding genes, and genes encoding specific proteins. Five potato cultivars recommended by the PEI Potato Board, including 3 drought tolerant (Satina, Caribou Russet, and AAC Red Fox) and 2 drought sensitive (Goldrush and Russet Burbank) cultivars, were used to evaluate the potential gene markers using RT-qPCR. The identified gene markers were further validated by screening two field grown potato cultivars (Caribou Russet and Russet Burbank) from Cavendish Farms field trials in PEI. Gene expression levels were estimated using the $2^{-\Delta\Delta CT}$ method and analyzed using one-way ANOVA and Tukey's HSD test. The principal component analysis (PCA) was applied to analyze the relative gene expression data and physiological data. Satina was the most drought tolerant cultivar, followed by Caribou Russet as the second drought tolerant cultivar. AAC Red Fox exhibited lower drought tolerance, followed by Goldrush, while Russet Burbank has the least drought tolerance. The PCA loading plots revealed that two genes (***CuZnSOD2*** and ***DREB1*****)** were less variable and have broader involvement in regulatory networks under drought stress. In contrast, four genes (***ERECTA***, ***GA20OX***, ***WRKY3***, and ***ABP*****)** were highly responsive, playing a primary role in the drought response among the eighteen genes selected as potential markers. This study found that the dehydration responsive element binding gene (*DREB1*; NCBI Acc. No. JN125862.1) and auxin-binding protein gene (*ABP*; NCBI Acc.No. XM_006361277.2) can serve as gene markers for selecting drought tolerant potato varieties; however, the *DREB1* gene was the most reliable indicator across all potato varieties. The *DREB1* gene was upregulated in drought tolerant (Satina, Caribou Russet, and AAC Red Fox) varieties under drought stress while it was downregulated in the drought sensitive (Goldrush and Russet Burbank) varieties. In the Cavendish Farms samples, the *DREB1* gene was upregulated in Caribou Russet but downregulated in the drought sensitive Russet Burbank cultivar. This study provides insights for potato breeding programs, while also further enhancing the gene mechanisms involved in drought stress responses.

Effects of Elevated CO_2 on Photosynthetic Performance, Water Use Efficiency and Potato Yield

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As a fourth major food crop, potato could fulfill the nutritional demand of the growing population. Understanding how potato plants respond to predicted increase in atmospheric CO_2 at the physiological, biochemical and molecular level is therefore important to improve potato productivity. Thus, the main objectives of the present study are to investigate the effects of elevated CO_2 on the photosynthetic performance, water use efficiency and tuber yield of various potato cultivars combined with biochemical and molecular analyses. We grew five potato cultivars (AC Novachip, Atlantic, Kennebec, Russet Burbank and Shepody) at either ambient (400 µmol CO_2 mol^{-1}) or elevated (750 µmol CO_2 mol^{-1}) CO_2 in the growth chambers at Fredericton Research and Development Centre, Fredericton, Canada. The plants under both ambient and elevated CO_2 conditions were grown at 22/16°C day/night temperature regimes, photosynthetic photon flux density (PPFD) of 300 ± 15 µmol photons m^{-2} s^{-1}, a 16 h photoperiod and at 50 ± 5% relative humidity. Compared to ambient CO_2-grown counterparts, elevated CO_2-grown Russet Burbank and Shepody exhibited a significant increase in tuber yield of 107% and 49% respectively, whereas AC Novachip, Atlantic and Kennebec exhibited a 16%, 6% and 44% increment respectively. These differences in CO_2-enhancement of tuber yield across the cultivars were mainly associated with the differences in CO_2-stimulation of rates of photosynthesis. For instance, elevated CO_2 significantly stimulated the rates of gross photosynthesis for AC Novachip (30%), Russet Burbank (41%) and Shepody (28%) but had minimal effects for Atlantic and Kennebec. Elevated CO_2 significantly increased the total tuber number for Atlantic (40%) and Shepody (83%) but had insignificant effects for other cultivars. Average tuber size increased for AC Novachip (16%), Kennebec (30%) and Russet Burbank (80%), but decreased for Atlantic (25%) and Shepody (19%) under elevated versus ambient CO_2 conditions. Although elevated CO_2 minimally decreased stomatal conductance (6-22%) and transpiration rates (2-36%), instantaneous water use efficiency increased by up to 79% in all cultivars suggesting that enhanced water use efficiency was mainly associated with increased photosynthesis at elevated CO_2. The effects of elevated CO_2 on leaf chlorophyll and protein content varied across the cultivars. We did not observe any significant differences in plant growth and morphology in elevated versus ambient CO_2-grown plants. Taken all together, we conclude that the CO_2-stimulation of photosynthetic performance, water use efficiency and tuber yield of potatoes is cultivar dependent.

Common Scab On The Genetic Grid Of Diploid Potatoes

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Common scab leads to high economic loss and food waste, and its effects will likely be exacerbated by frequent drought episodes due to climate change. Recently, we uncovered the genetic architecture for maturity and drought tolerance traits in a panel of 384 diploid potato germplasm. Using the same germplasm panel, we have conducted a genome-wide association study to dissect and uncover the genetic architecture for common scab's coverage, severity, and incidence traits. We identified common scab-resistant diploid potato clones and the genomic regions and genes associated with each trait. The study demonstrated that common scab resistance is polygenic in diploid potatoes, that some associated markers are pleiotropic on at least two of the traits, and that the more a clone carries scab-associated QTL/QTN markers, the more it is resistant to common scab in the field conditions. The data suggest that some of the clones herein identified can be used as common scab mitigation solutions either in breeding programs and/or as diploid varieties in the wake of climate change, and while reducing crop waste and economic losses to growers.

Examination and Genetic Analysis of a Novel Yellow-Green Leaf Mutant of Potato

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Leaf color mutants generally have reduced photosynthetic efficiency, which has extremely negative impacts on crop growth and economic product yield; however they can be useful as a marker or guard plant in research trials or for ornamentals in home gardens. Several yellow-green potato plants were found in a breeding population grown in Benton, New Brunswick in the summer of 2021. Tubers harvested from the mutant plants were grown in the greenhouse to confirm the phenotype, and a single mutant clone with stable colouration and good plant vigor (F20028-FG) was chosen for further study. Crosses were made with AC Blue Pride, a variety with normal leaf colour, and a population of 180 F_1 progeny was produced. Leaf colour of the F_1 population varied between yellow-green, light green and mid-green. Under controlled greenhouse conditions, colourimeter L*-a*-b* values of the leaves strongly correlated with chlorophyll content, suggesting that the mutant is chlorophyll-deficient. To study the trait further, the population was genotyped using the 2000 SNP DArTag platform. Genetic analysis indicated that this trait is controlled by a single nuclear gene located on chromosome 4, which is distinct from similar genes or quantitative trait loci previously identified in potato. The range of variation in the chlorophyll-deficient plants suggests that there are further genetic factors influencing this trait which have not been identified. Under field conditions, while there was correlation between leaf colour and Chlorophyll *a* fluorescence levels, there was no impairment of gross photosynthesis. Observed tuber yield for some F_1 light green clones was similar to checks. Understanding the genetic factors underlying this trait and the physiological responses to the chlorophyll deficiency may lead to strategies for improving abiotic stress tolerance in potato.

True potato seed – what's old is new again

Helen Tai
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The potato tuber is an underground vegetative organ that is both consumed and used as "tuber seed" to cultivate the crop. The crop produced is clonal and genetically uniform, however, tuber seed carries pathogens picked up during the growing season that can be passed on to the next growing season and to other farms. For this reason, tuber seed is monitored and certified by regulatory agencies (e.g. CFIA and APHIS) to reduce spread of diseases. Tuber seed production starts with tissue culture plantlets followed by multiple generations of tuber increase. Tuber seed increase to commercial levels of production can take 5-10 years after variety release from the breeder. This long lag time for release of new varieties to the market can hamper ability of the potato industry to take advantage of new market trends and technological innovations for crop production and processing. An alternative to tuber seed is true potato seed (TPS), which are produced from the pollination of flowers. Advantages are the low level of pathogens harbored by TPS. Thus far, only viroids can be passed on through TPS. Additionally, TPS can be multiplied early on at higher levels reducing the time needed for seed increase. In South America, where potato originated, ancient Indigenous farmers used both TPS and tuber seed to propagate, which led to successful domestication of the crop. In developing regions of the world, TPS has provided a means for distribution of the crop to remote areas promoting food security. There is currently growing interest in further developing TPS for potato production. The cultivated potato is a tetraploid crop with high levels of genetic complexity, so with every pollination each TPS is genetically distinct. Breeders rely on this genetic variation to develop new varieties, however, crop uniformity is needed for commercial crop production. Recently, tetraploid intercrossed TPS varieties have been developed and released that have acceptable levels of crop uniformity. There is also growing interest in diploid hybrid breeding. In diploid breeding there are only two sets of chromosomes instead of four. Due to the reduced genetic complexity diploids can be inbred if they are self-compatible. Inbred diploid lines are genetically uniform and can be used in controlled hybrid crosses. The seed from these hybrid crosses are genetically uniform and can be used to produce TPS crops. Methods for commercial level TPS production are under development and various strategies and knowledge gaps will be discussed.

Post harvest tuber phenotyping using large data and artificial intelligence.

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Many scientific studies examining environmental impacts, genetic screening or agronomic management practices focus on in field and at harvest measurements but often do not assess post-harvest tuber traits or storability. Here we provide an update on methods to assess potato tuber quality using large datasets and artificial intelligence/machine approaches; with a focus on processing markets and how they can be incorporated into crop and storage management on farms. Case studies looking at effects of adopting soil health building practices (intercropping, cover cropping, reduced nitrogen inputs) will be presented.

Spray-Induced Gene Silencing (SIGS) as a Potential Tool to Control Wireworms (*Agriotes spp*.) in Potatoes

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Spray-induced gene silencing (SIGS) is an emerging technology based on exogenous application of double-stranded RNA (dsRNA) to plant tissues, to induce gene silencing. The method works through RNA interference (RNAi) mechanisms, is easy to apply and less time-consuming, does not require genetic transformation as in transgenic crops, and thus, is considered more environmentally sustainable and target-specific than chemical pesticides. Wireworms are the soil-dwelling larvae of click beetles and feed on underground plant tissue such as seeds, roots, and tubers. These destructive pests cause significant damage to a wide range of vegetable crops worldwide. Their damage to potatoes is commonly seen as shallow to deep holes in the tubers and leads to reduced potato tuber quality and marketability.

This research aims to provide proof-of-concept for the use of SIGS in controlling wireworms (*Agriotes* spp.) in potatoes, using dsDNA or dsRNA on tissue culture plantlets. The potato cultivar Russet Burbank and the transgenic potato P2-F7-16-eGFP expressing eGFP, were used as plant materials. To assess and quantify the translocation of exogenous dsDNA throughout the plants, the plasmid DNA carrying eGFP gene was diluted in ddH_2O and applied to potato cultivar Russet Burbank by foliar spray and root dipping treatments. Samples were collected from the upper and lower parts of the plantlets, including stem, leaves and roots, at 3 hours, 1 day, and 3 days post-treatment with dsDNA. RT-qPCR was used to quantify the translocation of the sprayed targets.

Based on the dsDNA experiments, the translocation was more efficient using the root dipping method compared to leaf spray. In the root dipping method, the dsDNA was detected in all parts of the plant. Higher amounts of dsDNA were detected in the lower parts of the plant compared to the upper parts after 1 day, and then decreased, suggesting distance- and time-dependent effects on the translocation. In the leaf spray method, limited translocation was detected in the lower parts of the plant at 3 hours post-treatment, and no signals were detected in roots at any time points. The overall dsDNA translocation efficiency in the potato plantlets will be presented and discussed.

The Colour and the Shape: genomewide association analysis of tuber colour and shape variability in a genetically diverse population of potato varieties.

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Here we presents results of genomewide association analysis (GWAS) on tuber skin and flesh colour and tuber shape variability across a population of tetraploid potato varieties. The population was a subset of the AAFC potato germplasm collection and consisted of 400 unique clones, including heritage varieties, breeding lines and commercially released varieties. The population was genotyped at ~109000 single nucleotide polymorphism markers using a sequence based genotyping approach. The population was grown in two replicates at two sites in 2022-2023, and the tubers were phenotyped for skin and flesh colour with a Hunter Lab colourimeter. Tuber shape was measured manually on an ordinal scale, and via an optical grader. GWAS identified genetic markers associated with the major loci controlling tuber colouration on chromosome 2, 3, and 11 and the major locus controlling pigment deposition in the tuber skin on chromosome 10. In addition to the major loci, numerous loci of smaller effect were identified as possible colour modifier loci. For tuber shape GWAS consistently identified markers associated with the major locus known to control tuber roundness on chromosome 10 and an additional locus on chromosome 2, using manual or machine scored phenotypes. Using optical grader data on shape variability we also identified markers associated with tuber shape uniformity on chromosome 2, 3 and 10. The use of these markers for marker assisted selection is discussed.

Examining the Use of Minuet® Biopesticide for Control of Common Scab in Processing Potato Varieties

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Common scab, caused primarily by *Streptomyces spp.* bacteria, continues to be a significant source of loss in marketable yield for Prince Edward Island potato producers. Recent research indicates that the use of the in-furrow biopesticide Minuet® may help suppress common scab symptoms. Minuet® is a biological fungicide labelled in Canada for suppression of Rhizoctonia root rot, black scurf and other tuber skin quality diseases. Positive results in field trials on PEI in 2023 led to five additional trial fields being added in 2024 to further investigate the potential for Minuet® to suppress common scab symptoms under commercial conditions. At planting, approximately 10 acres (4 ha) of potatoes were planted per field with Minuet® applied in-furrow at the label rate, with the rest of the field planted without Minuet® (grower standard practice). At harvest, ten-foot yield samples were collected in both treatment and control sections of each field and stored for subsequent grading. Following grading for yield and size, a random subset of 25 tubers from each sample were graded for scab incidence and severity. There was no difference in total yield observed, consistent with 2023 results. A significant reduction ($p<0.001$) in common scab incidence in the Minuet® treatment (4.7%) compared with the control (16.3%) was observed when pooling samples from all fields; however, the largest difference was observed in one trial field (Ranger Russet variety), where a 72% relative reduction in scab was observed in favour of the Minuet® treatment. There was not a corresponding reduction in scab severity. There was also a significant reduction ($p<0.001$) in Rhizoctonia black scurf symptoms in the Minuet® treatment compared to the control. In addition, there was a significant increase ($p=0.018$) in the percentage of 10-ounce tubers in the treated acres (15.0% for Minuet®, 8.1% for control). Based on two years of field trials using susceptible varieties, there appears to be a trend toward a reduction in common scab symptoms through use of Minuet®.

Impacts Of Primary Non-inversion Shallow Tillage And Moldboard Plowing On The Potato Early Dying Disease Complex In Prince Edward Island, Canada

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Conservation tillage has shown potential to improve soil health and enhance crop productivity in various cropping systems. Moldboard plowing (MP) in the fall prior to the potato phase is a conventional practice in Prince Edward Island (PEI), Canada, which leaves the soil prone to erosion and soil organic matter decline. Potato early dying disease complex (PED) is a major yield limiting factor in potato production in PEI. The objective of this four-year (2019–2022) study conducted in 14 commercial fields was to determine the effect of non-inversion shallow tillage (ST) in comparison with MP on PED pathogen population density in the spring at potato planting time and in the fall post-potato harvesting, and on PED disease severity. Root lesion nematodes (*Pratylenchus spp*., RLN) were detected in all fields. *Verticillium dahliae* was the predominant species in all fields, while *V. albo-atrum* was sporadically detected in a few samples. The population density of the RLN and *V. dahliae* varied among the fields. In the spring samples, *V. dahliae* density was significantly higher in 5 of the 14 fields with the ST treatment compared with MP. RLN density was significantly higher in one of the 14 fields with the ST. When averaged across all fields, *V. dahliae* density was 1.8-fold higher with ST than with MP ($p = 0.018$), but no differences were detected for RLN density between ST and MP. In the fall after the potato harvest, only two fields had significantly higher *V. dahliae* density with the ST than with MP, and no differences were detected for RLN density between ST and MP. When combined data across all fields were analyzed, no differences in pathogen population levels were detected between ST and MP for both *V. dahliae* and RLN. Higher PED severity was detected in three fields associated with ST. However, when disease ratings were averaged across all fields, no PED severity difference was detected between ST and MP. The PED severity was significantly positively related to the spring population density of *V. dahliae* and RLN, but not with the tillage regimes in this study. Further study is needed to determine the long-term effect of tillage regimes on soil health, disease development, soil disease suppressiveness, pathogen population dynamics and PED development in potato production

Evolving Dynamics: Shifting of Bacterial Species in the Potato Blackleg and Soft Rot Disease Complex over a Decade in the Northeastern U.S.

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Potato blackleg and soft rot (PBSR), caused by species within the genera *Dickeya* and *Pectobacterium*, has been a threat to potato production, resulting in substantial economic losses due to seedling emergence failure, stem rot, and storage decay. This study aimed to identify and characterize the bacterial species responsible for PBSR outbreaks in the Northeastern U.S. and assess their genetic diversity, pathogenicity, and ecological adaptations. A total of 300 symptomatic potato samples were collected from the Northeastern region of the United States between 2021 and 2023. Using polymerase chain reaction (PCR), average nucleotide identity (ANI), and digital DNA-DNA hybridization (dDDH) analyses, we identified at least eight *Pectobacterium* species, with *Pectobacterium parmentieri* and *P. versatile* being the most prevalent, detected in 44.34% of samples. Additionally, *Pectobacterium punjabense* and *P. parvum* were found as PBSR pathogens in the U.S. for the first time. *Dickeya dianthicola* was detected in three genotypes, with genotype I being the predominant strain. Over time, the population of *D. dianthicola* has been declined but that of *P. parmentieri* and *P. versatile* increased.

Co-infections involving multiple PBSR species were common. From the disease samples, mixed pathogens *P. parmentieri + P. versatile* and *P. atrosepticum + P. versatile* were the most frequently observed combinations. These interactions may influence disease severity, competition, or synergistic pathogenic effects, highlighting the complexity of PBSR epidemiology. Whole-genomic sequencing results also revealed diverse virulence factors, including plant cell wall-degrading enzymes (PCWDEs), secretion systems, and quorum-sensing mechanisms, that contribute to bacterial adaptation, survival, and spread in host plants and the environment.

The findings also raise concerns about the potential influence of climate change and agricultural practices on the evolving dynamics of PBSR pathogens. This study provides valuable insights into the genetic and ecological characteristics of PBSR-causing bacteria, aiding in the development of targeted control measures and sustainable potato disease management strategies.

Biological Control Mechanisms and Their Role in Managing Potato Diseases: Insights into Pathogen Lifestyle

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Over the past few decades, modern agriculture is increasingly looking into production systems that are more sustainable and ecologically sound. Biological control methods against different plant pathogens, as one of the cornerstones of integrated pest management (IPM), can help achieve this goal. There were significant progress in using different microorganism species as biological control agents (BCAs) and in assessing their efficacy against diseases of different pathosystems as well as in understanding the mechanisms involved in biological control approaches of plant pathogen. Previous research found that BCAs, microbial or non-microbial, are able to interact with pathogens indirectly by inducing plant resistance, defense priming and nutrient competition, or directly via sophisticated antagonism by the BCAs such as hyperparasitism and antibiosis inhibiting the growth of the pathogens. Many studies solely focused on how different BCAs interfered with one or more aspects of the disease triangle i.e. interactions among environment, plant and pathogen, however, the role of pathogen lifestyles (biotrophic, hemibiotrophic and necrotrophic) was often overlooked. To address this knowledge gap, the mechanisms of biological control against different diseases were revisited, uncovering the importance of pathogen lifestyles in influencing the selection and efficacy of BCAs when it comes down to a specific pathosystem. Using the potato crop as an example, which is highly susceptible to a wide range of fungal, bacterial, and viral diseases, we explored how pathogen lifestyles may dictate the success of biological control strategies. By integrating insights from recent studies, we propose that a deeper understanding of pathogen lifestyles can significantly enhance the development and application of tailored biological control approaches for more sustainable and effective disease management in potato production.

Harnessing Machine Learning and Deep Learning for Potato Disease Identification: A Climate-Resilient Approach to Sustainable Agriculture

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A single crop disease outbreak can devastate an entire harvest, threatening food security and economic stability. Due to dynamic weather conditions, the risk of crop diseases continues to rise, resulting in substantial crop losses. In major potato-producing regions such as the Atlantic Provinces, including Prince Edward Island (PEI), New Brunswick (NB), and Maine, United States of America (USA), diseases like Early Blight, Gray Mold, Late Blight, and Stem Rot pose persistent challenges. Traditional disease identification approaches are reactive and often ineffective, leading to significant yield losses. This research introduces an Artificial Intelligence (AI) driven predictive framework that integrates Machine Learning (ML), Deep Learning (DL), and climate-based modeling to detect and mitigate potato disease outbreaks before they escalate. By examining weather data with disease outbreaks, the proposed models achieve over 90% accuracy. For the examination of disease patterns with weather data, both group disease models and individual disease-specific models are developed. Moreover, a cross-regional disease prediction approach is conducted for comparative disease identification across Canada and the USA, enhancing the robustness and scalability of the framework. A prototype named ‘Potato Insight Catalyst’ was also developed for PEI to provide warnings and enabling farmers to take preventive actions, reduce reliance on agrochemicals, and optimal resource utilization. The findings reveal that AI holds the capability to transform precision agriculture by assisting farmers with advanced decision-making tools. Additionally, it contributes to enhanced yield resilience, promotes sustainable agricultural practices, and ensures food security. Bridging the gap between innovation and sustainability, the proposed approach sets a new standard for smarter, more resilient, and more adaptive farming practices.

Quantifying Rates of Resistance to Common Pyrethroid and Neonicotinoid Insecticides in New Brunswick Aphid Populations

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Aphid populations in agricultural systems face increasing selection pressure from insecticide applications, leading to widespread resistance. While multiple resistance mechanisms exist, genetic mutations conferring target-site insensitivity are particularly concerning, as they confer a high degree of resistance and persist in populations even without continued insecticide pressure. As part of an ongoing survey of insecticide resistance in New Brunswick (NB), aphids were collected through the provincial Aphid Alert monitoring program and analyzed for resistance mutations to pyrethroid and neonicotinoid insecticides. This occurs in the context of a shifting aphid community in NB, with substantial population increases over the past decade and the rise of once-rare outbreaks of the most concerning species, Green Peach Aphid (*Myzus persicae*). DNA was extracted from preserved aphid specimens and screened via PCR and DNA sequencing for known resistance mutations. Due to complexities in amplifying insect genomic DNA, a new mRNA extraction and reverse transcription sequencing method was developed to include screening for neonicotinoid resistance. Previous surveys focused exclusively on pyrethroid resistance, revealing near-saturation levels (>90%) in GPA, now reaching nearly 100% in NB. GPA mostly occur late in the season, while other aphids are exposed to insecticides throughout. Resistance in other Aphid Alert-sorted species (e.g., Potato Aphid, Raspberry Aphid) and unsorted aphids (e.g., Paper Birch Aphid *Euceraphis papyrifericola*) remains lower (~20% as a group). These species exhibit distinct resistance patterns, with Potato Aphid, for example, showing low pyrethroid resistance (~13%) but high neonicotinoid resistance (80%), suggesting that non-GPA species may be developing resistance differently depending on insecticide exposure timing. Pyrethroid resistance in non-GPA species increases through the season, from 12% in early-season to 27% in late-season populations, likely due to continued insecticide application selecting for resistant individuals over time. Neonicotinoid resistance follows a different pattern, being only moderate in GPA (~53%) but very high (70-80%) in other aphid species. This may result from the systemic nature of neonicotinoids, which are applied at planting and provide constant exposure throughout the season. In season-long species like Potato Aphid, neonicotinoid resistance reached 80%, far higher than in GPA, which appears primarily late in the season, months after widespread neonicotinoid application. These seasonal and species-specific resistance patterns are still being refined, with further sequencing efforts ongoing. DNA barcoding of cytochrome oxidase I (cox1) sequences was performed alongside resistance screening, confirming species identity in provincially sorted specimens and identifying novel resistance-carrying species in unsorted "other" aphids. Our findings emphasize the urgent need for diversified insecticide strategies and real-time resistance monitoring to guide in-season management decisions. Future work aims to streamline RNA extraction and sequencing workflows to provide timely resistance estimates as a supplement to Aphid Alert bulletins, enabling growers to adjust pest management strategies dynamically. The continued rise in resistance highlights the necessity of integrated pest management approaches to sustain insecticide efficacy in NB's potato production systems.

Effects Of Successive Soil Fumigation With Metam Sodium On Verticillium Wilt Of Potato

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Potatoes (*Solanum tuberosum*) are among the top three staple crops produced worldwide, supporting over a billion people worldwide. *Verticillium dahliae*, a soilborne pathogen responsible for Verticillium wilt of potato or the potato early dying complex, is one of the most economically impactful pathogens. This is due both to the reduction impacts on tuber yield as well as the high cost associated with soil treatment. The most common treatment for managing *V. dahliae* is chemical fumigation with metam sodium. However, rising disease pressure and decreased efficacy of fumigation after repeated applications have led to increased fumigation frequency and rates in recent years. This study aims to examine the effects of successive fumigation treatments on Verticillium wilt of the potato and disease impacts related to yield, as well as to determine the efficacy of three fumigation-rotation treatments in managing this disease. Data were collected over three years in a field trial in Presque Isle, Maine, with four fumigation-rotation groups: a control, Group 0 (no fumigation), Group 1 (fumigated once), Group 2 (fumigated twice), and Group 3 (fumigated three times). The results showed non-significantly higher total and marketable yields in fumigated plots across all three years, but there was no significant difference in disease incidence, severity, or yield due to fumigation-rotation treatment. The findings suggest that multiple successive fumigation treatments do not provide significant benefits over one time fumigation, and may reduce treatment efficacy over time, as is evidenced by a decrease in tuber yields. Thus, a single fumigation event with metam sodium in a three-year period is comparably effective in managing Verticillium wilt.

A Robotic Solution for Automating the Rouging Process in PVY-Affected Potato Fields

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Early and accurate detection of plant diseases is essential for maximizing crop health, minimizing yield losses, and ensuring sustainable farming practices. This study focuses on addressing the challenge of managing Potato Virus Y (PVY) in potato cultivation through the development of an autonomous electric robotic system designed for real-time disease detection. The robotic platform is equipped with high-resolution RGB cameras to capture plant images and a high-precision GPS-RTK system, which geo-tags each image during acquisition. This capability enables the generation of an infestation map that visually highlights the precise locations of infected plants, providing valuable insights for targeted disease management.

Field data for this study was collected from commercial potato fields in New Brunswick and Prince Edward Island, where PVY infection rates ranged between 1% and 3%. The robot systematically navigated these fields, capturing high-quality images of potato plants in varying growth stages and environmental conditions. The collected images were manually labeled to create a dataset of healthy and infected plants, which was then used to train and validate a deep learning model based on the YOLO architecture. The model achieved a classification accuracy of 75%, with a mean Average Precision (mAP) of 78.5% and an F1-score of 0.76 during testing. These results indicate the model’s strong capability to distinguish infected plants from healthy ones, even under diverse lighting and environmental conditions.

The integration of robotics, computer vision, and artificial intelligence in this system demonstrates a scalable and efficient approach to disease monitoring in large agricultural settings. By reducing labor demands associated with manual scouting and enabling precise disease localization through GPS-based mapping, this technology supports more effective and data-driven disease management strategies. The findings from this study highlight the potential of autonomous robotic solutions in advancing precision agriculture, ultimately contributing to increased crop productivity and more sustainable farming practices.

Exploring the Potential of Metagenomic Approaches for the Detection and Confirmation of *Clavibacter sepedonicus.*

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Bacterial ring rot is caused by *Clavibacter sepedonicus*, a Gram-positive coryneform bacterium, and primarily manifests as tuber vascular ring decay. It also induces interveinal chlorosis, yellowing of leaflets, necrosis, and systemic wilt in potato plants, leading to significant economic losses in potato production. Due to its severe impact in seed potato industry, countries like Canada, the United States, and many European nations enforce zero tolerance for this disease. At Charlottetown lab, wehave reclassified *Clavibacter* subspecies based on whole-genome and multi-locus sequence typing (Li et al., 2018), and identified two novelspecies, *C. zhangzhiyongii* sp. nov. (Tian et al 2021) and *C.lycopersici* sp. nov. (Osdaghi et al., 2023).

This study aims to explore metagenomic sequencing methods for the detection and confirmation of *Clavibacter sepedonicus*. We extracted DNA from diagnostic tuber samples tested positive in specific qPCR assay for the presence of bacterial ring rot, and sequenced the DNA library using the Illumina MiSeq platform. The raw sequences were cleaned using the Atria program, and the clean sequences were processed through our in-house PolyChrome Classifier and Detector pipelines to identify *Clavibacter sepedonicus*-specific sequences and recover the nearly whole genome using Unicycler and Ragtag. The identified sequences were confirmed using Clasnip, our online classification and Multi-Locus Sequencing Typing program, and further validated with CCMetagen, a metagenomics profiling tool.

From the MiSeq platform, we generated 6.1 million clean sequences, with 15% mapping to the reference genome of *Clavibacter sepedonicus*, each with fewer than two mismatches, insertions, or deletions. The mean sequencing depth was 21x the 3.4 million bp reference genome, covering 98.8% of the genome at least once and 94.6% at least five times. We successfully assembled a scaffold-level genome with nine contigs, the largest contig and N90 being 2.9 million bp. Clasnip and PolyChrome results support the initial detection results using qPCR and ELISA, and confirmed classification of *Clavibacter sepedonicus*, and CCMetagen identified 4% of markers as belonging to *Clavibacter sepedonicus*, comprising 80% of the bacterial genome content.

This exploratory study demonstrates the potential of metagenomic approaches for the detection and classification of regulatory and quarantine pathogens like *Clavibacter sepedonicus*.

Managing Potato Common Scab with the synthetic auxin 2,4-D and the biopesticide Minuet

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Common scab of potato causes important economic losses every year in North America. Common scab (CS) is notoriously difficult to control as no specific chemical pesticides are available. Broad-spectrum soil fumigation is sometimes used to control CS, however, it has serious human health and environmental consequences. A low dose of the synthetic auxin **2,4-dichlorophenoxyacetic acid** (2,4-D) and the beneficial bacterium *Bacillus subtilis* (Minuet, Bayer) were previously shown to reduce CS. However, there are still questions about the most effective 2,4-D application rate on different potato genotypes and the efficacy of combining 2,4-D and biopesticides. The objectives of this study were to evaluate the effects of different 2,4-D application rates on three potato cultivars and the efficacy of Minuet, either used alone or in combination with 2,4-D. In 2021 and 2023, two foliar 2,4-D applications (a total of 157 of the active ingredient (a.i.) ha^{-1}) decreased CS severity compared to the untreated control at the MB and NB sites. Interestingly, the reduction of CS severity at the NB site was accompanied by a decrease in the abundance of the CS pathogen in the rhizosphere and tuberosphere soils compared to the untreated control. This suggests that the induction of a systemic plant defense response by 2,4-D might lower their abundance. However, 2,4-D failed to control CS in NB in 2021 and PEI sites in 2021 and 2022. The lack of reproducibility among sites and years suggested that climate and (or) soil properties were influencing the effectiveness of 2,4-D in controlling CS. In 2022, 2,4-D applied at 157 a.i. ha^{-1} decreased CS severity and increased marketable yield in three out of six potato varieties evaluated in MB. We hypothesized that greater 2,4-D application rates in some potato genotypes might be required to control CS. Two applications of 2,4-D at 157, 196 and 326 g a.i. ha^{-1}were applied on the foliage of Green Mountain, Norland, and Yukon Gold. There was a significant decrease in CS severity in Norland and Yukon Gold compared to the control, however, in Green Mountain the opposite effect was observed. Marketable and total yields of plants treated with 2,4-D were similar to the control however, in Yukon Gold there was a significant increase in marketable and total yield with plants treated with 100 ml/acre compared to the control. The biopesticide Minuet applied in-furrow significantly reduced CS compared to the control. Minuet (2024) or 2,4-D (2023) provided disease control, but the combination of both did not improve the result. The application of 2,4-D and Minuet to potato crops shows promise in reducing economic losses due to CS.

DNA-Based Profiling of Microbial Diversity in Four Streams of Agricultural Landscape in Atlantic Canada

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Background & Motivation: The advent of shotgun metagenomic sequencing has revolutionized our ability to study microbial distribution and occupancy in ecosystems with remarkable detail. Traditional culture-based methods are limited by their reliance on culturable organisms, selective growth conditions, time-intensive processes, and inability to capture the full diversity and functional potential of microbial communities. Metagenomic sequencing allows us to overcome these numerous challenges, enabling the characterization of microbes with higher accuracy. By analysing the composition, diversity, and functional potential of microbial communities, this approach has significantly deepened our understanding of how ecosystems respond to environmental disturbances and how to maintain their essential functions. In this study, we c investigated the microbial consortia that constitute these riverine ecosystems, aiming to understand the diversity within these communities.

Methodology: From 2020 to 2022, we collected water samples from four tributaries of the Dunk River in Prince Edward Island, Canada, totalling 87 samples. These were subjected to filtration, DNA extraction, shotgun DNA sequencing using Illumina short-read sequencing technology, and nitrate, chloride, and dissolved phosphorus analysis. Quality checks and improvements were conducted for these reads. Taxonomic profiling was performed using Kraken followed by Bracken to estimate relative taxon abundances.

Results: Across 87 river metagenome samples, representing diverse stream sites and time points, the estimated average species richness was approximately 5428 species, indicating a substantial level of microbial diversity within these freshwater ecosystems. Taxonomic profiles of the stream water samples predominantly featured with ~67.5% the phylum Psuedomonadota (formerly Proteobacteria), with families Comamonadaceae, Flavobacteriaceae, Pseudomonadaceae, and Burkholderiaceae being the most prominent. *Flavobacterium* (~ 9.08%) was the most abundant genus, with *F. ammonificans* and *F. ammonigenes* as dominant species. These species are involved in nitrogen cycling, especially ammonia production, and can break down complex organic matter. Their predominance may suggest a high organic load, either natural (e.g., leaf litter) or anthropogenic (e.g., pollution).

The microbial profile exhibited a characteristic pattern of uneven species abundance, with a limited number of taxa dominating the community while a substantial proportion of species were present at low relative abundances. For instance, species like *Leptospirillum ferrooxidans* and *Leptospirillum ferriphilum* were identified in lower abundances across samples. Nitrospira were the most abundant within the Nitrospiraceae family, indicating their dominance and crucial role in the nitrogen cycle, particularly in nitrite-to-nitrate conversion. While *Pectobacterium* is a genus well-known for its plant-pathogenic members, analysis revealed a typical long-tail distribution, with established pathogens like *P. carotovorum* and *P. wasabiae* occurring as rare taxa at low relative abundances across sites.

Conclusion: This study highlights the power of shotgun metagenomic sequencing in revealing the complex microbial diversity of riverine ecosystems. Dominant genera like *Flavobacterium* suggest significant roles in nitrogen cycling and organic matter breakdown, while rare genera such as *Leptospirillum* and *Pectobacterium* may serve as bioindicators of specific environmental conditions. These findings contribute to a growing understanding of the crucial role of microbial communities in freshwater ecosystems like rivers. They emphasize that microbial diversity is not just a descriptive feature but is deeply intertwined with ecosystem functioning and environmental conditions. It also raises questions about the drivers of this diversity and the interactions within this complex community.

The Impact Of Diversifying Potato Crop Production Systems With Perennial Multispecies On Soil Health And Greenhouse Gas Emissions

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Building soil health not only assures that the soil can sustain food production through increased soil organic matter and improved nutrient cycling, but it also aids in reducing nutrient loss to the environment, particularly nitrogen (N). Traditional potato production systems are particularly harsh on soil health. Management strategies such as reducing the frequency of potato crops in the rotation and diversifying potato production systems by incorporating multispecies cover crop mixtures enhance soil health by improving soil organic carbon (SOC) and nutrient supply, particularly N, and hence, crop productivity. In this study, we determine how the short-term impact of diversifying cropping systems using perennial multispecies mixtures affects soil health and greenhouse gas (GHG) emissions. The field site was at the McCain Food's Farm of the Future in Florenceville, New Brunswick. Soil samples were collected from 2021 to 2023 at 0-15 cm depths from four crop production systems, including rotations of a conventional 2-year potato-barley (P-B), a 2-year potato-multispecies mix (P-M), a 3-year potato-barley with barley underseeded with a mix of timothy, alfalfa, ryegrass, and double-cut red clover, and the underseeded left to grow in year 2, followed by potato in spring of year 3 (P-Bm-M), and a 3-year potato-multispecies mix with the multispecies mix (oats, field pea, alfalfa, timothy, ryegrass, red clover, and annual tillage radish) grown for two years followed by potato in year 3 (P-M-M). Soil biochemical health indicators (permanganate oxidizable carbon (POXC), particulate organic matter C (POMC) and N (POMN) were measured throughout the three years, while nitrous oxide (N_2O) and carbon dioxide (CO_2) emissions were measured in the third year when all four crop production systems were in the potato phase. Cumulative N_2O emissions were reduced by 59% in the P-M (5.31 kg N ha^{-1}), and 54% in the P-Bm-M (5.94 kg N ha^{-1}), compared to P-B (12.8 kg N ha^{-1}). Cumulative CO_2 emissions were 58-74% greater under P-B (3.69 Mg CO_2-C ha^{-1}) than in rotations with perennial multispecies mixtures (2.33 Mg CO_2-C ha^{-1} for P-M-M; 2.26 Mg CO_2-C ha^{-1} for P-Bm-M; 2.12 Mg CO_2-C ha^{-1} for P-M). POXC, POMC and POMN in the P-B and P-M were significantly lower in the third year (2023), when all crop production systems were in the potato phase compared to 2021. In the P-Bm-M, POMN increased in 2023 compared to 2021, while it did not show a significant difference for P-M-M. These findings suggest that diversifying rotations with multispecies while reducing the frequency of potato crops in the rotation improves biochemical soil health indicators and reduces N_2O and CO_2 emissions compared to conventional potato-barley rotation, which is critical for long-term agricultural sustainability.

Dacom the New Brunswick Experience

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Since 2009, McCain has been using the Dacom program to support scheduling fungicide applications for late blight protection. The program relies on weather data from two weather stations in Florenceville and Drummond, NB. Participating growers provide local data by measuring factors such as emergence, crop cover, crop growth, and the chemicals applied.

Dacom program generates recommendations based on this data, which are shared with growers in advance of significant weather events. This allows for timely fungicide applications that utilize the appropriate modes of action.

The presentation will highlight the Dacom experience in New Brunswick from 2023 and 2024, detailing the challenges and successes that growers faced. The eastern region of North America experiences more rainfall than the western region, which increases the risk of late blight for growers. By incorporating Dacom recommendations into their decision-making processes, McCain growers can better manage the risk of late blight before it occurs. Participation in the Dacom program is voluntary, and growers use the information as one of several tools for managing late blight.

Improving Potato Production: How do Bacterial and Mycorrhizal Inoculants Work for You?

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It is now widely recognized that soil microorganisms play an important role in plant growth and subsequent yields. These microorganisms can be bacteria or fungi. The best-known group among fungi is probably mycorrhizae, which establish a symbiotic relationship with plant roots. By exploring the soil, the mycorrhizal fungus' intense hyphal network enables better assimilation of water, phosphorus, nitrogen and other mineral elements. This promotes better plant growth and resistance to biotic and abiotic stresses, while also playing a major role in the soil's physical and microbiological characteristics. In fact, the carbon exuded into the soil by hyphae supports the growth of bacterial communities.

Natural populations of mycorrhizae can often be very low, as certain agricultural practices such as intensive tillage are detrimental to their survival. At the same time, the interaction between bacteria and mycorrhizal fungi is often strain-dependent, meaning that not all bacteria can take advantage of hyphal exudates, and the full potential of bacteria is only possible if they have access to significant sources of available carbon (energy).

Bacterial biostimulation mechanisms are often complex. In some cases, the metabolites produced by bacteria will improve the availability of soil nutrients. In other cases, the bacteria will induce the transcription of plant genes, which in turn will have beneficial effects on mineral uptake or stress resistance. We will present some of these mechanisms and the genes involved.

To validate the impact of these mechanisms in real crop situations, 16 experimental trials have been set up in Quebec, Ontario and Prince Edward Island, from 2021 to 2024. Three treatments were applied: an untreated control (standard practices), a treatment receiving a commercial mycorrhizal inoculant (AGTIV® REACH) and a treatment receiving the same commercial inoculant supplemented with a biostimulant bacterium (AGTIV® STIMULATE). The results showed that inoculation with the mycorrhizal fungus resulted in a significant increase in yield, while simultaneous inoculation with the mycorrhizae and bacteria significantly doubled this increase. The two microorganisms therefore have a synergistic effect on improving marketable tuber yields.

Results obtained under actual growing conditions demonstrate that joint inoculation of a mycorrhizal fungus and a compatible bacterium result in a profitable increase in yield for the grower. The use of biostimulant microorganisms in agriculture is in line with a sustainable agriculture approach, enabling better use of water and nutrients in the soil.

An Improved Meteorological Drought Forecast Model Leveraging SPEI Time Series Decomposition For Atlantic Canada

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Abstract

Drought represents a significant natural hazard that can profoundly impact various aspects of human activities. Improved drought models with a high level of accuracy, especially at multiple timescale horizons, can provide significant benefits for sustainable water resources management. However, the noisy nature (non-stationarity and nonlinearity) of drought data proves challenging and makes accurate forecasting complex. This study introduces a regression-based framework in combination with variational mode decomposition (VMD) preprocessing and metaheuristics optimization to improve multistep drought predictions. With decomposed standardized precipitation evapotranspiration index (SPEI) data, three machine learning models—Extra Tress Regression (ET), K-Nearest Neighbors (KNN), and Kernel Ridge Regression (KRR)—were modeled in two approaches [decomposed and non-decomposed data] to predict the $SPEI_{12}$ (timescale of 12 months) meteorological drought index. The analysis focused on three Atlantic Canadian stations (Charlottetown, Prince Edward Island; Saint John, New Brunswick; Sydney, Nova Scotia), where agricultural activities mostly reliant on rainfall can be susceptible to drought. The dataset for the study spans from 1980 to 2022. Lagged datasets of decomposed and non-decomposed $SPEI_{12}$ were generated. Autocorrelation and Partial autocorrelation functions were applied to determine effective input lags. The Sand-Cat swarm optimization technique (SCSO) was integrated into the kernel ridge regression, to determine the optimal global solution. Model evaluation with statistical metrics such as the root mean square error (RMSE) and the correlation coefficient (R) demonstrated that the VMD-KRR-MPY model provided the most accurate multistep ahead predictions (1, 3, and 6 months forecast horizon) for the $SPEI_{12}$ drought index at all stations. During the model testing phase, this model achieved the highest precision, predicting 1-month $SPEI_{12}$ with ($R > 98\%$) and ($RMSE < 14\%$), at all locations. For the hydrological-based measure of Nash-Sutcliffe Efficiency (NSE), this model performed best (NSE: 88% - 98%) at all forecast horizons for every location. Model accuracy declines slightly as the forecasting horizon increases, however, compared with other models, the VMD-KRR-MPY can improve the accuracy of drought prediction in the region, providing a reference for coping with drought occurrence and early warning in advance.

Machine Learning-Driven Precision Irrigation: A Novel Approach to Optimizing Potato Crop Coefficient (*K_c*) for Enhanced Water Use Efficiency

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Abstract

Accurate crop coefficient (K_c) estimation is essential for optimizing water use efficiency and irrigation scheduling. Traditional empirical models often struggle with environmental and crop variability. This study employs an advanced machine learning approach, integrating Extreme Gradient Boosting (XGBoost) with the Chaos Game algorithm to predict K_c for potatoes (**Solanum tuberosum L.**). SHapley Additive exPlanations (SHAP) values enhance interpretability, identifying key influencing factors. Using meteorological, soil, and crop management data from multiple sites, three input scenarios were tested: comb1 (all data**),** comb2 (only soil data), and comb3 (only meteorological data). The Chaos Game algorithm optimized XGBoost, improving accuracy and convergence speed. Results show the comb2 model achieved superior performance (R = 0.9978, RMSE = 0.02151, MAPE = 1.63%). SHAP analysis revealed soil moisture and field capacity as major influences. This method enhances Kc prediction accuracy, aiding farmers in refining irrigation strategies and promoting sustainable water management. It is adaptable for other crops across diverse climates and soil conditions.

Posters

Mitigating Soil Organic Carbon Loss in Intensive Agriculture: Long-Term Effects of Woodchip Applications on Carbon and Nitrogen Dynamics

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Abstract:
Intensive potato production in New Brunswick has led to a decline in soil organic carbon due to frequent soil disturbance and limited organic matter inputs. This study, conducted at the Agriculture and Agri-Food Canada Fredericton Research and Development Centre, investigates SOC loss in a field over multiple growing seasons of potato production after switching from forage production and whether incorporating willow woodchips into topsoil can mitigate SOC loss. Results indicate that SOC declined 0.06 kg C m^2 per year on the control plots after the switch. However, the woodchip treatment consistently reduced carbon losses, highlighting its potential as a sustainable soil management strategy in intensive cropping systems.
Keywords: potato production, beneficial management practices, woodchip application, soil organic matter, soil degradation, Atlantic Canada.

Evaluating the Efficacy of Biochar, Compost, Wood Ash, and Sugar Kelp as Natural Soil Amendments on Potato Growth, Leaf Gas Exchange, and Yield

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Abstract

Sustainable agricultural practices are essential for improving crop productivity while reducing dependence on synthetic fertilizers. Natural soil amendments, such as biochar (BC), compost (COM), wood ash (WA), and sugar kelp (SK), have gained attention due to their potential to enhance soil health and plant growth. This study investigates the effects of these alternative soil amendments on potato (*Solanum tuberosum*, Russet Burbank variety) growth traits, leaf gas exchange, tuber characteristics, and overall yield. Understanding the effectiveness of these amendments can provide valuable insights into optimizing soil management strategies and promoting resilient, high-yielding crop systems. A small-scale box experiment was conducted using a Randomized Complete Design (RCD) at the Bioresource Lab, University of Prince Edward Island, to evaluate the effectiveness of these natural amendments. The experimental treatments included SK, WA, COM, BC, and fertilized control (CK), each replicated four times. Key physiological and yield-related parameters were measured, including plant height, stem diameter, number of stems, fresh and dry biomass, number of tubers, tuber grading (marketable vs. non-marketable), chlorophyll content, and Normalized Difference Vegetation Index (NDVI). Additionally, leaf gas exchange parameters net photosynthesis rate (*Pn*, μmol m^{-2} s^{-1}), transpiration rate (*E*, mol m^{-2} s^{-1}), intercellular CO_2 concentration (*Ci*, μmol mol^{-1}), and stomatal conductance (*Gs*, mol m^{-2} s^{-1}) were evaluated. The results indicated that SK was not effective in enhancing plant growth, leaf gas exchange, tuber development, yield, and biomass compared to CK. In contrast, BC, WA, and COM significantly improved plant growth traits, enhanced leaf gas exchange efficiency, increased tuber quantity and quality, and boosted overall potato yield relative to CK. Among these, BC exhibited the highest efficiency across all measured parameters. These findings underscore the potential of alternative natural amendments, particularly WA, COM, and BC, to enhance plant physiological responses, improve crop resilience, and reduce reliance on synthetic fertilizers. Further field trials are essential to validate these results and assess their long-term impact on potato productivity and sustainable soil management.

Integration Of GeoAI With Drone Imagery To Forecast Potato Crop Health Indices In Prince Edward Island, Canada

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Forecasting the potato crop health indices using input red-green-blue (RGB) images from the drone is necessary to optimize yield and addressing food security. While previous methods primarily relied on multispectral sensors, these are often costly and lack accuracy for yield monitoring. Recent advancements in Geospatial analysis and Artificial Intelligence (AI) have led to the novel introduction of Geospatial Artificial Intelligence (GeoAI) techniques for image processing. By leveraging GeoAI techniques and high-resolution RGB imagery from the drone, a cost-effective and accurate method for assessing crop health has been implemented throughout the growing season. The study based in Prince Edward Island, Canada, aims to ensure optimal potato crop health at different stages throughout the growing season: vegetation (15-30 DAP; days after plantation), tuber formation (30-45 DAP), tuber bulking (75-110 DAP), and tuber maturation (> 110 DAP) which is critical for maximizing yield. By analyzing RGB spectrum vegetation indices and correlating them with ground truth values, a robust framework has been developed for predicting potato crop health indices. This study addresses critical gaps in predicting potato crop health indices and yield monitoring by offering a cost-effective, high-resolution alternative to traditional multispectral methods. Future directions include optimizing computational efficiency and extending the framework to other crops. The findings highlight the potential of GeoAI image processing techniques to transform precision agriculture and mitigate yield losses in the context of increasing climate change.