79th Annual Meeting of the

Northeastern Division

American Phytopathological Society

Program and Abstracts
March 11-13, 2020

The Hotel Northampton
36 King Street
Northampton, Massachusetts 01060
NED-APS 2020 Sponsors

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Local Arrangements 2020

Robert Wick


Program Design:

K. Peter and A. Gould
# AGENDA

## WEDNESDAY, March 11, 2020

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<tr>
<td>10:00 am – noon</td>
<td><strong>BREAKFAST</strong> (On Your Own)</td>
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<tr>
<td>12:00 pm – 6:00 pm</td>
<td>CAREERS 101 WORKSHOP – Grand Ballroom (pre-registration required)</td>
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<tr>
<td>12:00 – 1:00 pm</td>
<td><strong>REGISTRATION</strong> – Lobby</td>
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<tr>
<td>1:00 – 5:00 pm</td>
<td><strong>INDUSTRY/ EXTENSION MEETING</strong> – Grand Ballroom</td>
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<td>Presiding: Heather Faubert, Lisa Beirn and Ann Hazelrigg</td>
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<tr>
<td>5:30 – 9:00 pm</td>
<td><strong>WELCOME RECEPTION</strong> – Grand Ballroom/Atrium</td>
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## THURSDAY, March 12, 2020

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<tr>
<td>6:30 – 8:00 am</td>
<td>CONTINENTAL BREAKFAST (included) – Grand Ballroom</td>
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<tr>
<td>7:30 am – 5:00 pm</td>
<td><strong>REGISTRATION</strong> – Lobby</td>
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<tr>
<td>8:15 – 8:30 am</td>
<td><strong>WELCOME AND OPENING REMARKS</strong> – Grand Ballroom</td>
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<td>Geunhwa Jung, <em>NED-APS President</em></td>
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<tr>
<td>8:30 – 11:00 am</td>
<td><strong>GRADUATE STUDENT COMPETITION</strong> – Grand Ballroom</td>
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<td>Presiding: Susan Scheufele</td>
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<tr>
<td>8:35 am</td>
<td><strong>Distribution and pathogenicity of Dickeya aquatica causing potato blackleg and soft rot</strong></td>
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<td></td>
<td>F. EKBATANIAMIRI¹, N. F. Marangoni¹, T. Ge¹, S. Johnson², R. P. Larkin³ and J. Hao³, (1)School of Food and Agriculture, University of Maine, Orono, ME, (2)University of Maine Cooperative Extension, Presque Isle, ME, (3)USDA-ARS, New England Plant, Soil, and Water Lab, Orono, ME</td>
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<tr>
<td>8:50 am</td>
<td>Characterizing mutated succinate dehydrogenase proteins to explain differential sensitivity to SDHIs in Clarireedia spp.</td>
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<td>N. PUNSARA GALLALA GAMAGE, J. Lee, M. Elliott and G. Jung, University of Massachusetts, Amherst, MA</td>
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<tr>
<td>9:05 am</td>
<td><strong>Genotyping Dickeya dianthicola causing potato blackleg and soft rot in Northeastern America for inferring the source of inoculum</strong></td>
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<td>T. GE¹, S. Johnson², R. P. Larkin³ and J. Hao³, (1)School of Food and Agriculture, University of Maine, Orono, ME, (2)University of Maine Cooperative Extension, Presque Isle, ME, (3)USDA-ARS, New England Plant, Soil, and Water Lab, Orono, ME</td>
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<tr>
<td>9:20 am</td>
<td>Evaluation of potato germplasms for pink rot resistance</td>
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<td>Time</td>
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<tr>
<td>9:35 am</td>
<td><strong>Efficacy and resistance risk of Aprovia and Elatus in controlling Verticillium dahlia</strong></td>
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<tr>
<td>9:50 – 10:15 am</td>
<td><strong>BREAK</strong></td>
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<tr>
<td>10:15 – 11:00 am</td>
<td><strong>GRADUATE STUDENT COMPETITION (continued) – Grand Ballroom</strong></td>
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<tr>
<td>10:15 am</td>
<td><strong>Characterization of oomycetes and fungi from the substrate of marijuana (Cannabis sativa L.) plants</strong></td>
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<tr>
<td>10:30 am</td>
<td><strong>Improved genome assembly and annotation of Clarireedia spp. following Nanopore MinION sequencing</strong></td>
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<tr>
<td>10:45 am</td>
<td><strong>Role of rice PIRIN gene in regulating rice defense against Magnaporthe oryzae</strong></td>
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<tr>
<td>11:00 – 1:00 pm</td>
<td><strong>LUNCH (On Your Own)</strong></td>
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<tr>
<td>1:00 – 5:30 pm</td>
<td><strong>CONTRIBUTED PAPER SESSION I – Grand Ballroom</strong></td>
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<tr>
<td>1:05 pm</td>
<td><strong>CURE-based discovery of genetic interactions governing PdhS-DivK-CtrA pathway activity in Agrobacterium tumefaciens</strong></td>
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<td>1:20 pm</td>
<td><strong>Higher aggregation of Cercospora leaf spot is a common spatial pattern in table beet fields in New York</strong></td>
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<tr>
<td>1:35 pm</td>
<td><strong>A forward genetic screen to identify genes regulating pathogenicity and cercosporin production in Cercospora beticola</strong></td>
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</table>
1:50 pm  **Dickeya dadantii** differentiates into two subpopulations to multitask on virulence and growth during the infection of potato
Z. Cui and Q. Zeng, The Connecticut Agricultural Experiment Station, New Haven, CT

2:05 pm  Detection of multiple grapevine viruses in New England vineyards
D. Borges¹,², S. Preising¹,³, M. M. Ambrósio² and W. L. DA SILVA¹, (1)The Connecticut Agricultural Experiment Station, New Haven, CT, (2)Universidade Federal Rural do Semi-Árido - UFERSA, BRAZIL, (3)Southern Connecticut State University, New Haven, CT

2:20 pm  **New and re-emerging diseases of hops (Humulus lupulus) in Connecticut**
E. B. ALLAN-PERKINS¹, D-W. Li¹, N. P. Schultes² and J. A. LaMondia¹, (1)Connecticut Agricultural Experiment Station, Windsor, CT, (2)The Connecticut Agricultural Experiment Station, New Haven, CT

2:35 pm  Fungal associates of Nitidulid Beetles from oak wilt positive sites in Northeastern USA
I. A. MUNCK¹, K. Dodds¹, M. DiGirolomo¹ and J. Cancelliere², (1)USDA Forest Service, Durham, NH, (2)NYSDEC, Delmar, NY

2:50 pm  Rhizosphaera needle cast of landscape conifers: Species diversity and management.
N. J. BRAZEE, University of Massachusetts, Amherst, MA

3:05 – 3:30 pm  **BREAK**

3:30 – 5:30 pm  **CONTRIBUTED PAPER SESSION II** – Grand Ballroom
Presiding: Beth Gugino and Ann Hazelrigg

3:30 pm  **Temporal and spatial dynamics in the apple flower microbiome in the presence of the phytopathogen Erwinia amylovora**
Q. ZENG, Z. Cui and B. Steven, The Connecticut Agricultural Experiment Station, New Haven, CT

3:45 pm  **Diversity of seed-borne fungi in wheat grains sampled from all over Egypt in 2019**
Y. M. SHABANA¹, K. Ghoneem², N. Arafat¹, Y. Rashad³, D. Gamil Aseel³, B. Fitt⁴, A. Qi⁴, B. Richard⁴ and H. Sayed⁴, (1)Faculty of Agriculture, Mansoura University, El-Mansoura, EGYPT, (2)Plant Pathology Research Institute, Agricultural Research Center, Giza, EGYPT, (3)City of Scientific Research and Technological Applications, Alexandria, EGYPT, (4)University of Hertfordshire, Hatfield, Hertfordshire, UNITED KINGDOM

4:00 pm  **Field populations of Botrytis cinerea from strawberry simultaneously resistant to both azoxystrobin and boscalid**
Y. WANG¹, T. Qu², J. Hao³, S. Yuan⁴ and Y. Jin¹, (1)Jilin University, Changchun, CHINA, (2)Qingdao Agricultural University, Qingdao, CHINA, (3)School of Food and Agriculture, University of Maine, Orono, ME, (4)Institute for the Control of Agrochemicals, Beijing, CHINA
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| 4:15 pm | **Investigation on the sensitivity of *Stemphylium vesicarium* of pear to SDHIs**  
K. GAZZETTI¹ ², E. L. Diaconu³, A. Ciriani², I. M. Nanni², M. Menghini² and M. Collina⁴, (1)CREA-GB, Fiorenzuola D'Arda, Emilia-Romagna, ITALY, (2)University of Bologna, Department of Agricultural and Food Science, Bologna, ITALY, (3)Istituto Zooprofilattico Sperimentale del Lazio e della Toscana “M. Aleandri”, Rome, ITALY, (4)Università Di Bologna, Department of Agricultural and Food Science, Bologna, ITALY |
| 4:30 pm | **Field assessment of six unique succinate dehydrogenase (SDH) mutations conferring differential resistance to SDHI fungicides in *Clarireedia* spp.**  
M. ELLIOTT¹, J. Lee¹, T. Yamada² and G. Jung¹, (1)University of Massachusetts Amherst, MA, (2)Hokkaido University, Sapporo, JAPAN |
| 4:45 pm | **Fungicide SYP-14288 inducing multi-drug resistance in *Rhizoctonia solani***  
X. Cheng¹, X. Man¹, Z. Wang¹, P. LIU¹ ² and J. Hao², (1)Department of Plant Pathology, China Agricultural University, CHINA, (2)School of Food and Agriculture, University of Maine, Orono, ME |
| 5:00 pm | **Introducing Howler, an innovative, multi-site fungicide**  
B. MCINNES, AgBiome Innovations, Hahira, GA |
| 5:15 pm | **Engineered mesoporous silica nanoparticles for suppression of Fusarium wilt of watermelon.**  
W. H. ELMER, Y. Shen and J. C. White, The Connecticut Agricultural Experiment Station, New Haven, CT |
| 5:30 – 6:30 pm | **GRADUATE STUDENT AWARD COMMITTEE** – Hampshire |
| 6:30 – 7:30 pm | **UNDERGRADUATE POSTER SESSION/ RECEPTION** – Grand Ballroom/Atrium |
|  | **Efficacy of biofungicides on the control of root rot and wilt caused by *Pythium myriotylum* on *Cannabis sativa* L. ‘Wife’**  
M. ARUNATEGUI, C. Shields McGehee and R. E. Raudales, University of Connecticut, Storrs, CT |
|  | **Biocontrol of postharvest fungal infection of Asian pears (*Pyrus pyrifolia*) by locally isolated bacterial antagonists**  
Y. GRYNYSHYN, R. MCHUGH, K. Bonner and M. A. Borsick Herman, St. John Fisher College, Rochester, NY |
|  | **Investigation of potential sources of overwintering inoculum for cranberry fruit rot**  
R. JAHRLING and L. S. Uppala, University of Massachusetts-Amherst-Cranberry Station, East Wareham, MA |
|  | **Survey of plant parasitic nematodes in Massachusetts cranberry bogs**  
M. MILLER, S. Sree and R. L. Wick, University of Massachusetts Amherst, Amherst, MA |
Improved assay for evaluating potato resistance to *Rhizoctonia solani* assisted by toxin-based analysis
X. Zhang¹, X. Xing¹, J. Hao², X. ZHANG², D. Li³ and Z. Yu³, (1)College of Hort. & Plant Protect., Inner Mongolia Agricultural University, Hohhot, CHINA, (2)School of Food and Agriculture, University of Maine, Orono, ME, (3)College of Agronomy, Inner Mongolia Agricultural University, Hohhot, CHINA

| 7:30 – 9:30 pm | BANQUET & AWARDS – Grand Ballroom |

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**FRIDAY, March 13, 2020**

| 7:00 – 9:00 am | CONTINENTAL BREAKFAST (included) w/ NED-APS BUSINESS MEETING – Grand Ballroom
Presiding: Geunhwa Jung |
| 9:30 – 12:00 pm | SYMPOSIUM: *Artificial Intelligence for Plant Pathology* – Grand Ballroom |
| 9:30 am | OPENING REMARKS Presiding: Anissa Poleatewich |
| 9:30 – 10:05 am | In-situ and imaging spectroscopy for grape disease detection, differentiation, and monitoring
K. M. GOLD, Cornell University, Geneva, NY |
| 10:05 – 10:40 am | Computer vision quantification of foliar disease severity
L. CADLE-DAVIDSON, USDA-ARS, Geneva, NY |
| 10:40 – 10:55 am | BREAK |
| 10:55 – 11:30 am | TBD
M. DESANTIS, Bloomfield Robotics, Pittsburgh, PA |
| 11:30 am – 12:00 pm | DISCUSSION |
| 12:00 pm | CLOSING REMARKS |
New and re-emerging diseases of hops (*Humulus lupulus*) in Connecticut

E. B. ALLAN-PERKINS¹, D-W. Li¹, N. P. Schultes² and J. A. LaMondia, (1)Connecticut Agricultural Experiment Station, Windsor, CT, (2)The Connecticut Agricultural Experiment Station, New Haven, CT

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.

Efficacy of biofungicides on the control of root rot and wilt caused by *Pythium myriotylum* on *Cannabis sativa* L. ‘Wife’

M. ARUNATEGUI, C. Shields McGehee and R. E. Raudales, University of Connecticut, Storrs, CT

In the recent years, the production of hemp (*Cannabis sativa* L.) in soilless media in greenhouses has expanded in the Northeastern United States. The objective of this project was to assess the efficacy of biofungicides on root rot caused by *Pythium myriotylum* on hemp seedlings. The experimental unit consisted of 10 two-week-old *Cannabis sativa* L. cv. Wife plants, with three repetitions per experimental run. The experiment was conducted twice. The experiment was a full factorial (2 x 3) with *Pythium myriotylum* (plus or minus) and biofungicides (*Trichoderma harzianum* T-22 with *Trichoderma virens* G-41, *Bacillus amyloliquefaciens* D747, or untreated). Two days after applying the biofungicides, the plants were inoculated with *P. myriotylum* at 4.7 x 10³ oospores per mL. After 16 days, disease incidence and severity, shoot and root weight, and relative greenness were recorded. On day 10, all plants treated with *P. myriotylum* were wilted. The dry shoot and root biomass of the positive control plants (inoculated with *P. myriotylum*, no biofungicides) were 84.6% and 93.4% smaller than the negative control plants (no *P. myriotylum*, no biofungicides). Plants inoculated with *P. myriotylum* and amended with biofungicides had between 77.8-81.1% less shoot and 88.6-89.1% less root dry weight than plants treated with biofungicides without *P. myriotylum* present. The biofungicides did not reduce the incidence and severity of root rot caused by *P. myriotylum* on hemp seedlings.
Detection of multiple grapevine viruses in New England vineyards

D. Borges¹,², S. Preising¹,³, M.M. Ambrósio² and W. L. DA SILVA¹, (1)The Connecticut Agricultural Experiment Station, New Haven, CT, (2)Universidade Federal Rural do Semi-Árido - UFERSA, BRAZIL, (3)Southern Connecticut State University, New Haven, CT

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.

Rhizosphaera needle cast of landscape conifers: species diversity and management.

N. J. BRAZEE, University of Massachusetts, Amherst, MA

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.

Computer vision quantification of foliar disease severity

L. E. CADLE-DAVIDSON, USDA-ARS, Geneva, NY

The challenge of quantitative visual assessment of disease severity has been at the center of plant pathology research for decades. Subjectivity, bias, fatigue, variable lighting, and lost information through categorization are some of the limitations to human visual disease assessment. In the VitisGen2 grape breeding project, we used microscopy and quantitative genetics to develop gold-standard visual phenotyping techniques for powdery mildew resistance.
assessment, but each experiment required 1-2 months of data collection. However, the accumulated knowledge and structured protocols allowed the development of a high-throughput imaging robot coupled with neural network quantification of disease severity. We call this lab robot Blackbird. A single Blackbird robot can analyze 2500 samples each day, with accuracy similar to manual microscopy. We are expanding the applications of Blackbird to other foliar traits and pathosystems, using artificial intelligence to quantify disease with high throughput and accuracy, enabling experiments on a scale previously unimaginable.

Fungicide SYP-14288 inducing multi-drug Resistance in Rhizoctonia solani

X. Cheng¹, X. Man¹, Z. Wang¹, P. LIU¹,² and J. Hao², (1)Department of Plant Pathology, China Agricultural University, CHINA, (2)School of Food and Agriculture, University of Maine, Orono, ME

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 (EC₅₀) on mycelial growth, was established with mean of 0.0055 ± 0.0030 μg/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 EC₅₀ 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.

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

Z. CUI and Q. Zeng, The Connecticut Agricultural Experiment Station, New Haven, CT

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 (<10μm), the rest elongated as filamentous cells (>10μm). 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.

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

M. ELLIOTT¹, J. Lee¹, T. Yamada² and G. Jung¹, (1)University of Massachusetts Amherst, MA, (2)Hokkaido University, Sapporo, JAPAN

Dollar spot, caused by *Clarireedia* 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 *Clarireedia* 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 *Clarireedia*, 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 *Clarireedia* spp.

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

F. EKBATANIAMIRI¹, N. F. Marangoni¹, T. Ge¹, S. Johnson², R. P. Larkin³ and J. Hao¹, (1)School of Food and Agriculture, University of Maine, Orono, ME, (2)University of Maine Cooperative Extension, Presque Isle, ME, (3)USDA-ARS, New England Plant, Soil, and Water Lab, Orono, ME

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 not evidence to support that bacteria in surface water was associated with the recently occurred outbreak.
Engineered mesoporous silica nanoparticles for suppression of Fusarium wilt of watermelon.

W. H. ELMER, Y. Shen and J. C. White, The Connecticut Agricultural Experiment Station, New Haven, CT

Silicon can be engineered into mesoporous structures at a nanoscale (<100 nm). When these mesoporous Si nanoparticles (MSN) are sprayed onto watermelon, they can promote growth and suppress Fusarium wilt (Fusarium oxysporum f. sp. niveum). MSN can also be coated with other molecules of interest, such as chitosan, which induces disease resistance. When chitosan coated MSN was sprayed (500 mg/l) onto 4-wk old watermelon transplants and planted in Fusarium infested microplots, biomass, and fruit production was increased in noninfested soils but not Fusarium infested microplots. In greenhouse trials, chitosan coated MSN was associated with larger plants in infested soils and a 27 to 40 % reduction in AUDPC values. When MSN was engineered to 20, 35, 68, or 93 nm, the 20 nm sized MSN suppressed disease better than larger sized MSN presumably due to greater surface area and greater dissolution of Si into the plant. MSN was then engineered to release silicic acid at different rates. When sprayed onto watermelon, faster dissolving MSN were superior to slower dissolving MSN and to the controls in suppressing disease in the greenhouse. In microplots, faster dissolving MSN increased fruit yield by 45% and reduced disease severity by 51%. These findings demonstrate the value of nano-engineering and highlights the utility of a single application of MSN to young transplants in proving season long disease resistance and increased yields.

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

N. PUNSARA GALLALA GAMAGE, J. Lee, M. Elliott and G. Jung, University of Massachusetts Amherst, MA

Clariereedia 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 Clariereedia 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 Clariereedia 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.
Investigation on the sensitivity of *Stemphylium vesicarium* of pear to SDHIs

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Brown spot of pear (BSP) is a disease caused by the fungus *Stemphylium vesicarium* (Wallr.) Simmons. Symptoms consist of necrotic lesions on pear fruits, leaves and twigs, producing high economical losses in pear-production areas. Many fungicide applications are required from petal fall to fruit ripening to protect orchards from BSP. In Italy, the fungus showed field resistance toward key products as dicarboximides, strobilurins and fludioxonil. To date boscalid, pencyhiopyrad, fluopyram, fluxapyroxad and isopyrazam have been authorized in Italy against BSP. In 2019, the first *S. vesicarium* genome sequence was deposited in GenBank under the accession number: QXCR00000000. The genome annotation pipeline led to predict 12,309 gene models, and the functional annotation provided information about COGs, GO terms, KEGG pathways, and SMART/Pfam domains for each group. Among predicted genes, we identified orthologous of genes known in other plant pathogenic ascomycetes as involved in fungicides resistances. Efficacy field tests on SDHIs were conducted in a pear experimental orchard located in Emilia-Romagna region. The *S. vesicarium* strains isolated from the plots were tested for their in vitro sensitivity. Overall, the results highlighted the onset of problems related to the efficacy of SDHIs in fields. Molecular and bioinformatic analysis made it possible to discover amminoacidic substitutions conferring SDHIs resistance to the *S. vesicarium* of pear.

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.
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.

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.

Evaluation of potato germplasms 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 trails 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.

**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 beet 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.

**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.

**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.

**A forward genetic screen to identify genes regulating pathogenicity and cercosporin production in Cercospora beticola**

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*Cercospora beticola* Sacc. is one of the most destructive foliar pathogens of table beet, sugar beet, and Swiss chard in the United States. Traditionally the pathogen is controlled with fungicides, however, development of fungicide resistance, especially to single site modes of action (e.g. FRAC 11), has impeded the durability of the approach. Despite the importance, little is known about its biology and pathogenicity on table beets. In order to understand the regulation of pathogenicity and cercosporin production, a forward genetic screen was undertaken. A population of 1,169 random insertional mutant strains were generated using *Agrobacterium tumefaciens* mediated transformation of *C. beticola* Tb14-085 and were screened for their ability to infect table beet cv. Ruby Queen and produce cercosporin *in-vitro*. We have identified 22 avirulent mutants, and 30 mutants with reduced virulence compared to the wild type isolate Tb14-085. Additionally, six mutants displayed increased production of cercosporin *in-vitro* compared to the wild type isolate. Some mutants also displayed abnormal morphological phenotypes on V8 medium. Currently, a target-enrichment sequencing method is being developed to identify the site/s associated with the phenotype/s. Taken together our
findings provide a framework for understanding the genetic bases of virulence and cercosporin production in C. beticola and aid towards the development of management strategies of this important pathogen.

**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.

**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.

**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.

**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.

**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.

Characterization of oomycetes and fungi from the substrate of marijuana (*Cannabis sativa* L.) plants

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We isolated fungi and oomycetes from coconut coir and rockwool collected from containers with marijuana plants (*Cannabis sativa* L. cv. Silver and Citron) with visual root rot symptoms from a commercial growing facility in Connecticut. The objectives of this project were to identify the isolates collected from the substrates using morphological and molecular techniques, determine the pathogenicity of the isolates by measuring incidence and severity of root rot and wilting on hemp seedlings *in vitro* and *in vivo*, and evaluate the pathogens’ sensitivity to mefenoxam. The mitochondrially-encoded cytochrome oxidase genes were used to identify *Pythium* and *Globisporangium* isolates. The translation elongation factor (EF-1α) region was used for *Fusarium*. Three isolates were *Globisporangium irregulare* (formerly *Pythium irregulare*), 21 isolates were *Pythium myriotylum*, and one was *Fusarium oxysporum*. All of the isolates tested were pathogenic to hemp *in vitro* and *in vivo*. Hemp plants infected with isolates presented between 6.7-100% disease incidence and were smaller by 32% or more compared with the non-inoculated control. All *Pythium* and *Globisporangium* isolates presented some degree of sensitivity to mefenoxam. Our study indicates that multiple pathogenic isolates may be present in soilless substrates in Cannabis.

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

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Dollar spot, caused by causal agent of *Clarierea* 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 underlie detoxification. Our research objective is to improve the existing genome assembly of *Clarierea* spp, launch genome annotation and identify additional detoxification-related candidate genes. Here, we report an improved genome assembly of two *Clarierea* 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 >1.3Mb contig N50 and >3.2Mb 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.

**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.

**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 >10⁷ 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.

**Improved assay for evaluating potato resistance to Rhizoctonia solani assisted by toxin-based analysis**

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*Rhizoctonia solani* is the causal agent of potato stem canker. Conventional assays for evaluating potato resistance using *R. solani* inoculum can be reliable but time consuming. To improve the method of resistance evaluation, 20 potato cultivars were examined using both *R. solani* inoculum and *R. solani*-derived toxin (RS toxin). In field trials during 2009 and 2010, wheat-bran-based inoculum of *R. solani* was incorporated at either 2, 3 or 4 g per seed piece in the soil prior to planting. Stem canker was evaluated during the growing season. For a quick assay of resistance screening, potato seedlings were obtained through tissue culture on Murashige and Skoog media. Seedlings at 12-cm height were transferred into agar medium amended with RS toxin and incubated for eight days. The inhibition caused by RS toxin was positively correlated with toxin concentration. The inhibition of potato cultivars ranged from 33% to 100% on stems sections, and from 32% to 148% on seedlings. Potato responses to toxin-based treatment were highly correlated with the field data using *R. solani* inoculation (*r* = 0.731, *P* < 0.01). Thus, the toxin-based assay could improve efficiency and speed of disease resistance evaluation and can be used for screening large numbers of potato clones before field evaluation. Both assays showed that the ‘Desiree’ cultivar was most tolerant, whereas ‘Atlantic’, ‘Favorita’, and ‘Shepody’ were highly susceptible to *R. solani*.

**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*.