PROGRAM

2024 Northeastern Division Meeting

Northeastern Division 83rd Annual Meeting

The American Phytopathological Society

6-8 March 2024

Ithaca, NY

2023-2024 NED-APS OFFICERS

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Thanks to Syngenta and OPS Diagnostics for their sponsorship.

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WEDNESDAY, MARCH 6

8:00 – 9:00 AM **Breakfast (Ithaca/Cayuga Rooms)**

9:00 AM – 12:00 PM **Fieldtrip** (Carpool to Campus| Pre-registration required)
Coordinator: Gary Bergstrom
Cornell Plant Pathology Herbarium and Botanic Gardens – On Campus Walking Tour (lunch on your own)

1:00 – 3:00 PM **Cover Letters 101 Workshop (Ithaca/Cayuga Rooms)**
Moderator: Anissa Poleatewich (Pre-registration required)

The APS Careers 101 workshop series is designed to support plant pathology professionals as they embark on their careers. This year, our focus is on cover letters. Cover letters often serve as the first page of a job application and are the first thing that future employers see. They demonstrate a candidate's qualifications, help put the CV into context, and showcase candidates written communication skills. This workshop includes evaluation of effective and ineffective cover letters, as well as practice creating cover letters. The workshop is intended for early career professionals, postdocs, and students.

Registration is free – but is required to attend. For more information about this event, please contact Anissa Poleatewich (anissa.poleatewich@mycorrhizae.com).

3:00 – 5:00 PM **Joint Extension/Industry meeting (Ithaca/Cayuga Rooms)**
Moderator: Nick Brazee (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.

5:00 – 7:00 PM **Division Social (Ithaca/Cayuga Rooms)**
Appetizers and non-alcoholic beverages will be served.
Cash bar available for alcoholic beverages

Hosts: Nick Brazee & Craig Austin

THURSDAY, MARCH 7

7:00 AM – 8:00 AM **Breakfast (Ithaca/Cayuga Rooms)**

Session 1: Graduate Student Symposium (**Ithaca/Cayuga Rooms**; Moderator: Craig Austin)

8:00 AM Welcome & Opening Remarks
8:10 AM Juliana Gonzalez-Tobon, Cornell University
8:30 AM Jamie Spychalla, Pennsylvania State University
8:50 AM Pratibha Sharma, Cornell University
9:10 AM Veedaa Soltaniband, Université Laval
9:30 AM Aliyah Brewer, Cornell AgriTech/PPPMB
9:50 AM Mariah Sophia Kidd, Pennsylvania State University

10:10 – 10:30 AM: Morning Break

10:30 AM Karen Luong**,** Pennsylvania State University
10:50 AM Elizabeth Indermaur, Cornell University
11:10 AM Fatemeh Ekbataniamiri, Cornell University
11:30 AM Daniel Cerritos-Garcia, University of Connecticut
11:50 AM Kensy Rodriguez, Cornell University

12:15 – 1:15 PM: Lunch (Ithaca/Cayuga Rooms)

Session 2: Graduate Student Symposium (cont.) (**Ithaca/Cayuga Rooms**; Moderator: Elena Karlsen-Ayala)

1:30 – 3:10 PM: Graduate Student Symposium
1:30 PM Natalia Piñeros-Guerrero, Cornell University
1:50 PM Sergio Manuel Gabriel Peralta, University of Connecticut
2:10 PM Robetauli Mastiur Simangunsong, Cornell University
2:30 PM Quyen Hoang, Franklin & Marshall College
2:50 PM Radhika D. Patel, Rutgers University

3:10 – 3:30 PM: Afternoon Break

3:30 PM Alexandra Carabetta, University of Connecticut
3:50 PM Jocelyn Schwartz, Cornell University
4:10 PM Amelia Martin, University of Connecticut
4:30 PM Isabella Magna Yannuzzi, Cornell University
4:50 PM Olanrewaju Michael Shittu, Pennsylvania State University

6:00 – 9:00 PM: Banquet and Awards Ceremony (Ithaca/Cayuga Rooms; Hosts: Nick Brazee & Craig Austin)

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

FRIDAY, MARCH 8

7:00 – 8:30 AM Breakfast & Business Meeting (Ithaca/Cayuga Rooms; Moderator: Nick Brazee)

7:30 – 8:30 AM

Welcome: Nick Brazee, President
Treasurer's report: Anissa Poleatewich, Treasurer/Secretary
Division Forum update: Jianjun Hao (Jay), Division Forum Rep
Old & New Business
APS Council Update – Niklaus Grünwald

8:30 – 9:15 AM Keynote speaker – Niklaus Grünwald, USDA-ARS

Novel tools and approaches to infer processes and patterns of pathogen emergence

Z.S.L. FOSTER(1), M. SUDERMANN(2), C. PARADA-ROJAS(2), F. IRUEGAS-BOCARDO(2), R. ALCALÁ BRISEÑO(2), C.M. PRESS(1), V.J. FIELAND(2), J.H. CHANG(2), and N.J. GRÜNWALD(1)
(1)Horticultural Crops Disease and Pest Management Research Unit, USDA ARS, Corvallis, Oregon, USA, (2) Dept. Botany and Plant Pathology, Oregon State University, Corvallis, Oregon, USA

Pathogens continue to emerge worldwide as species new to science or novel variants of existing pathogens. Many processes can lead to pathogen emergence including hybridization, migration, recombination, loss of heterozygosity, horizontal gene transfer, mutation, etc. This talk will provide insights into our approaches to automate pathogen genomics for detection of novel variants, develop variant specific diagnostics from whole genome data, and apply these approaches to monitoring pathogen emergence. Rapid and automated analysis of plant pathogen genome sequences is essential for more effective responses to disease outbreaks. We developed the pipeline PathogenSurveillance to diagnose individuals or groups of pathogens and their diversity within populations from whole genome data. PathogenSurveillance analyzes raw reads derived from eukaryotic or prokaryotic pathogens. The pipeline automatically processes sequence data and determines the taxonomic placement, finds the closest reference genome sequence, maps sequence reads, calls variants, identifies core genes, and reports back the population and species phylogenetic relationships. We also developed the python package krisp to find primers and diagnostic sequences that differentiate groups of samples from each other at any taxonomic scale, using either unaligned genome sequences or a variant call format (VCF) file as input. The validity of krisp results has been demonstrated in the laboratory with the successful design of SHERLOCK assays to diagnose the sudden oak death pathogen *Phytophthora ramorum*. Our pipelines automate and accelerate analysis of whole genome sequence data essential for rapid analysis and diagnoses of disease outbreaks.

Niklaus J. Grünwald is a Research Plant Pathologist with the Horticultural Crops Disease and Pest Management Research Laboratory, USDA Agricultural Research Service, in Corvallis, Oregon and Professor in the Department of Botany and Plant Pathology and the Center for Quantitative Life Sciences at Oregon State University. He received his Ph.D. in plant pathology from the University of California at Davis and conducted postdoctoral research at Cornell University. His principal research interests include the ecology, genetics, evolution, and management of emerging Phytophthora diseases with a special emphasis on the Sudden Oak

Death pathogen *Phytophthora ramorum* and the Irish famine pathogen *P. infestans*. More recently, he has started working on development of computational and bioinformatics tools for comparative genomics, genotyping-by-sequencing, population genomics, metabarcoding, metagenomics and diagnostics based on CRISPR-Cas. Grünwald has served as associate editor, senior editor and editor-in-chief for Phytopathology and PhytoFrontiers, editor for Plant Pathology, and currently serves as founding editor-in chief for CABI Agriculture and Bioscience. He currently is the president of the American Phytopathological Society (APS). He is a recipient of the 2006 USDA ARS Early Career Scientist of the Year award, the 2007 APS Syngenta award, the 2015 APS Ruth Allen Award recognizing outstanding, innovative research contribution that have changed the direction of research in any field of plant pathology and became APS fellow in 2016 and American Association for the Advancement of Science (AAAS) fellow in 2019.

9:15 – 9:30 AM: Morning Break

Session 3: Contributed Papers (Ithaca/Cayuga Rooms; Moderator: Nick Brazee)

9:30 AM Elliot McGinnity Schneider, Cornell University
9:45 AM Bo Liu, University of New Hampshire
10:00 AM Jason Heindl, Rowan University
10:15 AM Jiyeong Choi, Cornell University
10:30 AM Erica A. Fealko, Bioworks
10:45 AM Kathryn E. Bushley, USDA
11:00 AM Kathryn E. Bushley, USDA
11:15 AM Xing Ma, Cornell University
11:30 AM Patrick Fardella, Rutgers University
11:45 AM Elena Karlsen-Ayala, USDA
12:00 PM Roy Ladell Davis, University of Connecticut
12:15 PM Judith Kolkman, Cornell University

~~~GRADUATE STUDENT SYMPOSIUM ABSTRACTS~~~

Characterizing environmental sensing mechanisms in *Dickeya dadantii*

J. GONZALEZ-TOBON(1), P. STODGHILl(1,2) and M. FILIATRAULT(1,2)
(1)Cornell University, Ithaca, NY; (2)USDA-ARS, Ithaca, NY

Many bacteria sense their surrounding environment and move accordingly via chemoreceptor proteins in a process known as chemotaxis. Members of the *Dickeya* genus, which 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 these MCPs in *Dickeya*. We hypothesized these regions harbor small non-coding RNAs (ncRNAs). Transcription start sites (TSSs) were identified using Cappable-seq and aligned well with the areas being transcribed (detected via RNAseq and validated via qRT-PCR). Using biocomputational methods we identified their potential promoters and terminators. Together these results suggest that these regions are being transcribed independently from the genes terming them Regions of Activity (ROAs). Mutants lacking the ROAs or the MCP genes, were constructed and tested for their ability to swim and swarm *in vitro*, their chemotaxis

capability towards serine, and their virulence in potato stems and tubers. Differences were found between some of the mutants and the wild-type. Based on the results, three mutant pairs (ROA and MCP) were selected as candidates for further analysis. Our results provide new insight into the sensing and signaling mechanisms used by *Dickeya* and may provide targets for disease control.

A Story of Air and Water: Aerial Fungal Microbiome Dispersal in a Michigan Vineyard
J. SPYCHALLA(1), L. HEGER(2), T. MILES(2) and S. CRANDALL(1)
(1)Pennsylvania State University, University Park, PA, (2)Michigan State University, East Lansing, MI

Fungal pathogens can cause disease on grapevine by aerial spore infection. Spore dispersal mode (air via wind or rain), collection time, and canopy height are environmental factors that may confound which fungi are reported. Aerial mycobiota were captured from three rows of the *Vitis* interspecific hybrid 'Vignoles' using passive rainwater samplers and rotating-arm air impaction at varying heights (0.6, 1.4, and 1.8 m with two traps at each height) in Clarksville, Michigan, USA. Samples were collected weekly from July to September 2022. DNA was extracted and metabarcoding was conducted (ITS 1,2) (n = 108). Beta diversity as well as fungal community similarity was visualized with a PCoA test using Bray-Curtis distances. PERMANOVA results indicated three major results. First, there were significant differences found in fungal composition based on sampling method and rainwater contained more *Basidiomycota* than air samples (R2 = 43.48, p=0.001). Second, the aerial mycobiota varied strongly by week when collected from the air and rainwater respectively (R2 = 48.63, p=0.001; R2 = 0.05, p=0.001). Third, air sampler height had little effect on airborne fungal communities (R2 = 1.13, p=0.316) or those from rainwater (R2 = 1.54, p=0.016). These results indicate that variation in fungal genera was dependent upon both the collection method and time of collection. Vertical height was of no consequence, suggesting similar communities of fungi circulated at all canopy levels.

Genetic and functional diversity of *Globisporangium irregulare* isolated from industrial hemp soils in south central Pennsylvania
Q. HOANG and J.E. BLAIR
Franklin & Marshall College, Lancaster, PA

The revival of industrial hemp cultivation in Pennsylvania after nearly a century of absence poses unique challenges for the identification and management of soilborne diseases. In this study, we sampled soils from six industrial hemp production locations across south central PA at multiple time points during summer and fall of 2022, with an overall goal of assessing oomycete diversity and disease potential. Isolates of known pathogens, including *Globisporangium irregulare, G. ultimum*, and *Pythium aphanidermatum* were identified from both seed/fiber and CBD production fields. Focusing on *G. irregulare*, we assessed genetic diversity among the collected isolates using a combination of sequence analysis (COI, ITS) and nuclear microsatellite genotyping. To examine functional diversity, we performed seed germination assays using both soy and corn as potential hosts, as well as hairy vetch as a non-host control. Our results show high levels of genetic diversity among our *G. irregulare* isolates, with four major COI haplotypes and 4-7 alleles across four microsatellites, as well as variation in germination reduction across the isolates tested. We are currently examining the impact of community composition on germination reduction via co-inoculation experiments with *G. irregulare* and potential mycoparasites, *G. acanthophoron* and *G. nunn*. Overall this study advances our knowledge of oomycete diversity associated with industrial hemp under modern agricultural conditions.

Salts and eastern hemlock extract to stimulate plant defenses and control phytopathogenic bacteria
V. SOLTANIBAND, A. BARRADA, M. DELISLE-HOUDE, M. DORAIS, R.J. TWEDDELL and D, MICHAUD
Département de phytologie, Université Laval, Québec, QC, CANADA

Numerous studies have reported on the antibacterial activity of sodium bicarbonate and sodium benzoate, two 'generally recognized as safe' (GRAS) salts used in the food industry. Eastern hemlock (EH; Tsuga canadensis) twig extract was recently shown to also exhibit antibacterial activity, via a stimulating effect on the onset of host plant natural defenses and/or a direct toxic effect on bacteria. The aim of this study was to evaluate the effects of sodium bicarbonate and sodium benzoate, alone or in combination with the EH-twig extract, on both the activation of plant defenses and the control of phytopathogenic bacteria populations, using *Pseudomonas syringae* pv. *tomato* DC3000 (Pst) and transgenic Arabidopsis reporter line, PR1::GUS, as a model pathosystem. The two salts and the EH extract were evaluated *in vitro* and *in vivo* for their effects on GUS expression patterns in the reporter line, defense gene transcription, leaf senescence, callose deposition, and *Pst* populations in inoculated leaf tissue. Our results show that salts and the EH extract, alone or in combination, stimulate the expression of genes associated with the salicylic acid pathway in Arabidopsis and reduce the *Pst* populations in inoculated leaves. These findings highlight the potential of sodium bicarbonate, sodium benzoate, alone or in combination with EH-twig extract, as stimulators of host plant defenses for the control of phytopathogenic bacteria.

Untapped Downy Mildew Resistance in Grapevine
A. BREWER(1), A. UNDERHILL(2), S.D. SAPKOTA(3) and L.E. CADLE-DAVIDSON(2)
(1)Cornell AgriTech/PPPMB, Geneva, NY, (2)USDA Grape Genetics Research Unit, Geneva, NY, (3)USDA, Kearneysville, WV

Grapevine downy mildew (DM) is devastating in humid regions when disease management fails. While the international research community has discovered dozens of DM resistance loci (called RPV, Resistance to *Plasmopara viticola*), there is little knowledge of resistance alleles in US grape breeding programs. However, the NIFA-funded *Vitis*Gen projects established a framework for resistance breeding via accessible DNA marker systems and automated microscopy phenotyping. This research aims to integrate DM knowledge into US breeding programs by translating existing microsatellite DNA markers to rhAmpSeq haplotype markers, which are transferable across *Vitis* species and breeding programs. To study allele effect size and race-specificity of resistance alleles, an RPV evaluation vineyard is being developed and replicated in NY and WV. Because the Eastern US is a center of diversity for *P. viticola*, alleles published as effective in other places may be less effective in the region. Each RPV will be represented by four unique vines of diverse background genetics, where the vines only have one known RPV allele in their genome. Through collaboration, in 2024 this RPV evaluation vineyard will already represent 10 RPVs, serving as a resource for grape breeding and for research regarding downy mildew resistance and pathogen biology. Any resulting new varieties would complement existing management strategies mostly based on fungicides, leading to a more sustainable US grape industry.

Using nematodes to investigate relationships among soilborne pathogens and to study ecological soil health in soybean fields
M.S. KIDD(1), D.K. WEERASOORIYA(2), A. MURILLO-WILLIAMS(3), A.A. COLLINS(4) and P. ESKER(2)
(1)The Pennsylvania State University, State College, PA, (2)The Pennsylvania State University, University Park, PA, (3)Penn State University, Bellefonte, PA, (4)Penn State University, Manheim, PA

Plant parasitic nematode (PPN) populations have increased across Pennsylvania, but contributing factors remain unknown. There is a need for novel knowledge about the soil microbiome, including micro-inhabitants and their relationships with soil health and other microorganisms, particularly those surrounding PPNs. This project aims to explore the associations between PPN with soil health parameters, soilborne pathogens, and field history attributes. We hypothesize fields with a history of tillage, *Fusarium* diseases, and inconsistent crop rotations will have higher and more diverse PPN populations. Specific objectives are to (i) determine if PPN abundance and species diversity can provide a more comprehensive outlook on biological soil health than traditional tests, (ii) explore relationships between PPN and *Fusarium* species, and (iii) investigate correlations between PPN abundance and diversity with field history facets. Since 2018, we have collected 765 samples across 50 counties for PPNs in Pennsylvania. For many samples, growers submitted a field history form covering growth practices, common weeds, and past and current diseases. Using Pearson's correlation coefficient, we observed a weak positive correlation between crop rotation and pin nematodes (r=0.017, n=227), and a weak negative correlation between tillage and dagger and pin nematodes (r=0.0138 and r=0.0266 respectively, n=152). These results will help improve long-term management recommendations for PPNs.

Surveying Best Management Practices for White Mold Disease in Soybeans in Pennsylvania
K. LUONG and P. ESKER, The Pennsylvania State University, University Park, PA

White mold (WM), caused by *Sclerotinia sclerotiorum*, can cause significant yield and economic loss in soybeans. Although numerous management tactics exist, varying factors, such as differing microclimates, WM field histories, production practices, and accessibility of management tools, pose a need for tailored strategies that are economically feasible and effective for each farm. This study aims to elucidate growers' knowledge and perception of WM risk and the constraints of current management practices. During the winter of 2022 and 2023, paper surveys were distributed at extension workshops to examine the extent of the issue of WM and growers' perception of its importance. Grower discussion meetings were held throughout Pennsylvania with three to twelve participants to understand current production practices, WM history, management practices and limitations, and research needs. Paper survey data were analyzed in R, and qualitative content data analysis was performed in NVivo. Initial analyses of the paper survey show that 75% of participants correctly identified WM symptoms , with 40% having WM for at least one year and 20% being unsure. Five major themes revealed by the content data analysis were 1) production practices, 2) production challenges, 3) decision-making factors, 4) current WM management practices, 5) limitations to WM practices, and 6) perceptions and experience with extension. These insights can help us develop tailored management recommendations.

Will Disease Impact the Expansion of Rhubarb Production in the Northeast?
E. INDERMAUR(1), C.T. COLIN DAY(2) and C.D. SMART2
(1)Cornell University, Geneva, NY, (2)Plant Pathology and Plant-Microbe Biology Section, Cornell AgriTech, Geneva, NY

Rhubarb (*Rheum spp*.) is a more ancient crop than its culinary history in Europe and North America reveals. Native to the Tibetan Plateau and surrounding high-elevation tundra, the genus comprises more than 60 species of herbaceous perennials grown globally for culinary and medicinal purposes. Culinary rhubarb (*R. rhabarbarum*) is grown for the consumption of its fleshy leafstalk (petiole) that can be sold in fresh food markets or used in craft beverages and baked goods. Despite being well-suited for cultivation in the Northeast US, where markets are expanding, little is known about host genetics or pathology. Growers have sought recommendations on cultural and disease management practices to advance

regional production. The most common disease in the Northeast is rhubarb leaf spot (RLS), caused by the fungal pathogen *Didymella rhei*. The goal of this research is to advance rhubarb production by expanding our knowledge of pathogen biology, enabling the identification of management strategies to reduce disease incidence and spread. To date, 162 *D. rhei* isolates from five New York populations have been genotyped using single nucleotide polymorphisms discovered via genotyping-by-sequencing. Low genotypic diversity was observed between populations. Additionally, no evidence of sexual reproduction has yet been found. The implications of a suggested clonal population structure in the pathogen on disease management will be discussed.

Unraveling Dynamics Governing Strain Divergence in *Pectobacterium* Species
F. EKBATANIAMIRI
Cornell University, Ithaca, NY and Bryan Swingle, USDA ARS, Ithaca, NY

Phylogenetic analysis of *Pectobacterium* species responsible for soft rot diseases in US potato growing regions during 2015-2022 shows that levels of diversity differ between species. The levels of diversity (i.e., branch lengths) are generally believed to correspond to length of time, based on the assumption that related species have similar mutation rates. We tested this assumption using the Luria–Delbrück fluctuation assay to estimate mutation rates in *Pectobacterium parmentieri* and *Pectobacterium versatile*, two soft rot species with very different levels of diversity. The method examines the number of spontaneous rifampicin resistant mutants in parallel cultures, presenting results as the mutation rate per *rpoB* locus per generation. The mutation rate per nucleotide is then multiplied by the chromosome size to obtain the mutation rate per genome per generation. We hypothesize that similar mutation rates between these species (or higher mutation rates in the less diverse species) would support more recent introduction of the species with lower diversity. Conversely, finding that the more diverse species has a higher mutation rate would suggest that diversity is not directly related to time. This study contributes to understanding the dynamics of plant pathogenic bacterial diversification, aiding in more useful interpretation of phylogenetic trees.

Managing Septoria Leaf Spot of Hemp, Caused by the Fungus *Septoria cannabis*
J. SCHWARTZ(1), T. GORDON(2), Z. STANSELL(2) and C.D. SMART(3)
(1)Cornell University, Ithaca, NY, (2)USDA-ARS, Geneva, NY, (3)Plant Pathology and Plant-Microbe Biology Section, Cornell AgriTech, Geneva, NY

Septoria cannabis is an economically important disease of hemp (*Cannabis sativa*), yet it is an understudied pathosystem. To test the efficacy of fungicides commonly used to control Septoria leaf spot, a field trial was conducted in New York State. Hemp plants sprayed with Quadris, which is not labeled for use on hemp, had the lowest levels of Septoria leaf spot with a mean of 0.5% disease severity and performed significantly better than the untreated control, which had a mean disease severity of 33%. Curezin, a product in development by VM Agritech, had a mean of 6% disease severity and performed significantly better than the untreated control. Regalia, Double Nickel, and Cease could not be distinguished from the untreated control. As hemp growers have limited options for chemical control of Septoria leaf spot, 79 accessions from the USDA National Plant Germplasm System's hemp collection were tested in the field to identify potential sources of disease resistance. Further screenings in the greenhouse and the field will be used to validate the 2023 findings.

Squash bug preference for cucurbit species and its influence on vectoring *Serratia marcescens* causing Cucurbit Yellow Vine Disease in New York

K. RODRIGUEZ(1), S.J. PETHYBRIDGE(2), C.T. COLIN DAY(3), B.A. NAULT(4), B. SWINGLE(5) and C.D. SMART(4)
(1)15 Castle Creek Dr, Geneva, NY, (2)Plant Pathology & Plant-Microbe Biology Section, Cornell University, Geneva, NY, (3)Plant Pathology and Plant-Microbe Biology Section, Cornell AgriTech, Geneva, NY, (4)Cornell University, Geneva, NY, (5)USDA ARS, Ithaca, NY

Cucurbit yellow vine disease is caused by the bacterium *Serratia marcescens*, a disease affecting most commercially available cucurbits. This bacterium is vectored by the squash bug (*Anasa tristis*), a serious pest of cucurbits. CYVD symptoms include yellowing, scorching of leaves, and discoloration of the stem. Squash bugs acquire *S. marcescens* by feeding on the phloem of infected plants and can persist in the insect's hemocoel through molting and overwintering. This project aimed to determine the preference of the squash bug for different Cucurbit species and their relationship with CYVD incidence in the field. We tested this by using 12 cultivars from six cucurbit species (two cultivars per species). Every week, we collected data on the number of adults, nymphs, and eggs per plot and the number of CYVD-diseased plants. We found that the number of squash bugs was highest on July 31st, 2023, which was followed by a high CYVD incidence on August 9th, 2023. There was a significant difference in the average number of squash bugs per species, with *Cucurbita pepo* (acorn and zucchini) and *C. maxima* (squash and winter squash) the most preferred and *Citrullus lanatus* (watermelon) and *Cucumis melo* (melon) the least preferred. The incidence of CYVD was also significantly different and highest in *C. pepo* and *C. maxima*. These findings help document the squash bug population dynamics in New York, their preference for different cucurbit species, and the risk of CYVD incidence.

Determining the contribution of onion volunteers to the population genetics of *Stemphylium vesicarium* in New York using microsatellite markers.

N. PIÑEROS-GUERRERO(1), F. HAY(1), D.W. HECK(1), A. KLEIN(1), C.A. HOEPTING(2) and S.J. PETHYBRIDGE(3)
(1)Cornell University, Geneva, NY, (2)Cornell University, Albion, NY, (3)Plant Pathology & Plant-Microbe Biology Section, Cornell University, Geneva, NY

Stemphylium leaf blight (SLB), caused by the fungus *Stemphylium vesicarium*, is one of the most important foliar diseases affecting onions (*Allium cepa* L.) in the northeastern United States. Volunteers, plants regrowing from onion bulbs left in the field the previous season, may play an important role in the dissemination of the pathogen. However, no studies have been conducted assessing the effect of volunteers on SLB epidemics. In 2022, volunteer plants were collected prior to planting from four fields located in Elba region, NY (B1, B3, B4 and MG). A total of 37 single-spore isolates were obtained from these volunteers (B1 = 8, B3 = 7, B4 = 9, and MG=13). At the end of the season, onion leaf samples showing SLB symptoms were collected prior to lodging from B1, B3 and B4 fields. Ten isolates per field were obtained from leaf samples (n=30). A total of 67 isolates were used to characterize the genetic diversity in *S. vesicarium* populations using nine microsatellite (SSR) markers. The population of *S. vesicarium* isolates obtained from onion plants prior to lodging was highly diverse based on Evenness, Nei's allelic diversity, Shannon-Wiener, and Stoddart and Taylor's genotypic diversity indices. Minimum spanning network (MSN) showed that *S. vesicarium* populations sampled from volunteers highly contributed to the multilocus genotypes (MLGs) found at the end of the season prior to lodging, indicating that volunteers might be an important source of SLB inoculum.

Identifying antimicrobial resistance in *Erwinia amylovora* using selective media, CRISPR profiles, and genetic markers
I.M. YANNUZZI(1) and K.D. COX(2)
(1)Cornell University, Ithaca, NY, (2)Cornell University, Geneva, NY

Fire blight, caused by the bacterium *Erwinia amylovora*, is an economically devastating disease of pome fruit. Modern integrated management programs focus heavily on antibiotics including the aminoglycoside antibiotic streptomycin. However, populations of streptomycin resistant *E. amylovora* complicate management. To assess the prevalence of antibiotic resistance, *E. amylovora* isolates from commercial farm across New York state were collected, isolated, and evaluated in vitro. Between the years 2020 and 2023, 388 isolates of *E. amylovora* were collected from 19 different New York counties. Of the 388 isolates we determined that 163 (42%) were resistant to streptomycin. From that sampling effort whole genome sequencing was conducted for a subset of isolates with covering a range of phenotypes and genotypes to complete CRISPR profiling and screen for genetic elements responsible for resistance. Through understanding the presence and spread of antibiotic resistant *E. amylovora* we can streamline fire blight disease management and optimize grower recommendations.

Morphology and Multi-Gene Phylogeny of *P. betae* (syn. *Neocamarosporium betae*) populations in New York and Washington States, USA
R.M. SIMANGUNSONG(1), L. KOENICK(2), S. MURPHY(2), and S.J. PETHYBRIDGE(2)
(1)Cornell University, Ithaca, NY, (2)Cornell University, Geneva, NY

Phoma betae Frank is a hemibiotrophic pathogen causing various diseases in *Beta vulgaris.* Noteworthy *P. betae* cultures include CBS 523.66 and CBS 109410. Addressing the polyphyletic nature of Pleospora and related genera, Ariyawansa et al. (2015) elucidated Pleosporaceae's evolutionary relationship. CBS 109410, IMI 156653, and ICMP 10945, initially designated as *P. betae*, were reassigned to the Neocamarosporium clade based on SSU, LSU, and RPB2 genes. Notably, all the SSU, LSU, RPB2 NCBI accession numbers (EU754079, EU754178, GU371774) correspond to CBS 109410. IMI 156653 and ICMP 10945 lack associated NCBI accession numbers in Ariyawansa et al.'s (2015) reference organism sequence list supplementary document. CBS 523.66, another *P. betae* reference strain, mentioned by Boerema et al. (2004), wasn't included. For robust phylogenetic analyses, two or more informative genes are typically used. This study aims to delineate *P. betae* isolates' phylogenetic lineages from New York and Washington States, USA, by comparative analysis of *P. betae* reference isolates (CBS 523.66, CBS 109410, IMI 156653, ICMP 10945) and a multigene phylogeny using ITS, LSU, SSU, RPB2, Tub2, and Tef1-a gene markers will be conducted. Accurate nomenclature is crucial in discussions related to fungal plant pathogens, as inaccurate species names may lead to unnecessary control measures, restrictions, or inadvertent introductions of fungal plant pathogens.

Residue management as an alternative to manage cercospora leaf spot of table beet and its effects on the soil microbiome.
P. SHARMA(1), E. BRANCH(2), S. MURPHY(1), J. KIKKERT(3) and S.J. PETHYBRIDGE(1)
(1)Plant Pathology & Plant-Microbe Biology Section, Cornell University, Geneva, NY, (2)North Dakota State University, Fargo, ND, (3)Cornell Cooperative Extension, Canandaigua, NY

Infested leaf residue is one of the primary sources of *Cercospora beticola* inoculum that causes Cercospora leaf spot (CLS) in table beet. CLS has potential to negatively impact the foliar health of table beets, leading to substantial economic losses. Current management relies on in-season fungicides, but the rapid development of fungicide resistance, as a function of high genetic diversity of *C. beticola,* poses a

significant challenge. Management of infested leaf residue can potentially delay the onset of disease by reducing soilborne primary inoculum. In a replicated field experiment, infested leaves were treated with various management methods. The experimental design was a completely randomized block with four replications for each treatment and nontreated controls. Treatments were applied in fall 2021 and table beets were planted in summer 2022. The results revealed that heat treatment of residue significantly decreased CLS severity and AUDPS by 45.3% and 51.8%, respectively, compared to the nontreated surface residue. Conversely, treatments involving $CaCO_3$ and a combination of chopping and plowing showed significantly higher CLS severity and AUDPS, increasing by 92.8% and 149.3%, respectively, compared to the no residue control. Other treatments were not significantly different from either control. Treatments did not significantly alter the soil microbiome compared to the no residue control; however, a seasonal effect was observed in soil microbial diversity.

Emergence of new taxonomic subgroups of *Xanthomonas arboricola* causing bacterial blight-like symptoms on hazelnut in New Jersey

R.D. PATEL, G. MASNY, D. SHAH, N. PATEL, J. CAPIK, T.J. MOLNAR and D. KOBAYASHI
Rutgers, The State University of New Jersey, New Brunswick, NJ

Bacterial blight (*Xanthomonas arboricola* pv. *corylina*) (*Xac*) is emerging as a major obstacle to hazelnut production globally. The disease is currently present in most hazelnut-producing regions, including Oregon and, the world's largest producer, Turkey. Bacterial blight-like symptoms have also been detected in the past decade in New Jersey with increasing incidence and severity over these years. Symptoms include stem twisting, leaf cupping, and necrotic lesions on the stems, calyx, and occasionally on nut surfaces. To identify the causal agent, bacteria were isolated from diseased hazelnut trees throughout New Jersey from 2020-2023. Multilocus sequence analysis identified these isolates as *X. arboricola*. Additional phylogenetic analysis with seven housekeeping genes indicates substantial genetic variation among these strains. Some isolates appear closely related to *Xac* isolated from France and the U.S. However, most New Jersey isolates form a single clade distinct from existing pathovars of *X. arboricola.* Collectively, these results suggest that a new taxonomic subgroup of *X. arboricola* is responsible for causing bacterial blight-like symptoms on hazelnut in the state.

All Together Now: The Relationship Between Predatory Protists and Multicellular Bacterial Structures in the Phyllosphere

A. CARABETTA(1), R.R. PATEL(2) and L.R. TRIPLETT(2)
(1) University of Connecticut, CT, (2) Connecticut Agricultural Experiment Station, New Haven, CT

Bacteria in the *Pantoea* genus have the ability to create symplasmata, which are clusters of hundreds of bacteria enclosed in a capsule. Symplasmata are formed when the bacteria are under stress, including in the phyllosphere environment. In this study, we tested the hypothesis that the large size of symplasmata may protect bacteria against predation. Protists are predators that can affect plants by triggering bacterial defense behaviors. *Colpoda sp.* are dominant protist members of the phyllosphere. I hypothesized that symplasmata would reduce the predation rate by *Colpoda*, and that symplasmata would form at higher rates when protists were present. To test this, I cultured *Pantoea agglomerans* in symplasmata inducing or non-inducing media. Cultures were incubated with *Colpoda*, and I measured the numbers of bacteria, protists, and symplasmata formed over the course of five days. Symplasmata formed at higher rates in cultures containing *Colpoda*, and symplasmata-containing cultures had a higher predation survival rate than symplasmata-free cultures, suggesting symplasmata formation protects bacteria from predation. Surprisingly, Colpoda formed cysts at a faster rate when symplasmata were present, suggesting that the symplasmata may have a toxic effect on the protist. This shows that

phyllosphere bacteria with the ability to form symplasmata may have better adaptive potential to avoid protist predation, which could influence the bacteria's fitness in the phyllosphere.

Fungicide sensitivity of *Alternaria spp*. to azoxystrobin reveals presence of resistance to QoIs in some broccoli producing states in the East Coast

D. CERRITOS-GARCIA(1), R..L DAVIS(2), A. MARTIN(3), M. FENTON(4), H. BETAW(5), C.D. SMART(5), C.A. HOEPTING(6), D.B. LANGSTON(7), S.L. RIDEOUT(8), K. PATEL(9), B. DUTTA(10) and S.E. EVERHART(2)
(1)University of Connecticut, Storrs Mansfield, CT, (2)University of Connecticut, Storrs, CT, (3)University of Connecticut, Vernon, CT, (4)University of Connecticut, CT, (5)Cornell University, Geneva, NY, (6)Cornell University, Albion, NY, (7)Virginia Tech, Suffolk, VA, (8)Virginia Tech, Blacksburg, VA, (9)University of Georgia, GA, (10)University of Georgia, Tifton, GA

Alternaria leaf blight and head rot is a devastating disease of broccoli mainly caused by *A. brassicicola*. Disease symptoms appear in the seedling stage and continue up to harvest, where even minimal black spots present in heads make them unmarketable. To manage this disease, conventional broccoli producers rely on fungicide applications using QoIs, but recent reports suggest that resistance may be present in GA and VA. To better understand why QoIs are failing in these states, we collected leaf samples from broccoli fields in 2021 and 2022 in GA, VA, NY, CT, and MA. We amassed a collection of 525 *Alternaria* spp. isolates, which were either identified as *A. brassicicola* (90.3%) and all others as *A. alternata* (9.7%). *A. alternata* was found in two fields in VA, one in NY, and one in CT. Sensitivity to azoxystrobin was estimated as inhibition of spore germination using a microplate assay based on optical density. We screened 350 isolates of *A. brassicicola* and 51 of *A. alternata* and calculated the effective concentration at which 50% of spores germinated (EC_{50}). The median EC_{50} of *A. alternata* (4.35 ppm) was 153 times greater than that of *A. brassicicola* (0.0284 ppm). Among 21 *A. alternata* sequenced at the *cytb* gene,19 isolates showed the mutation G143A that confers complete resistance to QoIs. Since symptoms of both pathogens are similar, this study may explain why QoIs have reportedly failed and enable us to make more informed disease management recommendations.

Comparative analysis on the optimal temperature and leaf wetness for disease development of three species of Alternaria

A. MARTIN(1), R.L. DAVIS(2), D. CERRITOS-GARCIA(3), D.B. LANGSTON(4), S.L. RIDEOUT(5), B. DUTTA(6) and S.E. EVERHART(2)
(1)University of Connecticut, Vernon, CT, (2)University of Connecticut, Storrs, CT, (3)University of Connecticut, Storrs Mansfield, CT, (4)Virginia Tech, Suffolk, VA, (5)Virginia Tech, Blacksburg, VA, (6)University of Georgia, Tifton, GA

Alternaria leaf blight and head rot is one of the most economically important diseases of brassicas in the United States. In a multi-state survey of symptomatic broccoli, identified were *A. japonica* and *A. alternata,* in addition to the usual suspect, *A. brassicicola.* Little is known about the disease etiology and epidemiology of these species as causal agents of ABHR and this study aimed to fill that gap. A growth chamber assay to quantify the effects of temperature and humidity on symptom development using detached broccoli leaves was developed and is currently being applied for representative isolates of each species. Leaves were inoculated and placed into a growth chamber with 99% relative humidity. A spore suspension was created and a single droplet used to inoculate leaves. The droplet was tapped off of leaves after 12, 24, 36, and 48 hours post inoculation. The experiment will be conducted at temperatures of 17, 21, 25, 29 and 33°C. Disease development will be recorded starting at 36 hours for 7 days using ImageJ software to measure lesion change over time. Results of the experiment will be used to determine

environmental factors conducive to disease caused by each species, which will enable the future development of predictive models and disease forecasting.

Deciphering the Genetic Diversity of *Gemmamyces piceae* in Alaska Using SSR

S.M. GABRIEL PERALTA(1), G.C. ADAMS(2), L. WINTON(3), K. CERNY(4), and S.E. EVERHART(4), Department of Biological Risks, Průhonice, CZECH REPUBLIC (1)University of Connecticut, Storrs Mansfield, CT, (2)University of Nebraska-Lincoln, Lincoln, NE, Alaska Forest Health Protection, Anchorage, AK, (3)Department of Biological Risks, Průhonice, CZECH REPUBLIC, (4)University of Connecticut, Storrs, CT

Gemmamyces piceae causing spruce bud blight disease has become an emerging and destructive disease in Central Europe and it is currently present in Alaska where it was not reported until 2014. To further understand these outbreaks, we examined the population structure using microsatellite loci. SSR loci were identified in one genome of *G. piceae* from Alaska and to find variable SSR loci these were aligned to 3 more genomes, after filtering less than 40 SSR loci sites were variable. Results of genotyping 86 isolates from four geographically separate locations showed 64 multilocus genotypes. Comparison of populations between populations showed the highest genotypic diversity within Fairbanks. Using Bruvo's distance, we compared populations using a Minimum Spanning Network (MSN) that revealed some genotypes were shared across multiple populations and others were unique. The population from Fairbanks was most highly clustered in the MSN and distinct when characterized using a Discriminant Analysis of Principal Components (DAPC). An AMOVA is currently underway to determine whether these differences are significant, which would support the idea that the populations were introduced long enough ago that each has become geographically established within these populations that were sampled. This is the first population genetic study to be conducted on this pathogen and provides important insights that are relevant to forest health management recommendations.

Assessing the Efficacy of On-Farm Fungicide Treatments for the Management of Fusarium Head Blight and Foliar Disease Complex.

O.M. SHITTU(1), T. MCFEATERS(2,3) and P. ESKER(2)
(1)Penn State University, Pennsylvania, PA, (2)The Pennsylvania State University, University Park, PA, (3)Penn State Department of Plant Pathology, State College, PA

Fusarium Head Blight (FHB), caused by *Fusarium graminearum*, infects wheat during flowering, reducing yield, quality and causing mycotoxin accumulation, posing food safety risks. Foliar diseases that occur around this stage also impact wheat yield. An Integrated Disease Management approach is used for managing FHB, applying fungicides only when predicted risk is high. In addition, fungicides effective against FHB are also labeled for foliar diseases. The aim of this study was to assess the effectiveness of fungicide treatments against FHB and foliar diseases in wheat using an on-farm approach. Three cooperators across Pennsylvania participated in this trial. Growers were provided their preferred fungicides to be applied during the flowering growth stage. Disease assessment for both FHB and foliar diseases occurred at the soft dough growth stage, with yield data collected at harvest. There was no significant difference between the FHB index of treated and untreated plots across the three farms. Foliar diseases varied: one farm had <10% severity, and another had 40% and 50% for treated and untreated plots, respectively. At harvest, two farms showed yield differences (9281 vs. 8541 kg/ha, 8003 vs. 7667 kg/ha), while the third showed no difference, with an average yield of 8373 kg/ha. Results from these on-farm trials provide knowledge for FHB and late-season foliar disease management, benefiting extension agents and wheat growers seeking cost-effective disease control.

Detection of gut sucrase gene expression from single vine mealybugs for RNAi applications
E.M. SCHNEIDER, V. HOYLE, H. MCLANE and M. FUCHS
Cornell University, Geneva, NY

The vine mealybug, *Planococcus ficus* (Hemiptera: Pseudococcidae), poses a serious threat to grapevine production. *P. ficus* is a phloem-feeding insect capable of transmitting most grapevine leafroll-associated viruses, the causative agents of grapevine leafroll disease. Prior work demonstrated the efficacy of RNA interference (RNAi) as a possible pest control tactic for mealybug species, and thus, for limiting the spread of leafroll viruses. These studies used pooled dissected guts from mealybugs to quantify RNAi-driven changes in gut gene expression and were designed to diminish osmotic function in the insect's gut. However, clean dissection of *P. ficus* guts is cumbersome and pooled samples do not allow for precise identification of changes in gene expression at the single insect level. Furthermore, whole-body insects tend to yield higher amounts and quality of RNA as compared to dissected guts alone. Thus, to optimize the previous experimental approach, we isolated total RNA from single whole insects, pooled whole insects, and pooled dissected guts to evaluate whether dissections are necessary for accurate sucrase (*SUC)* expression data analyses. No significant difference was observed in the amplification of *SUC* between these three sample types as shown by similar threshold cycle values in RT-qPCR. These findings suggest the feasibility of using single mealybugs without dissection in future studies on RNAi based management of *P. ficus*.

The emerging disease of blueberry leaf rust is caused by *Thekopsora minima* in New Hampshire
B. LIU
UNH Extension, Durham, NH; University of New Hampshire, Durham, NH

In the summer and fall of 2023, leaf rust was observed on highbush blueberry (*Vaccinium corymbosum* L.) throughout the farms in Merrimack, Hillsborough, and Strafford Counties in NH. Symptoms were found mainly on older leaves, and premature defoliation were observed with the varieties of Rubel, Jersey, Elliott, Liberty, and Brigitta. Purplish-brown necrotic spots were present on the adaxial leaf surface, while the abaxial leaf side exhibited orange to yellow colored uredinia. Urediniospores were broadly obovate with dark yellowish content and measured 19 to 25 × 16 to 20 µm (average 22 × 18 µm, n = 30). The spore walls were hyaline, echinulate, and 1.0 to 1.5 µm thick with obscure germ pores. Potential alternate hosts (Tsuga spp.) for blueberry leaf rust were present around the orchards. Leaf samples with rust symptoms were collected and stored at 4°C for molecular confirmation using ITS primers (ITS1 and ITS4). The sequences of around 500 bp fragments of ITS regions match the ITS sequences of blueberry leaf rust pathogens deposited in GenBank with 99% similarity, indicating the leaf rust pathogen is the emerging disease in NH. To our knowledge, this is the first report of *T. minima* on blueberries within NH, which could be related to significant summer and fall precipitation.

Regulation of developmental phenotypes in *Agrobacterium tumefaciens* by VtlR and the sibling RNAs AbcR1/AbcR2
J. HEINDL(1), J. ZEITLER(2), D. ARANGO-CARDONA(2) and S. ISLAM(2)
(1)Rowan University, Glassboro, NJ, (2)Rowan University, NJ

LysR-type transcriptional regulators (LTTRs) function in bacteria to alter gene expression in response to environmental stimuli. *Agrobacterium tumefaciens* is a plant pathogen of the class Alphaproteobacteria,

and the causative agent of crown gall disease. *A. tumefaciens* interacts with host tissues via unipolar attachment and biofilm formation at or near wound sites. We have previously shown that the LTTR-family transcriptional regulator, VtlR, contributes to regulation of developmental phenotypes important for pathogenesis including growth, motility, and biofilm formation. We have also previously shown VtlR-dependent regulation of over 200 genes, including the small regulatory RNA, AbcR1. Comparison of VtlR-dependent and AbcR1-dependent transcriptomes via RNA-seq highlighted overlap of some target genes as well as independent regulation of others. A second small regulatory RNA, AbcR2, located immediately downstream of AbcR1, shows only modest regulation by VtlR and has been shown to regulate few target genes. Our current work details the molecular mechanisms of VtlR- and AbcR1-dependent gene regulation. Our work also explores the differences between the sibling RNAs, AbcR1 and AbcR2, and their roles throughout the life cycle of the bacterium. Finally, we are evaluating biofilm architecture and within-biofilm gene expression to discern cellular processes controlled by the VtlR/AbcR regulatory axis that impact efficient biofilm formation.

Single amino acid mutations of proteins encoded by grapevine fanleaf virus alter their ability to suppress RNA silencing

J. CHOI and M. FUCHS
Cornell University, Cornell Agritech, Geneva, NY

Fanleaf degeneration is one of the most devastating viral diseases of grapevine (*Vitis* spp.). This disease can lead to substantial yield loss (< 80%) and reduce the productive lifespan of vineyards. Fanleaf degeneration is caused by grapevine fanleaf virus (GFLV). This virus encodes three silencing suppressors (VSRs) to counteract RNA silencing: protein 1A, protein $1B^{Hel}$, and the fused protein $1AB^{Hel}$. The three GFLV VSRs carry one or two of the canonical tryptophan-glycine (WG) and GW motifs. In this study, we explored the role of W in the WG and GW motifs in VSR activities by producing single amino acid substitutions (W to alanine) via site-directed mutagenesis. GFLV wildtype and mutant VSRs were introduced with an RNA silencing-inducing hairpin construct into transgenic *Nicotiana benthamiana* plants expressing (green fluorescent protein) GFP via agroinfiltration. Next, apical leaves were evaluated for the development and intensity of systemic suppression of GFP via UV imaging, measuring GFP fluorescence intensity, and via quantifying GFP transcripts and GFP siRNA abundance using RT-qPCR. Mutating the WG/GW motif led to a loss of suppression activity for some GFLV VSR mutants in conjunction with a loss of the ability to reduce siRNA accumulation and expression of *N. benthamiana* genes involved in RNA silencing. This research provided insights into the molecular mechanisms underlying the VSR function of three GFLV proteins for counteracting host antiviral immunity.

Developing IPM Strategies with Growers Through the BioWorks Product Compatibility Guide

E.A. FEALKO, M. BROWNBRIDGE and E. JACKSON
BioWorks, Victor, NY

Integrated Pest Management (IPM) programs can be a sustainable and economic approach to pest management. IPM programs use information related to life cycles of pests and their interaction with the surrounding environment to develop personalized programs for control. Growers may be attempting to control many pests at once which can create a complicated program. The BioWorks Technical Services team try to provide accurate information and assist growers in the decision-making process. One of the tools they use is our product compatibility guide. This guide provides information on the compatibility of BioWorks products with other crop inputs (fungicides, insecticides, fertilizers). This allows the grower to know if the products they would like to utilize in their program can be safely used together in a program, e.g., in rotation, and if they are 'tank mix' compatible and can be co-applied. Our Quality Control (QC)

department checks for both physical and biological compatibility (if applicable). Results are shared with growers via our Technical Services team, and is accessible on our website through our product compatibility tool. Working with the grower, our technical services team will discuss options and help the grower decide on whether or not to include those products in their IPM program.

Investigating microbiome metagenomics for soybean cyst nematode biocontrol
K.E. BUSHLEY
USDA, Ithaca, NY

Heterodera glycines, the soybean cyst nematode (SCN), is a pathogen damaging soybean crops across the globe. Soybean plant resistance to SCN has been weakening over the last few decades. While plant breeders are working on identifying new resistance loci and for breeding, this process is slow. Other treatments, like nematicides are extremely harmful to the environment and many have been banned over environmental or health concerns. Therefore, identifying novel biocontrol and biopesticide solutions is urgently needed. We have focused our research on microbial biocontrol organisms, bacteria and fungi, to kill or control SCN populations. Samples were collected in Waseca, Minnesota from field treatments that included long-term (40 yr) monoculture of SCN-resistant soybeans, SCN-susceptible soybeans, soybean fields with an annual rotation of corn and soy, and a field that had grown soybeans for 3 years. The long-term SCN-susceptible field has shown decreases in overall SCN populations over time, potentially a result of the buildup of nematode antagonistic microbes in the soil. We sequenced the microbiome of SCN, soybean roots, bulk soil and rhizosphere soil with community amplicon 16S & ITS. Illumina short read metagenomes were generated from SCN cyst samples and PacBio metagenomes from bulk and rhizosphere soil. We have identified taxa are conserved across sample types, and taxa differ between treatments.

Genomic and Germplasm Resources of the USDA-ARS Entomopathogenic Fungi Collection
K.E. BUSHLEY(1), M. WHEELER(2) and B. LOVETT(1)
(1)Robert Holley Center, Ithaca, NY, (2)USDA-ARS Robert Holley Center, Ithaca, NY

The USDA-ARS Entomopathogenic Fungi (ARSEF) culture collection houses over 14,000 fungi and protistan microorganisms isolated from insects, spiders, nematodes, mites, and other invertebrates. It serves as a germplasm resource for development of microbial biocontrol agents targeting invertebrate agricultural pests. Successful deployment of biocontrol agents requires identifying isolates with targeted host-specificity that are also non-toxic to humans and other wildlife. Metadata housed in ARSEF databases on insect host associations, substrate, and collection locations can guide the initial selection, but the predictive value of this information is currently limited. To understand the genetic basis of biocontrol phenotypes, a predictive phylogenomic framework for these fungi is required. We are synthesizing publicly available genomic, genetic, and biochemical resources for ARSEF isolates and developing best practices for the generation and sharing of biological control phenotypic data. We envision these resources will enable researchers to expedite selection of biocontrol isolates and facilitate genetic manipulations to improve their effectiveness.

Analysis of soft rot *Pectobacteriaceae* population diversity in US potato growing regions between 2016 and 2022
X. MA(1), and B. SWINGLE(2),
(1)Cornell University, Ithaca, NY, (2)USDA-ARS, Ithaca, NY

Soft rot *Pectobacteriaceae* (SRP) are globally dispersed pathogens that cause significant economic loss in potato and other crops. Our understanding of the SRP species diversity has expanded in recent years due to advances and adoption of whole genome sequence technologies. In the present study, we used whole genome sequence analysis to describe the current distribution and epidemiology of SRP responsible for diseases in commercial potato cropping systems in the United States. We collected 118 SRP strains isolated from diseased potato plants and tubers in 14 states between 2015 and 2022. As a result, we identified three *Dickeya* and eight *Pectobacterium* species responsible for diseases in potatoes. Especially, *D. dianthicola*, *P. parmentieri*, *P. carotovorum*, and *P. versatile* appeared to be the predominant species, constituting 83% of the isolates. Furthermore, all *D. dianthicola* strains studied here as well as 90% of US *D. dianthicola* isolates sequenced to date exhibit significant clonality. The prevalence of this specific group of *D. dianthicola*, temporally and geographically, aligns with the occurrence of blackleg and soft rot outbreaks in the northeastern US after 2014. The genomic diversity observed in *P. parmentieri* implies introductions to the US from at least four distinct sources, earlier than the arrival of the predominant group of *D. dianthicola*. In contrast, *P. carotovorum* and *P. versatile* appear to be widespread, long-term endemic strains in the US.

Digital PCR Quantification of Dollar Spot Disease from Creeping Bentgrass (*Agrostis stolonifera*) Turf at Fairway Height

P. FARDELLA, P. ZHANG, S. MUKHTAR, J. MURPHY and M.-Y. CHOU
Department of Plant Biology, Rutgers University, New Brunswick, NJ

Dollar spot disease, caused by the fungal pathogen *Clarireedia jacksonii*, is a detrimental disease of turfgrass necessitating costly fungicide applications. Accurate and timely quantification of *C. jacksonii* could allow field managers to precisely apply fungicides and reduce overall applications. Previously, it was shown that *C. jacksonii* could be quantified in pre- and post-symptomatic creeping bentgrass samples using qPCR targeting the internal transcribed spacer (ITS) sequence. However, this *C. jacksonii* qPCR assay yields relative amounts of the pathogen based on Ct values. Digital PCR (dPCR) provides absolute quantification of the targeted genetic marker and is not prone to PCR inhibitors and background noise biases. To determine if dPCR could also detect and quantify *C. jacksonii*, samples taken from a creeping bentgrass field managed at fairway height were analyzed. The results showed that the Ct values derived from qPCR and copy numbers derived from dPCR were significantly and exponentially regressed ($R^2 = 0.98$ and p-value < 0.001), such that decreasing Ct values represent an increasing number of copies of the ITS marker. This supports that dPCR can be used as a molecular diagnostic tool for *C. jacksonii* from field samples. Additionally, modifications in sampling methods for turfgrass collection and primers and probes for the molecular quantification of dollar spot disease will increase the efficiency of these molecular-based decision support tools.

Salt challenges across ecosystems: insights from the mycorrhizal associations in the Florida pine rocklands

E. KARLSEN-AYALA(1), M. JUSINO(2), M. SMITH(3), and R. GAZIS(4)
(1)USDA, Northern Research Station, Hamden, CT, (2)USDA, Northern Research Station, Center for Forest Mycology, Madison, WI, (3)University of Florida, Gainesville, FL, (4)University of Florida, Homestead, FL

Increased salt intrusion due to sea level rise is a growing concern for coastal forests such as the south Florida pine rocklands, a critically endangered ecosystem with a monodominant canopy of Florida slash pine (*Pinus densa*). Little is known about how resilient the ectomycorrhizal (ECM) communities within this ecosystem are to increased soil salinity. In this study we sampled roots from ten mature trees in eight

pine rocklands forests to assess how the natural soil salinity gradient shapes ECM communities in adult trees. We selected three of these sites and experimentally tested the effect of sublethal salt concentrations (0, 25, 50, and 75 mM) on seedling ECM communities. We used Illumina MiSeq of the fungal ITS1 to assess the ECM community on mature pine trees and experimental seedlings. Results show that ECM species richness with mature trees was significantly negatively correlated with soil salinity and that soil salinity and pH were significant predictors of ECM community composition. For the experimental seedlings, only soil salinity was a significant predictor of ECM communities, and higher salt treatments resulted in higher seedling mortality. Additionally, higher salt concentrations generally resulted in shifts towards contact exploration types except in the saltiest treatments. A better understanding of the diversity and ecology of ECM fungi in areas that are highly impacted by salt is an important component for land management and conservation.

Koch's Postulates to confirm pathogenicity of *Alternaria alternata* and *Alternaria japonica* on broccoli
R.L. DAVIS(1), D. CERRITOS-GARCIA(2), A. MARTIN(3) and S.E. EVERHART(1)
(1)University of Connecticut, Storrs, CT, (2)University of Connecticut, Storrs Mansfield, CT, (3)University of Connecticut, Vernon, CT

Alternaria brassicicola is a major fungal pathogen and the causal agent of Alternaria blight and heat rot (ABHR) of broccoli and other brassicas. Typically, *A. brassicicola* is controlled using quinone outside inhibitor fungicides, such as azoxystrobin, however recently there are concerns of potential fungicide resistance. While there is potential for *A. brassicicola* to develop heritable fungicide resistance, there may be other factors affecting sensitivity and this observation. During a multistate survey to describe the population genetics of *A. brassicicola*, leaf lesions were collected from Connecticut, New York, Virginia, and Georgia. From these leaf lesion, *A. alternata* was isolated from broccoli in one field Connecticut and two fields in Virginia. To confirm pathogenicity of these *A. alternata* isolates, and *A. japonica* collected in a previous study, we performed Koch's Postulates using broccoli. Results of our experiment showed that isolates of both *A. alternata* and *A. japonica* were pathogenic and able to cause disease symptoms on broccoli. It remains to be known whether either of these species are able to cause economically limiting disease under field conditions; further studies are underway.

Genome-wide association analysis of resistance to *Rhynchosporium commune* in winter malting barley
J. KOLKMAN, K. KUNZE, S. SEPP, G.C. BERGSTROM and M. SORRELLS
Cornell University, Ithaca, NY

Barley scald, caused by *Rhynchosporium commune*, is a major foliar fungal pathogen affecting winter barley production in New York and worldwide. Genetic resistance to scald includes both qualitative and quantitative resistance genes. We assessed resistance to scald in a large population of winter barley breeding lines and varieties that encompassed the preliminary yield trials for the winter malting barley breeding program at Cornell University. Approximately 400 genotypes were grown in two locations in Tompkins Co., NY in both 2021, and 2022, and each location had a history of scald occurrence and natural inoculum of *R. commune*. Plants were scored for winter survival, heading date, plant height, and scald severity. Genome wide association mapping was utilized to identify regions of the genome associated with resistance to scald in this population using Mixed Linear Models in Tassel5.0 with 20,770 SNPs. SNPs associated with resistance to scald included a region of along chromosome 3H, which contained previously identified resistance loci including the *Rrs1* gene. Additional regions across the genome were also identified which harbored both previously known and unknown resistance loci. Understanding the genetic architecture of resistance to scald in NY, and its relationship to agronomic traits, provides a platform to move forward in breeding for durable resistance.