CANADIAN PHYTOPATHOLOGICAL SOCIETY

ATLANTIC REGION MEETING 2025

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

Atlantic Region Meeting
October 2, 2025
St. John's Research and Development Centre, St. John's, NL

INTRODUCTION

Welcome to St. John's and to the 2025 Canadian Phytopathological Society (CPS) Atlantic Region Meeting. It is our pleasure to host this year's CPS regional meeting, and we are looking forward to a stimulating afternoon of scientific discussion and fellowship.

There are 14 oral presentations and three poster presentations on various topics in phytopathology scheduled for the afternoon. A dinner will take place at The Fish Exchange, 351 Water St., St. John's, NL following the meeting.

We are pleased to welcome **Dr. Adam Foster,** Charlottetown Research and Development Center, Agriculture and Agri-Food Canada, as our keynote speaker. Dr. Foster is a research scientist working on Fusarium head blight and his talk is entitled, "Battling Fusarium head blight in the Maritimes: integrated disease management and molecular approaches".

We look forward to welcoming in-person participants to the newly renovated St. John's Research and Development Center, and we are grateful that many participants who are unable to travel will take the time to join us virtually. Thank you for making the time to participate in this meeting.

This booklet contains abstracts of oral and poster presentations in the order in which they will be presented. All abstracts will subsequently be published in an upcoming issue 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 Atlantic Canada.

Rick Peters, Atlantic CPS Rep
Linda Jewell and Dawn Bignell, Co-chairs, Local Arrangements Committee

The Canadian Phytopathological Society Atlantic Region Meeting 2025

Thursday, 2 October 2025
Multipurpose Room, SJRDC, Agriculture and Agri-Food Canada, St. John's, NL

13:00-13:10 **Introduction/Welcome:**
Dr. Rick D. Peters (Research scientist, AAFC St. John's) – CPS representative, Atlantic region
Dr. Dawn Bignell (Professor, Memorial University of Newfoundland) – Co-chair of local arrangements committee
Dr. Linda Jewell (Research scientist, AAFC St. John's) – Co-chair of local arrangements committee

Session A: Moderator: Linda Jewell, AAFC-SJRDC

13:15-13:45 **Keynote Speaker: Dr. Adam Foster. Battling Fusarium head blight in the Maritimes: integrated disease management and molecular approaches.** *Charlottetown RDC, Agriculture and Agri-Food Canada, Charlottetown, PE*

13:45-14:00 **Improving management practices to reduce oat lodging and disease.** Dustin MacLean, *Department of Plant, Food, and Environmental Sciences, Faculty of Agriculture, Dalhousie University, NS*

14:00-14:15 **Cultivation and genomic characterization of soil microorganisms for potential biocontrol of *Fusarium graminearum* using iChip technology.** Hailey Hill, *Agriculture and Agri-Food Canada, Charlottetown Research and Development Centre, PE*

14:15-14:30 **Diversity and virulence of scab-causing *Streptomyces* in Newfoundland.** Artho Baroi, *Department of Biology, Memorial University of Newfoundland, NL*

14:30-14:45 **Identification of novel regulators of *Streptomyces scabiei* plant pathogenicity using an untargeted approach.** Wanyue Li. *Department of Biology, Memorial University of Newfoundland, NL*

14:45-15:00 **Elucidating the role of the concanamycin phytotoxins in the virulence of the potato common scab pathogen *Streptomyces scabiei*.** Corrie Vincent, *Department of Biology, Memorial University of Newfoundland, NL*

15:00-15:30 Nutrition Break/Poster Presentations

Posters: **Using comparative genomics to understand the regulation of plant pathogenicity in *Streptomyces.*** Stacey Follett, *Department of Biology, Memorial University of Newfoundland, NL*

Burn-pruning supports robust fruit yields but does not provide long-term suppression of *Exobasidium*-caused diseases in lowbush blueberry (*Vaccinium angustifolium*). Linda Jewell, *Agriculture and Agri-Food Canada, St. John's Research and Development Center, NL.*

High resolution mapping of potato late blight risk using gridded weather data. Tobias Laengle, *Agriculture and Agri-Food Canada, Pest Management Center, St. John's, NL*

Session B: Moderator: Dawn Bignell, Memorial University of Newfoundland

15:30-15:45 **A quarter century of research on the late blight pathogen (*Phytophthora infestans*) in Canada.** Rick Peters, *Charlottetown RDC, Agriculture and Agri-Food Canada, Charlottetown, PE*

15:45-16:00 **Comparative genomics of *Clavibacter sepedonicus* reveals mutational signatures and virulence determinants in potato bacterial ring rot.** Qifan Yang, *Canadian Food Inspection Agency, Charlottetown Laboratory, PE*

16:00-16:15 **Clasnip 2: An online phylogenetic and classification tool for the differentiat of closely related eukaryotes.** Jiacheng Chuan (Eric), *Canadian Food Inspect Agency, Charlottetown Laboratory, PE*

16:15-16:30 **Characterization of virulence factors in *Golovinomyces ambrosiae*, the causal agent of powdery mildew in cannabis.** Madeline Breton-Séguin, *Université de Moncton, Moncton, NB*

16:30-16:45 **Identification of novel powdery mildew resistance genes in cannabis.** Youssef Moutahir, *Université de Moncton, Moncton, NB*

16:45-17:00 **Revisiting fire blight threats to apple and management strategies in the Atlantic region.** Shuanglong Huang, *Department of Agriculture, Province of Prince Edward Island.*

17:00-17:15 **Study of resistance to Colorado Potato Beetle in wild potato species maintained in the Canadian potato gene resources collection- results of larvae feeding assays.** Benoit Bizimungu, *Agriculture and Agri-Food Canada, Fredericton Research and Development Centre, NB*

17:15-17:30 **Concluding remarks: Rick Peters**.

18:00-20:00 **Dinner:** Fish Exchange, 351 Water St., St. John's, NL

Note to presenters: please ensure that your presentation has been sent to the moderator in advance of your presentation

Abstracts in order of presentation

Battling *Fusarium* head blight in the Maritimes: integrated disease management and molecular approaches. A. FOSTER, E. JOHNSTONE, A. SAUNDERS, T. K. TURKINGTON, D. MACLEAN AND H. HILL *Agriculture and Agri-Food Canada, Charlottetown Research and Development Centre, 440 University Ave, Charlottetown, PE C1A 4N6, Canada; (A.S.) Department of Biology, Dalhousie University, 1355 Oxford St, Halifax, NS B3H 4R2, Canada; (T.K.T.) Agriculture and Agri-Food Canada, Lacombe Research and Development Centre, 6000 C&E Trail, Lacombe, AB T4L 1W1, Canada; and (D.M.) Department of Plant, Food, and Environmental Sciences, Dalhousie University, Agricultural Campus, Truro, NS B2N 5E3, Canada*
Fusarium head blight (FHB), caused by various *Fusarium* species, is a devastating disease of cereal crops. It can result in significant yield reduction and mycotoxin contamination of grain, which poses a health risk to humans and livestock. FHB remains one of the most significant threats to cereal production in Canada. A decade of research dedicated to understanding and mitigating FHB's impact on regional wheat, barley, and oat production has been conducted. The research has advanced on several fronts, beginning with foundational work in host resistance and pathogen epidemiology. Through the long established FHB nursery screening, this pathology work has directly supported cereal breeding programs in Canada. Concurrently, population genetic studies have clarified the understanding of the causal agents, identifying *Fusarium graminearum* Schwabe as a primary, though not always the most prevalent, species of concern. Translating this knowledge into practice, field-level management strategies were evaluated, including crop rotation, residue management, and seeding rate manipulations, with mixed outcomes. To provide producers with real-time data, a partnership with industry validated and launched a regional FHB forecasting model, available as an online tool. Additionally, novel molecular techniques, using CRISPR-Cas9 for rapid virulence factor identification, a process which in turn revealed important, unanticipated effects of gene editing and qPCR methods for detecting the novel ANX chemotype of *F. graminearum*. New research projects explore novel control strategies such as the use of iCHIP technology to discover novel soil bacteria for biopesticide development and an investigation into the surprising link between Fusarium species and oat lodging.

Improving management practices to reduce oat lodging and disease. D. MACLEAN, E. JOHNSTONE, N. MCLEAN, A. MILLS, Y. JIANG, A. FOSTER. *Department of Plant, Food, and Environmental Sciences, Faculty of Agriculture, Dalhousie University, 50 Pictou Road, Truro, NS, Canada B2N 5E3; and (E.J., A.M., A.F.) Charlottetown Research and Development Centre, Agriculture and Agri-Food Canada, 440 University Avenue, Charlottetown, PE C1A 4N6, Canada.*
Oat lodging, the permanent displacement of stems due to internode buckling or root displacement, can render large field areas non-harvestable, especially under heavy rain, high winds, excess nitrogen, or plant pathogen pressure. This study aimed to manage oat lodging and disease through precision fungicide applications, identifying optimal fungicide modes of action and spray timings, and evaluating fungicide x timing interactions for lodging control. Field trials were conducted in Truro, NS, and Harrington, PEI, in 2023 and 2024, using a Latin square split-split design with nitrogen rates (50, 100, 150 kg ha^{-1}) as the main plot factor,

fungicide x timing (Quadris® and Prosaro XTR® at ZGS32 and ZGS39), and cultivars (AAC Excellence, CDC Orrin) as subplot factors. Cultivar, nitrogen rate, and their interaction significantly affected lodging incidence across both years and sites, but fungicide application only reduced lodging in Harrington, PEI, in 2024. Additional trials in 2025 and planned for 2026 at both sites used a randomized complete block design (RCBD) with cultivar CS Camden and a nitrogen rate of 75 kg ha^{-1}. Three fungicide x timing applications (Acapela® at ZGS 12-22, Tilt 250E® at ZGS 30-39, Miravis Ace® at ZGS 51-69) were tested singly or in combinations. These trials aim to identify the most effective fungicide and timing strategies to minimize lodging and maximize oat yield.

Cultivation and genomic characterization of soil microorganisms for potential biocontrol of *Fusarium graminearum* using iChip technology. H. HILL, B. FOFANA, A. GRUNWALD, T. CLARK, B. WAGNER AND A. FOSTER. *Agriculture and Agri-Food Canada, Charlottetown Research and Development Centre, 440 University Avenue, Charlottetown, PE C1A 4N6, Canada; (H.H., T.C., B.W.) University of Prince Edward Island, 550 University Avenue, Charlottetown, PE, C1A 4P3, Canada*
Fusarium Head Blight (FHB), primarily caused by the fungal pathogen *Fusarium graminearum*, is a devastating disease that impacts cereal crops by significantly reducing both yield and grain quality. In addition to crop damage, FHB can result in the accumulation of harmful mycotoxins, posing serious health risks to humans and livestock when consumed. While various management strategies exist, such as crop rotation and fungicide application, they are often insufficient. For example, the use of fungicides may cause the pathogen to develop resistance, while other techniques simply do not provide adequate control. A major challenge in discovering alternative solutions is that a large majority of microbes in the environment are difficult to culture using conventional methods. To address this, we optimized and employed isolation chip (iChip) technology to aid in the discovery of previously unculturable soil bacteria with potential antagonistic activity against *F. graminearum*. These bacterial isolates were first screened in vitro against a green fluorescence protein (GFP)-labeled strain of the fungus to identify candidates exhibiting suppressive activity. Promising isolates will undergo further characterization, including chemical profiling via ultra-performance liquid chromatography-mass spectrometry (UPLC-MS) to identify the specific bioactive compounds responsible for the observed suppressive effects against the fungal pathogen.

Diversity and virulence of scab-causing *Streptomyces* in Newfoundland. A. BAROI AND D. R. D. BIGNELL. *Department of Biology, Memorial University of Newfoundland, St. John's, NL, Canada.*
Streptomyces are filamentous actinomycetes renowned for their ability to produce antibiotics. Although widespread across terrestrial and aquatic environments, only a small proportion of species have been identified as plant pathogens. Common scab (CS) is an economically important disease caused by certain *Streptomyces* species that impairs the quality and market value of root crops worldwide. CS symptoms include raised, pitted, or superficial scab-like lesions, which may coalesce to cover large areas, causing significant economic damage. In addition to CS, some *Streptomyces* species can cause netted scab (NS), which is characterized

by net-like lesions on tubers and, in severe cases, necrosis of fibrous roots. CS is mainly associated with the production of a phytotoxic metabolite called thaxtomin A, whereas the development of NS may rely on the production of another phytotoxin called fridamycin E. Additional factors, including secreted proteins and phytohormones, may also contribute to disease severity. *Streptomyces europaeiscabiei* is prevalent in Europe and is associated with both CS and NS of potato. In Newfoundland, this species was previously identified as a causative agent of CS, whereas *Streptomyces scabiei* and other known CS pathogens were not detected despite being reported in other parts of eastern Canada. Given the prior study's limited sampling, a broader survey is needed to define the diversity of pathogenic *Streptomyces* in Newfoundland. This study aims to isolate and characterize plant pathogenic *Streptomyces* from scab lesions on root crops across Newfoundland, providing new insights into CS and NS and supporting strategies to reduce their impact on growers.

Identification of novel regulators of *Streptomyces scabiei* plant pathogenicity using an untargeted approach. W. LI AND D. R. D. BIGNELL. *Department of Biology, Memorial University of Newfoundland, St. John's, NL, A1C 5S7, Canada*
Streptomyces scabiei is a Gram-positive, filamentous soil bacterium that serves as a key causative agent of potato common scab (CS) disease. CS is characterized by the presence of brown, scab-like lesions on the tuber surface, and these lesions result in significant economic losses to growers by decreasing the quality and marketability of affected crops. The principal pathogenicity factor responsible for CS development by *S. scabiei* is a phytotoxic specialized metabolite called thaxtomin A. Additionally, *S. scabiei* produces other phytotoxins (e.g. concanamycins) that are known or supposed to contribute to its pathogenicity. The production of thaxtomin A is controlled by multiple regulators, including the cluster-situated regulator TxtR, five members of the *bld* gene family, the cellulose utilization repressor CebR, and two members of the leucine-responsive regulatory protein family. As there are more than 800 predicted regulatory genes present in the *S. scabiei* genome, we hypothesize that there are additional regulatory genes that modulate the production of thaxtomin A and other virulence factors in *S. scabiei*. To investigate this, *S. scabiei* was cultured in triplicate on three different agar media that support different thaxtomin A production levels (low, high, none). Total RNA was extracted from the cultures at 2, 4, and 7 days post-inoculation and was subjected to RNA-seq in order to identify regulatory genes that are upregulated (activators) or down-regulated (repressors) under thaxtomin A-inducing conditions. Candidate regulatory genes identified will be subjected to gene deletion and overexpression to confirm their role in controlling the plant pathogenic phenotype of *S. scabiei.*

Elucidating the role of the concanamycin phytotoxins in the virulence of the potato common scab pathogen *Streptomyces scabiei*. C. V. VINCENT AND D. R. D. BIGNELL. *Department of Biology, Memorial University of Newfoundland, St. John's, NL, A1C 5S7, Canada*
Potato common scab (CS) is an economically important crop disease afflicting potatoes worldwide. The presence of CS lesions on potato tubers reduces the quality and market value of the crop, leading to significant financial losses for growers. The soil-dwelling bacterium *Streptomyces scabiei* is distributed worldwide and is the best-characterized causative agent of

CS. The cellulose biosynthesis inhibitor thaxtomin A (ThxA) is the principal pathogenicity factor produced by *S. scabiei* and is essential for CS development. In addition, *S. scabiei* synthesizes the virulence-associated phytotoxin *N*-coronafacoyl-L-isoleucine (CFA-Ile), which is predicted to function as a jasmonic acid hormone mimic, and it produces the concanamycin phytotoxins, which function as inhibitors of vacuolar-type ATPases. Previous research suggests that concanamycin production may impact the virulence of *S. scabiei,* though their exact role in host-pathogen interactions has not been established. This research examined the contribution of the concanamycins to the virulence of *S. scabiei,* alone and in conjunction with ThxA and CFA-Ile. *S. scabiei* mutants that are altered in the production of concanamycins, ThxA, and/or CFA-Ile were constructed and used in plant bioassays to assess the virulence phenotype of each compared to wild-type *S. scabiei*. In addition, the role of concanamycins and other phytotoxins in the colonization of plant root tissue by *S. scabiei* was examined using confocal laser scanning microscopy along with green fluorescent protein-labeled mutant strains. The results of this study provide new insights into the molecular mechanisms of CS disease and *S. scabiei*-host interactions.

Using comparative genomics to understand the regulation of plant pathogenicity in *Streptomyces*. S. FOLLETT AND D. R. D. BIGNELL. *Department of Biology, Memorial University of Newfoundland, St. John's, NL A1C 5S7, Canada.*
Streptomyces are soil-dwelling actinobacteria known for their complex life cycle and ability to produce a wide range of bioactive metabolites. While most *Streptomyces* species are saprophytic, a small number have evolved into plant pathogens responsible for economically important diseases such as common scab, which affects potatoes and other root crops. Pathogenic *Streptomyces* typically produce Thaxtomin A (ThaxA), a phytotoxin that disrupts plant cell wall biosynthesis and serves as a key virulence factor. ThaxA production is encoded by a mobile pathogenicity island that can be horizontally transferred between strains. However, not all strains that acquire the ThaxA biosynthetic cluster (BSC) are capable of producing ThaxA, suggesting that host-specific regulatory factors may be involved in the activation of this virulence factor. This project aims to use a comparative genomics approach to identify novel regulators associated with ThaxA production. By comparing the genomes of ThaxA-producing and non-producing species, we aim to identify regulatory genes that are conserved in producers and are absent in non-producers. Candidate regulatory genes will be subjected to deletion and overexpression in the best studied plant pathogen, *Streptomyces scabiei,* to validate their role in modulating ThaxA biosynthesis and plant pathogenicity. Ultimately, this research aims to define how the genetic background of different *Streptomyces* species influences their capacity for plant pathogenicity following acquisition of the ThaxA BSC, thereby providing insights into the molecular mechanisms underlying the emergence of novel plant pathogenic species in natural environments.

Burn-pruning supports robust fruit yields but does not provide long-term suppression of *Exobasidium*-caused diseases in lowbush blueberry (*Vaccinium angustifolium*). K. COMPTON, L. O'QUINN, J. WHITTAKER, L. E. JEWELL, AND T. LAENGLE. *St. John's Research and Development Center, Agriculture and Agri-Food Canada (AAFC), St. John's, NL, Canada; and (J.W., T.L.) Pest Management Center, AAFC, St. John's, NL, Canada*

Commercial lowbush blueberry (*Vaccinium angustifolium* Ait.) fields are pruned every 3-4 years to encourage berry production. This has historically been accomplished through controlled burn; however, burn-pruning is expensive (e.g., fuel costs), logistically challenging (e.g., weather-related limitations), and carries safety and environmental risks. Burn-pruning has been largely supplanted by mowing despite producing higher crop yields and reducing the incidence and/or severity of several diseases, pests, and weeds, minimizing the need for pesticide applications. Diseases caused by fungi of the genus *Exobasidium,* such as red leaf, are of increasing importance in blueberry production, but the impact of burn-pruning on their incidence is unclear. To evaluate burn-pruning as a strategy to reduce red leaf, an experiment was conducted at a commercial lowbush blueberry farm in a field scheduled for pruning in spring 2024. A randomized complete block design was utilized wherein each plot (4 m × 4 m) within a block was assigned a pruning treatment (burned or mowed) applied in May 2024. Red leaf incidence was recorded weekly from May – Sept. in 2024 and 2025, and in the first fruiting year (2025), the berries from each plot were harvested and graded. Although burned plots generally had lower red leaf incidence through 2024 and produced significantly (2×) more berries than the mowed plots, red leaf incidence did not differ between treatments in 2025, and Exobasidium fruit spot incidence was higher on berries from burned than mowed plots. Spore traps in nearby burned or mowed fields may provide insight into these unexpected disease dynamics.

High resolution mapping of potato late blight risk using gridded weather data. C. PARSONS, J. WHITTAKER, L.E. JEWELL, AND T. LAENGLE. *Pest Management Center, Agriculture and Agri-Food Canada (AAFC), and (LEJ) St. John's Research and Development Center, AAFC, St. John's, NL, Canada*

Potato late blight (PLB), caused by the oomycete *Phytophthora infestans*, is one of the most damaging potato diseases in the world, and growers rely on frequent fungicide sprays to protect crops. While this approach has been effective, it does not always reflect actual disease risk and can lead to unnecessary costs, environmental impacts, and resistance issues. Newfoundland and Labrador's (NL) cool, humid climate is well-suited to the disease, and PLB is observed in most growing seasons, but growers do not have access to reliable tools to inform timing of fungicide applications to protect their crop. Forecasting models such as BLITECAST and NEGFRY are designed to guide spray decisions using weather and crop data but because of the spatial distance between many farms and available weather stations, these tools lack reliable inputs in NL and other parts of Atlantic Canada. To address this data gap high-resolution gridded weather data from Environment and Climate Change Canada's High Resolution Deterministic Prediction Systems (HRDPS) were evaluated as model inputs. Disease risk maps were then created in ArcGIS to visualize disease risk, and we undertook a two-year field trial that compared model-based and calendar-based spray programs. This work will evaluate the existing potato late blight forecasting models in Newfoundland and Labrador and determine if forecasting models could be a practical and sustainable alternative to traditional potato late blight management practices in the region.

A quarter century of research on the late blight pathogen (*Phytophthora infestans*) in Canada.

R. D. PETERS, A. MACPHAIL, D. GREGORY, K. MACDONALD AND B. CRANE.
Charlottetown Research and Development Centre, Agriculture and Agri-Food Canada, 440 University Avenue, Charlottetown, PE, C1A 4N6, Canada

Late blight, caused by the oomycete *Phytophthora infestans* (Mont.) de Bary, is a disease of global significance. Yield losses in both potato and tomato crops have been annual occurrences in Canada in recent years. In the last 25 years, surveys of pathogen populations in Canada have recorded genetic changes in populations driven by dramatic shifts in prevalent genotypes following their introduction into a growing region. The introduction of novel genotypes has occurred via movement of air-borne sporangia, and the transport of infected potato seed and tomato transplants. In addition to population displacement, circumstantial evidence for recombination generating novel genotypes was observed in specific growing regions in some years. Pathogen population shifts have necessitated alterations in disease management strategies, to account for fungicide resistance and host preferences of new strains. In recent years, tomatoes grown in home/community gardens have become increasingly important as a source of pathogen inoculum infecting commercial potato crops. Continued monitoring of pathogen populations will be critical to document changing pathogen characteristics and epidemiology, which can then provide the basis for informed disease management.

Comparative genomics of *Clavibacter sepedonicus* reveals mutational signatures and virulence determinants in potato bacterial ring rot.

Q. YANG, J. CHUAN, D. HAMMILL, A. PROUD, S. SPRINGER AND X. LI. *Canadian Food Inspection Agency, Charlottetown Laboratory, PE C1A 5T1, Canada; and (S. S.) Department of Biology, University of Prince Edward Island, PE C1A 4P3, Canada*

Bacterial ring rot (Brr) is a major regulated potato disease in Canada. It causes the decay of the vascular ring in potato tubers and foliage wilt. *Clavibacter sepedonicus*, the causal pathogen of Brr, establishes infection by secreting lytic enzymes and exopolysaccharides, and by expressing key virulence genes such as *celA*, *pat-1*, and *chp-7*. Recent advances in genomic diagnostics have refined the classification of the genus *Clavibacter*, leading to the recognition of novel species. In this study, we performed comparative genomics on *C. sepedonicus* isolates, integrating historical reference strains with Brr-infected potato samples. We achieved reliable detection and confirmation of *C. sepedonicus,* even from datasets with low sequencing depth, using our in-house classification pipelines: Clasnip and Polychrome Classifier and Detector. A newly identified Canadian isolate contained more than 177 insertions/deletions (indels) or single-nucleotide polymorphisms (SNPs) relative to historical strains, including changes in genes directly linked to pathogenicity and virulence. In comparison, a recent U.S. isolate exhibited 696 indels/SNPs, considerably more than the Canadian strain, suggesting that the Canadian isolates evolve more slowly, or separated more recently from the historical strain. This is potentially due to Canada's uniform nationwide Brr management regulations, in contrast to the varied state-regulated measures in the U.S. The continuous accumulation of mutations could give rise to strains with higher virulence, altered pathogenicity, or wider host ranges. To better understand the effects of this divergence,

we will analyze new *Clavibacter* isolates to track mutational trends, examine their pathogenicity, and develop rapid, reliable diagnostic tools to support Brr management.

Clasnip 2: An online phylogenetic and classification tool for the differentiation of closely related eukaryotes. J. CHUAN, Q. YANG, D. L. HAMMILL, D. PRESTON AND X. Li. *Charlottetown Lab, Canadian Food Inspection Agency* (*CFIA*)*, 93 Mt Edward Rd, Charlottetown, PE C1A 5T1, Canada*

Distinguishing closely related bacteria, virus and fungi that harm human health, crops, or ecosystems is challenging due to their genetic similarities. Misidentification can delay responses to diseases or invasions. Clasnip 2 (www.clasnip.com) is a user-friendly, web-based tool designed to accurately identify pathogenic organisms, supporting public health, food safety, and environmental protection.

Clasnip 2 uses cutting-edge bioinformatics methods to analyze DNA sequences from bacteria (e.g., those causing foodborne illnesses or crop diseases like potato zebra chip), virus, and fungi. It acts as a platform to allow users to build curated sequence databases of their interests, upload genetic data, and view reports with classification results, phylogenetic trees, and variation lists. Accessible to researchers and regulators, it works with various sample types, from a single genomic region to a whole genome.

Clasnip 2 successfully identifies plant pathogens and is used in CFIA Charlottetown Lab as a pathogen classification and confirmation tool. It classifies potato rot and golden nematodes using *Ditylenchus* (18S) and *Globodera* (rRNA collections) databases, and rust fungi with *Puccinia* (ITS2) database, achieving high accuracy across diverse genetic datasets. The platform's intuitive design simplifies complex analyses, making it practical for labs and has the potential for human pathogens.

Clasnip 2 enhances Canada's ability to detect and manage agricultural and health threats. It can speed up pathogen identification, improving outbreak responses and food safety. For Canadians, it supports safer food, healthier communities, and economic stability by protecting agriculture, a key economic sector. It also strengthens biosecurity, helping prevent invasive species that harm ecosystems. By fostering scientific innovation, Clasnip 2 aligns with national goals for public health and environmental sustainability.

Characterization of virulence factors in *Golovinomyces ambrosiae*, the causal agent of powdery mildew in Cannabis. M. BRETON-SÉGUIN AND D. L. JOLY. *Université de Moncton, Moncton, NB, E1A 3E9*

The use of cannabis dates back thousands of years, for therapeutic, industrial, and ritual purposes. Native to Central Asia, this plant from the Cannabaceae family is now cultivated and utilized worldwide, particularly for its medicinal and industrial applications. However, like all plants, cannabis is susceptible to various infections caused by pathogens such as bacteria and fungi. Among these, powdery mildew caused by *Golovinomyces ambrosiae* poses a significant threat to cannabis crops. This biotrophic fungus secretes virulence factors (effectors), which are small proteins that manipulate plant immune system, allowing the pathogen to bypass host defenses and facilitate infection. The main objective of this study is to characterize these virulence factors, with a focus on the role of effectors in interacting with plant defense mechanisms. The first part of the research aims to initiate the functional characterization of

effector mechanisms within plant cells by determining their subcellular localization. To achieve this, effectors will be transiently expressed in plant cells via agroinfiltration, and their localization will be observed using confocal microscopy. The second part of the study will assess the impact of these effectors on specific plant defense responses, such as reactive oxygen species (ROS) production and callose deposition. To this end, *Arabidopsis thaliana*, a model plant, will be genetically transformed to stably express individual effectors. These plants will then be subjected to various stress conditions, including exposure to other pathogens and to *Golovinomyces ambrosiae* itself.

Identification of novel powdery mildew resistance genes in cannabis

Y. MOUTAHIR AND D. L. JOLY. *Université de Moncton, Moncton, NB, E1A 3E9*

Cannabis production is increasingly challenged by phytopathogens, among which powdery mildew (*Golovinomyces ambrosiae*) is one of the most severe threats. This disease causes major yield losses and compromises product quality. With the global expansion of the legal cannabis industry, breeding resistant cultivars has become a priority to ensure stable and sustainable production. Our screening efforts, conducted under high inoculum pressure, revealed substantial variation in resistance among *Cannabis sativa* cultivars. Some accessions displayed complete resistance, others partial resistance, while certain cultivars showed transient resistance that was lost during flowering.

From a genetic perspective, two resistance genes, *PM1* and *PM2*, have already been reported in cannabis. However, our results indicate that resistance in several of our cultivars cannot be explained solely by these known genes or by the *CsMLO1* insertion, previously associated with loss of susceptibility. The data indicates that other unidentified resistance loci appear to play a critical role, pointing to a more complex resistance architecture than initially anticipated. This project aims at characterizing these novel resistance genes, through a combination of phenotype-based selection with molecular approaches to unravel the full spectrum of resistance mechanisms in cannabis. Ultimately, this knowledge will support the breeding of durable, resilient cultivars with effective protection against powdery mildew.

Revisiting fire blight threats to apple and management strategies in the Atlantic region.

S. HUANG, C. ANDERSON, A. MACLEOD AND S. LIU. *Department of Agriculture, Government of Prince Edward Island, 5th Floor Jones Building, 11 Kent Street, Charlottetown, PE, C1A 7N8, Canada*

Fire blight, caused by *Erwinia amylovora*, a Gram-negative bacterium with a wide host range of over 200 plant species, remains a persistent and devastating threat to apple production in the Atlantic region. Climatic conditions characterized by warm, humid springs are highly conducive to fire blight disease development, which could lead to significant economic losses from blossom, shoot, fruit and rootstock infections, as well as other different forms. While established integrated pest management (IPM) strategies exist, the evolving challenges of climate change, shifts in popular cultivar susceptibility, and the development of antibiotic resistance ultimately contribute to the regionally periodic nature of fire blight outbreaks in apple orchards. In this context, the primary drivers of fire blight risk specific to the Atlantic climate, including the potential integration of modern forecasting models like Cougarblight and Maryblyt© to better time management interventions will be revisited. The current efficacy of core control tactics, including the use of biological controls (e.g., Pantoea agglomerans), chemical options like copper and the strategic use of antibiotics, and the vital role of

cultural practices and sanitization will be reviewed. Potential threats such as the latent streptomycin-resistant strains will also be discussed. Taken together, the goal of this revisiting is to provide apple growers and industry stakeholders in the Atlantic region with an updated practical framework for mitigating the risk of fire blight, as well as to initiate proactive discussions for future research needs to help safeguard the productivity and sustainability of Atlantic apple orchards.

Study of resistance to Colorado Potato Beetle in wild potato species maintained in the Canadian Potato Gene Resources Collection - results of larvae feeding assays. B. BIZIMUNGU, I MUHAMMAD. AND S. BROWNE. *(B.B., I.M, S.B.) Agriculture and Agri-Food Canada, Fredericton Research and Development Centre, Fredericton, New Brunswick, Canada E3B 4Z7, Canada; (I.M.) University of New Brunswick, Fredericton, New Brunswick, Canada*

Potato (*Solanum tuberosum* L.) is an important staple food in Canada and around the world. The crop is however, susceptible to many pests and pathogens and its production often requires the use of chemical protectants in the absence of natural resistance. Wild potato species are known to harbour many useful genes that could be used to breed potato cultivars with disease and pests resistance. We investigated the collection of wild species genotypes vegetatively maintained as part of the Canadian Potato Gene Resources in Fredericton, NB, as potential source of resistance to Colorado potato beetle (CPB) (*Leptinotarsa decemlineata*), one of the most important insects of potato. Tests were conducted in the laboratory using larvae feeding assays on cut leaves. Preliminary results indicated a wide range of variation of reactions to CPB among wild species clones in terms of percentage of defoliation relative to untreated controls. A number of clones showed relatively low defoliation than *Solanum tuberosum* cultivar included in the experiments as a check, whereas some others showed higher damage. Promising genotypes as potential sources of resistance include *Solanum gandarillasii, S. megistacrolobum* and *S. microdontum*. Further tests will be required to confirm reactions in the field environment and using adult insects.