2018 NORTHEAST POTATO TECHNOLOGY FORUM

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2018 Northeast Potato Technology Forum

The Northeast Potato Technology Forum is an annual event that provides potato researchers and extension specialists from Atlantic Canada and Northeast United States an opportunity to discuss potato research and promote collaboration and information exchange. The 25th annual Northeast Potato Technology Forum was held March 21-22, 2018 at the Crowne Plaza Lord Beaverbrook Hotel in Fredericton, New Brunswick.

The 2018 program was comprised of 28 oral presentations and three posters. The research presented included cropping systems, crop management, diseases and disease control, soil health, genomics, potato virus Y, soil fumigation and insect pests.

Many thanks are extended to the session chairs, presenters and all participants of the Forum. Our appreciation and thanks go to Syngenta for sponsoring the evening reception; McCain Foods (Canada) for publication of this booklet; Gilles Moreau for compiling the abstracts; Robert Gareau for technical assistance, and the New Brunswick Department of Agriculture, Aquaculture and Fisheries for support resources. We also extend thanks and appreciation to our sponsors for their support.

This booklet contains the abstracts of the 28 oral presentations and three posters of the Forum. The research represented by these papers is integral to the growth and sustainability of the potato industry in the Northeast region.

Thank you for making the 2018 Northeast Potato Technology Forum a success.

Loretta Mikitzel

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Preferential Spread of Novel Recombinant PVY Strains, and Their Effects on Symptom Expression, Yield and Tuber Quality in Popular Potato Varieties

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Potato virus Y (PVY; family Potyviridae, genus Potyvirus) is a major cause of yield and quality loss in potato crops. PVY exists as a complex of many strains, and in recent years around the world, populations of PVY have shifted dramatically toward recombinant strains such as PVY^{NTN}, PVY^{N:O} and PVY^{N-Wi}. A 2010 to 2016 survey of PVY strains in commercial fields of New Brunswick (NB), Canada, the traditionally dominant PVY^O dropped from 82% of infections in 2010 to 14% in 2016, replaced mostly by PVY^{NTN} (64%) and PVY^{N:O} (22%). Preliminary data from the 2017 harvest has shown the predominance of PVY^{NTN} to be continuing. Several hypotheses have been put forth to explain how these recombinant strains have been rising in PVY populations. Since 2014, our research group has undertaken five experimental field trials tracking PVY spread in NB and Manitoba¹, and to quantify the relative rates of spread of PVY^O, PVY^{N:O} and PVY^{NTN}. In these trials with Russet Burbank and Goldrush varieties, PVY^{NTN} spread far more effectively than PVY^{N:O} and especially PVY^O. The different potentials of each strain to spread in the field were mostly expressed at the plant-to-plant transmission level with little strain-related difference in transduction to tubers in infected plants. Strain-specific PVY spread also varied between Russet Burbank and Goldrush varieties, possibly due to selective PVY^O resistance in Goldrush.

In general, the major recombinant strains $PVY^{N:0}$ and PVY^{NTN} typically show more mild and cryptic foliar symptoms in potato plants, hampering their detection and management in the field. Also, different potato varieties have distinct symptom expression profiles in response to infection by different PVY strains. Since 2014, we have catalogued foliar symptom expression and effects of PVY^o, PVY^{N:0} and PVY^{NTN} infection on tuber yield and guality in both primary (leaf infection) and secondary (tuber-borne) infection in 30 varieties important to the Canadian potato industry. Replicate plants of each variety were grown in the greenhouse from virus-free plantlets, then artificially inoculated with PVY strains and symptoms followed through plant maturity, tuber production and storage and growth of a second generation of plants from infected tubers. In general, we have confirmed that foliar symptoms and yield reduction in most varieties is most severe in PVYo-infected plants. Foliar symptom severity is not a consistent predictor of yield reduction across strains and varieties, however. Indeed, yield reduction was only significantly correlated with a qualitative symptom severity scale in PVY⁰-infected plants, and not in PVY^{N:0}- or PVY^{NTN}-infected plants. On average, yield reduction was lower in secondary-infected plants, though not always significantly and not universally across all tested potato varieties. PVYNTN is also known to cause very damaging necrotic ringspots in tubers of susceptible varieties, though in our screening, we only found four varieties of 30 tested (AC Chaleur, Envol, Pacific Russet and Yukon Gold) in which this was the case.

¹MacKenzie, T. D., Lavoie, J., Nie, X., & Singh, M. (2018). Differential Spread of Potato virus Y (PVY) Strains O, N:O and NTN in the Field: Implications for the Rise of Recombinant PVY Strains in New Brunswick, Canada. Am J Potato Res, 1-10. <u>https://doi.org/10.1007/s12230-018-9632-6</u>

Introduction of Molecular Diagnostic Methods for the Rapid and Sensitive Detection of Potato Viruses in Support of CFIA Seed Potato Certification Program

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Over 50 viruses have been reported to infect potato naturally and 10 of them have been confirmed as present in commercial potato lots in Canada. They are; potato viruses A, M, S, X, Y (PVA, PVM, PVS, PVX, PVY), *Potato leafroll virus* (PLRV), *Potato mop-top virus* (PMTV), *Potato latent virus* (PotLV), *Tobacco rattle virus* (TRV) and *Alfalfa mosaic virus* (AMV). One of the most efficient approaches for the control of potato diseases induced by viruses is to use virus free seed potatoes. There is a requirement for indexing seed potatoes for some, or all these viruses, in various potato regulatory testing schemes under the Seed Potato Certification Program administered by the Canadian Food Inspection Agency (CFIA).

A wide range of diagnostic methods has been developed and employed for the diagnosis of potato diseases induced by viruses and for the identification of virus species or even strains types. Of these methods, serological procedures targeting viral proteins have been employed for many years because they are cost effective for indexing samples on a large scale. Nucleic acid based technologies targeting virus genomes or gene segments, particularly the methods based on polymerase chain reaction (PCR) have gained wide acceptance and have been implemented broadly for the detection and identification of potato viruses in various potato samples including tubers, leaves, true potato seeds and *in vitro* microplants.

During the last 10 years, the Charlottetown Lab (CL) has developed, evaluated and validated molecular diagnostic procedures for indexing seed potatoes. Several of these molecular tests have been implemented in the CL and in CFIA approved diagnosis labs in support of potato regulatory testing. The standard molecular diagnostic protocols implemented include reverse transcription (RT) PCR and real-time quantitative RT-PCR for primary screening and restriction fragment length polymorphism (RFLP) and sequence analysis (from automated cycle sequencing) for confirmation/ verification. The molecular methods have demonstrated to be superior to serological methods in regards to sensitivity, specificity and simplicity.

Experiments have been conducted in the CL to make molecular diagnostic procedures safe, simple, rapid and automated. Magnetic bead based technology has been introduced to replace the chemical based methods for extracting nucleic acid (NA) from various plant tissues. Additionally, the use of the KingFisher platform in combination with magnetic bead extraction solution, allows for automated NA extraction thereby increasing the CL's capacity for regulatory testing in emergency situations. Safe and sensitive NA staining dyes, GelRed, GelGreen and SYBR Green, have replaced the highly toxic ethidium bromide (EB) in agarose gel electrophoresis (AGE) for visualization of PCR amplicons. Procedures for capillary analysis based on the use of the QIAxcel platform have been implemented in the CL to replace AGE; the capillary analysis has also shown to be ideal for high throughput testing (HTT).

Studies have been conducted for evaluating loop-mediated DNA amplification (LAMP in short) technology for the detection of potato viruses. Reverse transcription of viral RNA followed by LAMP DNA amplification under isothermal conditions provides a specific, sensitive, rapid and cost-effective test for detection. Virus specific primers have been designed and evaluated in the CL for the isothermal detection of PMTV and TRV. LAMP may be utilized as an alternative test when there is a need for rapid confirmation or verification.

New CL research projects have been launched in recent years to assess the application of next generation sequencing (NGS) technology in plant regulatory testing. A MiSeq sequencer(Illumina), and the necessary accessories (equipment for assessing NA quality, normalization etc.) have been acquired and experiments have been conducted for developing appropriate pipelines for detecting a wide range of potato pathogens in various testing samples from the potato post entry quarantine (PPEQ), seed potato certification, potato nuclear stock certification and plant pest surveillance programs. Appropriate methods/kits for extracting high quality NA (high index number) were assessed and selected. Sequence reads were obtained in NGS runs from the paired-end sequencing and used for *de novo* assembly using CLC Genomics Workbench. After filtration against the host genome sequence, assembled contigs were then blasted against all known sequences available in the NCBI database. Complete sequences of a number of viruses including AMV, PLRV, PVM, PVS, PVY (various strain types), *Tomato chlorosis virus* (ToCV) and *Potato aucuba mosaic virus* (PAMV) were obtained. The NGS results were then validated by one or more diagnostic methods, e.g. bioassay, RT-PCR and RT-qPCR using gene specific primers and probes.

The molecular and genome based methods have proven to be superior to ELISA and some other diagnostic methods. The evaluations conducted in the CL and elsewhere have shown the wide application of molecular and genome technologies for the detection of plant viruses. NGS followed by PCR/qPCR confirmation provides a powerful tool for the rapid and reliable detection and confirmation of plant viruses which is extremely important for regulating phytosanitary issues.

High Resolution DNA Melting (HRM) Assay for Detection of Rx1 and Rx2 for Rapid High-Throughput Selection for Extreme Resistance to Potato Virus X in Potato

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Potato selections are regularly assessed for their response to Potato virus X (PVX) infection prior to their release by AAFC's potato breeding program. Extreme resistance (ER) to PVX has been detected in many potato breeding clones and advanced selections. Assessment of the existing PCRgel electrophoresis based methods for detection of Rx1 and Rx2, the genes that independently control ER to PVX, indicated that the 5Rx1F/5Rx1R primer pair led to reliable detection of Rx1 whereas the 106Rx2F/106Rx2R primer pair detected Rx2 despite some non-specific reactions in potato clones/cultivars without Rx2. However, the methodology is time consuming and does not differentiate the absence of Rx1/Rx2 from a failed PCR reaction. A newly designed primer pair that targets Rx1 and Rx2 as well as rx1 and rx2 produced an amplicon for all alleles. When the primer pair was combined with 5Rx1F/5Rx1R, respective amplicons were produced, although they were not distinguishable by regular agarose gel electrophoresis. When subjected to a high resolution DNA melting (HRM) assay, two distinct melting profiles for Rx1 and rx1, respectively, were detected. Triplex PCR-gel electrophoresis and -HRM assay for detection of Rx1, Rx2 and rx1/rx2 were also performed. The efficacy of the HRM assays were validated in potato cultivars/clones with known phenotypes, indicating its potential for high-throughput selection of potato clones/cultivars carrying Rx1 or Rx2. Duplex PCR-HRM assays of over 600 progeny from 12 crosses involving various parents correctly detected the presence or absence of Rx1 in each progeny, allowing accurate prediction of the phenotype. Progeny that tested positive for Rx1 by HRM exhibited ER to PVX whereas progeny that tested negative for Rx1 were susceptible to PVX infection. The genotype of each parent and the possible presence of Nx in two Rx1-possessing parents are also discussed.

Photosynthetic Characteristics of Potato Plants Varying in Verticillium Wilt Resistance

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The potato early dying disease caused by fungus *Verticillium dahliae* Kleb. poses a major constraint to potato production in temperate regions. The pathogen causes wilting, chlorosis and premature vine senescence leading to poor plant performance and significant reduction in tuber yield and quality. Our preliminary study has revealed a decline in photosynthetic rates in *Verticillium* infected plants, which was associated with early vine senescence. A study is underway to better understand the mechanism of the photosynthetic decline under *Verticillium* infection. The information will be used to develop strategies for managing early dying and offsetting tuber losses from *V. dahliae* infection. CO₂ gas exchange rates, stomatal conductance, water use efficiency and other photosynthetic parameters will be measured in combination with molecular and biochemical analyses. The study will be carried out in infected and control potato plants varying in *Verticillium* wilt resistance.

Applying Real-Time PCR to Rapidly Detect and Quantify Verticillium Species in Soil Samples

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The Verticillium genus contains fungal pathogen species including Verticillium dahliae and Verticillium nonalfalfae (previously known as Verticillium albo-atrum group one). These species cause Verticillium Wilt in potato crops by infecting the plant tissue and blocking the xylem responsible for carrying water from roots to the stems and leaves. This results in wilt, stunted growth, death of plant tissue, and reduced tuber production. Verticillium is a soil-borne fungus, whose reproductive structures can persist [for several years] in agricultural soils and potentially infect later planted potato crops. Therefore, being able to rapidly and accurately assess the pathogen load of crop soil is essential for planting and management decisions.

Traditionally, soil pathogen load assessment has been done via soil plating on selective media and allowing fungal colonies to grow for at least 3 weeks before performing counts. This is time consuming and requires expertise in identification to perform the counts; additionally, several *Verticillium* species look very similar to *V. dahliae* anatomically, which may lead to misidentification and miscounting. In the case of *V. nonalfalfae*, microsclerotial resting structures are not formed, making accurate counts even more difficult. The use of real-time quantitative PCR with well designed, species-specific primers can avoid uncertainty and reduce throughput time considerably, as DNA can be extracted from soil and subjected to real-time PCR in as little as one day.

Working with soil and fungi on a molecular level is not without challenges. Soil is a complex matrix containing inhibitory compounds that must be removed before efficient PCR can be performed, and diverse microbial communities requiring highly discriminating DNA-based detection techniques. Also, the genome of *Verticillium* may contain multiple copies of the same target DNA sequence, or these sequences may be very similar between species, making PCR primer design critical for accurate species detection. The development and optimization of a quantitative real time PCR test for *Verticillium dahliae* and *Verticillium nonalfalfae*, along with the advantages of this testing process, will be discussed.

Improving Resistance of Existing Varieties to Common Scab using Somaclonal Variation

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Common scab is responsible for important economic losses in New Brunswick every year. In some areas, common scab is limiting production. The pathogen causing common scab produces phytotoxins named thaxtomins that are responsible for the brownish lesions on tubers. Several potato varieties are resistant to common scab, however several of the varieties used in niche market are susceptible to this disease and growers are limited in their choice of varieties that they can grow for processing industry. Somaclonal variation uses the natural ability of plants to change under stress, and is often observed in tissue culture (Evans, 1989). Somaclonal variation can be used as a tool for potato improvement since it is not considered genetically modified (GM) because the variation occurs within the plant and no external DNA is added. The changes are often stable and heritable. There are several possible explanations for what causes the changes, including changes in the sequence of the genes or changes in the expression/ regulation of genes.

Somaclonal variation has produced commercial varieties, most of which are ornamental plants (e.g. geranium). There are also commercial varieties of crop plants (rice, sugarcane, sweet potato, alfalfa) and medicinal plants (Citronella, *Brassica juncea, Lathyrus sativus*) produced by somaclonal variation. Research in somaclonal variation in potato has been carried out for over 30 years. Somaclonal variation was documented for several traits in potato including agronomic traits (ex. plant maturity and vigour, yield, tuber number, size, and shape) (Heeres et al. 2002; Thieme & Griess, 2005) and disease resistance (late blight and common scab) (Sebastiani et al., 1994; Beaudoin et al. 2013; Wilson and Tegg 2010). Most traits in potato may be altered by this method if the genetic variation exists and if variation can be induced in the cultivar. The number of commercial varieties created by somaclonal variation is most likely under reported as many breeders choose not to disclose the method of development.

The overall objective of this project was to induce somaclonal variation to create lines more resistant to common scab from existing varieties Shepody and Red Pontiac. These varieties were chosen because they are publicly available and are currently used by growers in New Brunswick. The first step was to determine what growth media would induce production of calli and regenerate plantlets from stem or leaf pieces. Five media with different growth regulator types and concentrations were tested. Red Pontiac and Shepody produced calli on different medium and regenerated 2.2 plantlets per stem and 0.6 plantlets per leaf, respectively.

Pathogenic *Streptomyces* produces plant toxins named thaxtomins that act like cellulose inhibitor. Thaxtomin was used as a screening tool to kill cells that were very susceptible possibly resulting in a greater number of plantlets resistant to common scab compared to untreated calli. A reduction of up to 96% and 52% of the number of plantlets regenerated was observed between thaxtomin treated and untreated calli for Red Pontiac and Shepody, respectively. Fifty plantlets per variety were selected. Mini-tubers were produced in greenhouse and planted the next summer in a site infested with common scab pathogen. The experimental site was planted as a completely randomized block design with four replicates. Five parental lines were tested as controls. Preliminary results showed that about 10% of the variants were more resistant than the parental lines. A 2-fold decrease in common scab severity was observed in variants of Red Pontiac and Shepody compared to their respective parental lines. The decrease in disease severity resulted in 6% to 52% increase in marketable tubers (i.e. with less than 5% of the surface with lesions) in variants of Red Pontiac and a 20 to 38% increase in marketable tubers in variants of Shepody. This could represent substantial gain for the growers. Reproducibility and the stability of the variants will need to be further tested in the future.

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Candidate Gene Expression Biomarkers for Potato Growth and Storage Quality

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Monitoring for issues limiting vine growth, impacting yield and tuber quality during the growing season and long term storage occurs regularly. This information gives an indication that a problem has occurred but usually does not provide enough notice to effectively counter the identified issue. Living organisms respond to stressors at a gene expression level extremely quickly. By measuring these changes in gene expression we can determine if a stressor is present before it has a negative effect on tuber yield or tuber quality. The current presentation examines the use of gene expression as a management and research tool and how it can be implemented as a biomarker based predictor of potato performance and storability. Resistance to cold-induced sweetening (CIS) will be used as an example of how this technology could be used by growers and storage managers as a management tool and by potato breeders and researchers as a tool to guide and augment breeding and storage trials. We evaluate different algorithms for predicting CIS during the storage season based on gene expression measurements taken after harvest, prior to cold storage. From this data we classify CIS resistance, based on data collected at harvest, in different lines and perform a risk assessment as to whether a given lot of potato tubers will be above a sweetening threshold mid-way through the storage season. Finally we present a framework for how gene expression biomarkers can be applied to different agronomic issues and traits in potato.

Application of Sequence Based Genotyping for Genomics Assisted Breeding in Potato

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One goal of applied agricultural genomics is to develop high throughput genetic markers that can be used to screen large breeding line populations in an efficient, cost effective manner. Here we describe the application of the genotyping by sequencing (GBS) approach to marker discovery and genotyping on a population of diverse potato varieties included in the Canadian Potato Genetic Resources (CPGR) collection. By employing several minor modifications to the standard GBS protocol, including the use of a novel restriction enzyme, and the use of an in-house bioinformatics pipeline we have identified approximately 30000 single nucleotide polymorphism markers across 175 potato varieties. We illustrate the utility of these markers for potato germplasm collection curation, and in the detection of population structure and relatedness among varieties. We also illustrate the potential use of these markers for marker assisted selection (MAS) by combining the marker genotypes with historical trait data available for the CPGR collection.

Genetic Mapping of Colorado Potato Beetle Resistance-Related Metabolites in Potato

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Colorado potato beetle (CPB), Leptinotarsa decemlineata (Say), is one of the economically important pests of potato. All the larval stages and adult insects feed on potato foliage that can cause significant yield reduction. Chemical pesticides such as imidacloprid are mainly used to control CPB, but pesticide resistant populations are emerging. Thus, there is an urgency to develop alternative methods of pest management. Secondary metabolites present in plants can provide protection against pests and diseases. Steroidal glycoalklaoids (SGAs) are the most abundant secondary metabolites in members of Solanaceae family, including potato. Wild solanum species, S. chacoense and S. oplocense (recently reclassified as S. brevicaule), contain leptines and dehydrocommersonine, respectively, which are associated with potato resistance against CPB. SGA biosynthesis is controlled by genetic factors, and, therefore, efforts have been made to transfer genes controlling biosynthesis of resistance-related metabolites to cultivated potato by crossing or somatic hybridization with wild species. Recently, evaluation of CPB defoliation in the progenies of S. oplocense x S. tuberosum and selection of metabolite markers led to identification of dehydrocommersonine and another novel SGA identified as solanidenol-chacotriose to be related to host resistance and susceptibility respectively. Metabolite profiling of SGAs was used to phenotype a mapping population to find genes controlling production of SGAs controlling CPB resistance and susceptibility. Mapping population 17139 was developed from a cross between S. tuberosum cv Shepody and 13213-07, which is an F1 hybrid containing S. oplocense as one of the parents. Using genotyping by sequencing (GBS) and bulk segregant analysis, we identified loci in the genome responsible for SGAs in a marker region on chromosome 1 of potato. Genes in this region have functions related to oxidation-reduction reactions that correspond to biosynthetic steps that can give rise to SGA associated with CPB susceptibility.

N-Responsive Gene Expression Biomarkers for Predicting Tuber Yield and Specific Gravity

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Optimizing fertilizer application to maximize crop yield is a goal for growers to reduce fertilizer losses to the environment and costs for production. Optimal fertilizer application can also lead to improved tuber quality. Current methods target estimation of crop N status by utilizing optical sensing of chlorophyll or chemical testing of petiole N. Accuracy of these methods is not sufficient and improved methods are needed. An improved method for crop monitoring and yield prediction was developed using gene expression. Transcriptome sequencing was used to assess gene expression across the potato genome for a replicated trial with 0 and 180 kg N/ha treatments for varieties Atlantic, Shepody and Russet Burbank at two developmental and four sampling time points. Gene expression that was responsive to N rates was identified and used to develop a gene expression biomarker for estimating yield potential. Expression of 63 candidate genes was measured using Nanostring nCounter over seven field trials at five sites that had variable N treatments. The field trials showed yield responses to N treatments and variation in specific gravity. A total of 439 samples were collected. RNA was extracted and quantified using nCounter. Gene expression predictive of plot-level relative yield (yield per plot/maximal yield for trial), specific gravity and total N uptake was analyzed using regression analysis and supervised machine learning algorithms. The accuracy of prediction provided by gene expression models was superior to that provided by petiole N.

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Impact of Chloropicrin Soil Fumigation in Potato Production Systems

Chad Hutchinson* and Jeff Douglas

Chloropicrin soil fumigation is a relatively recent disease control practice adopted in potato production. However, chloropicrin soil fumigation has been used safely and effectively in agricultural production for over 50 years to suppress a broad range of soil born disease. In potato production, chloropicrin soil fumigation is gaining acceptance because it suppresses troublesome diseases such as common scab ad Verticillium wilt. There are many long-held assumptions regarding soil fumigation such as 1. soil fumigation sterilizes the soil, and 2. once a farmer starts soil fumigation, the practice cannot be stopped. New research into disease suppression and soil health following chloropicrin soil fumigation in potato production by examining the cultural practices and equipment required for chloropicrin application; disease suppression, tuber yield and quality; and the soil health benefits will be presented. University research and on-farm research trials will be shared.

Soil Health and Soil Borne Disease Management in Michigan Potato Production

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Potato production in Michigan ranks seventh nationally in potato production with a farm gate value of nearly \$208 million annually. Approximately 70% of production in the state goes towards the chip processing industry. Over the last decade some Michigan growers in certain production areas have been experienced declining yields and marketability issues. These quality problems have reduced marketable output. Soil borne disease complexes such as Verticillium wilt caused by Verticillium dahliae and potato common scab caused by Streptomyces spp. are recognized as a major cause of yield and quality declines. Nearly 90% of major diseases that impact crops (including potato) are caused by soil borne pathogens. Many of the available soil borne disease management tools can be spatially and temporally inconsistent. Research in soil borne disease management in Michigan has focused on the effects of soil treatments (e.g. fumigation, amendments, cultural practices) on soil health and the soil microbiome. Recent research approaches utilizing modern molecular analyses of microbial communities in potato systems, GIS, geostatistics, and traditional field studies will be presented.

Relating Apparent Soil Electrical Conductivity to Soil Properties in Commercial Potato Fields in Eastern Canada

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Apparent electrical conductivity (ECa) of the soil can be used as an indirect indicator of a number of soil physical and chemical properties. As a precision farming diagnostic tool, ECa can be used more efficiently if the factors influencing its spatial variability are understood. Many soil properties such as soil texture, moisture and organic matter have been shown to be closely related with the ECa. Moreover, these properties can often be related to yield potential. The objective of this research was to characterize the spatial variability of soil properties using a soil ECa sensor in commercial potato fields in eastern Canada. Soil ECa was measured for two depths (0-30 cm [EC30] and 0-100 cm [EC100]) using the Veris, a commercially available proximal soil sensor. The study was conducted on two commercial field sites: a 21 ha field in in New Brunswick (referred as NB1) and an 8 ha field in Prince Edward Island (referred as PEI1). Soil samples (0-0.15 m) were densely collected for 109 and 154 georeferenced sampling points at PEI1 and NB1, respectively, to determine soil spatial variability of soil properties (soil organic matter, pH, and Mehlich-3 extractable elements). Correlations of ECa with intrinsic factors, such as soil particle size and soil organic matter, were significantly and strongly correlated with ECa in both sites. Soil proximal sensors such as the Veris can be used for fields under potato production, and the measured ECa is closely related with soil texture. Given that soil texture is closely linked to water holding capacity, drainage and often linked with potato yield, mapping of fields for ECa using proximal sensors may be useful in implementing precision agriculture strategies.

Spatial Variation of Indices of Soil Health in a Commercial Potato Field in New Brunswick

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Healthy soil is critical to the sustainability of potato production. As a result, there has been increased interest in recent years in quantifying soil health in commercial fields or under various management practices. However, there is no single direct measurement of soil health which can be made, and as a result a number of indices of soil health have been proposed which relate to different attributes of a healthy soil. This assessment of soil health is mostly done at a field scale, and the within-field spatial variation of such indices of soil health is generally unknown. An improved understanding of the within-field spatial variation in indices of soil health would assist in the development of appropriate sampling strategies and in the interpretation of results.

Soil samples were collected from 0-15 cm depth in the spring prior to planting or fertilizer application from a commercial potato field in New Brunswick. This field site was previously mapped for spatial variation in soil apparent electrical conductivity (ECa), and the ECa was used to identify soil management zones. These management zones were found to be related to tuber yield and soil texture. Samples were collected from 154 geo-referenced grid points, and used to assess soil properties (e.g., soil pH, soil texture) and a suite of indices of soil health. The indices included soil organic C and total N by combustion, permanganate oxidizable C, particulate organic matter C and N, 24 hr burst test, soil respiration, labile N by aerobic incubation, soil aggregate stability, and soil water holding capacity.

Most soil properties and indices of soil health had significant spatial variation, and exhibited a strong spatial structure. As might be expected, several parameters had similar spatial patterns. For example, the spatial pattern of permanganate oxidizable C and particulate organic matter C was similar to that of soil organic C. Some parameters, such as the 24-hr burst test and soil aggregate stability differed significant with management zones identified using ECa, however, not all parameters varied significantly between management zones. The relationships among indices of soil health and soil properties, and their implications for sampling and interpretation, will be discussed.

Enhancing Ground Cover in Potato Production Systems with Nurse Crops and Winter Cover Cropping in Prince Edward Island

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The soil cropped to potato is susceptible to erosion in spring between seeding and potato emergence and in fall after potato harvest. This loss of organic-rich surface soil by erosion can lead to soil organic matter decline. Maintaining a living crop as long as possible is an effective management practice for reducing soil erosion, and can offer multiple other benefits. The objectives of this study were to evaluate: i) the effects of intercropping potato with nurse crops on potato performance and nitrogen dynamics; and ii) the feasibility of growing winter cover crops at different timings after potato harvest. Trials were conducted in small plot experimental trials as well as at a field scale in commercial fields.

Nurse crop study

A nurse crop is a crop seeded at around the time of potato planting which grows quickly and protects the soil until the potato crop emerges. During nurse crop screening phase in 2015, four nurse crop species (buckwheat, winter rye, oat and brown mustard) were compared with a no nurse crop control, and the nurse crop growth was controlled mechanically though hilling. In 2016, two nurse crop species (winter rye and root max ryegrass), and two ways of controlling nurse crop growth (mechanical control through hilling and the use of a grass selective herbicide) were compared with a no nurse crop control. In 2017, two nurse crop species (winter rye and spring barley) and 3 ways of controlling nurse crop growth (mechanical control through hilling, a grass selective herbicide, and a non-selective herbicide) were compared with a no nurse crop control.

Results from these three years demonstrated that hilling without the use of an herbicide is not efficient to stop nurse crop growth. There is a chance for regrowth of the nurse crop to occur when a grass selective herbicide is used, depending on the seeding rate and on the growth stage of the nurse crop. Winter rye and winter barley were the suitable candidates to be used as nurse crop, and a non-selective herbicide was more efficient than the grass selective herbicide (Figure 1). Future studies should test different seeding rates, and different timing to stop nurse crop growth, to identify the rate and time that would increase potato yield over the control. A yield increase would be sufficient to justify the extra cost associated with growing the nurse crop, and would protect the soil from erosion prior to emergence of the potato crop.





Note: mechanical control and grass selective herbicide application happened at the time of hilling (3-4 weeks after planting), whereas the non-selective herbicide was applied at around 15 days after planting.

Winter cover cropping study

In 2015, a broad range of winter cover crops were seeded after potato harvest at two dates (end of September and mid-October): winter rye, winter peas, winter rape, tillage root max, tillage radish, and Italian ryegrass. We observed a poor emergence of the crops seeded late except for winter rye. In 2016 and 2017, only 4 treatments were compared (spring barley, winter rye, winter wheat plus a no winter cover crop control) with two seeding dates (September 27 and October 4). Winter cereal (winter rye and winter wheat) were left to grow and parameters associated to yield were determined in the following summer. Grain yield and thousand kernel weight were statistically higher for winter wheat than winter rye but the effect of seeding date was not significant.

Winter cereals (winter rye or winter wheat) are the most suitable winter cover crops after early potato harvest. Spring barley could represent an interesting option due to its fast germination if the main objective is to establish a ground cover. We observed a trend towards reduced nitrate concentrations under winter cover crops compared with a no winter cover crop control (Table 1). This indicates that winter cereals are good scavengers of residual soil nitrate after potato harvest, and thus could offer economic and environmental benefits to growers. Seeding as earlier as end of September or by the first week of October would allow a good emergence and good yield of winter cereals. Table 1. Winter cover crop trial in a commercial field in 2016. The treatment effect on soil nitrate availability was measured at different time periods as nitrate desorbed from anion exchange membranes (AEM) over winter.

Nitrate measured at different periods (mg kg-1)									AEM over winter
	Oct. 6 th , 2016 Nov		Nov. 7 ^t	Nov. 7 th , 2016		May 8 th , 2017		Sept. 14th, 2017	
Control versus winter rye									
	0-15 cm	15-30 cm	0-15 cm	15-30 cm	0-15 cm	15-30 cm	0-15 cm	15-30 cm	µg cm ⁻² day ⁻¹
Control	40.2a	33.4a	13.7a	14.7a	29.2a	20.3a	5.15b	4.4a	0.39a
Winter rye	29.4b	23.6b	10.3a	9.4b	19.8b	11.6b	12.03a	7.8b	0.20b
Control versus winter wheat									
Control	46.6a	39.6a	11.6a	12.5a	35.7a	31.6a	5.3a	5.8	0.87a
Winter Wheat	25.9b	24.6b	15.6a	15.0a	30.8a	24.2b	8.4a	8.1	0.65b

Note: values within a group with different letters are statistically significant at 0.05 probability level.

The Use of Nurse Crops in Potato Production in NB

Sheldon Hann*, Josée Owen, Judith Nyiraneza, Bernie Zebarth and Sherry Fillmore

Historically, potato production systems in New Brunswick include intensive cultivation practices and produce very little soil cover during the planting to canopy closure phase. These aspects contribute to decreases in soil quality as well as increases in soil erosion. The use of "nurse cropping" in potato production can potentially help mitigate these factors. Nurse crops are companion plantings meant to fill in and reduce soil erosion in the period between planning and canopy cover. They can provide a fundamental role in the improvement of soil quality. Nurse crop stems can trap sediments by reducing surface runoff and intercepting rainfall by reducing rain drop impact; roots anchor the soil, contribute to organic matter, improve soil structure and improve the movement of air and water through soil. From 2015 to 2017, four trials were established at the Fredericton Research and Development Centre in Fredericton, New Brunswick, with the objective of evaluating the use of various nurse crops (field pea, winter rye and barley) at multiple seeding rates (high and low) as well as the application of multiple herbicide treatments prior to potato hilling (prism, paraguat and no kill) on potato productivity. The experimental results showed significant effects of treatment factors (nurse crop, seeding rate and herbicide treatment) on potato yield components in terms of size classes, marketable and total tuber yields Conclusions from the field trials describe that nurse crops can provide a mechanism to improve soil guality and benefit potato productivity.

Comparing Whole Seed with Cut Seed for Processing Potato Production in Prince Edward Island

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In 2016 and 2017, on-farm trials were conducted to assess the performance of whole seed tubers from a series of Prince Edward Island seed lots in comparison with a representative sample of cut seed pieces from the same seed lots. This work has been initiated to assess whether whole seed will produce similar or better returns per acre than cut seed lots. Seed was not grown under a management system to produce seed lots for whole seed, but whole tubers of two sizes (1.5 to 2.5 oz; 2.5 to 4.0 oz) were collected from each seed lot. These two seed sizes were then planted at two different seed spacings, depending on the variety (Russet Burbank in 2016, Russet Burbank and Prospect in 2017). Seed was evaluated at three plot locations in each year. In both years, significant differences were observed between the seed sources. Over the two years for Russet Burbank variety, performance of the 1.5 to 2.5 oz small seed was not markedly different from the cut seed control. Performance of the 2.5 to 4.0 oz whole tubers retuned approximately \$200/acre more than the cut seed control. Marketable yields were consistently higher for the whole seed treatments, with slight reductions in the percentage of 10 ounce tubers. More work is proposed for 2018. This trial was sponsored by the PEI Agronomy Initiative for Marketable yield (AIM).

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Planting Early Makes Money - for Both Seed and Processing Growers

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The objective of this study was to determine the impact of seed crop planting date on yield, physiological age and performance of the tubers in the subsequent year.

2016 - Seed Production year

Whole 56-85 gram Russet Burbank seed tubers were warmed to 10°C until the day of planting. The early planting date was May 21, 2016 (seed warmed for two weeks) and the late planting date was June 15, 2016 (seed warmed for 5 weeks). All tubers were planted 30 cm apart and the late planted tubers were desprouted prior to planting.

Early planted seed was at 100% emergence on June 15, 2016 and the late planted seed reached full emergence on July 5, 2016. Stem number was not affected by planting date. Tuber initiation occurred on July 13, 2016 for the early planted seed and on July 22, 2016 for the late planted seed. The plots were topkilled on September 1, 2016 and harvested three weeks later. Harvested tubers were graded into the following categories (by diameter): <35 mm, 35-45 mm, 45-55 mm, 55-70 mm, >70 mm, and rough.

Total and marketable yield from early planted seed were significantly higher than those from late planted seed, 150 cwt/acre more and 138 cwt/acre more, respectively (Table 1). Planting seed early resulted in higher yield of tubers 55-70 mm and >70mm in diameter. Late planting resulted in more 35-45 mm tubers. Average tuber weight was greater (p<0.05) for early planted seed (116.5 grams) than late planted seed (85 gram average).

Planting date	Total yield	Market- able*	< 35 mm	35-45 mm	45-55 mm	55-70 mm	>70 mm	Rough
Early	373.3 a	353.3 a	3.4	33.0 b	121.8	180.2 a	18.3 a	16.5 a
Late	223.4 b	214.7 b	4.8	48.0 a	116.8	48.7 b	1.2 b	3.8 b
p-value	0.001	0.005	0.255	0.033	0.660	0.001	0.016	0.011
Lsd 0.05	39.1	52.1		12.8		32.4	11.2	3.2

Table 1. Harvested Russet Burbank seed yield (cwt/acre) as affected by planting date.

* marketable seed yield = >35mm and no rough

Value of the seed crop was calculated using the price of \$15/cwt. The marketable yield from the early planting was worth more than \$2,000 more per acre than the marketable yield from the late planting.

Determining seed physiological age

After harvest, tuber samples from each seed planting date were held in the dark at room temperature and monitored to determine time of dormancy break. Seed that was planted on May 21, 2016 broke dormancy 112 days after harvest, on January 11, 2017, while seed that was planted June 15, 2016 broke dormancy on January 30, 2017, 131 days after harvest. Tubers from the late

planting date had a longer dormancy period and therefore were physiologically younger that those from the early planting date.

A spring sprouting test confirmed that the tubers from the late planting date were physiologically younger. In April, 2017, 25 tubers were cut into apical and basal halves, planted in peat moss and sprouted in the dark for 3 weeks. Sixty percent of the tubers from the early planted sample produced 3, 4 or 5 sprouts per seed piece, and 40% produced 1 or 2 sprouts. In the sample from the late planting date, 20% of the seed pieces produced 3 or 4 sprouts, and 80% produced only 1 or 2 sprouts. Increased stem numbers are indicative of older tubers.

2017 - Processing crop production year

After tuber harvest and grading, all the seed was stored at the McCain Research Farm storage at 4°C. The seed was cut just before planting on May 18, 2017. The seed pieces were planted at 38 cm inrow spacing, grown as a processing crop and harvested 130 days after planting.

Tubers from the seed that was planted early (May 21, 2016), when compared with the seed from the late planting (June 15, 2016), emerged faster, produced fewer stems per plant, more tubers per plant and yielded higher total and marketable yields with less tubers >10 ounces (Figure 1).





Calculated crop value of the tubers from the early 2016 planting date was 142/acre higher than from the late 2016 planting date primarily due to a higher yield of tubers in the 1% - 10 ounce size category.

Length of growing season in the seed production year influences seed yield and age, and the effects on age are carried over into the subsequent production season. Planting early results in older seed which preforms better in our short growing season and is of increased value to both the seed grower and process grower.

DualEM Sensor Based Management Zones for Site-specific Nutrient Management in Potato Fields

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Potatoes are a high value cash crop, which relies heavily on agrochemicals. Currently, crop management practices are implemented uniformly with inadequate attention being given to the spatial variability in soil properties and tuber yield which not only increases the production cost but also adversely affects the tuber yield, quality and environment. This study was designed to characterize and quantify the spatial variation in soil properties and tuber yield and to delineate management zones for site-specific nutrient management. Three fields were selected in New Brunswick, and a grid pattern was established at experimental sites to collect soil and yield samples. Soil samples were analyzed for soil physical and chemical properties. The volumetric moisture content and ground conductivity data were also recorded at the same grid points. The location of the sampling points and field boundaries were marked with a global positioning system.

Results of classical statistic and geo-statistical analysis suggested substantial spatial variability in soil and crop characteristics, indicating the influence of these parameters on yield. The mapping in geographical information system (GIS) also showed significant variability in collected data for selected fields. Regression analysis suggested that the sensor conductivity was able to explain >50% variability in tuber yield within selected fields. Furthermore, DualEM sensor conductivity was significantly correlated with moisture content, organic matter, and major nutrients. The cluster analysis was performed to group soil, crop, sensor and potato yield into five groups as very poor, poor, good, very good, and excellent and MZs were delineated in GIS. Multiple means were compared for delineated MZs for the influential soil and crop variables having significant impact on yield. Results showed higher yield in highly productive areas and vice versa. Preliminary results of this study showed a great potential for the DualEM sensor to be used for developing MZs for site-specific nutrient management.

Keywords. Ground conductivity, management zones, spatial variability, variable rate fertilization, potato production.

Potatoes: From Seed to Seed - Can We Change the Approach?

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The path for potato germplasm development is littered with pitfalls. Many breeding lines with good yield potential or disease resistance end up with poor quality and/or marketability. Similarly, some popular cultivars are not environmentally friendly in terms of nutrients and water use efficiency. Self-incompatibility is usually observed in potatoes, especially in popular cultivars such as Russet Burbank, hindering the purge of unwanted mutations. Consequently, the ultimate resort is outcrossing to enlarge the genetic background. The From seed to seed presentation will share and discuss ideas and approaches towards creating self-compatible potato germplasm while contributing to correcting some undesirable traits in elite cultivars such as Russet Burbank.

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New Insights on Wireworm Biology

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Agriotes sputator is the principal insect pest species confronted by the agricultural industries in PEI. Due to the lack of effective control methods and mounting population pressure, this pest has become a major concern not only in potato, but also many other crops. The present study was aimed at improving our knowledge of the biology of the dominant wireworm species in PEI, so that more effective pest management strategies can be developed. The research indicated that more than 95% eggs were deposited in the upper two cm of soil under laboratory condition, and the average body size of newly hatched wireworms was measured at around 1.95 mm. During the first year of larval development, the body size reached up to 12 mm with the average value at 8.4 mm. Travel ability of neonate wireworms in the soil was tested with four distances. Results showed that, the longest distance that newly hatched larvae moved within 24 h was 12 inches, while one day later, 25 % of individuals traveled 18 inches to reach a food source. Horizontal movement of wireworm was determined with three sizes of larvae, small, medium, and large. Results demonstrated that larvae of all three sizes traveled 3.6 m within 24 h. This study provided insights into the biology of this pest that could be used to develop new control methods.

Potato Early Dying - Survey and Disease Management

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Potato early- dying disease complex (PED) is often called Verticillium wilt of potato and is considered one of the most economically devastating diseases in potato producing areas worldwide. The severity of the disease greatly increases with the association of the soil borne pathogens Verticillium dahliae & V. albo-atrum and the root lesion nematode (Pratylenchus sp.). Recently, an increase in wilt disease symptoms and a sharp decrease in marketable tuber yields were observed in New Brunswick (NB), Canada. A survey of 71 fields including 8 fields sampled before and after fumigation was carried out in order to determine and quantify nematodes and Verticillium in the soil. Techniques used included plate counts for Verticillium (CFU/g soil); Real-time gPCR for V. dahliae (cell/g soil); and nematode identification and counts (# of nematodes/kg of soil). The survey results of the 71 fields revealed that only 55 fields had Verticillium sp. ranging from 2-66 CFU/g soil sample by plate methods; 68 fields had high V. dahliae ranging from 261-27471 cell/g soil by RT-gPCR method. All fields had high numbers of root lesion nematode ranging from 560-14240 nematodes/kg soil sample (nematode count). There was an uneven distribution of PED incidence in potato fields at various locations of NB. Fumigation with chloropicrin drastically reduced the numbers of root lesion nematode by 34.1%-99.0%; Verticillium sp. CFU/g soil by 50%-100 %; and V. dahliae cell/g soil by 38%-91% in all of the 8 fumigated fields. Management of potato early dying complex with various pest management products under field condition was also studied in a field plot trial setup. The nematicide 'Velum' applied in-furrow at the recommended rate decreased the numbers of root lesion nematode by up to 66% compared to other products. The combination of both 'Velum + Aprovia', and the application of Ammonium-lignosulfonate highly reduced V. dahliae by 190.95 % and 274.24%, respectively, compared to other products. The fungicide 'Aprovia' applied in-furrow at the recommended rate for the management of Verticillium wilt highly reduced Verticillium sp. CFU/g soil in treated soil by 73.3% compared to other products and the untreated control. All pest management products increased potato marketable yield in the range of 27.38%-97.74%.

Potato Cultivar Effects on Pathogenic Streptomyces spp. Abundance and Bacterial Communities

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Common scab (CS) is caused by filamentous gram-positive bacteria of the genus Streptomyces. Common scab is an economically important disease of potato (Solanum tuberosum L.) worldwide. This disease does not usually have significant effects on plant vigour or tuber yield. However, CS does cause important economic losses due to cosmetic factors in the table market (i.e., tubers with more than 5% lesions cannot be sold), to declassification in seed production, and to losses of fry quality during potato processing. There is a lack of effective management strategies for CS. Although some methods to control CS were tested in the past, the success of these methods is highly variable from site to site and year to year. The pathogenic Streptomyces population abundance in soil is heterogeneous spatially and temporally however it is unclear how the abundance of pathogenic Streptomyces spp. is affected by potato cultivar over time. The objective of this study was to evaluate the effects of potato cultivar on pathogenic Streptomyces spp. abundance and diversity of bacterial communities in three spatial locations over the growing season: 1) soil close to the plant (SCP); 2) rhizosphere (RS); and 3) geocaulosphere (GS). The experiment was conducted in a naturally CS infested field located at Fredericton, NB, Canada for two summers. Two tolerant (Goldrush, Hindenburg) and two susceptible cultivars (Green Mountain, Agria) were tested. Abundance of pathogenic Streptomyces spp. population was measured using quantitative PCR targeting a gene involved in the plant toxin thaxtomin biosynthesis (txtC).

The abundance of pathogenic Streptomyces spp. significantly increased in late August compared with other dates in RS of susceptible cultivars in both years. Abundance of pathogenic Streptomyces spp., when averaged over locations and time, was significantly greater in susceptible cultivars compared with tolerant cultivars. Principal component analysis showed that SCP and RS soil properties (pH, organic carbon and nitrogen concentrations) explained 68% and 76% of total variation in Streptomyces spp. abundance among cultivars in 2013, respectively, suggesting that cultivars influenced CS pathogen growth conditions.

Potato cultivars influence the diversity of bacterial community which could explain changes in the abundance of pathogenic Streptomyces spp. To evaluate this, the diversity of bacterial communities was determined in four potato cultivars during potato growth using Illumina MiSeq Next-Generation sequencing targeting the 16S rRNA gene. A total of 26,861 operational taxonomic units (OTU) were observed for two summers. Only 30 and 28 % OTUs were shared among the four potato cultivars in 2013 and 2014, respectively. The alpha-diversity of bacterial communities as measured by Shannon diversity index was significantly greater in tolerant cultivar Hindenburg compared to both susceptible cultivars in 2014, whereas in 2013 α -diversity was significantly greater in Hindenburg compared to Agria and Goldrush. Beta-diversity of bacterial communities was significantly different among spatial locations (i.e., SCP, RS and GS) and over time. There were no significant differences in β -diversity among potato cultivars according to a Permutational Multivariate Analysis of Variance (PERMANOVA), however, differences in relative abundances of OTUs classified as Streptomyces, Actinobacteria subgroup 6, Bradyrhizobium, and Pseudarthrobacter among cultivars were observed in SCP, RS and GS. The results suggest that abundance of pathogenic Streptomyces spp. in the SCP, RS or GS may be

influenced due to differences in the quantity or composition of exudates among potato cultivars rather than due to a change in the diversity of soil bacterial communities, although it cannot be ruled out that specific bacterial species may have synergistic or antagonistic effects on pathogenic Streptomyces spp growth.

Current Research Progress in Potato Zebra Chip Disease

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With symptoms of internal necrosis resulting in severe discoloration of processing crisp chips, potato Zebra Chip Disease (ZCD) was originally discovered in Mexico in 1994 (Secor et al 2009). The disease has been observed since 2000 in Guatemala and the southern United States, and has spread further northward into most central areas of the US and New Zealand. The disease has devastated the potato industry due to losses in the commercial value of harvested potato tubers with necrotic symptoms, and has caused millions of dollars in losses to potato growers. The causal agent of ZCD, 'Candidatus Liberibacter solanacearum' (CLso) transmitted by potato/tomato psyllid (*Bactericera cockerel*), was not identified until 2009 (Liefting et al., 2009; Secor et al., 2009) due to the fastidious nature of the plant pathogen. Subsequently, CLso was also shown to cause similar phloem-borne diseases on carrot and celery in northern Europe vectored by carrot psyllids (Trioza apicalis). CLso causes carrot and celery yellowing in Finland, Sweden, Norway, Spain, and France. More recently, the pathogen in potato-tomato psyllids causing potato ZCD has been discovered on the Norfolk Island between New Zealand and Australia during a major guarantine survey. The insect and the disease would be major threats to Australian potato industry. There are strict quarantine measures in place for movement of goods between Norfolk Island and Australia; however, potato/tomato psyllids (Bactericera cockerel) were indeed observed in Western Australia according to a recent report (http:// www.interstateguarantine.org.au/).

Studies based on phylogenetic analysis using the combination of the 16S rRNA, 16S-23S rRNA intergenic spacer region (ISR), and 50S ribosomal protein gene sequences revealed that the CLso pathogens found in different geographic regions were diverse and could be assigned to five separate clades: haplotypes A, B, C, D, or E, with various host plants. In New Zealand, Mexico, and the US, haplotypes A and B were identified as associated with ZCD of potatoes and psyllid yellows of tomato and capsicum (Munyaneze et al 2016) with tomato/potato psyllid (*B. cockerel*) as the vector. Subsequently, CLso haplotypes C, D, and E were identified in northern Europe. CLso haplotype C associated with carrot yellowing disease in Finland, Sweden, Norway, and Germany was transmitted by the carrot psyllid (*Trioza apicalis*). CLso haplotypes D and E were described in carrot and celery in Spain, Morocco and France, and the psyllid (*B. trigonica*) was considered the vector.

The ZCD symptoms on potato tubers are characterized by collapsed stolons, browning of vascular tissue concomitant with necrotic flecking of internal tuber tissues, and streaking of the medullary ray tissues, which result in severe internal necrosis of potato tuber tissue that becomes dark blotches, stripes, or streaks after being processed into chips, causing it to lose its commercial value (Secor et al 2009). Infected potato plants exhibit plant stunting, shortened internodes, yellowing and upward curling of leaves, pinkish discoloration, and growth of lateral shoots and aerial tubers, leading to plant wilting and sudden death. Infected tubers often fail to sprout. Our greenhouse observations indicated the formation of secondary tubers from infected tubers which then sprout to form plants with delayed emergence (Li, X. and Nie, J. unpublished data). Some of the early foliar symptoms resemble purple top caused by phytoplasmas, which, like the liberibacter, are obligatory

plant pathogens and cannot be cultured on laboratory media. ZCD symptoms on potato foliage can also appear similar to psyllid yellows attributed to a toxin released by psyllids feeding on potato/ tomato. However, tubers from plants with psyllid yellows do not normally exhibit internal tuber necrosis and are negative by PCR assay specific to CLso (Sengoda *et al.*, 2010).

Table 1 lists the etiology of the diseases, 'Ca. L. solanacearum', and its current distribution, vectors, and hosts. The actual list of host plants may extend further to many solanaceous weeds species. In tomato, CLso was reported for the first time in New Zealand, causing mottling, yellowing, deformation of the leaf lamina, and sudden death of the plant (Liefting et al., 2009). In Mexico and the US, CLso caused tomato decline with the symptoms of chlorosis of apical shoots, lanceolate leaflets with epinasty and margins with purple coloration, necrosis and abortion of flowers, mature leaves brittle and rolled up, reduced internodes, and reduced growth (Rojas-Martínez et al 2016). Under greenhouse conditions, some tomato varieties (vars. Money Maker and Roma) were latent carriers of CLso haplotype A (Li, et al 2013). Tomato plants graft-inoculated with scions from CLso haplotype A-infected tomato plants remained symptomless, but tested positive in a CLso-specific PCR assay. In contrast, potato plants (cultivars Jemsam, Atlantic, Shepody, Frontier Russet, and Russet Norkotah) grafted with scions from the same latently infected tomato plants showed typical symptoms of purple top, leaf scorch, formation of aerial tuber, and plant wilting to death after being grafted. However, many attempts to graft CLso haplotype B infected tomato or potato plants to the same varieties of tomato (vars. Money Maker and Roma) often caused tomato decline symptoms, resulting in plant death. In other words, the tomato varieties tested were not considered to be latent carriers of CLso haplotype B. It remains unclear what and how the pathogenicity variations of these two haplotypes in tomato are reflected at the genome level, and a study is in progress at the Charlottetown Lab in which comparative genomics analysis is being done among the genome sequence data from haplotypes A, B and C (Figure 2) on the basis of their pathogenicity on tomato. To date, we have identified 11128 Single-Nucleotide Polymorphisms (SNPs) for genome differentiations among CLso haplotype A, B, and C (Figure 2). Association of the signature SNPs and the functional genes or transcription factors with the virulence on individual host plant would help unveil the pathogenicity characteristics.

Currently, seven genome sequences with multiple contigs were deposited in GenBank by various research groups. Some of the source materials originated from potato-tomato psyllids while others were isolated from either tomato or carrot. To date, none of the source materials originated from potato, presumably due to the lethality of the CLso to potato plants after its transmission by psyllids or grafting (Lin et al 2011, Thompson et al 2015, Wang et al 2017). Comparative genomics analyses of various CLso haplotypes from different geographic locations suggests that the genomes of CLso haplotype A, B, and C from the U.S., New Zealand and Finland demonstrate significant genome plasticity within the species (Thompson et al 2015, Wang et al 2017). However, none of these studies focused on the pathogenicity variations among the three haplotypes on their hosts.

Recently, we have obtained CLso haplotype C strain maintained in carrot seeds from Finland. The carrot plants containing CLso were successfully grafted to tomato plants, and the grafted tomato plants showed no obvious symptoms, but tested positive using CLso-specific PCR assay followed by sequencing confirmation. Whether the CLso haplotype C can be grafted to potato and cause ZCD remains to be studied at the CFIA Charlottetown Lab. However, a very low percentage (3%) of transmission of CLso haplotype C by carrot psyllids (*B. trigonica*) was observed (Teresani et al 2017). Interestingly, a similar low transmission rate was observed while CLso haplotype A and B were used to

inoculate carrots by potato psyllids (Munyaneza et al 2016). They concluded that "potato psyllid is unlikely to transmit CLso (haplotype A and B) to carrots under normal field conditions".

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Haplotypes	Host plant	Distribution	Vector
A and B	Potato (Solanum tuberosum), Tomato (S. lycopersicum), Chilli (Capsicum annuum), Eggplant (S. melongena), Tomatillo (Physalis ixocarpa), Tamarillo (S. betaceum), Cape gooseberry (Physalis peruviana), Wolfberry (Lycium barbarum), Nightshades (S. elaeagnifolium, S. ptychanthum).	Mexico, Western and Central USA, Guatemana, Nicaragua, New Zealand	Potato/Tomato psyllid (<i>Bactericera</i> <i>cockerelli</i>)
C, D, and E	Carrot (Daucus carota subsp. sativus), Celery (Apium graveolens)	Finland, Sweden, Norway, Spain, France, New Zealand	Carrot psyllid (<i>Trioza</i> <i>apicalis, B.</i> <i>trigonica</i>)

Table 1 'Candidatus Liberibacter solanacearum', its distribution, and vectors



Figure 1. World distribution of 'Candidatus Liberibacter solanacearum'. Picture from CABI website (https://www.cabi.org/).



Figure 2. Mauve alignment of the three 'Candidatus Liberibacter solanacearum' haplotypes A (NZ1) and B (ZC1) and B and C (FIN 114) genomes.

Potato Performance and Nitrogen Cycling as Impacted by Drip Irrigation and Different Crop Rotations

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Potato yield have been stagnant in Prince Edward Island partially due to soil quality decline and/or to drought spell. This study initiated in 2015 and 2016 in two adjacent fields explored the impacts of novel crop rotations with and without supplemental irrigation on potato performance, selected soil quality parameters and nitrogen dynamics. Soil moisture was maintained at 90-95% of field capacity via an onsite drip irrigation system during July-August. Three rotations were compared; (ROT1) barley under seeded with red clover (year 1)-red clover (year 2) - potato (year 3); (ROT2) soybean (year 1)- brown mustard (year 2)-potato (year 3); (ROT3) grain corn (year 1)-sorghum sudan grass (year 2)-potato (year 3) with and without drip irrigation. During potato phase, the main plot was split in two sections; one with no N application and the other half receiving 190 N, P₂O₅, and K₂O kg ha⁻¹. Potato tuber internal defects were assessed by quantifying the percentage of tubers showing brown heart, hollow heart, dry or soft rot and vascular discoloration from a subsample of tubers per each treatment.

Before potato seeding in spring 2017, soil samples were taken and sent to Cornell soil laboratory to analyze soil health-related parameters. Not statistical differences among rotation systems were observed on soil quality parameters measured by Cornell soil laboratory. However, soil respiration was 24 to 35% higher with the rotation including red clover and sorghum sudan grass than the rotation including mustard. Active carbon was 6% higher with red clover than with other two rotations. Similar trends were observed with aggregate stability and organic carbon. The rotation including red clover has lower surface hardening than other rotations although not statistically significant at 5% probability level.

There was an effect of rotation and N rate on potato marketable yield but the effect of irrigation was not significant. The rotation including mustard and sorghum have statistically higher marketable yields than red clover and yield increase by irrigation were around 10% higher than without irrigation. Internal defects were assessed and hollow heart was not affected by rotation and irrigation. However, the percentage of tubers showing hollow heart was twofold higher with- than without irrigation. Comparing rotation systems among them, the rotation system including sorghum sudan grass was associated with lower percentage of tubers showing hollow heart, dry and soft rot and vascular discoloration than the other rotations but the differences were not statistically significant at 0.05 probability level.

Nitrate dynamics during potato phase from soil extraction or measured by anion exchange membranes showed trends towards higher nitrate under the rotation including red clover and lower nominal values associated with the rotation including sorghum sudan grass even if not statistically significant at 0.05 probability levels. These preliminary results will be validated in 2018 in an adjacent field where a similar trial was initiated in 2016.

Developing Sustainable Varieties- Late Blight Resistance in Advanced Potato Selections

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Late blight, caused by *Phytophtora infestans*, is the most important disease of potatoes. Recent changes in *P. infestans* populations have increased the risks and costs of potato production worldwide. The utilization of resistant cultivars is an important component of potato disease management strategies. An important objective of Agriculture and Agri-Food Canada (AAFC) potato breeding program is to incorporate genetic resistance into adapted cultivars to facilitate reduced use of pesticides in order to increase agricultural productivity and enhance environmental performance of potato production systems. Sources of resistance identified in *Solanum tuberosum* germplasm and related wild species from South and Central America have progressively been incorporated into AAFC potato breeding program. In-house hybridization efforts are also supplemented with exchange of breeding populations and parental lines from collaborating institutions in order to increase genetic diversity and base for selection. Late blight resistant clones with acceptable quality traits for processing or fresh market uses are progressing into various stages of cultivar development. A number of advanced selections have been released to industry for evaluation and potential commercial release. Other promising selections are recycled in the breeding program as crossing parents to further develop superior cultivars.

Evaluation of the Link Between Soil Microbial Communities Structure and Potato Field Production

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Prince Edward Island (PEI) Potato Board represents more than 200 potato growers in the province, and represents the interests of the PEI potato industry to various levels of government. PEI potato growers have been experiencing significant problems with understanding the factors that affect potato yield and disease development. Despite significant efforts, little is conclusively known about how soil biological and physical characteristics are linked to high and low potato yields. In preliminary studies supported by the Potato Board looking at yield variability within fields, researchers have seen indications that soil compaction, certain nutrient deficiencies, and soil-borne pathogens such as *Verticillium*, root lesion nematodes, and common scab can have significant effects on marketable yield. The goal of this research is to evaluate a link between potato yield and disease occurrence and the diversity and structure of soil microbial communities in potato fields. This will provide a foundation for the development of an affordable method for prediction of field production potential, allowing the grower to test the soil in the fall before potato planting and adjust the cropping strategy for maximum yield and profit.

Screening of Potato Cultivars for Heat Tolerance

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Potato is a crop that is very sensitive to heat stress, likely because the origin of the potato crop is the cold highland of Andes. Presently the potato crop is mainly in relatively low temperature regions or low temperature seasons in the world. Despite being a North American country, Canada can still have very hot summer due to the global climate change. According to Statistics Canada (2016), as a result of extreme heat stress in summer of 2016, the potato yield in Ontario decreased 17.2% in 2016 compared with the production in 2015 (Statistics Canada, 2016). To identify potato cultivars that are relatively tolerant to heat stress, we screened 55 potato cultivars for heat tolerance under heat stress conditions (35 ± 1 °C in the daytime and 28 ± 1 °C at night) in greenhouses in comparison with plants growing under non-heat-stressed conditions. This experiment was conducted in the Fredericton Research and Development Centre, Agriculture and Agri-Food Canada, Fredericton, New Brunswick, Canada. Tubers were harvested from plants after three months. The tuber number, tuber fresh weight, and tuber dry weight were scored. The results and data interpretation will be presented.

POSTERS

Bug Off: Developing Green Antimicrobial Agents & Pesticides

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Our research team has been working for over twenty years on the generation of several families of compounds that have potent antifungal, antibacterial and antiparasitical properties with the ultimate goal of designing an *environmentally-friendly pesticide*. Compounds containing boron (boric acid and borax derivatives) are particularly promising as they are relatively harmless to mammals and higher life forms but are toxic to smaller life forms such as microbes and insects. An additional benefit to boron compounds is that upon metabolism they degrade into boric acid, an essential plant food. Interest in small molecule boron pharmaceutical chemistry has grown tremendously in recent years as researchers continue to discover new and remarkable applications for these interesting molecules. We will present some of our findings in this area along with a novel group of compounds based on the food additive maltol, which is found in the bark of larch trees, in pine needles, and in roasted malt.



Variation of Organelle DNA Content and Dry Matter Content During Tuber Development in Shepody and Russet Burbank

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Potato dry matter (solids) content is critically important for the quality of French fries. Dry matter in potato tubers is mainly starch, which is synthesized in cellular organelles called plastids. Starch synthesis likely required support of cellular energy from mitochondria (location for respiration). However, it is unclear whether the contents of plastid DNA and mitochondrial DNA in potato tubers are involved in dry matter accumulation in tubers. The present study analysed the relationship between the contents of these DNAs and the contents of dry matter in the two tuber ends (stem end and bud end) in potato cultivars 'Shepody' and 'Russet Burbank', two important French fry cultivars that have high-dry matter contents in tubers. We found that the contents of both dry matter and these organelle DNAs at the two tuber ends increased during tuber development. Starch content was also higher when dry matter content was higher. The results suggest that the increased starch synthesis in tubers during tuber development required increased contents of organelle DNAs. This study provided insights into the relationship between the dry matter and organelle DNA contents in potato tubers.

Genome Editing in Potato Plants by Agrobacterium-Mediated Transient Expression of TALENs

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Genome editing (also known as targeted mutation) has promise for molecular breeding because the genetic variation is from gene mutation rather than transfer of genes. There are two major tool systems in genome editing -- the CRISPR/Case9 system and the transcription activator-like effector nucleases (TALEN) system. Compared with the CRISPR/Cas9 system, the TALEN system has likely a lesser off-target rate in genome editing. Both a rapid test system for the functionality of designed TALENs and an effective delivery system for introducing the TALENs to plants for induction of mutation are critical to successful target mutation. TALENs have usually been tested in protoplasts (the cells after the cell wall was removed enzymatically) or introduced to plants with viral vectors. However, plant regeneration from protoplast culture can generate extensive somatic cell variation. Viral vectors are not always available and usually require containment during experiments. In addition, plants edited by viral vectors require virus elimination. Here, we used a non-viral, Agrobacterium-mediated transient expression approach, to serve both rapid test and effective delivery of TALENs into two vegetatively propagated cultivars Russet Burbank and Shepody of potato (Solanum tuberosum). TALENs designed to target two endogenous genes -- starch branching enzyme (expected to increase resistant starch content if mutated) and an acid invertase (expected to increase the tuber resistance to cold sweetening if mutated) by Agrobacterium-mediated infiltration (agroinfiltration) into leaves of potato plants. The DNA from infiltrated-leaves was analyzed using restriction-site loss assay and subsequent DNA sequencing. Deep sequencing of these tetraploid cultivars was also conducted to determine the zygosity at the targeted chromosomal loci. We successfully induced mutations at the cellular level at both targeted loci.

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