2020 Northeastern Division Meeting Abstracts

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Field populations of *Botrytis cinerea* from strawberry simultaneously resistant to both azoxystrobin and boscalid

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Botrytis cinerea is an economically important pathogen of strawberry that has been primarily controlled by fungicides. To investigate possible occurrence of resistance to azoxystrobin and boscalid in field populations of *B. cinerea*, 119 isolates were obtained from strawberry fields and greenhouses in Shangdong, China. In fungicide sensitivity analysis, 68 isolates showed resistance, including 56 isolates resistant to both azoxystrobin and boscalid (type AB), 9 isolates (type A) resistant to azoxystrobin only, and 2 isolates (type B) resistant to boscalid only. *Botrytis cinerea* isolates did not show cross-resistance between azoxystrobin and boscalid, iprodione, or pyrimethanil, nor between boscalid and iprodione or pyrimethanil. Compared to sensitive isolates, most resistant isolates had a higher or same level of fitness regarding mycelial growth, sporulation, conidial germination, and sclerotial formation. By analyzing cDNA sequences of mitochondrial cytochrome b gene (*cytb*), a unique mutation was detected at the position G143A in all type-AB and -A isolates. Point mutations were also found at either H272Y, H272R, P225F or N230I on the *sdhB* gene in some type-AB isolates. In two type-AB isolates, a new point mutation (V9A) was detected on *sdhD* gene, along with mutations detected on G143A of *cytb* and N230I of *sdhB*. Thus, most likely G143A mutation corresponded to azoxystrobin resistance and mutations at other points corresponded to boscalid resistance.

Rhizosphaera needle cast of landscape conifers: Species diversity and management

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Rhizosphaera needle cast can be a significant disease of spruce in landscape and Christmas tree farm settings. While blue (*Picea pungens*) and white spruce (*P. glauca*) are most severely affected by the disease, *Rhizosphaera* can be found on nearly all members of the Pinaceae. To date, little is known about *Rhizosphaera* species diversity and host preference. Additionally, there is a need for systemic fungicide control in landscape settings that avoids aerial spraying. Based on field collections and conifer samples submitted to the UMass Plant Diagnostic Lab, over 70 isolates have been obtained from seven host genera: *Abies*, *Cedrus*, *Picea*, *Pinus*, *Pseudotsuga*, *Sequoiadendron* and *Tsuga*. Using conidial measurements, cultural characteristics and sequence data (ITS & *tef1*), at least seven species are present in the region. *Rhizosphaera kalkhoffii* occurs primarily on *Picea*, with *Abies* as a secondary host, while several other species exhibit a broad host range. The ITS and *tef1* datasets have revealed potentially undescribed species, collected from *Abies*, *Pinus* and *Sequoiadendron*. The efficacy of systemic fungicides (phosphites, propiconazole and paclobutrazol) will be tested on three-year-old spruce seedlings (*P. abies*, *P. glauca* and *P. pungens*) inoculated with *R. kalkhoffii*. The effects of drought stress on disease severity will also be tested. If systemic fungicides can be effectively delivered via trunk or soil drench, this could aid in management and reduce fungicide use.

Introducing, Howler, an innovative, multi-site fungicide

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AgBiome discovers and develops innovative biological and trait products for crop protection utilizing its proprietary Genesis™ discovery platform. This innovative discovery platform has enabled AgBiome to efficiently capture, fully sequence, and screen the most diverse and unique microbial collection for fungal, nematode, and insect control. Through this process, AgBiome has developed and commercialized Howler fungicide. Howler's novel, multi-site, mode-of-action controls soilborne and foliar diseases to include Rhizoctonia, Botrytis, downy mildew, powdery mildew, and soil-borne Phytophthora.

Improved genome assembly and annotation of *Clariireedia* spp. following Nanopore MinION sequencing

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Dollar spot, caused by causal agent of *Clariireedia* spp. (formerly *Sclerotinia homoeocarpa*), is the most economically important fungal pathogen on golf courses and has developed resistance to four classes of fungicides as well as multidrug resistance (MDR). Conferred by xenobiotic detoxification, MDR is a vital worldwide problem demanding prompt solutions. Therefore, it is crucial to gain a better understanding of the genetic mechanisms that underline detoxification. Our research objective is to improve the existing genome assembly of *Clariireedia* spp, launch genome annotation and identify additional detoxification-related candidate genes. Here, we report an improved genome assembly of two *Clariireedia* spp. strains previously sequenced using Illumina HiSeq and PacBio CLR platforms: the multi-drug sensitive HRS10 and the multi-drug resistant HRI11. High-coverage long reads were obtained by Nanopore MinION sequencing. In addition to previous data, the assembly contiguity was doubled with >1.3 Mb contig N50 and >3.2 Mb longest contig for both strains. Genomic completeness was measured by Benchmarking Universal Single-Copy Ortholog (BUSCO) and >98% conserved fungi gene were identified. Genome annotation with Illumina HiSeq RNA-seq data will be completed for both strains in the presence and absence of a DMI fungicide. This high-quality genome assembly and annotation will serve as an important resource for a genome-wide understanding of MDR as well as other important research.

Biocontrol of postharvest fungal infection of Asian Pears (*Pyrus pyrifolia*) by locally isolated bacterial antagonists

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Fresh produce is susceptible to rot-causing fungi that can infect while growing, at harvest, during handling, storage, transport and marketing, or even after purchase by the consumer. Postharvest produce losses are estimated between 10 to 30% per year, despite use of modern storage facilities, sanitation techniques, and fungicides. Concerns regarding food safety, environmental harm, and fungicide resistance are driving a need for alternative control measures such as biological control. During the summer of 2017, 256 bacterial strains were isolated and identified from leaves, fruit, and soil of Asian pears (cultivar 'Olympic') at Ontario Pear Farm in Ontario NY. *Pseudomonas fluorescens* and *Pantoea vagans*, two known species of biocontrol bacteria, were tested for control of two postharvest fungal pathogens, *Rhizopus stolonifer* and *Botrytis cinerea*. Biocontrol efficacy was assessed *in vivo* using Asian pear cultivar 'Shinseki'. Efficacy of control by *P. fluorescens* and *P. vagans* was assessed using a repeated measures ANOVA.

Diversity of seed-borne fungi in wheat grains sampled from all over Egypt in 2019

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Knowledge on distribution and diversity of the seed-borne fungi in wheat is important to protect the crop and to sustain food supply for an increasing population under climate change in Egypt. From all 25 wheat-cultivating governorates in Egypt, wheat grain samples were collected. In each governorate, four districts/counties at least 15 km apart were chosen. Then, in each county, two villages and one wheat field from each village was selected for sampling. Each sample weighed one kg of wheat grains. At each sampling site, the crop information was recorded and the location was georeferenced using the global positioning system (GPS). In total, two hundred samples of wheat grains (i.e. 25x4x2) were collected in 2019 and stored in fridges. They were subsequently screened for their seed-borne mycoflora. A total of 16 genera and 24 species of fungi were recovered from the seed samples using the deep-freezing blotter method. The 16 genera identified were: *Alternaria*, *Arthrobotrys*, *Bipolaris*, *Cephalosporium*, *Cladosporium*, *Curvularia*, *Epicoccum*, *Fusarium*, *Mucor*, *Nigrospora*, *Penicillium*, *Rhizopus*, *Stemphylium*, *Trichothecium*, *Ulocladium*, and *Verticillium*. Among the 16 genera, eleven genera of seed-borne fungi consisting of 81 strains, which are known to be plant pathogens, were tested for their pathogenicity and transmission on wheat seedlings. Washing and embryo count tests were also done on all wheat grain samples to detect smut fungi.

Fungal associates of Nitidulid Beetles from oak wilt positive sites in northeastern USA

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Oak wilt, first detected in New York in 2008, is a deadly vascular disease caused by a fungus (*Bretziella fagacearum*) that affects all native oak trees. The pathogen produces fungal mats that release a sweet odor which attracts sap-feeding beetles (Coleoptera: Nitidulidae). Nitidulids coated with sticky spores can spread the disease as they disperse to healthy trees. Our objective was to characterize fungi associated with Nitidulids in the Northeast. During May-June of 2018, Nitidulids were collected weekly in wind oriented traps baited with wort and pheromones from 3 sites in New York where oak wilt has been detected and one site in New Hampshire where oak wilt has not been detected. Fungi on Nitidulids were isolated by serial dilution plating. DNA was extracted from representative isolates. The internal transcribed spacer (ITS1-5.8s-ITS2) region of the rDNA was amplified. Fourteen Nitidulid beetle species were trapped. Of these, *Colopterus truncatus*, a principal oak wilt vector, was the most frequently collected. The oak wilt pathogen was not recovered which is not surprising given that oak wilt-positive trees from New York sites had been removed within months of detection. Thirty five fungal species, most plant pathogens or endophytes, were recovered from beetles suggesting that in addition to the oak wilt pathogen, Nitidulids are also vectoring other plant pathogens.

Investigation of potential sources of overwintering inoculum for cranberry fruit rot

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Cranberry (*Vaccinium macrocarpon* Ait.) fruit rot, a disease complex associated with more than ten fungi is the most prevalent disease problem that cranberry growers face from season to season. If left uncontrolled, fruit rot could cause 100% yield losses. At present, there is no research literature on the sources of overwintering for fruit rot inoculum. During various cultural operations (due to machinery and human movement) some host plant structures (leaves, stems/uprights and berries) get separated from the plants. The common practice in cranberry growing states is that farmers gather a significant portion of the detached debris during harvest or winter cleaning and pile them next to the bogs as trash piles. We hypothesized that the debris that was left on or near the cranberry bogs may serve as fruit rot fungal inoculum sources for the next cropping season. In April 2019, we collected samples (berries, uprights and leaf debris left on and within 100 feet (30.5 meters) from the bog as trash piles) from nine cranberry bogs in Massachusetts, to investigate their role in the survival/overwintering of fruit rot fungi from one season to the other. Samples were surface sterilized and incubated in humid chambers for two weeks. At the end of the incubation period, samples were evaluated for fruit rot pathogen conidia under a high-content light microscope. Prevalence and distribution of fruit rot pathogens differed among the bogs and tissue samples and will be presented.

New and re-emerging diseases of hops (*Humulus lupulus*) in Connecticut

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Commercial hop (*Humulus lupulus*) production has returned to Connecticut to meet increased demand for local ingredients from the growing craft brewing industry. Hop growers in the state require information on hop diseases and management strategies, including those employed in other hop growing regions that may be adapted for use in Connecticut. In 2018, the presence of powdery mildew, caused by *Podosphaera macularis*, was confirmed in Connecticut by morphological identification coupled with DNA sequencing and phylogenetic analysis. The presence of only one mating type was confirmed using DNA sequencing. In August of 2018, a new pathogen was found infecting hop cones and leaves at two locations in Connecticut. Morphological and molecular analysis demonstrated that this disease was caused by a taxon of the genus *Diaporthe*, previously unreported on hops. Three fungicides were evaluated for efficacy in vitro for this fungus, and two of the chemistries show promise for controlling this pathogen. Research into new and re-emerging pathogens is important to give Connecticut farmers tools for identifying and managing hop diseases to prevent loss of hop yield and quality for this growing market.

In-situ and imaging spectroscopy for grape disease detection, differentiation, and monitoring

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Disease is one of the greatest threats to the environmental, financial, and societal sustainability of grape production worldwide, and is expected to become of greater and more dire importance as the negative effects of climate change continue to intensify. Advanced disease detection methods that can identify infection at low intensity or before the onset of visual symptoms would greatly improve management by reducing disease potential and spread. *In-vivo* and imaging spectroscopy have been shown to be effective for rapid, early, real-time disease detection in grape and other specialty crops, and for characterizing the underlying physiological differences that engender this capacity. Infection on a relatively small part of a plant will trigger the cascade release of defense compounds, regardless of whether or not the individual plant succumbs to disease. This leads diseased plants to have different physiology and biochemistry than non-diseased plants, both pre- and post-symptom development. Early quantification of these differences could lead to earlier management intervention and an increased understanding of the spatial and temporal variability associated with disease. In this talk, the

opportunities and challenges facing in the use of this approach for grape disease detection, differentiation, and management will be discussed, as well as the use of satellite-based imaging spectroscopy for grape and broader specialty crop disease detection.

Temporal and spatial dynamics in the apple flower microbiome in the presence of the phytopathogen *Erwinia amylovora*

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Plant microbiomes have important roles in plant health and productivity. However, despite flowers being directly linked to reproductive outputs and serve as a natural opening for pathogen invasion, little is known about the microbiomes of flowers and their potential interaction with pathogen. Here, we investigated the temporal dynamics and spatial traits of the apple stigma microbiome when challenged with a phytopathogen *Erwinia amylovora*, the causal agent of fire blight. We profiled the microbiome from the stigmas of a single flower, greatly increasing the resolution at which we can characterize shifts in the composition of the microbiome. Individual flowers harbored unique microbiomes at the OTU level. However, taxonomic analysis of community succession showed a population transition from more diverse at the beginning of bloom to a less diverse population dominated by *Enterobacteriaceae* and *Pseudomonadaceae* at the later stage of bloom. Flowers inoculated *E. amylovora* established large populations of the phytopathogen, with pathogen counts of $>10^7$ in 90% of the flowers. Yet, only 42% of inoculated flowers later developed fire blight symptoms. This reveals pathogen amount on the stigma is not sufficient to predict disease outcome. Our data demonstrate that apple flowers represent an excellent model to characterize how plant microbiomes establish, develop, and interact with biological processes such as disease progression in an experimentally tractable plant organ.

Fungicide SYP-14288 inducing multi-drug resistance in *Rhizoctonia solani*

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Rhizoctonia solani is a widely distributed soilborne plant pathogen accounting for significant losses to many crops. The newly developed fungicide SYP-14288 is highly effective against *R. solani*. To examine the sensitivity of natural populations of *R. solani* to SYP-14288, 112 *R. solani* isolates were collected from infected rice plants. An established baseline sensitivity, calculated from the effective concentration for 50% inhibition (EC_{50}) on mycelial growth, was established with mean of 0.0055 ± 0.0030 $\mu\text{g/mL}$. All wild-type strains of *R. solani* were sensitive to SYP-14288. To examine the risk of fungicide resistance, 20 SYP-14288-resistant mutants of *R. solani* were generated on agar plates amended with SYP-14288. The EC_{50} values of mutants were 11.3 to 119.4-fold higher than the wild-type parents. Most of the mutants remained at a consistent level of resistance after 10 transfers, and possessed a relative higher level of pathogenicity, although their fitness was slightly lower than the wild parental strain. A cross-resistance assay demonstrated that mutants resistant to SYP-14288 were also resistant to some select fungicides: fluazinam, fentin chloride, fludioxonil, difenoconazole, cyazofamid, chlorothalonil and 2, 4-dinitrophen. These test fungicides had different modes of action, indicating that SYP-14288 induced a multi-drug resistance in *R. solani*, which could be concerning by increasing the spectrum of resistance in *R. solani* to commonly used fungicides.

Field assessment of six unique succinate dehydrogenase (SDH) mutations conferring differential resistance to SDHI fungicides in *Clariireedia* spp.

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Dollar spot, caused by *Clariireedia* spp. (formerly *Sclerotinia homoeocarpa* F.T. Bennett) is the most economically important turfgrass disease causing considerable damage on golf courses. While cultural practices are available for reducing dollar spot infection, chemical fungicide use is often necessary for maintaining optimal turf quality. Since the release of boscalid in 2003, the succinate dehydrogenase inhibitor (SDHI) class has become an invaluable tool for managing dollar spot, however, resistance to this class has recently been reported. Following SDHI field failure on 4 golf courses and 1 university research plot, the UMass Turf Pathology Lab has identified a total of six unique SDH mutations conferring differential in-vitro sensitivity to SDHIs in *Clariireedia* spp. In 2018 and 2019 turf research plots at the Joseph Troll Turf Research Facility in South Deerfield, Massachusetts were inoculated with sensitive, non-mutated isolates of *Clariireedia*, as well as resistant isolates harboring each unique mutation. Field efficacy trials were conducted on inoculated plots to assess differential sensitivity to 5 SDHI active ingredients (boscalid, fluxapyroxad, isofetamid, fluopyram, pydiflumetofen) across mutations under field conditions. Results indicate unique mutations are associated with distinct SDHI sensitivity profiles. This information will be useful in providing sustainable management recommendations for controlling resistant populations of *Clariireedia* spp.

Role of rice *PIRIN* gene in regulating rice defense against *Magnaporthe oryzae*

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The *PIRIN* gene plays a key role in regulating plant defense mechanisms through programmed cell death and abscisic acid signaling pathways. Through screening of a RNAi-mutant library, the *PIRIN* gene in rice (*OsPIRIN*) was responsible to ROS accumulation. To test the role of *OsPIRIN* in rice defense against *Magnaporthe oryzae* that causes rice blast, two constructs were transformed into *Oryza sativa* L. spp. *Japonica*: the first was a construct that targets endogenous *OsPIRIN* by using clustered regularly interspaced short palindromic repeats (CRISPR-*OsPIRIN*), and the second was an overexpression OE-*OsPIRIN* construct. RNA was extracted from these two genetically modified and wild-type (WT) rice plants. Analysis of transcriptomic profiling showed that CRISPR-*OsPIRIN* up-regulated the expression of *OsPR1a*, which belongs to the pathogenesis-related class 1 (PR1) gene family. On the other hand, OE-*OsPIRIN* significantly down-regulated *OsPR1a*. To confirm the above results, quantitative real-time polymerase chain reaction (qRT-PCR) was performed using the extracted RNA by targeting *OsPR1a* and *OsPIRIN* genes. Transcriptomic sequencing analysis and targeted qRT-PCR results were found to be comparable. After *M. oryzae* inoculation on rice, the severity of rice blast was in the order from low to high in these plants: CRISPR-*OsPIRIN* > WT > OE-*OsPIRIN*. Therefore, *OsPIRIN* might involve in plant-pathogen interaction and indirectly regulate *OsPR1a*.

***Dickeya dadantii* differentiates into two subpopulations to multitask on virulence and growth during the infection of potato**

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Necrotrophic plant pathogens acquire nutrients from dead plant cells, which requires the disintegration of the plant cell wall and tissue structures by the pathogen. Infected plants lose tissue integrity resulting in exposing the nutrient rich, decayed tissues to the environment. One challenge for the necrotrophs to successfully cause secondary infection is to effectively utilize the released nutrients to build up a large population before other saprophytes come. In this study, we observed that the necrotrophic pathogen *Dickeya dadantii* exhibited heterogeneity in cell length in an isogenic population during infection of potato tuber. While some cells were regular rod-shape (<10 µm), the rest elongated as filamentous cells (>10 µm). Short cells are virulent and motility, whereas filamentous cells did not engage in virulence and were non-mobile. However, compared to the short cells, the filamentous cells displayed upregulated metabolic genes and increased growth, which may benefit the pathogens to build up a large population necessary for the secondary infection. The segregation of the two subpopulations was dependent on differential production of the bacterial alarmone ppGpp. When exposed to fresh tuber tissues, filamentous cells quickly divided into short virulent cells. The pathogen adaptation of cell length heterogeneity identified in this study presents a model for how some necrotrophs balance virulence and vegetative growth to maximize fitness during infection.

Higher aggregation of *Cercospora* leaf spot is a common spatial pattern in table beet fields in New York

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Understanding how diseases are distributed in fields is the first step to develop efficient management strategies. *Cercospora* leaf spot (CLS), caused by *Cercospora beticola*, is the most common foliar disease in table beet fields in New York. The objective of this study was to analyze the spatial pattern of CLS in table beets fields in New York. Disease assessments were performed in 2017 (N = 16 fields) and 2018 (N = 15 fields). In each field, three transects with 51 sampling locations were evaluated. The sampling locations were separated by 0.3 m within each transect and 100 m between transects. Six leaves at each sampling location were assessed for the presence or absence of CLS symptoms. Maps were constructed to visualize the distribution of diseased plants in fields and spatial pattern analyses were used to quantify the degree of aggregation. Incidence ranged from 16.6 to 74.2%, with a median of 30.1%. Fisher's aggregation index (*D*) for binomial data detected aggregation in all fields ($D > 1$; $P < 0.001$). *D* values ranged from 1.88 to 4.69 with a median of 3.94. Aggregated patterns were also detected by ordinary and median runs analyses for 38.7% and 51.6% of the fields, respectively. Autocorrelation analyses demonstrated significant correlation between diseased plants up the 5th spatial lag (~ 1.52 m) within most fields. Results of this study demonstrate that CLS is highly aggregated within table beet fields in New York.

Characterizing mutated succinate dehydrogenase proteins to explain differential sensitivity to SDHIs in *Clariireedia* spp.

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Clariireedia spp. (formerly *Sclerotinia homoeocarpa* F.T. Bennett) is the causal agent of dollar spot disease on turf grasses of golf courses and is one of the most economically important turfgrass pathogens in North America. The most effective strategy for dollar spot control is repeated application of multiple classes of fungicides. However, it is well known that repeated fungicide application influences the development of fungicide resistance. Succinate dehydrogenase inhibitors (SDHI) are a widely used fungicide class for the management of dollar spot as well as many other plant pathogenic fungal diseases impacting a variety of crops. Our lab has identified 6 succinate dehydrogenase (SDH) subunit mutations conferring resistance to SDHIs in *Clariireedia* spp. Recent research has indicated that different mutations confer differential sensitivity profiles for each SDHI active ingredient. However, not much is known about the protein conformational changes caused by each SDH mutation and how those structural changes contribute to this variable sensitivity. Therefore, the objectives of this research are to 1) characterize the structure of 6 mutated SDH proteins conferring SDHI resistance in *Clariireedia* spp. 2) utilize this structural characterization to support the chemical industry in screening and designing novel fungicides for control of each mutation and 3) develop management strategies for resistant populations of plant pathogenic fungi.

Detection of multiple grapevine viruses in New England vineyards

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Vineyards in the Connecticut and Rhode Island were surveyed for the occurrence of grapevine viruses. Ten vineyards were visited and a total of 62 composite samples of leaf with petioles were collected from symptomatic plants. All samples were assayed by DAS-ELISA using antibodies specific for four major grapevine leafroll-associated viruses (GLRaV-1, GLRaV-2, GLRaV-3, and GLRaV-4), grapevine fanleaf virus (GFLV), tobacco ringspot virus (TRSV), and tomato ringspot virus (ToRSV). ELISA positive samples were further tested by RT-PCR using primers specific for each of the viruses to confirm the ELISA results. Twenty-two samples were infected with at least one of the viruses tested. GLRaV-3 (24.19%) was the most frequent virus detected followed by GLRaV-1 (12.90%), ToRSV (3.23%), and GLRaV-2 and TRSV (1.61%). This is the first study reporting the presence of grapevine viruses in New England, extensive surveys are on the way to evaluate the prevalence and economic impact of these viruses to the vineyards in the region.

Genotyping *Dickeya dianthicola* causing potato blackleg and soft rot in Northeastern America for inferring the source of inoculum

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The outbreak of blackleg on potato in the Northeastern US that started from 2015 has resulted in significant economic losses. *Dickeya dianthicola* was the primary cause, although it was not clear how the outbreak initially occurred. To elucidate the factors in promoting the epidemics, infected potato samples were collected in northeastern region from 2015 to 2019. *Dickeya dianthicola* isolates were investigated for their diversity. Fingerprinting using BOX-PCR and phylogenetic analysis based on sequences of 16S rDNA and *gapA* genes indicated that *D. dianthicola* isolates were divided into three genotypes (Type I, II, and III). The majority of isolates from Maine were Type I, except a few isolates from 2016 and 2018 that were Type II, which was continuously present through the five years across the select states but with a relatively lower percentage than Type I. Type III *D. dianthicola* was found in Pennsylvania, New Jersey and Massachusetts, but never detected in Maine. It was inferred that Type I was associated with Maine origination, but Type II may be indigenous in other states. Type III may be related to movement of fresh plant materials. Overall, this work provides evidence that outbreak of blackleg of potato in the Northeastern US was caused by multiple types of *D. dianthicola*, representing multiple origins. Therefore, the outbreak could be promoted by contaminated seed distribution and exacerbated by locally existing pathogens and favorable weather conditions.

Efficacy and resistance risk of Aprovia and Elatus in controlling *Verticillium dahliae*

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Verticillium dahliae causes potato early dying (PED), accounting for significant yield losses in potatoes. To evaluate the effects of fungicides, Aprovia (a.i. benzovindiflupyr) and Elatus (a.i. azoxystrobin and benzovindiflupyr) in controlling PED, a field trial was conducted in Maine in 2019. Prior to planting, *V. dahliae* inoculum cultured on autoclaved barley seeds were air dried and sprinkled in furrow at 20 g per foot row with an 8-inch span, followed by the application of fungicides. Fungicide-free plots were used as a control. Potato plants were evaluated for symptoms of PED three weeks before harvest and on tubers postharvest. Both fungicides significantly reduced in-season disease incidence. Although not statistically significant, Elatus-treated plots resulted in 19.6% higher yield than control. Benzovindiflupyr was evaluated for inhibition of *V. dahliae* conidial germination in potato dextrose broth. Effective concentration for 50% inhibition (EC₅₀) of benzovindiflupyr ranged from 0.07 to 8.39 µg/ml. To determine the risk of fungicide resistance, *V. dahliae* mutants resistant to benzovindiflupyr were generated on benzovindiflupyr-amended potato dextrose agar plates. EC₅₀ values for the mutants were 78- to 150-fold higher than parental strains. Therefore, soil treatments with Aprovia and Elatus had some effect on managing PED. However, the risk of resistance to fungicides should be considered in disease management.

Evaluation of potato germplasm for pink rot resistance

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Pink rot of potato caused by *Phytophthora erythroseptica* continues to be a factor for significant tuber decay and yield losses. To examine potato germplasm for disease resistance, field trials were conducted at Aroostook Research Farm, Presque Isle, ME from 2016 to 2019. Potato materials including 6 commercial varieties and up to 35 clones were tested, with some clones changed each year. Field plots were arranged in a randomized complete block design with three replications, and 10 seed pieces were planted per germplasm per plot. Inoculum was prepared by incubating *P. erythroseptica* in mushroom spawn bags containing 6 L of vermiculate and 3 L V8 broth of four weeks at 22°C. The inoculum was hand distributed at 200 ml/ft in furrow, followed by hand placing the seed pieces. Plants were maintained using standard practices including fertilization and pest control. Emergence and vigor of potato plants were evaluated four

weeks after planting. Harvested potato tubers were evaluated for pink rot and yield four weeks after harvest. Results indicated that the varieties Pike, Snowden, and Atlantic and breeding clones AF4648-2 and AF5484-3 demonstrated resistance to pink rot.

CURE-based discovery of genetic interactions governing PdhS-DivK-CtrA pathway activity in *Agrobacterium tumefaciens*

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Throughout the Alphaproteobacteria, including *Agrobacterium* species, the PdhS-DivK-CtrA regulatory pathway influences multiple developmental phenotypes including the cell cycle, attachment to surfaces, and swimming motility. The facile nature of generating and screening for suppressor mutations affecting swimming motility and exopolysaccharide production makes this system ideal for participation and completion by undergraduate researchers. Using sensitized PdhS-DivK-CtrA pathway mutant strains in the context of a course-based undergraduate research experience (CURE), we have identified novel genetic interactions governing pathway activity and phenotypic outputs. Newly uncovered pathway components include the *A. tumefaciens* CpdR2 homologue (Atu3663), the *A. tumefaciens* SpbR homologue (Atu0923), a dual-function diguanylate cyclase-phosphodiesterase (Atu3207), and a two-component system (Atu0970/Atu0971). Importantly, validation of these newly isolated pathway components extends to phenotypes beyond those used for screening. These results highlight that use of an upper-level undergraduate laboratory course for mutant generation and phenotypic screening allows for accelerated discovery of mechanisms regulating the PdhS-DivK-CtrA pathway and its outputs.

Distribution and pathogenicity of *Dickeya aquatica* causing potato blackleg and soft rot

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Blackleg and soft rot (BSR) of potato is caused by various *Dickeya* and *Pectobacterium* species, which have caused a significant loss to potato production in the Northeastern US since 2015. To understand the role of surface water in the epidemiology of BSR, water samples were collected from rain, pond, stream, and well water sources. Bacteria were concentrated by centrifugation and isolated on crystal violet pectate agar. Genomic DNA was extracted from both water samples and bacterial cultures. The detection and identification of pathogen was performed using polymerase chain reaction (PCR) with species-specific primers and sequencing analysis of target genes of 16S rDNA and *gapA*. Among the detected bacteria, *Dickeya aquatica* was a predominant species found in pond and stream water with 30.7% of the total samples. Pathogenicity tests of a representative strain of *D. aquatica* 174/2 was conducted using tuber inoculation and stem injection on potato. Results showed that *D. aquatica* was a pathogenic species with a greater virulence than *D. dianthicola*. This is the first report of *D. aquatica* causing BSR of potato in the US, yet there is no evidence to support that bacteria in surface water was associated with the recently occurred outbreak.

Survey of plant parasitic nematodes in Massachusetts cranberry bogs

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A study was done to determine the genera of plant parasitic nematodes and their distribution in Massachusetts cranberry bogs. The survey included 35 commercial bogs owned by independent growers (27 conventional, 8 organic) located in Wareham, Middleboro, Carver, Rochester, and Plymouth, Massachusetts. Nematodes were extracted from the soil to assess genera present. Nematode genera observed included *Hemicycliophora*: (sheath nematode), *Helicotylenchus* (spiral nematode), *Tylenchus*, *Mesocriconema* (ring nematode), *Hoplolaimus* (lance nematode), *Trichodorus* (stubby root nematode), and various genera of free-living nematodes. Additionally, two plots at the University of Massachusetts Cranberry Research Station located at 1 State Bog Road, East Wareham, MA were used for a season-long study of nematode population dynamics. For the population dynamics study, two 100 sq. ft. plots were established, one with cv. Howes and the other cv. Early Black. The plots were sampled approximately every two weeks during the growing season. *Hemicycliophora* was found in 100% of samples. Plant parasitic nematodes greatly outnumbered free living nematodes in conventional bogs. In organic bogs, populations of plant parasitic and free-living nematodes were nearly equal.