CANADIAN PHYTOPATHOLOGICAL SOCIETY

MARITIME REGION MEETING 2013

Crops and Livestock Research Centre
Agriculture and Agri-Food Canada
Charlottetown, Prince Edward Island

November 28, 2013

Canadian Phytopathological Society
Maritime Region Meeting
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INTRODUCTION

Welcome to Charlottetown and to the 2013 Canadian Phytopathological Society Maritime Region Meeting. It has been a full year since we got together as a group, and I look forward to a stimulating afternoon of scientific discussion and fellowship.

There are 12 oral presentations on various topics in phytopathology scheduled for the afternoon. A dinner and presentations will take place at **Hunter's Ale House** following the meeting.

I am pleased and honoured to welcome Dr. Richard A. Martin, active scientist with Agriculture and Agri-Food Canada in Charlottetown, as our keynote speaker. Dr. Martin is renowned for his work on pathogens of cereal and oilseed crops, in particular, *Fusarium* spp. causing head blight of cereal crops. His presentation is entitled: '**Fusarium Head Blight in the Atlantic Region: A 30 Year Retrospective**.'

Many thanks to all who attended the meeting. I would particularly like to thank the Canadian Phytopathological Society, represented by president Janice Elmhirst, for sponsoring this event and I'd like to thank Janice directly for making the time to attend our event. I trust we will be able to get together on a regular basis in future, and on that note, we will host the 2014 meetings in Fredericton, NB.

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

Rick D. Peters
CPS Maritime Region Rep

Canadian Phytopathological Society
Annual Maritime Region Meeting – 2013

Scientific Program
Thursday, November 28
Conference Rooms – Crops and Livestock Research Centre, Charlottetown, PE

1:00-1:10	**Welcome: Rick D. Peters,** CPS Rep-Maritime Region
1:10-1:30	**CPS Affairs: Janice Elmhirst, CPS President**
1:30-2:15	**Keynote Speaker: Dr. Richard A. Martin Fusarium Head Blight in the Atlantic Region: A 30 Year Retrospective**
Session A:	**Host/Pathogen Responses and Interactions**
2:15-2:30	Breeding for resistance to PVY- An update from the Potato Research Centre A.M. Murphy* and D.H. Wilson
2:30-2:45	Gene expression analysis of changes induced by phosphites in *Phytophthora infestans* T. Borza, G. Sakthivel, and G. Wang-Pruski*

2:45-3:00 The development of genetic markers as a screening tool for resistance to late blight (*Phytophthora infestans)* in potatoes (*Solanum tuberosum)*
J. Coffin*, R.H. Coffin, G. Wang-Pruski, R.D. Peters and A. MacPhail

3:00-3:15 PVX and PVY^{NTN} co-infections incite stronger synergistic reactions than mixed infections with PVX and other strains of PVY in solanaceous plants
X. Nie*, Z. Liang, and M. Singh

3:15-3:45 **Nutrition Break and Poster Session**

Session B: **Posters**

Session C: **Pathogen Detection**

3:45-4:00 Detection and quantification of *Verticillium dahliae* and *Verticillium albo-atrum* in soil and potato plants by real-time qPCR
X. Gao*, T. Borza, and G. Wang-Pruski

4:00-4:15 Comparative genomics of pectobacteria and development of species-specific assays against *Pectobacterium wasabiae*
K. Yuan*, W. Chen, C. Lewis, J. Tampong, and S. Li

4:15-4:30 Molecular detection and identification and phylogenetic study on *Heterobasidion* species complex
S. Li*, K. Yuan, J. Nie, H. Arsenault, S.F. Shamoun, and C. Hammett

Session D:	**Pathogen Characterization and Disease Management**
4:30-4:45	*De novo* assembly and analysis of the mRNA transcriptome in resting spores of the potato wart pathogen *Synchytrium endobioticum* D. Smith* and U. Singh
4:45-5:00	Modernization of Canadian potato post entry quarantine program - Validation and implementation of molecular diagnostic methods H. Xu* and S. Cody
5:00-5:15	Strawberry decline syndrome: an emerging threat to strawberry production in Atlantic Canada. P.A. Abbasi*
5:15-5:30	Metalaxyl-m sensitivity of *Phytophthora erythroseptica* causing pink rot of potato in Canada B. Crane, R.D. Peters*, K.A. Drake, A. MacPhail, D. Gregory and K. MacDonald
5:30-5:45	**Wrap-up**
6:30-10:00	**Dinner and Awards**

Fusarium head blight in the Atlantic Region: a 30 year retrospective. R.A. MARTIN*, H. VOLDENG, T.M. CHOO and Y. YAN. *Crops and Livestock Research Centre, Agriculture and Agri-Food Canada, 440 University Ave, Charlottetown PE C1A 4N6, and (H.V, T.M.C., Y.Y.) Eastern Cereal and Oilseed Research Centre, Agriculture and Agri-Food Canada, Ottawa ON.*

Fusarium head blight (FHB) (*as caused by Fusarium graminearum* Schwabe) has been an on-going important disease problem in cereals in the Atlantic Region of Canada, since the early 1980's. Severity has ranged from trace to highly severe between years and or between areas within the region; with mycotoxin (deoxynivalenol, DON) levels in excess of 10ppm. Spring wheat and barley have been the major affected cereals in the Region; and while infected oats is impacted to only a minor extent. Winter wheat cultivars are highly susceptible but the crop appears to miss critical infection periods and field issues are less than with spring cereals. The challenge has been to providing for adequate risk management strategies which address regional epidemic development patterns while being economically viable and address field symptoms and mycotoxin contamination. Primary emphasis in research and development has been directed towards the development of superior germplasm with resistance to FHB and resultant mycotoxin contamination. While a slow process, success with resistant germplasm has started to occurred, with release of cultivars with good resistance will maintaining high agronomic and other disease resistant characteristics; for example, AAC Scotia, breed in Charlottetown, with some of the best resistance available in a good high yielding and quality spring wheat line. In barley, research has consistently demonstrated that two row cultivars, Island particularly, are far superior to six row cultivars, and this has resulted in a heavier use of two row barley, in regional production. While fungicide studies have identified superior materials for foliar/head application for increasing yield in wheat and barley, the impact on FHB control has been disappointing, with DON reductions ranging from 0 – 50%. Some basic epidemiology studies have demonstrated that infection periods are not limited to anthesis but continue throughout the season; resulting in challenges to development of superior germplasm and other disease reduction strategies. This has meant that resistance strategies or germplasm developed in other regions are not always effective in the Atlantic Region.

Breeding for resistance to Potato Virus Y: An update from the Potato Research Centre. A.M. MURPHY*, D.H WILSON AND S. ALLABY. *Potato Research Centre (PRC) Agriculture and Agri-Food Canada* (*AAFC*), *850 Lincoln Rd., Fredericton, NB E3B 4Z7, Canada*

Several strategies have been used to increase the frequency of extreme resistance to PVY conferred by Ry genes in potato selections. Progeny from resistant parents were screened by mechanical inoculation followed by graft inoculation to verify extreme resistance. Extreme resistance is effective against all strains of PVY. However, several parents used to confer resistance to PVY were found to be highly susceptible to common scab. For this reason, a project was undertaken to develop improved parents which have both extreme resistance to PVY and common scab. Approximately 1000 clones from 12 families were subjected to common scab and PVY challenges over several cycles; survivors were retained on the basis of their disease reactions. These survivors were also assessed for the presence of a marker associated with resistance to golden nematode (*G. rostochiensis* (Woll.)). As of October 2013, twenty three selections have been retained, twenty of which have extreme resistance to PVY, fifteen have good scab scores and five carry a marker for golden nematode resistance. Their agronomic performance has been assessed and they will be evaluated for parental value. Several potato selections recently released through the Accelerated Release process have extreme resistance to PVY and are currently undergoing evaluation by industry participants.

Gene expression analysis of changes induced by phosphites in *Phytophthora infestans* (Mont.) de Bary. T. BORZA, G. SAKTHIVEL AND G. WANG-PRUSKI*. *Department of Plant and Animal Sciences, Faculty of Agriculture, Dalhousie University, 50 Pictou Road, Truro, NS B2N 5E3, Canada.*

Phosphite-containing fungicides are increasingly used to control the development of the fungal-like plant pathogens from the *Oomycetes* group. The oomycete *Phytophthora infestans* (Mont.) de Bary is responsible for the occurrence of late blight disease in potatoes, which causes enormous economic damage worldwide. Phosphites (Phi) inhibit oomycetes by two different modes of action; directly, by inhibiting pathogen's development, and indirectly, by inducing plant defense mechanisms. The way Phi suppresses the development of *P. infestans* in plants is still not well documented. With the aim to determine the effects of Phi on *P. infestans* we analyzed, using quantitative RT-PCR (qPCR), the expression pattern of 14 genes involved in pathogen-plant interaction, calcium-mediated signal transduction, energy production, oxidative stress, translational regulation and protein synthesis. *P. infestans* mating type A2, genotype US-8 was grown *in vitro*, on a pea medium. After five days of growth, two different concentrations of Phi, i.e. 100 µgl/mL and 150 µg/mL, were added to the medium. To ascertain the fungitoxic effects, samples were taken 24 h and 48 h after the addition of Phi. Both concentrations triggered a similar overall response pattern. After 24 h the expression of most genes was found to be down-regulated. A completely opposite trend was documented after 48 h, when the expression of nearly all genes was found to be up-regulated. A possible explanation for this pattern is that after a short period of stress, *P. infestans* aims to compensate the toxic effects by turning on the expression of a wide array of genes.

The development of genetic markers as a screening tool for resistance to late blight (*Phytophthora infestans)* in potatoes (*Solanum tuberosum).* J. COFFIN*, R.H. COFFIN, G. WANG-PRUSKI, R.D. PETERS and A. MACPHAIL. *Privar Farm Inc.*, 909 *Eliot River Road, North Wiltshire, PE, C0A 1Y0,Canada; (G.W-P.) Department of Plant and Animal Sciences, Dalhousie University, Truro, NS, Canada; and (R.D.P.) Agriculture and Agri-Food Canada, Charlottetown, PE, Canada*

Late blight (*Phytophthora infestans)* is a serious disease. The objectives were to develop genetic markers related to the late blight resistance genes in parental materials and to determine if these genetic markers could be used to distinguish breeding progeny for resistance. The late blight resistant material was derived from *Solanum bulbocastanum.* Two resistant lines, F02005 and F02006, were accessed from Agriculture & Agri-Food Canada, Fredericton, NB. Seven DNA markers were successfully developed within the two R genes. The two R genes, Rpi-BLB1 and Rpi-BT1, were tested using four pairs of primers for Rpi-BLB1 and three pairs of primers for Rpi-BT1. The 7 DNA markers successfully detected 2 of the functional R genes present in the 2 resistant parents, but not in the 2 susceptible ones. The next step was to see if the progeny produces the proper PCR products from the DNA markers, which confirms the progeny inherited the resistant genes. Progeny were selected from survivors of offspring of the resistant x susceptible cross by inoculation with a suspension of spores of *P. infestans*, A2-US8. Leaves were collected from the field grown progeny and immediately preserved in liquid nitrogen. Six of the 7 markers, 3 for the Rpi-BLB1 gene and 3 for the Rpi-BT1 gene were examined using the 4 parents and 9 offspring. Of the 9 progeny tested, 7 contain 2 functional R genes and 2 do not. This outcome indicates that these DNA markers can distinguish between progeny with the R genes and those without.

PVX and PVY^{NTN} co-infections incite stronger synergistic reactions than mixed infections with PVX and other strains of PVY in solanaceous plants. X. NIE*, M. SINGH, Z. LIANG and X. XIONG. *Potato Research Centre, Agriculture and Agri-Food Canada, 850 Lincoln Rd, Fredericton, NB E3B 8Z7, Canada; (M.S.) Agricultural Certification Services, 1030 Lincoln Rd, Fredericton, NB E3B 8B7, Canada; and (Z.L., X. X.) College of Horticulture and Landscape, Hunan Agricultural University, Changsha, China*

Post-harvest test of potato cv. Kennebec revealed a *Potato virus Y* (PVY) incidence at 15.8%, a rate that is unusually high for a cultivar possessing a high level of field resistance to the virus. Randomly selected tubers were planted in a field plot and the resulting plants were monitored. Approximate 16% plants developed symptoms ranging from mild mosaic to severe necrosis/rugosity/stunting. ELISA and RT-PCR analysis revealed that infections with *Potato virus S* (PVS), *Potato virus X* (PVX) and PVY, mostly in mixed-infections, occurred commonly in the 14-sampled plants. Two strains, namely PVY^{O} and PVY^{NTN} were identified in the PVY-positive plants. In general, mild mosaic was associated with infections with PVX and PVS; intermediated mosaic was associated with PVS and PVY^{NTN} infections; whereas severe leaf deformation/necrosis/drop were associated with PVY^{NTN} and PVX co-infections, or with PVY^{O} and either PVS or PVX co-infections. Virus-free plantlets were mechanically inoculated with PVX, PVY^{O}, and PVY^{NTN} alone or with PVX+PVY^{O} or PVX+PVY^{NTN} combination in the greenhouse. Infections with PVY^{O}, either alone or with PVX, or with PVX+PVY^{NTN} incited severe mosaic and systemic necrosis soon after the inoculation. The most severe symptoms occurred in the mixed-inoculation with PVX+PVY^{NTN}, demonstrating dramatic synergism between PVX and PVY^{NTN}. Profound PVX and PVY^{NTN} synergism was also found in tobacco, tomato and *Physalis floridana* plants, suggesting that the genetic makeup of PVY plays an important role in the level of synergistic reactions between PVX and PVY on solanaceous plants.

Detection and quantification of *Verticillium dahliae* and *V. albo-atrum* in soils and potato plants by qPCR. X. GAO*, T. BORZA, Z. GANGA and G. WANG-PRUSKI. *Department of Plant and Animal Sciences, Faculty of Agriculture, 50 Pictou Road, Truro NS B2N 5E3, Canada*

Verticillium wilt, mainly caused by the soil-borne pathogens *Verticillium dahliae* Kleb. and *V. albo-atrum* Reinke & Berth., is a vascular wilt disease causing declining yields in worldwide potato production areas. Pre-planting risk assessment of *Verticillium* pathogens in soils or early diagnosis of infection in potato plants are necessary to determine the best crop production management strategies. This study seeks to develop a rapid PCR-based *Verticillium* test system for detecting and quantifying both *V. dahliae* and *V. albo-atrum* in soils and potato plant tissues. Based on the ribosomal DNA (rDNA) intergenic spacer (IGS) and β-tubulin gene sequences, species-specific SYBR Green real-time quantitative PCR (qPCR) assays were modified or developed for the detection and quantification of *V. dahliae* and *V. albo-atrum*, respectively. Our results showed that the primer pairs can be used to distinguish the *V. dahliae* and *V. albo-atrum* pathogens grown in *in vitro* culture, or from soil and plant tissues samples. The lowest detection limits of *Verticillium* DNA in plant and soil samples are approximately 10 and 100 fg of DNA, respectively. These amounts are equivalent to less than one *Verticillium* cell in plant samples and to one to three cells in soil samples, depending on the genes (IGS or tubulin) used for identification. Repeated experiments confirmed that the methodology is sensitive, species-specific, and reliable. It can be widely used in field assessment, crop production and evaluation of treatment options.

Comparative genomics of pectobacteria and development of species-specific assays against *Pectobacterium wasabiae*. K. YUAN*, J. TAMBONG, W. CHEN, C. LEWIS, S.H. DE BOER and X. LI. *Canadian Food Inspection Agency-Charlottetown Laboratory (CFIA-CL), 93 Mount Edward Road, Charlottetown, PE C1A 5T1, Canada; and (W.C., C.L., J.T.) Agriculture and Agri-Food Canada (AAFC), 960 Carling Ave, Ottawa, K1A 0C6, Canada*

Pectobacterium wasabiae (previously classified as *Erwinia carotovora* subsp *wasabiae*) is one of the soft rot bacteria belonging to Gram negative *Enterobacteriacae* family and responsible for significant economic losses of potato and ornamental plants. *P. wasabiae* has unique features compared with other soft rot bacterial species and genera and is well suited for studying the ecology, speciation, and pathogenicity. Draft genome sequence of a Canadian potato isolate Pw1002 was generated using next generation sequencing technique, resulting in 42 scaffolds of a total size of 5.0Mb. Further analysis on the RAST server identified a number of predicted virulence factors. Comparative genomic analysis of *P. wasabiae* Pw1002 with two other potato strains, SCC3193 (Europe) and WPP163 (USA), and one horseradish strain, CFBP3304 (Japan), was executed using MAUVE (v2.3.1). Eighteen hypervariable regions bearing pathogenicity related factors were grouped to ten INDELs and eight highly diversified regions. Among these regions only six loci have unique sequences for developing specific assays using AlleleID7 (v7.8). *P. wasabiae* specificity test was performed in preliminary PCR amplificaton of all six loci on closely related species and subspecies of pectobacteria (P. *atrosepticum*, *P. carotovorum* subsp *brasiliense* , *P. carotovorum* subsp. *carotovorum* , *Dickeya spp (E. chrysanthemi*), *P. carotovorum* subsp. *odorifera*, and *P*. Followed evaluation indicated two loci could be used as targets for *P. wasabiae* specific realtime PCR assays. Further analysis of genome sequences of strains isolated from different hosts and geography regions have provided a template for phylogenetic and functional studies of this widely distributed pathogen.

Molecular detection and identification and phylogenetic study on *Heterobasidion* species complex X. LI*, K. YUAN, S.F. SHAMOUN, J. NIE, H. ARSENAULT, G. SUMAMPONG and C. HAMMETT. *Canadian Food Inspection Agency, Charlottetown Laboratory, Mount Edward Road, Charlottetown, PE, Canada, C1A5T1; and (S.F.S., G.S.) Canadian Forest Service, Pacific Forestry Centre, Victoria, BC, Canada V8Z 1M5*

Heterobasidion causing root and butt rot of coniferous trees is a species complex comprising of five species with various geographic distributions. In North America, *H. irregular* causes disease on pine trees and was known as the traditional P-intersterility group (P-ISG); and *H. occidentale* infects spruce and was named as the S-ISG. The other three species, *H. annosum sensu stricto* (s.s.), *H. parviporum* and *H. abietinum*, are widely distributed in European and Euroasian countries, known as P-ISG, S-ISG, and F-ISG (pathogenic on fir), respectively. Morphological differentiation among there species remains a long standing challenge for classification, and risk is, therefore, unknown for accidental introduction of a new, potentially more aggressive root and butt rot pathogen of coniferous trees via trading of forest products and commodities. In this study, we collected 22 Canadian isolates from British Columbia, Quebec and Ontario, and 55 European and Euroasian isolates for developing species-specific PCR, real-time PCR and loop-mediated isothermal amplification (LAMP) assays. A real-time PCR assay was modified and evaluated for detection and identification of all 5 species of Heterobasidion species complex while four LAMP assays were designed and evaluated for identification of *H. irregular*, *H. occidentale*, *H. annosum* (s.s.), and *H. abietinum* with various specificity. Phylogenetic data based on eight housekeeping gene markers indicated that ten isolates from British Columbia and fifteen from Quebec and Ontario formed two North American lineages, resembling *H. occidentale* and *H. irregulaire*, and three clades formed by all European isolates belonged to species of *H. annosum* (s.s.), *H. parviporum*, and *H. abietinum*, respectively. The phylogenic data also showed that the European and North American species formed two monophyletic sister clades: one consists of *H. abietinum*, *H. parviporum* and *H. occidentale*, and the other includes *H. annosum* and *H. irregulaire*. Both geographic separation and host specificity are the main factors contributed in species formation of Heterobasidion species complex.

De novo* assembly and analysis of the mRNA transcriptome in resting spores of the potato wart pathogen *Synchytrium endobioticum. D.S. SMITH* and U. SINGH. *Canadian Food Inspection Agency, Charlottetown Laboratory, 93 Mount Edward Road, Charlottetown, PE C1A 5T1, Canada*
Potato wart, caused by the soil-borne fungal pathogen *Synchytrium endobioticum* (Schilbersky) Percival, is a serious potato disease with the potential to cause significant economic damage. The overwintering stage of *S. endobioticum* is a resting spore, which can remain viable in soil for decades. *S. endobioticum* is a regulated, quarantine pest, and infested fields must be declared free from viable sporangia before they can be released from quarantine. The current viability test is a bioassay, which is labour-intensive and takes three months to perform. It has been proposed that a molecular test based on the detection of mRNA transcripts may provide a more efficient supplementary or replacement viability test for *S. endobioticum* in soil. A cDNA library from resting spore RNA was constructed and sequenced, generating 16 million 150 base paired-end reads. The reads were quality-checked and assembled *de novo* into 7,285 transcripts representing 6,663 loci. Four previously sequenced genes were found within the assembly, thus validating the sequence and assembly data. The vast majority of transcripts were expressed at a low level, and only 283 (0.04%) were expressed at 500 transcripts per million or higher. Of these, 166 sequences demonstrated significant homologies and could be annotated using blast2GO. Predominant biological processes and molecular functions associated with the more highly expressed transcripts included response to stress, signal transduction, intracellular transport, oxidoreductase activity, ribosome structure, and translation.

Modernization of Canadian potato post-entry quarantine program – Validation and implementation of molecular diagnostic methods. H. XU* and S. CODY. *Canadian Food Inspection Agency, Charlottetown Laboratory, 93 Mt. Edward Rd., Charlottetown, PE, Canada, C1A 5T1*

The importation of tuber-producing species of *Solanum* spp. either as true seed or plant parts for vegetative propagation, is prohibited from all countries and some regions of the United States of America. However, small quantities of *Solanum* spp. germplasm may be introduced into Canada, for vegetative propagation while minimizing the risk of introducing quarantine pathogens under the potato post-entry quarantine (PPEQ) program. Potato accessions entered into the PPEQ program are routinely propagated *in vitro* followed by multiplication in greenhouse before serial testing is conducted for detecting any possible potato pathogens. For a long time, the detection has relied on bioassay, ELISA and electron microscopy. R-PAGE was implemented in the 1990's for the detection of viroids. The entire process of the PPEQ testing is costly and time consuming. Efforts have been made in recent years to modernize the PPEQ program by introducing molecular diagnostic procedures. Since 2010, standard protocols based on RT-PCR and real-time PCR were validated and implemented for detecting *Potato mop-top virus* and *Clavibacter michiganensis* subsp. *sepedonicus* in potato germplasm. Projects have also been initiated for the evaluation and validation of multiplex RT-PCR procedures for detecting various viruses in microplantlets and grown out plants. Methods for the efficient extraction of nucleic acids from various potato tissues and for the verification of primary quarantine testing results have also been evaluated and incorporated into standard diagnostic protocols. These molecular methods are superior to the bioassay and ELISA in sensitivity, specificity and rapidity and their implementation will greatly improve the quality and efficiency of potato quarantine testing.

Strawberry decline syndrome: an emerging threat to strawberry production in Atlantic Canada. P.A. ABBASI*. *Atlantic Food and Horticulture Research Centre, Agriculture and Agri-Food Canada, 32 Main Street, Kentville, Nova Scotia B4N 1J5, Canada*

Strawberry nurseries in the Annapolis valley, Nova Scotia, are major suppliers of bare-root transplants or plug plants for the commercial growers in Canada and US. However in 2012 and 2013, acute decline symptoms appeared in strawberry plants in some of these nurseries, gravely threatening strawberry production in both countries. Strawberry growers noticed uneven growth patterns, stunted foliage, reddening of older leaves, and yellowing of leaf margins in their fields. The strawberry decline syndrome has also been reported from several US states and the source of infection was traced backed to infected plants from nurseries in Nova Scotia. Analysis of infected plants revealed the presence of two main viruses, *strawberry mild yellow edge virus* (SMYEV) and *strawberry mottle virus* (SMoV). Both these viruses are vectored by aphids in a persistent or semi-persistent manner. It was also confirmed that the samples showing severe decline symptoms were doubly infected by both SMYEV and SMoV. When the viruses are present by themselves in a plant, there is little to no disease development, but when they are both present, there is a sudden shift in severity of symptoms for unexplained reasons. Several strawberry plantings have already been discarded to prevent further spread and both strawberry fruit and nursery production sectors are at great risk to this disease. Characterization of interactions between strawberry viruses, host, and aphid vectors and their roles in acute decline disease would lead to development of disease management strategy to mitigate the economic losses to the national strawberry industry.

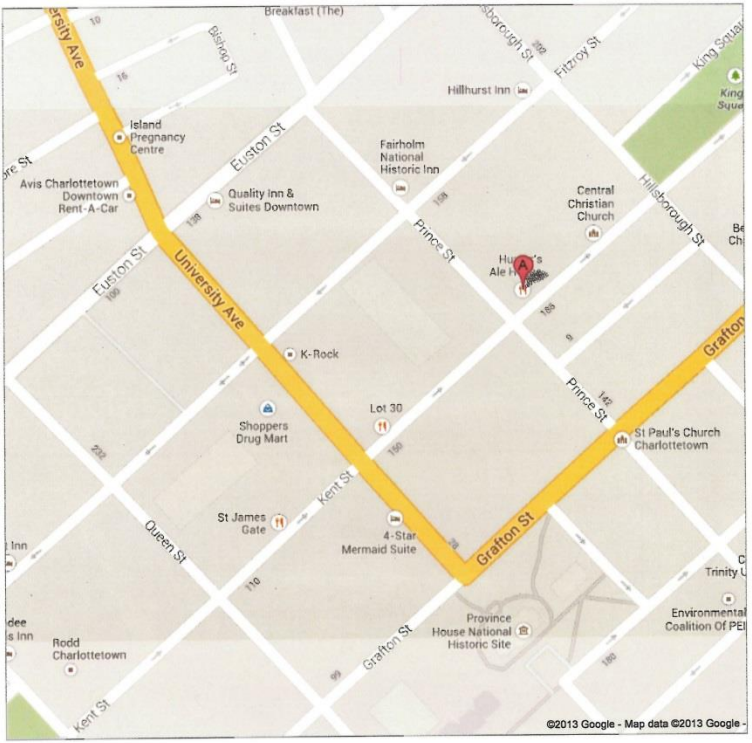
Resistance to metalaxyl-m in populations of *Phytophthora erythroseptica* causing pink rot of potato in Canada. B. CRANE, R.D. PETERS*, L.M. KAWCHUK, A. MACPHAIL, K.A. DRAKE, D. GREGORY and K. MACDONALD. *Agriculture and Agri-Food Canada, Crops and Livestock Research Centre, 440 University Ave., Charlottetown, PE C1A 4N6, Canada; (L.M.K.) Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB T1J 4B1, Canada.*
Pink rot, caused by *Phytophthora erythroseptica*, is a common disease of potatoes in Canada. It is particularly prevalent when high levels of moisture in autumn contribute to pathogen spore release and tuber infection. Management of pink rot has relied heavily upon application of metalaxyl-m (Ridomil Gold ®), either at planting or as a foliar spray during the growing season. In recent years, isolates of *P. erythroseptica* with resistance to metalaxyl-m have been recovered in New Brunswick and in 2012, resistant strains of the pathogen were found in Prince Edward Island. A national survey to assess the distribution of resistant strains of *P. erythroseptica* was initiated in 2013. Samples of infected tubers from across Canada were used to obtain isolates of the pathogen for subsequent testing for metalaxyl-m sensitivity using an *in vitro* agar assay. To date, isolates of *P. erythroseptica* with resistance to metalaxyl-m have been recovered from Prince Edward Island, Nova Scotia, New Brunswick, Ontario and Manitoba. Therefore, an expansion of the range and distribution of metalaxyl-m resistant isolates of the pink rot pathogen is occurring in Canada. The widespread occurrence of metalaxyl-m resistance raises concerns about the efficacy of applications of Ridomil Gold ® for pink rot control and may add importance to the role played by phosphites in the management of this disease.

Notes

Notes

Directions to Hunter's Ale House, Charlottetown

Leaving the Research Centre, turn LEFT onto University Ave. As you head downtown, you will encounter a number of stop lights. Turn LEFT at the Kent St. lights. Continue a short distance to Hunter's Ale House (185 Kent St.). The pub is on the corner of Kent and Prince streets and there is parking along the road of both streets.



A. **Hunter's Ale House**
185 Kent St, Charlottetown, PE C1A 1P1
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4.0 ★★★★☆ 25 reviews