



PROGRAM

2023 Northeastern Division Meeting
Northeastern Division 82nd Annual Meeting
The American Phytopathological Society
8-10 March 2023
Southbury, CT

2022-2023 NED-APS OFFICERS

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8-10 March 2023
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WEDNESDAY, MARCH 8

7:00 AM – 8:30 AM **Breakfast** (Heritage Room)

8:00 AM – 12:00 PM **Fieldtrips** (Meeting in Hotel Lobby)

Coordinator: Robert Marra

1. APHIS-Quarantine Facility, or
2. White Flower Farm

Lunch will be provided at the Heritage Hotel upon return.

1:00 – 2:30 PM **Careers 101 Workshop: Networking 101** (Constitution Room)

Moderator: Anissa Poleatewich (Pre-registration required)

Collaborations and job prospects can be based upon whom you meet and how you communicate. Networking early in your career is the key to making those connections and keeping relationships open. This workshop is an introduction to some of the networking skills that are essential for both early career and sustained productivity. Workshop is intended for early career professionals, postdocs, and students.

2:45 – 5:30 PM **Joint Extension/Industry meeting** (Constitution Room)

Moderators: Ann Hazelrigg (Pre-registration required)

An informal gathering to share and discuss recent trends in plant health, pathogen identification, and disease management. Open to anyone interested in applied plant pathology.

6:00 – 8:00 PM **Division Social** (Garden Room)

Appetizers and non-alcoholic beverages will be served.

Cash bar available for alcoholic beverages

Hosts: Robert Marra & Rosa Raudales

THURSDAY, MARCH 9

Session 1: Graduate Student Symposium (Constitution Room; Moderator: Nicholas Brazee)

- 8:00 AM Welcome & Opening Remarks
- 8:10 AM Liza DeGenring, University of New Hampshire
- 8:30 AM Radhika Patel, Rutgers University
- 8:50 AM Ryan Spelman, Pennsylvania State University
- 9:10 AM Patrick Fardella, Rutgers University
- 9:30 AM Shayli Morris, University of Maine
- 9:50 AM Michelle Paukett, Pennsylvania State University

10:10 – 10:30 AM: Morning Break

- 10:30 AM Veedaa Soltaniband, Université Laval
- 10:50 AM Karen Luong, Pennsylvania State University
- 11:10 AM Liga Kalnina, Cornell University
- 11:30 AM Xiuyan Zhang, University of Maine
- 11:50 AM Daniel Cerritos-Garcia, University of Connecticut

12:15 – 1:15 PM: Lunch (Constitution Room)

Session 2: Graduate Student Symposium (cont.) & Contributed Papers (Constitution Room; Moderator: Rosa Raudales)

1:30 – 3:10 PM: Graduate Student Symposium

- 1:30 PM Juliana Gonzalez-Tobon, Cornell University
- 1:50 PM Katherine Ashley, University of Maine
- 2:10 PM Sergio Peralta, University of Connecticut
- 2:30 PM Pingyuan Zhang, Rutgers University
- 2:50 PM Felicia Millett, University of Connecticut

3:10 – 3:30 PM: Afternoon Break

3:30 – 5:00 PM: Contributed Papers

- 3:30 PM Washington Da Silva, Connecticut Agricultural Experiment Station
- 3:45 PM Bond McInnes, AgBiome Innovations
- 4:00 PM Renee Smith, Connecticut College
- 4:15 PM Raja Thangavelu, Connecticut Agricultural Experiment Station
- 4:30 PM Roy Davis, University of Connecticut
- 4:45 PM Nicholas Brazee, University of Massachusetts

6:00 – 9:00 PM: Banquet and Awards Ceremony (Garden Room; Hosts: Rosa Raudales & Robert Marra)

Dinner and non-alcoholic beverages included with registration. Cash bar available.

FRIDAY, MARCH 10

7:30 – 9:30 AM Breakfast & Business Meeting (Constitution Room; Moderator: Rosa Raudales)

8:00 – 9:00 AM

Welcome: Rosa E. Raudales, President

Treasurer's report: Craig Austin, Treasurer/Secretary

Division Forum update: Jianjun Hao (Jay), Division Forum Rep

Old & New Business

9:00 – 9:30 AM APS Council Update – Amy Charkowski, APS Immediate Past President, APS Council

9:30 – 9:45 AM: Morning Break

Session 3: Contributed Papers (cont.) & Keynote Presentation (Constitution Room;
Moderator: Rosa Raudales)

9:45 AM Wade Elmer, Connecticut Agricultural Experiment Station

10:00 AM Xiaowei Fan, University of Maine

10:15 AM Quan Zeng, Connecticut Agricultural Experiment Station

10:30 AM Daniel Heck, Cornell University

10:45 AM Ross Sousa, University of Maine

11:00 AM Lijie Teng, University of Maine

11:15 AM Ravikumar Patel, Connecticut Agricultural Experiment Station

11:30 AM – 12:30 PM Keynote speaker - Amy Charkowski, Colorado State University

Has the quest for healthy potatoes led to spread of plant disease?

Description: Plant disease is a complex problem and improving plant health requires integrating research and education and working in multidisciplinary teams. Dr. Charkowski will describe the evolution of her career in plant pathology and how her work with farmers affected her career trajectory and interest in education. This presentation will weave together the story of three attempts to improve plant health. First, she will describe recent discoveries in how plants resist soft rot bacteria as an example of how discussions with a plant breeder and a chemist led to one mechanism that was obvious in retrospect and a second mechanism that was a complete surprise. Next, she will share the story of an accidental discovery in potting mix that may explain how a soil-borne potato virus became endemic in the US. Finally, Dr. Charkowski will describe how her work with farmers and undergrad researchers motivated her to help start two new undergrad programs and she will share a bit about the process of developing these programs.

Bio: Amy Charkowski is a Professor of Plant Pathology and Department Head at Colorado State University. She earned her B.S. from the University of Wisconsin-Madison and Ph.D. from Cornell University. From 2001-2016, she served as a faculty member in the Plant Pathology Department at the University of Wisconsin-Madison and as the administrative director of the Wisconsin Seed Potato Certification Program. Dr. Charkowski's research is mainly on plant pathogens that affect seed potato production or trade, including potato viruses, *Spongospora*, and soft rot bacterial pathogens of potato. She teaches graduate and undergraduate classes in IPM and plant pathology. She led her department in development of a new undergraduate major in Agricultural Biology and a minor in Agricultural Data Science at Colorado State University.

ABSTRACTS

Improving soil health and disease suppression through cultural practices in potato production

K. ASHLEY, J. Hao, R. Larkin

University of Maine, Orono, ME, USA

Successful field crops require adequate soil health for soil fertility, structure, and disease control. To understand the impacts of different management strategies on soil health, twelve treatments modeled after common potato production practices were implemented in two-year and three-year rotations in Maine and monitored over four years from 2019 to 2022. Rotation crops, green manures, compost amendments, and soil fumigants were applied to the production of potato varieties 'Caribou Russet' and 'Russet Burbank'. Soil was sampled periodically to quantify soil microbial community dynamics, nematode populations, soil fertility, and other soil properties. Incidence and severity of soilborne diseases and yield data were collected from harvested tubers. For microbial community analysis, soil DNA was extracted and regions of the bacterial 16S rRNA and fungal ITS region were sequenced. Results indicated that plots amended with compost had significantly higher yields than other treatments, followed by fumigated plots. For the soilborne disease *Verticillium* wilt, compost-amended plots showed the lowest severity and fumigated plots had the most severe symptoms. Early sequencing results from 2019 and 2020 did not indicate significant differences among treatments for bacterial and fungal community characteristics, however, plots amended with compost showed some deviation from nonamended treatments.

Diplodia shoot blight (*Diplodia gallae*) of northern red oak (*Quercus rubra*) in the northeastern United States.

N. BRAZEE (1), I. Munck (2), K. McLaughlin (3), S. Ferreira (4), N. Keleher (5)

(1) University of Massachusetts, Amherst, MA, USA; (2) USDA Forest Service, Durham, NH, USA; (3) New York State Department of Environmental Conservation, Delmar, NY, USA; (4) Vermont Department of Forests, Parks and Recreation, Randolph Center, VT, USA; (5) Massachusetts Department of Conservation and Recreation, Amherst, MA, USA

The 2015–2018 outbreak of spongy moth (*Lymantria dispar*) in southern New England initiated a severe oak decline and mortality event. While defoliation was a primary driver, increased secondary pest and pathogen activity contributed to decline and death. Following this event, *Diplodia* was frequently recovered from northern red oaks (*Quercus rubra*) exhibiting shoot tip blight throughout the canopy. Given the many recent reports of *D. corticola* on oak in eastern North America, it was presumed to be the causal agent. To confirm, a limited survey was conducted from five states in the region (Maine, Massachusetts, New Hampshire, New York, and Vermont). Based on ITS, *tef1* and *tub2* sequences generated from 28 isolates collected primarily from northern red oak, *D. gallae*, two potentially novel *Diplodia* species and *D. sapinea* were identified. Surprisingly, *D. corticola* was not found in this study. ITS sequences alone failed to discriminate among isolates of *D. gallae* and *D. corticola*, creating uncertainty over previous reports of *D. corticola* in eastern North America. Only a combined ITS+*tef1* dataset successfully distinguished *D. gallae* and *D. corticola* along with two other closely related species that also occur on oak (*D. quercicola* and *D. quercivora*). Identification of *Diplodia* isolates from non-*Quercus* hosts also detected *D. neojuniperi* on two ornamental hosts (*Juniperus chinensis* and *Microbiota decussata*), which has not been reported previously in North America.

Fungicide sensitivity of *Alternaria* causing leaf blight and head rot of brassicas in the eastern U.S. to QoIs using a high throughput microplate assay

D. CERRITOS-GARCIA (1), C. Smart (2), D. Langston (3), S. Rideout (4), R. Davis (1), B. Dutta (5), S. Everhart (1)

(1) University of Connecticut, Storrs, CT, USA; (2) Cornell University, Geneva, NY, USA; (3) Virginia Tech University, Blacksburg, VA, USA; (4) Virginia Tech Eastern Shore Agricultural Research and Extension Center, Painter, VA, USA; (5) University of Georgia, Tifton, GA, USA

Brassica growers in the eastern U.S. rely on chemical control to manage *Alternaria* leaf blight and head rot (ABHR) using quinone outside inhibitors (QoI) fungicides such as azoxystrobin. In the eastern U.S., ABHR is mainly caused by *A. brassicicola*, but recently a second species, *A. japonica*, was reported in SC and GA. Our recent study found that *A. japonica* is less sensitive than *A. brassicicola*. We found a 100-fold difference in the effective concentration at which only 50% of spores germinate (EC_{50}). The conventional method to test the sensitivity of *Alternaria* to QoI fungicides is spore germination assays. This method is laborious and time-consuming, which limits its application to small numbers of isolates. A high throughput method is needed to evaluate a large number of isolates from different regions. In this study, we implement a microplate assay based on optical density measurements to estimate the inhibition of spore germination to azoxystrobin indirectly. Compared are two methods, one based on the colorimetric changes of a dye and one without the dye. Preliminary experiments using six isolates collected from GA, VA, and NY suggest that EC_{50} from the colorimetric method is correlated to the conventional method. Studies are still ongoing using the method without the dye. Development of a high throughput method will allow large-scale evaluation of *Alternaria* sensitivity to QoIs in the eastern U.S. and will be used to inform disease management recommendations.

Collection and isolation of *Alternaria brassicicola* samples to understand population structure along the east coast, United States

R. DAVIS (1), D. Cerritos-Garcia (1), A. Martin (1), M. Fenton (1), K. Patel (2), H. Betaw (3), C. Hoeping (4), S. Rideout (5), D. Langston (6), C. Smart (3), B. Dutta (2), S. Everhart (1)

(1) University of Connecticut, Storrs, CT, USA; (2) University of Georgia, Tifton, GA, USA; (3) Cornell University, Geneva, NY, USA; (4) Cornell Cooperative Extension, Albion, NY, USA; (5) Virginia Tech Eastern Shore Agricultural Research and Extension Center, Painter, VA, USA; (6) Virginia Tech Tidewater Agricultural Research and Extension Center, Suffolk, VA, USA

Alternaria brassicicola is a fungal pathogen of Brassicas and the main causal agent of *Alternaria* blight and head rot on the East Coast of the United States. In broccoli production, this disease is primarily managed using chemical intervention in the form of quinone outside inhibitor (QoI) fungicides, such as azoxystrobin. Recent reports, however, suggest that resistance to these QoI fungicides may be present in the pathogen population. To determine if there is resistance to these fungicides, samples of *A. brassicicola* were collected from Connecticut, New York, Virginia, and Georgia in 2022 as a part of a coordinated, multistate effort to analyze the population genomics of this pathogen. This multistate survey has resulted in a collection of 345 isolates. While previous studies related to the population genetics of *A. brassicicola* have indicated that there is ample genetic diversity to differentiate genotypes at field-scale, there are lingering questions surrounding the relative importance of sources of inoculum and whether regional differences exist within the pathogen population. Thus, this study followed a hierarchical pattern to collect lesion from the leaves of broccoli plants in fields, with about 10 miles separating each field in each state. The next steps of this research will be to employ an AmpSeq approach to be able to integrate existing genetic markers with a new set of polymorphic SNP loci to be mined from whole genomes.

Use of chitosan and biopesticides for management of postharvest apple diseases

L. DEGENRING (1), K. Peter (2), A. Poleatewich (1)

(1) University of New Hampshire, Durham, NH, USA; (2) Penn State Fruit Research and Extension Center, Biglerville, PA, USA

Management of tree fruit diseases is especially challenging in the Northeastern United States due to ideal climatic conditions for plant pathogens. To manage diseases successfully and sustainably, an integrated approach is necessary. Applications of the natural product chitosan have been shown to induce plant defenses and reduce postharvest plant disease severity in several crops. We hypothesized that combined applications of chitosan and biopesticides could have a synergistic effect on reducing disease. The objective of this research was to examine the efficacy of pre- and post-harvest applications of chitosan and biopesticide products for suppression of postharvest apples rots. Research orchard trials and New Hampshire on-farm trials were conducted to evaluate pre-harvest applications of chitosan and Serenade ASO (*Bacillus subtilis*) on suppression of post-harvest rots. Postharvest chitosan and biopesticide treatments reduced incidence of rots caused by *Penicillium expansum* and *Colletotrichum fioriniae* compared to the grower standard. Additionally, chitosan reduced lesion size of *P. expansum* and *C. fioriniae* on inoculated apples compared to the water control. Our results suggest that chitosan is an effective treatment to reduce postharvest apple rot and has the potential to be used as an alternative tool for integrated disease management of apple rots.

Nano copper for crop disease management

W. ELMER

Connecticut Agricultural Experiment Station, New Haven, CT, USA

Foliar applications of nanoscale copper oxides (CuO) improve plant health against diseases. We report that single foliar applications of nano Cu (500 ppm) convey season long protection from soilborne and foliar for a wide selection of ornamentals and vegetables including asparagus, basil, begonia, cyclamen, chrysanthemum, eggplant, pumpkin, soybean, tomato, watermelon, and zinnia. In experimental greenhouse and field plots, increases in biomass and yield were observed in all plants when a single application of nano-Cu was applied to the young transplants. Since many different fungal and bacteria disease were suppressed, a general mechanism of resistance was suspected. Transcriptomics and metabolic assays indicate that nano Cu operates through modulation of plant defense products. Specific enzymes associated with host defense such as polyphenol oxidase and phenylalanine ammonia-ligase were frequently upregulated early following Nano-Cu application. It was hypothesized that enhanced defense from nano-Cu early in crop growth might delay the onset of pathogen infection and symptom development long enough to allow more biomass, flowers, and yield. No evidence suggests a fungitoxic mechanism. The most striking finding is that single applications to small transplant were associated with season long protection from disease and increased yields.

Chemical control of potato early blight based on disease forecasting

X. FAN

University of Maine, Orono, ME, USA

Early blight (*Alternaria solani* and *A. alternata*) has been a severe problem to Maine potato production. To effectively control the disease, fungicide BAS 762 (mefentrifluconazole and boscalid) sprays were examined based on a modified tomato forecaster (TOMCAST) and physiological degree-day (P-Day) models. A field trial was established with the plots arranged using a randomized complete block design with four replications. Potato 'Caribou Russet' and 'Lamoka' were planted in a plot of 4-row and 25 plants per row. Weather data were collected through a weather station installed near the field. Fungal spores were collected using a Burkard spore trap. Fungicides were first applied when P-Day reached 300 and subsequently arranged based on TOMCAST thresholds or regular intervals, depending on the treatment. BAS 762 was applied at 10 and 15 fl oz/A. The disease was evaluated weekly. The results showed 'Lamoka' did not show early blight infection, indicating a level of resistance, but 'Caribou Russet' was susceptible to the disease. For 'Caribou Russet', while there were no yield differences among the treatments, BAS 762 reduced the disease-severity-based area under the disease progress curve compared to the untreated. Higher rates and frequency of application did not result in yield differences, which was possible due to a lower disease level.

Efficacy of the *Epichloë festucae* antifungal protein *Efe-AfpA* against *Clarireddia jacksonii*

P. FARDELLA, F. Belanger, B. Clarke

Rutgers University, New Brunswick, NJ, USA

Epichloë festucae is a clavicipitaceous endophyte found in some turfgrasses. In strong creeping red fescue (*Festuca rubra* subsp. *rubra*), the fungal endophyte provides resistance to dollar spot disease caused by the ascomycete pathogen *Clarireddia jacksonii*. Some turfgrasses such as creeping bentgrass (*Agrostis stolonifera*) do not have naturally occurring endophytes that provide such resistance. Understanding this endophyte-mediated resistance could lead to utilizing the underlying mechanism to protect other grasses from disease. Previously, we identified an *E. festucae* antifungal protein, *Efe-AfpA*, which was highly expressed *in symbio* and localized to the plant apoplast. *Efe-AfpA* was expressed in *Penicillium chrysogenum* and purified from the culture filtrate for downstream investigations of efficacy against plant pathogenic fungi. *Efe-AfpA* was highly inhibitory against *C. jacksonii* mycelium in plate assays, disrupting the plasma membrane. Applications of pure protein to pots of creeping bentgrass inoculated with dollar spot mycelium showed reduced disease severity. It is possible that purified antifungal proteins can be developed as fungicide alternatives or amendments to current fungicide programs. The resulting decreased use of chemical fungicides will decrease the selective pressure that can result in development of resistant strains of pathogens, and the environmental and financial cost these fungicide programs.

Characterizing environmental sensing mechanisms in *Dickeya dadantii*

J. GONZALEZ-TOBON, P. Stodghill, M. Filiatrault
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Many bacteria sense their surrounding environment and move accordingly via chemoreceptor proteins in a process known as chemotaxis. These proteins play essential roles during the disease cycle. Members of the *Dickeya* genus, that cause disease on numerous crops and ornamental plants, present notoriously more methyl-accepting chemoreceptors (MCPs) than other closely related bacteria. However, the functions and signals of many of these MCPs remain unknown. Interestingly, long untranslated regions exist upstream of the coding regions of MCPs in *Dickeya*. We hypothesized these regions harbor small non-coding RNAs (ncRNAs). Transcription start sites (TSSs) were identified using Cappable-seq and found to align well with the areas being transcribed, which were detected via RNAseq and validated via qRT-PCR, *in vitro* and *in planta*. Using biocomputational methods, we identified potential promoters, putative regulatory sequences, and terminators in these regions. Together these results showed that such intergenic regions and MCP genes are actively transcribed *in planta*. Mutants lacking these regions, as well as lacking the MCP genes, were constructed. Results showed differences in the ability to swim and swarm *in vitro*, as well as when causing disease in the potato stem, compared to wild-type bacteria. Our results provide new insight into the sensing and signaling mechanisms used by *Dickeya* and provide targets for disease control.

***Sampling*: a new iOS application to assess epidemics and decision making for integrated disease management**

D. HECK, S. Pethybridge
Cornell University, Geneva, NY, USA

Decision guides to underpin integrated pest management (IPM) practices rely on knowing the density of a pest population or disease intensity threatening the crop. The knowledge is gained by using sampling and scouting methods that prescribe how and when samples should be taken. Sequential sampling is an adaptive method that does not use a fixed number of sampling units and depends on a series of parameters, such as the objectives, precision desired, spatial heterogeneity, and pest density or disease intensity. We developed an iOS mobile device application, called *Sampling*, to be populated with sequential sampling plans for a variety of insect pests and plant diseases. The user can define the parameters, such as sampling objective, precision, or action threshold, navigate in the map to locate the field, and the app will access the appropriate sampling plan for that occasion. Users can start sampling and select the number of diseased individuals on the sampling unit, while the app algorithms will indicate when enough sampling units were collected to stop sampling. After sampling, a decision is made if a management practice is needed in the field (or not) according to the action threshold selected. All of the sampling units are georeferenced and the data can be shared for downstream analyses. *Sampling* is available for free download from the Apple Store (<https://apple.co/3pUiYKy>) and is compatible with iOS 14.0 or greater on iPhone or iPad.

Managing apple scab with the integration of biological controls and disease forecasting to reduce the reliance of multisite fungicides

L.A. KALNINA, K. Cox

Cornell University, Geneva, NY, USA

Apple scab, caused by *Venturia inaequalis*, requires regular fungicide applications to achieve adequate disease control. Multi-site fungicides such as mancozeb and captan are integral to chemical management programs due to resistance concerns. To reduce the reliance and mitigate regulatory concerns with multisite fungicides, there has been increased demand for more sustainable solutions. To reduce reliance on multisite fungicides, we attempted to integrate biopesticides in programs with single-site fungicides using disease forecasting to enhance efficacy in cvs. 'Gala', 'Jonagold' and 'Empire' plantings. Programs included; untreated control, conventional-calendar applications, biopesticide alternated with single-sites on calendar schedule, biopesticide alternated with single-sites using one of three different disease forecasting tools (NEWA, RIMpro, or a weather app). Disease incidence was rated biweekly and relative area under the disease progress curve was calculated and analyzed. No significant differences were observed among management programs suggesting that integrated programs would be viable and that any forecasting based timing can be just as effective as a calendar schedule.

Understanding how climate, soil, and field histories influence the genotypic diversity of *Sclerotinia sclerotiorum* in Pennsylvania and New York

K. LUONG (1), T. McFeaters (1), S. Pethybridge (2), P. Esker (1)

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White mold, caused by *Sclerotinia sclerotiorum*, is a significant disease in the Northeast USA. However, more knowledge of how climate, soil, and field histories drive population structure and genotypic and genetic diversity of *S. sclerotiorum* at a regional level is needed. This study aims to determine *S. sclerotiorum* population diversity across six soybean production regions in Pennsylvania (PA) and compare these populations with those from a snap bean production region in New York (NY). Sclerotia were collected from diseased soybean and snap bean plants and soil samples from 25 fields from 2019 through 2021. A total of 258 hyphal-tipped isolates were obtained, 177 from PA and 81 from NY, respectively. Multilocus genotypes (MLGs) were determined using nine microsatellite markers and analyses were performed using the *poppr* package in R. Climate, soil, and field history data were obtained using online and paper maps and surveys. Our results show that the PA/NY *S. sclerotiorum* population is predominantly clonal, with a clonal fraction of 85.56%. There are 37 MLGs with two predominant MLGs shared between both states. There is no significant differentiation between regions and climate types, but differentiation between soil types within regions may explain high genotypic diversity in certain regions. The impact of field histories is still being analyzed. With this knowledge, we hypothesize that edaphic factors contribute most to genotypic and genetic diversity.

Introducing Howler® and Theia® fungicides for fruit and vegetable production

B. MCINNES

AgBiome Innovations, Hahira, GA, USA

Fruit and vegetable growers need effective, broad-spectrum fungicides for sustainable disease control. AgBiome's novel biological fungicides, Howler and Theia, provide superior performance and resistance

management while addressing increasingly stringent regulatory requirements and consumer demands for quality produce. In 2022 University trials, Howler and Theia were evaluated for disease control in apples, grapes, potatoes, and vegetables. Howler or Theia demonstrated equal or better control than commercial standards applied in an alternating program or tank mixture.

The genomic region matters when synthesizing dsRNA for plant virus suppression via RNAi

J.S. Milagres, K.A. Barroso, R. Thangavelu, W. DA SILVA

Connecticut Agricultural Experiment Station, New Haven, CT, USA

The application of dsRNAs is a strategy that can mitigate the losses caused by viruses in agriculture. These molecules are the precursors of small interfering RNAs (siRNA) via RNA interference (RNAi) - a mechanism in eukaryotic cells that helps to control viral infections. The objective of this study was to evaluate the performance of dsRNA derived from three potato virus Y (PVY) genomic cistrons to suppress PVY infections. DsRNAs were synthesized in vitro from three different cistrons. Fifty µg of each dsRNA was applied per leaf to a total of two leaves per tobacco plant. Plants were mechanically inoculated with PVY either, at one or five days after dsRNA treatment (five plants per cistron inoculated each day). Experiments were replicated three times and the status of infection (checked by ELISA) and symptoms were evaluated two weeks after PVY inoculation. Twenty percent of the plants treated with region 1-derived dsRNA displayed symptoms when inoculated one day after dsRNA treatment, none of the plants treated with the other dsRNAs showed symptoms. For plants inoculated five days after treatment with dsRNA from 1, 2, and 3 cistrons, the infection rates were 73, 33, and 7%, respectively. Our results show that dsRNA treatment can protect plants for up to five days against PVY infection and that the viral genomic region matters when designing dsRNA for protection against the target virus.

Abscission points of glandular and non-glandular trichomes are host entry points of the fire blight pathogen on apple leaves

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Plant surfaces are covered with a cuticle layer, which acts as a barrier and a first line of defense against many plant pathogens. Unlike fungal pathogens, which can penetrate plant cuticles, bacterial plant pathogens enter plants either through natural openings or artificial wounds caused by wind, rain or piercing-sucking insects. Abscission is a natural process by which organs such as leaves, flowers or fruit are shed from a plant. Whether bacterial plant pathogens can take advantage of the naturally occurring wounds during plant abscission as host entry points has not yet been described. During an investigation of the host entry points of the fire blight pathogen *Erwinia amylovora* in apple leaves, we determined that *E. amylovora* preferably colonizes two leaf surface structures: glandular trichomes (GT) and non-glandular trichomes (NT). Through confocal, scanning, and transmission electron microscopy, we demonstrated that *E. amylovora* not only grows epiphytically on GT and NT, but also enters through such structures into plant tissues. We observed an increase of host cell damage on GTs during leaf maturation, which eventually leads to the abscission of GTs. We provided evidence showing that the level of damaged host cells on GTs is in correlation with the level of *E. amylovora* colonization. This research provides a new mode of entry of bacterial plant pathogens into plant hosts, which is through natural injuries that occur during the abscission process.

Managing potato early dying using multi-facet strategies

S. MORRIS (1), K. Ashley (1), J. Hao (1), S. Johnson (2)

(1) University of Maine, Orono, ME, USA; (2) University of Maine Aroostook Farm, Presque Isle, ME, USA

Potato early dying, caused by *Verticillium dahliae*, is a major threat to the Maine potato industry. To determine the best practice in managing this disease, chemical and biological products were applied for soil treatment in Maine in 2022, including Majestene (*Burkholderia* sp.), Stargus (*Bacillus amyloliquefaciens*), Regalia (*Reynoutria sachalinensis* extract), Double Nickel (*Bacillus amyloliquefaciens*), MBI-306 (*Burkholderia rinojensis*), and Elatus (azoxystrobin and benzovindiflupyr). The inoculum of *V. dahliae* was prepared in an oat-seed-based medium. At planting, the inoculum was spread in the furrow at 10 ml per foot, followed by immediate soil treatments or soil drenching after planting. In a separate trial, soil was fumigated with metam sodium at 50 gal/A followed by applying biological products in various combinations and timing. DNA was extracted and sequenced targeting regions of the 16S rRNA and fungal ITS genes via an Illumina sequencing system. These sequence data were compared to that of similar field trials previously done. In all trials, yield and disease were measured post-harvest. Soil samples were collected at planting, one month, and two months after planting. Results indicated that plots with biological control treatments primarily had the highest yields, while Elatus was more effective in reducing disease incidence. Plots with biological products added post-fumigation had lower disease severity and higher yield compared to fumigation-only plots.

Quorum sensing mediated bacterial interspecies communication in soybean rhizosphere

S. Mukhtar, M.A. Hassani, S. Nason, Q. ZENG

Connecticut Agricultural Experiment Station, New Haven, CT, USA

Rhizosphere bacteria play an important role in plant development, growth, and health. Quorum sensing (QS) is an important microbial communication method although to what extent it is used for interspecies communication within rhizosphere microbiome, and its role in plant fitness is unknown. Using shotgun metagenomic sequencing, we identified that several QS systems such as AHL, HSQ, and COM class were highly enriched in soybean rhizosphere as compared to the bulk soil. A diverse group of AHL molecules were identified within rhizosphere soil, including C4, C6, C8-AHL and 3-oxo-C8, 3-oxo-C10-AHL which are also enriched in soybean rhizosphere as compared to bulk soil, suggesting they may convey beneficial functions during plant-microbe interactions. LC-HRMS analysis of individual bacterial strains isolated from the soybean rhizosphere showed that C4, C6 and C8 AHLs were detected in all bacterial strains but 3-oxo-C12 was detected only in *Pseudomonas* strains. Some of the identified AHL molecules induce plant growth promoting traits, such as phosphate solubilization, nitrogen fixation, indole acetic acid and siderophores production. Findings from this study suggests microbes within plant rhizosphere can communicate at interspecies level using QS, which provides beneficial functions to plants.

Emerging *Xanthomonas arboricola* populations causing bacterial blight-like symptoms on hazelnut in New Jersey

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Bacterial blight, caused by *Xanthomonas arboricola* pv. *corylina*, is becoming one of the most important diseases affecting hazelnut production worldwide. Symptoms appear on leaves and twigs as leaf spots and girdling stem cankers, ultimately resulting in dieback of young shoots, stunted growth, delayed production, and sometimes death of the tree. Over the past decade, a bacterial disease similar to bacterial blight has emerged in New Jersey and has increased in both incidence and severity on hazelnuts throughout the state. However, the disease appears less destructive and some symptoms differ from those typically described for the disease, including stem twisting, leaf cupping, and necrotic lesions on the stems, calyx, and occasionally on nut surfaces. Bacteria isolated from diseased hazelnut trees throughout the state between the growing seasons of 2020 to 2022 were tentatively identified as *X. arboricola* using a multilocus sequence approach. Genetic variation was observed among bacterial strains causing disease on hazelnut in New Jersey, and isolates varied in pigment intensity and growth rate in culture. Furthermore, phylogenetic analysis using seven housekeeping genes indicated strains isolated in New Jersey are genetically distinct from those present in Oregon and Europe. Collectively, these results suggest a new taxonomic subgroup of *X. arboricola* is responsible for causing bacterial blight-like disease on hazelnut in the northeastern US.

Physiological and genetic mechanisms associated with antibiotic persisters of *Pseudomonas syringae* pv. *phaseolicola*

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Persister cells are a small proportion of bacterial population that can survive antibiotics by entering a physiologically tolerant state. Persistence can cause antibiotic treatment failure in human pathogens, and could potentially contribute to treatment failure in agriculture. Using *Pseudomonas syringae* pv. *phaseolicola* (*Pph*), a model plant pathogen, we asked whether bacterial persisters survive membrane-active biocontrol treatments as well as antibiotics, or whether biocontrols might be better for controlling persisters. We discovered that about 1 in 2000 *Pph* cells is tolerant to streptomycin or to the biocontrol protein tailocin. Microscopy and cell sorting revealed that while culturable streptomycin persisters are dormant, tailocin persisters were different and physiologically active. Accordingly, the two treatments effectively killed one another's persisters. To identify possible mechanisms, high-persistence mutants to tailocin and streptomycin were selected. Eleven independent streptomycin persistence mutants mapped to a single toxin, while tailocin mutants were all associated with lipopolysaccharide clusters. These findings point to antibiotic persistence as an active process mediated by specific genes in a fraction of cells, and suggest that persistence could be manipulated to improve the efficacy and lifespan of chemical controls.

Soil microbiomes during early soybean development under *Pythium* disease pressure

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Suppressive soils, characterized by abiotic factors and microbial composition, provide a long-term sustainable plant pathogen management strategy for farmers. This research identifies bacterial and fungal abundance and diversity profiles in soil during the first two weeks of soybean development to determine if specific compositions correlate to *Pythium* disease severity. One field and two greenhouse experiments conducted in 2021 and 2022 used novel 3D-printed rhizoboxes, filled with field-collected soil, to enable non-destructive daily soil sample collection for a continuous assessment of soil microbiome changes. Abiotic soil treatments, selected to impact *Pythium*, included soil pH, soil type, soil saturation, and fungicide seed treatment. Prior to planting, rhizoboxes were inoculated with *Pythium sylvaticum* on 1/2-PDA plugs, with controls receiving organism-free plugs. Straw soil probes were collected daily and, on day 14, plant roots and shoots were rated for disease symptoms to compare soil microbiome profiles of healthy and diseased plants. DNA was extracted from the soil samples and MiSeq of the 16S and ITS regions identified the soil microbiome profiles of bacteria and fungi, respectively. Network and co-occurrence analyses were used to highlight key microorganisms and specific soil microbiome profiles predictive of *Pythium* disease severity, which can inform future farmer decision-making tools for *Pythium* disease management using suppressive soils.

Whole-genome sequencing of *Gemmatomyces piceae* from Alaska reveals differences to European populations

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Gemmatomyces piceae causes bud blight disease of spruce (*Picea* spp.). Although its status as a native or exotic pathogen has not been elucidated, *G. piceae* has been detected in Alaska. Despite the psychrophilic nature and difficulty to obtain pure cultures of *G. piceae*, four genomes (40 Mb) from Alaska were sequenced from single conidiospores after amplification by a REPLI-g® Single Cell Kit. *De novo* assemblies were obtained using SPAdes and statistics using Quast. Genome sizes ranged from 40.5 Mbp to 78.2 Mbp. N50 from 19.9 Kbp to 52.0 Kbp. BUSCO was used to measure the completeness of the assemblies based on single copy ortholog genes. From 6641 ortholog genes in the Pleosporales database a range from 5495 to 5609 were found, missing from 933 to 995, single from 5589 to 5598, duplicated from 9 to 102, fragmented from 94 to 151, missing from 933 to 995; resulting in an overall percentage of BUSCOs greater than 80% in all genomes analyzed. Initial Sanger sequencing of the ITS, LSU, Btub, Rpb2 and Tef1 genes of *G. piceae* from Alaska could not detect nucleotide differences to *G. piceae* from Europe. Genes extracted from WGS data were aligned to genes from European *G. piceae* and indels and SNP were observed along the aligned regions, except in the SSU gene. Genomes will be used to identify Short Sequence Repeat (SSR) microsatellite loci and polymorphic SNPs. An AmpSeq approach will be used to genotype 91 isolates of *G. piceae* that were collected in the summer of 2021.

Identification of yeasts from apple flower microbiome for the induction of systemic induced resistance in apple trees

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Fire blight is one of the most devastating diseases for apple and pear trees caused by the bacterial pathogen *Erwinia amylovora*. Many of the current control strategies are becoming ineffective and are unsustainable. Previously, it has been determined that systemic acquired resistance and expression of pathogenicity related (PR) genes in apple flowers can be triggered by treatment of cultured *Aureobasidium pullulans*, a naturally occurring yeast in the microbiome of apple flowers. This led us to the hypothesis that other yeast-like fungi found on the microbiome of apple blossoms may also induce plant host immunity and could be used as a biocontrol for fire blight. Seventy-six strains of yeasts were isolated, purified and identified by sequencing the internal transcribed spacer (ITS). Of the 18 yeasts tested, six yeasts induced the expression of PR2 in treated flowers more than fivefold. In addition, *Aureobasidium pullulans* that induced SAR in treated apple flowers can also cause russetting on fruits, a cosmetic defect on the cuticle of fruits although did not affect the size or weight of the fruits. Overall, this study suggests that yeasts from the natural flower microbiome may induce systemic induced response in apple trees and have potential to be utilized as biological controls against fire blight, although the risk of causing fruit russetting needs to be considered.

Ethanol extracts from tree residues: Antibacterial activity and stimulation of plant defense mechanisms in *Arabidopsis thaliana*

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Large quantities of lignocellulosic wastes from timber/forestry operations and urban forestry/greening are generated worldwide each year. These residues could be valorized in high-value products for sustainable agriculture. This study aims to provide new insights into the exploitation of lignocellulosic residues to control plant diseases. Ethanol extracts from residues of four tree species, namely eastern hemlock (*Tsuga canadensis*), eastern red cedar (*Juniperus virginiana*), English oak (*Quercus robur*), and red pine (*Pinus resinosa*) were first evaluated *in vitro* for their antibacterial activity against *Pseudomonas syringae* pv. *tomato* DC3000 (*Pst-LUX*). Their capacity to activate plant defense mechanisms was then assessed *in vitro* with an *Arabidopsis thaliana* transgenic reporter line expressing the PR1- β -glucuronidase (PR1::GUS) promoter fusion. Finally, the effects of the extracts were evaluated *in vivo* by spraying transgenic PR1::GUS plants at the blooming stage, two days before inoculation with a *Pst-LUX* suspension (1×10^8 CFU mL⁻¹). One week after the inoculation, GUS expression patterns, senescence, and *Pst-LUX* populations were determined in the leaves. Our results show that the tested tree extracts have antibacterial activity as well as the potential to stimulate plant defense mechanisms and partial resistance to bacterial populations in leaf tissues.

Effects of lobster shell meal for suppressing *Verticillium* wilt and improving potato growth

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The potato (*Solanum tuberosum*) is the most economically important crop in Maine, but has been challenged by many soilborne diseases such as potato early dying (*Verticillium dahliae*) as well as constrained by poor soil health. Compost and lobster shell meal (LSM) have been used to fertilize crops, and there is evidence that these soil amendments can promote beneficial microbial communities that may suppress pathogens. To explore the combined effect of LSM and compost as a disease suppressive tool, a greenhouse study was established, using potato 'Shepody' and treatments using various combinations of compost, LSM, and *V. dahliae* inoculum. Plants were evaluated for emergence, disease symptoms, height over time, and biomass after harvest. Initial results have shown there was little difference in plant emergence and plant height between treatments. However, compost with or without LSM was found to increase root biomass. LSM alone showed a decrease in the number of tubers, yet an increase in total tuber mass. Stem lesions caused by *V. dahliae* were larger on the compost treatments, while all treatments had similar disease ratings. However, further investigation will be required to determine if LSM is a useful tool in *V. dahliae* management.

Can cover crop legacy impact mycotoxin accumulation and fusarium disease in maize?

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Fusarium (*Fusarium verticillioides*) and Gibberella (*Fusarium graminearum*) ear and stalk rot are toxicologically important diseases of maize in the Northeast. While *Fusarium* infection can reduce maize yield, the mycotoxins produced by these pathogens (fumonisins and DON) are a significant concern, threatening human and animal health. Management is limited to the use of genetic resistance via transgenic *Bt* maize, which is inaccessible to organic producers. Cover cropping is an accessible alternative practice with potential for *Fusarium* management. Cover crops are known to modify nutrient cycling, soil biological activity, and plant defense pathways. Mycorrhizal colonization is also influenced by cover crop legacy and has previously been found to activate plant defense against insect herbivory and soilborne pathogens; yet more research is needed to understand how these modifications influence above ground fungal pathogens. We aim to identify the effect of various cover crop species legacies (triticale, oat, radish, canola, pea, and clover) and mycorrhizal colonization on maize disease severity and mycotoxin contamination by *Fusarium spp.* Preliminary results from the 2021 season indicate that mycorrhizal colonization may increase stalk rot severity. However, cover crop type did not influence ear rot disease severity or fumonisin accumulation. Understanding the impact of cover crops for *Fusarium* management will enhance our knowledge of the benefits that they provide.

Investigating the use of nanocarriers for targeted gene therapy in plant pathogen control

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The use of nanocarriers for targeted gene therapy has gained significant attention in recent years as a potential solution for controlling plant pathogens. Plant disease can cause significant economic losses in agriculture and food production worldwide and traditional methods of disease control, such as chemical pesticides, have been found to be ineffective and harmful to the environment. In this regard, targeted gene therapy using nanocarriers has emerged as a promising alternative. Nanocarriers, particularly protein nanocarriers, are small particles that can be engineered to target specific cells in plants and deliver genetic material, such as disease-resistance genes, to those cells. These particles offer a more targeted and effective way to control plant pathogens compared to traditional methods. At this conference, we will present our latest research on investigating the use of nanocarriers, specifically protein nanocarriers, for targeted gene therapy in plant pathogen control. We have characterized the physical and chemical properties of different nanocarriers and evaluated their ability to protect and deliver nucleic acid to plant cells. Our results show that the protein nanocarriers have high stability, are able to protect the genetic material from degradation, and efficiently deliver it to the target cells. However, further studies are needed to optimize the design of these nanocarriers for efficient and specific delivery of nucleic acid to plant cells.

Evaluating adjuvants for reducing potential phytotoxicity in aerial application of propiconazole

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Unmanned aerial vehicles (UAVs) can be used for fungicide applications. Due to weight limitations, this technology involves spraying chemicals with a small volume and high concentration, which may result in potential phytotoxicity. To evaluate the safety of UAV-delivered chemicals, rice plants were sprayed with propiconazole emulsifiable concentrate (EC) at 250 g/L mixed with various adjuvants and applied at a low volume, which contained the fungicide at concentrations equivalent to or higher than that used in UAV application. Four spray adjuvants were used for comparison along with the fungicide. Potential phytotoxicity on rice plants was examined based on surface tension and crop growth. Additives suitable for a low-volume spray of propiconazole were further studied on three rice varieties for phytotoxicity. In the result, rice leaves showed abnormal growth after 72 hours of fungicide application at 2, 4, and 8 times the recommended dose of 7500 µg/mL for UAVs spray. The dry weight of rice significantly decreased 21 d after application. Phytotoxicity was evaluated on three rice varieties 5 d after spraying propiconazole EC at 2 × recommended dose with one of the spray adjuvants. The addition of adjuvant 1% YS-20, Biaopu, TriTek, and Yipinsongzhi significantly augmented the phytotoxicity. However, both AgriSolv-C100 and Hongyuyan significantly mitigated the phytotoxicity, therefore could be used for UAV application.

Autumn-applied fungicide timing effects on the development of dollar spot during the subsequent growing season

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Anecdotal evidence suggests that autumn-applied fungicides may reduce dollar spot, caused by *Claviceps jacksonii*, the following season. Eight autumn-applied fungicide treatments and a non-treated control (NTC) were arranged in a randomized complete block design to evaluate the suppression of dollar spot the subsequent growing season. The trial was conducted on a '007' creeping bentgrass (*Agrostis stolonifera*) maintained as fairway turf in North Brunswick, NJ. Dollar spot developed naturally and was suppressed before the study started in early September 2019 and 2020. Seven treatments received a tank mix of fluazinam + propiconazole once (three timings), twice (three timings), or thrice (one timing) in September, October, and/or November 2019 and 2020. An eighth treatment received chlorothalonil thrice. The area of dollar spot symptoms was assessed every 1-7 days during study. Leaf tissue was collected in November 2019 and 2020 to quantify the pathogen population using q-PCR. Fluazinam + propiconazole delayed disease onset and suppressed disease severity the subsequent season in both years compared to the NTC; whereas, chlorothalonil resulted in reduced (2020) or no (2021) suppression. The tank mix applied in September-October and September-October-November provided the best disease suppression in both years. Suppression of the *C. jacksonii* population in autumn correlated with reduced disease severity the subsequent year.

Taxonomic components and infectiousness of bacteria causing potato blackleg and soft rot in the northeastern U.S.

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Potato blackleg and soft rot (PBSR) is caused by *Dickeya* and *Pectobacterium* spp., which related to the 2015 outbreak in the northeastern region of the US. To understand the epidemiology of PBSR, the taxonomy of the pathogens present after the outbreak and the dynamics of infectiousness throughout the tuber storage period were determined. Bacteria were isolated from potato samples showing PBSR from 2019 to 2022 in the northeastern region, especially Maine. Multi-locus sequence analysis was performed using the *recA*, *gapA* and *dnaX* genes of isolates' DNA. Results showed that *D. dianthicola* and *P. parmentieri* were isolated at a lower percentage than other *Pectobacterium* species in the outbreak. *Pectobacterium versatile* was more frequently isolated than *Dickeya* or other *Pectobacterium* species, and *P. brasiliense* and *P. parvum* isolates were found. To examine the infection process, 'Lamoka' potato tubers were inoculated with *D. dianthicola* isolate at three different time points from December to May. The inoculated tubers were grouped in storage as either 100% infested or 50% infested (mixed with 50% un-inoculated tubers). Following storage, the tubers were planted in the field. Results showed that plant emergence and yield were negatively correlated with disease intensity. The earlier the tuber was inoculated, the higher the disease level was observed. In addition, healthy tubers could be infected by contacting the inoculated tubers in storage.