CANADIAN PHYTOPATHOLOGICAL SOCIETY

ATLANTIC REGION MEETING 2018

ST. JOHN’S RESEARCH AND DEVELOPMENT CENTRE
AGRICULTURE AND AGRI-FOOD CANADA
308 BROOKFIELD RD, ST. JOHN’S, NL

Atlantic Region Meeting
August 30, 2018
St. John's Research and Development Centre, St. John's, NL

INTRODUCTION

Welcome to St. John's and to the 2018 Canadian Phytopathological Society (CPS) Atlantic Region Meeting. This is the first time in over 20 years that the Atlantic Region Meeting has been held in St. John's, and we are pleased to welcome you to this afternoon of presentation and discussion.

There are four oral presentations and four poster presentations on various topics. A dinner will take place at the Fish Exchange, 351 Water St., St. John's, at 6 pm following the meeting. We hope that you will join us to continue the day's discussions in a relaxed atmosphere.

I am pleased to welcome **Dr. Dawn Bignell,** Memorial University of Newfoundland, as the keynote speaker this afternoon. Dr. Bignell's work has focused on characterizing the biosynthesis of phytotoxins by *Streptomyces*. Her presentation is entitled: "**Molecular mechanisms of plant pathogenicity: the dark side of *Streptomyces*.**"

I am also very pleased to welcome **Dr. Dilantha Fernando**, President of the Canadian Phytopathological Society for sponsoring and attending this event. He will also be delivering a presentation about his research entitled **"'Designer Genes'? Resistance labels as a new management tool to growers to combat Blackleg in Canola"**. We hope that Dr. Dilantha and the other visitors will enjoy the unique things that our province has to offer during their stay.

This booklet contains the abstracts of oral and poster presentations. The abstracts for the oral presentations are listed in the order in which they will be presented; the poster abstracts are in no particular order, and I hope that you will take the time to meet with all of the poster presenters. All abstracts will subsequently be published in an upcoming edition of the Canadian Journal of Plant Pathology

I hope you have an enjoyable and stimulating afternoon!

Linda Elizabeth Jewell
Chair local arrangements committee

The Canadian Phytopathological Society Atlantic Region Meeting 2018
Thursday, 30 August, 2018
Provincial Boardroom, St. John's Research and Development Centre, St. John's, NL

13:15-13:30	**Registration, Poster Setup**
13:30-13:45	**Introduction/Welcome:** **Dr. Rick D. Peters**, CPS representative – Atlantic region **Leanne Wilson,** Associate Director, Research, Development and Technology, St. John's Research and Development Centre, St. John's, NL
13:45-14:15	**Dr. Dilantha Fernando**, President, Canadian Phytopathological Society **President's Address and Presentation** **"Designer Genes"? Resistance labels as a new management tool to growers to combat Blackleg in Canola**
14:15-15:00	**Keynote Speaker: Dr. Dawn Bignell,** Memorial University of Newfoundland **Molecular mechanisms of plant pathogenicity: the dark side of Streptomyces**
15:00-15:30	Nutrition Break/Poster Presentations
15:30-15:45	**Fluctuating pathogen populations predicate the need for adjustment to potato late blight management strategies in Canada.** R.D. PETERS, K.I. AL-MUGHRABI, F. DAAYF, A. MACPHAIL AND L.M. KAWCHUK
15:45-16:00	**Applications of Next Generation Sequencing for large scale pathogen diagnoses in soybean.** G.A. DIAZ-CRUZ, C. M. SMITH, K.F. WIEBE, S.M. VILLANUEVA, A. KLONOWSKI, B.J. CASSONE. *DEPARTMENT OF BIOLOGY, BRANDON UNIVERSITY, BRANDON, MB R78 6A9, CANADA*
16:00-16:15	**Forage Diseases and Silage Spoilage on Avalon: A Poorly Characterized Problem.** K. COMPTON, W. MOLLOY, AND L. E. JEWELL
16:15-16:30	**Closing remarks:** Dr. Rick Peters
18:00-20:00	**Dinner** (Fish Exchange, 351 Water St., St. John's, NL)

Note to presenters: please ensure that your presentation is given to the audio/visual coordinator prior to the start of the meeting.

President's Address and Presentation

"Designer Genes"? Resistance labels as a new management tool to growers to combat Blackleg in Canola

D. FERNANDO

Department of Plant Science, University of Manitoba, Winnipeg, MB, Canada R3T 2N2

Leptosphaeria maculans is a hemi-biotroph that causes blackleg disease and remains a significant threat to canola (*Brassica napus*) cultivation. Qualitative resistance has been utilized in many breeding programs around the world with some adult plant resistance in their background to mitigate this disease. Although Blackleg was well managed for over 3 decades with good genetics in the Canadian canola industry, there's been a steady increase of resistance being eroded due to the presence of new races of the pathogen in grower fields. Rlm3 is the predominant gene found in Canadian canola cultivars. AvrLm3 gene has been disappearing rapidly in many fields enabling the pathogen to cause moderate to severe disease in grower fields. Canada has also had a trade embargo with China due to blackleg presence in Canada. The successful implementation of research over 5 years by the government and grower groups has helped Canada to adopt new strategies in the mitigation of the blackleg disease. The understanding of the R-genes in Canadian canola germplasm and the blackleg-pathogen races across the canola growing regions has helped the industry to introduce a new R-gene rotation strategy. The development of a diagnostic tool, Kompititive Allele Specific PCR (KASP) markers has helped the producers to identify the predominant races present in their fields. This would help them to strategically select the R-genes and their combinations to be selected in the variety they select to grow in the R-gene rotations. The seed companies are starting to label their varieties with the known R-genes and their combinations so growers can make a good selection of varieties that suits their needs. The adoption of major-gene resistance groups and the *L. maculans* race diagnostics test will provide producers with new tools to help manage and mitigate blackleg on their farms. The presentation will take you through the past, present and future of canola a 26 Billion dollar crop, and the mitigation of blackleg disease in Canada.

Keynote

Molecular mechanisms of plant pathogenicity: the dark side of Streptomyces.

D. R. D. BIGNELL.

Department of Biology, Memorial University of Newfoundland, 232 Elizabeth Avenue, St. John's, NL A1B 3X9, Canada

Bacteria from the genus Streptomyces are best known for their complex developmental life cycle and for their ability to synthesize a wealth of bioactive specialized metabolites with useful applications in medicine and in agriculture. However, there is a dark side to this genus in that certain species can additionally function as aggressive plant pathogens and cause economically important crop diseases, the most notable of which is potato common scab (CS). CS affects the quality and market value of seed, processing and table stock potatoes due to the formation of superficial, erumpent or pitted lesions on the tuber surface. Current management strategies are insufficient or unreliable in controlling the disease, and there are no commercial potato cultivars that display complete disease resistance. Among the factors that have hindered the development of effective CS control strategies is a limited understanding of the mechanisms by which phytopathogenic Streptomyces spp. form parasitic interactions with plants. My lab is interested in elucidating the microbial virulence determinants that contribute to host colonization and disease development by the best characterized CS pathogen, Streptomyces scabies. In this presentation, I will provide an overview of our work on specialized metabolites that are essential for or contribute to the pathogenicity of this organism, as well as recent work on an uncharacterized (cryptic) specialized metabolite that might play a role in plant-microbe interactions. In addition, I will briefly discuss some new work on a potential virulence determinant that resembles toxins produced by human pathogenic bacteria.

Oral Presentations

Fluctuating pathogen populations predicate the need for adjustment to potato late blight management strategies in Canada.

R.D. PETERS, K.I. AL-MUGHRABI, F. DAAYF, A. MACPHAIL AND L.M. KAWCHUK.

Agriculture and Agri-Food Canada, Charlottetown, PE, Canada; (K. A-M.) Department of Agriculture, Aquaculture and Fisheries, Wicklow, NB, Canada; (F.D.) University of Manitoba, Winnipeg, MB, Canada; and (L.K.) Agriculture and Agri-Food Canada, Lethbridge, AB, Canada

Late blight has been an annual disease issue for both potato and tomato crops in Canada in recent years. Plant tissue samples infected with the late blight pathogen collected in Canada from 2015-2017, have yielded multiple clonal genotypes of *Phytophthora infestans* that varied by production region. Pathogen isolates collected from British Columbia potatoes were either US-8 (A2; metalaxyl-insensitive) or US-11 (A1; metalaxyl-insensitive) genotypes. Samples of potato or tomato received from most other production regions, including Alberta, Saskatchewan, Manitoba, Ontario, New Brunswick and Prince Edward Island yielded isolates of the US-23 genotype, which is an A1 mating type and largely sensitive to metalaxyl. Samples of potatoes from Quebec yielded US-23 or US-24 (A1; metalaxyl-insensitive) genotypes. Although isolates of US-23 were often sensitive to metalaxyl early in the season, increased resistance to this chemical pesticide was documented as the season progressed. Greenhouse/storage trials revealed that US-23 was less aggressive on potato foliage than US-8 or US-24, but equally aggressive as the other genotypes on potato tubers. Conversely, US-8 and US-24 were less aggressive on tomato foliage than US-23. The US-23 genotype has become the predominant genotype in most growing regions across Canada in recent years. Identifying and managing disease in tomatoes (transplants and home gardens) have become critical components of successful late blight management strategies for potato crops with the spread of US-23 across Canada.

Applications of Next Generation Sequencing for large scale pathogen diagnoses in soybean.

G.A. DIAZ-CRUZ, C. M. SMITH, K.F. WIEBE, S.M. VILLANUEVA, A. KLONOWSKI, B.J. CASSONE.

Department of Biology, Brandon University, Brandon, MB, R7B 6A9, Canada

Soybean (*Glycine max* (L) Merr.) has become a very important crop in Manitoba, Canada, with a sustained increase in the acreage dedicated to this crop during the last decade. Due to its novelty in the province, scarce information about foliar diseases has been recorded. To describe the foliar pathogens affecting this legume, we conducted a comprehensive survey across Manitoba during the summer of 2016, divided into two time points, June (33 fields) and August (70 fields). At least 3 symptomatic leaves per field were collected, and total RNA was extracted from each sample. Field and regional pools were produced. Regional pools were analyzed using RNA-sequencing, and the sequences that mapped against the soybean genome were discarded. Un-mapped reads were then compared against the non-redundant database in NCBI. We successfully detected the presence of several previously-reported and new soybean pathogens for the region. Additionally, a large number of residual pathogens, pathogens of crops other than soybean, were detected in our surveys, as well as multiple types of Arthropods. Our study shows the great potential of Next Generation Sequencing (NGS) for detection of foliar pathogens at large scale, as a mean of characterizing the pathogenic foliar microbiome of soybean. Also, it provided the opportunity to obtain enough information to assemble small viral genomes obtained from infected samples. However, there are also some limitations regarding the availability of genomic resources to accurately detect microorganisms, as well as the complexity given by microorganisms closely related, and the costs of the technique, which challenge the implementation of NGS for routine diagnosis.

Forage Diseases and Silage Spoilage on Avalon: A Poorly Characterized Problem.

K. COMPTON, W. MOLLOY, AND L. E. JEWELL.

St. John's Research and Development Centre, Agriculture and Agri-Food Canada (*AAFC*),
308 Brookfield Rd., St. John's, Newfoundland and Labrador, Canada

Economical dairy and beef farming is dependent upon the availability of locally-produced forages, which are fed to animals fresh or after they have been converted to silage through a fermentation process. When insufficient forage or silage is available, farmers must import feed which, in the province of Newfoundland and Labrador (NL), is particularly undesirable due to high transportation costs. An exploration of the forage diseases present on the island of NL was undertaken during the growing seasons of 2016, 2017, and 2018, and a study of silage quality was undertaken during the early winter months of 2016. The most frequently observed diseases included purple eyespot (*Cladosporium phlei*) of timothy (*Phleum pretense*); snow molds (*Microdochium nivale, Typhula* sp.) on both grasses and legumes; and legume leaf spots (including *Pseudopeziza trifolii*, *Phoma medicaginis*, and *Cercospora medicaginis*). Corn was affected by eyespot (*Kabatiella zeae*) and northern corn leaf blight (*Exserohilum turcicum*). A variety of abiotic stresses caused by inappropriate nutrient application or climatic factors were also observed. Furthermore, forages stored as silage were found to be contaminated by yeasts on 6/9 farms tested, and by filamentous fungi on 4/9 farms tested, suggesting that post-ensiling spoilage is occurring, even on materials that are free from obvious signs of spoilage or damage. This preliminary study provides the first baseline information about forage and silage microbial contamination in the province of NL.

POSTER PRESENTATIONS

In vivo characterization of scabin, a novel mART toxin family member from the common scab pathogen *Streptomyces scabies*.

H. C. PERRY AND D. R. D. BIGNELL.

Department of Biology, Memorial University of Newfoundland, 232 Elizabeth Avenue, St. John's, NL A1B 3X9, Canada.

Common scab disease (CSD) is an extremely taxing problem in todays agricultural world. The disease caused by phytopathogenic *Streptomyces* species negatively impacts the marketability of many tuberous crops, most notably potatoes. Several virulence factors have been isolated and characterized from the best studied pathogen, *Streptomyces scabies*, including thaxtomin A and Nec1. Unfortunately, no potato cultivar that is fully resistant to CSD exists to date, and traditional treatments and strategies for disease control prove to be largely ineffective. Recently, a gene encoding a promising putative virulence factor has been identified in the *S. scabies* genome. The gene, *SCAB27771*, encodes a mono-ADP ribosyltransferase (mART) toxin named scabin. Many mART toxins serve as virulence factors for human bacterial pathogens such as *Bordetella pertussis*, which causes pertussis (whooping cough), and *Vibrio cholerae*, which causes cholera. Scabin shares homology with the Pierisin family of mART toxins that utilize DNA as their target molecule and cause apoptosis in mammal cells. The purpose of this study is to assess the contribution of scabin to CSD symptom severity and the overall pathogenicity of *S. scabies*. To test this, an overexpression strain of *S. scabies* 87-22 was created by cloning *SCAB27771* into the pIJ8641 plasmid, which contains the strong constitutive promotor *ermE*p*. The plasmid was then introduced into *S. scabies* 87-22 where it integrated into the chromosome. This overexpression strain will be used in future potato tuber tissue and radish seedling bioassays to look for an increase in tissue damage compared to the wild-type and empty vector strains.

Characterization of a cryptic secondary metabolite in the potato common scab pathogen *Streptomyces scabies.*

J. LIU AND D. R. D. BIGNELL.

Department of Biology, Memorial University of Newfoundland, 232 Elizabeth Avenue, St. John's, NL A1B3X9 Canada

Streptomyces scabies is one of the main the causative agents of potato common scab (CS) disease, which is characterized by the formation of superficial, raised or pitted lesions on the tuber surface. CS affects fresh market, processing and seed potatoes, and it reduces the quality and market value of potato crops worldwide. The disease is difficult to manage, and there are currently no control strategies that work consistently and reliably. The ability of *S. scabies* to cause CS is primarily based on the production of a phytotoxic secondary metabolite (SM) called thaxtomin A, which is an essential pathogenicity factor for the organism. In addition, *S. scabies* has the genetic potential to produce other SMs that might contribute to CS disease development; however, most of the genes predicted to be involved in production of these SMs are silent under laboratory conditions, and thus there is little known regarding the nature of these metabolites and their role in CS disease. The aim of this research is to characterize one cryptic (unknown) SM that is conserved in other pathogenic *Streptomyces* spp. The putative biosynthetic genes that produce this cryptic metabolite are expressed at low level or not at all under laboratory conditions, and therefore different strategies are being employed in order to activate or enhance expression of these genes in *S. scabies*. This presentation will discuss the strategies being used as well as our preliminary results of the bioassays being utilized to detect various bioactivities that might be associated with the cryptic metabolite.

TxtH is an important component of the thaxtomin biosynthetic machinery in the potato common scab pathogen *Streptomyces scabies.*

Y. LI, J. LIU, K. TAHLAN AND D. R. D. BIGNELL.

Department of Biology, Memorial University of Newfoundland, 232 Elizabeth Ave, St. John's, NL A1B 3X9, Canada

Streptomyces scabies causes potato common scab (CS) disease, which reduces the quality and market value of affected potato tubers. The principle pathogenicity factor produced by *S. scabies* is the thaxtomin A phytotoxin, which is essential for CS disease development. Thaxtomin A production requires the nonribosomal peptide synthetases (NRPS) TxtA and TxtB, which synthesize the thaxtomin backbone using the amino acids L-phenylalanine and 4-nitro-L-tryptophan as substrates, respectively. TxtA and TxtB both contain an adenylation domain (A-domain) that is responsible for selecting and activating the corresponding amino acid substrate. In addition, a small protein called TxtH is a member of the MbtH-like protein (MLP) family, which are typically required for the proper folding of NRPS A-domains, and/or they stimulate amino acid activation by the A-domains. The objective of this study was to investigate the importance of TxtH in thaxtomin A biosynthesis in *S. scabies*. Biochemical studies of TxtH showed that it is required for promoting the solubility of both the TxtA and TxtB A-domains *in vitro*, and amino acid residues were identified within TxtH that are essential for this activity. Deletion of *txtH* in *S. scabies* caused a significant reduction in thaxtomin A production, and deletion of two additional MLP homologs present in the *S. scabies* genome abolished phytotoxin production completely. Overexpression of the *txtH* gene in wild-type *S. scabies* did not cause any significant differences in thaxtomin A production levels. The results confirm that TxtH plays a key role in the biosynthesis of the thaxtomin A phytotoxin in *S. scabies.*

Microorganisms Associated with Lowbush Blueberry (*Vaccinium angustifolium* Ait.) on the Island of Newfoundland.

K. COMPTON[1], D. WISEMAN[1], D. MARTIN[1], D.B. MCKENZIE[1], T. FORGE[2], AND L. E. JEWELL[1].

[1]*St. John's Research and Development Centre, Agriculture and Agri-Food Canada* (*AAFC*), *308 Brookfield Rd., St. John's, Newfoundland and Labrador, Canada;* [2]*Summerland Research and Development Centre, AAFC, 4200 Highway #97, South, Summerland, British Columbia*

Lowbush blueberry (*Vaccinium angustifolium* Ait.) is a small shrub found throughout eastern North America, prized for its nutritious berries which contain high levels of antioxidants. The host of microorganisms living in association with blueberries in the province of Newfoundland and Labrador (NL) have not been well characterized. For this reason, a study was undertaken to collect and identify the microorganisms found in association with both apparently healthy and unhealthy lowbush blueberry plants found in the wild and on farms in NL. Root and soil samples were collected during the summer of 2016 from 8 sites on the island of NL. Soils were inspected for the presence of nematodes, whereas root samples were surface sterilized and plated onto potato dextrose agar and cornmeal agar in order to isolate associated fungi. In addition, samples of stems, fruits, and leaves displaying disease symptoms were collected during the summers of 2016, 2017, and 2018. Over 100 different types of fungi were cultured from the root samples alone. The most commonly isolates included *Trichoderma* sp., *Cladosporium* sp., and *Pezicula ericae*. Foliar diseases observed included Exobasidium fruit and leaf spot, red leaf, Valdensinia leaf spot, and Septoria leaf spot. Regional differences were also observed, with diseases caused by *Exobasidium* spp. observed much more frequently on the Avalon than on the western or central regions of the province. In addition, high levels of yet-unidentified ring nematodes were observed. Reinfection studies to validate and characterize the interactions between the root-associated fungi and plant health are currently underway.