2021 Southern Division Meeting Abstracts

Abstracts presented at the APS Southern Division meeting held virtually, February 15–19, 2021. The recommended format for citing division meeting abstracts, using the first abstract below as an example, is as follows:

Bennett, A., Waliullah, S., Ji, P., and Ali, E. 2021. Phylogenetic analysis of *Pseudoperonospora cubensis*, the causal agent of cucurbit downy mildew in eastern United States. (Abstr.) *Phytopathology* 111:S1.1. <https://doi.org/10.1094/PHYTO-111-9-S1.1>

The abstracts are published as a supplement to *Phytopathology* for citation purposes. They were not reviewed by the *Phytopathology* Editorial Board and were not edited by the APS editorial staff.

<https://doi.org/10.1094/PHYTO-111-9-S1.1>

© 2021 The American Phytopathological Society

Phylogenetic analysis of *Pseudoperonospora cubensis*, the causal agent of cucurbit downy mildew in eastern United States

A. BENNETT, S. Waliullah, P. Ji, E. Ali, University of Georgia, Tifton, GA, USA

Pseudoperonospora cubensis is the causal agent of downy mildew and the most economically destructive disease to cultivated cucurbits. This disease causes significant damage to cucurbit production in the United States as well as worldwide. A fine-scale molecular characterization of the oomycete pathogen is essential for effective control efforts. Isolates were collected from four states in the US with significant cucurbit production, Georgia, Tennessee, West Virginia, and Michigan, during the 2020 growing season. The isolates were identified as *Pseudoperonospora cubensis* using nucleic acid-based PCR method with species-specific primers. Genetic diversity of the isolates from different regions was assessed by analysis of internal transcribed spacers (ITS) and cyclooxygenase-2 (COX-II) of ribosomal and mitochondrial DNA sequences, respectively. Phylogenetic trees were constructed and the relationship between genetic groups and geographic distribution of the isolates were analyzed. Phylogenetic analysis revealed significant genetic variability among the *P. cubensis* isolates. The study provides valuable information for better understanding of the diversity of the pathogen, and further research can be conducted using other molecular markers or whole genome sequence analysis.

Efficacy of sanitizers in reducing plant-to-plant transfer of *Calonectria pseudonaviculata* conidia on cutting tool blade

R. BIKI (1), F. Baysal-Gurel (1), W. E. Copes (2), (1) Tennessee State University, McMinnville, TN, USA; (2) USDA ARS, Poplarville, MS, USA

The conidia of *Calonectria pseudonaviculata* can be transferred from infected boxwood plants to healthy plants via cutting tool blade during pruning and harvesting, if tools are not properly sanitized. The objective of this study was to identify sanitizers that limit plant-to-plant transfer of *C. pseudonaviculata* propagules on cutting tools blade. In vivo studies were conducted in a BSL-2 room at the TSUNRC to determine efficacy of twelve commercial disinfectants and detergents in stopping plant-to-plant transfer of infective propagules on Felco 19 shear / cutting tool used in this study. Disease severity was assessed weekly for a month period on the pruned plants. All the treatments significantly reduced plant-to-plant transfer of *C. pseudonaviculata* compared to the non-treated inoculated control in both trials. Green-Shield (55.9 mL/L), Simple green d pro 3 plus (15.6 mL/L), Simple green d pro 5 (15.6 mL/L), KleenGrow (7.8 and 15.6 mL/L) and ZeroTol 2.0 (1:100 v/v) were the most effective treatments in reducing plant-to-plant spread of the boxwood blight disease. The non-treated inoculated shear consistently resulted in the highest disease severity and disease progress of pruned plants, indicating the critical need for sanitizing the tools during pruning and harvesting operations. The findings of this study will help growers successfully limit the mechanical transmission of the boxwood blight pathogen during production.

Determining baseline fungicide sensitivity in *Cercospora* spp. with DMI and QoI inhibiting fungicides

A. L. LANCASTER (1), J. C. Rupe (1), T. R. Faske (2), A. Rojas (1), (1) University of Arkansas, Fayetteville, AR, USA; (2) University of Arkansas, Lonoke, AR, USA

Cercospora foliar diseases are one of the most yield limiting factors for soybean in Arkansas, and its control is mainly based on the use of fungicides and tolerant cultivars. However, farmers have used extensively different fungicides to manage the disease. The use of fungicides has the potential to induce resistance, leaving this management method useless. The aim of this study was to establish a *Cercospora* spp. baseline of sensitivity against DMI fungicides such as Domark (Tetraconazole) and QoI fungicides like Quadris flowable (Azoxystrobin). Symptomatic leaves for *Cercospora* foliar diseases and seeds with purple seed stain were sampled from fields from six different counties in Arkansas. Isolates were obtained with single spore isolation or hyphal tipping. Clean isolates were grown for 7 days, and a plug was taken from the edge of the colony and transferred to plates amended with either tetraconazole at six concentrations (0–50 mg/L) or azoxystrobin at seven concentrations (0–10 mg/L). Isolates were evaluated in triplicates and plates incubated for 7 days at 27°C. Diameter was measured at both 5 and 7 days. The results of this continuing study so far are that *Cercospora* shows signs of resistance to Tetraconazole, and there was a difference in growth from 5 to 7 days. Based on the results found, the conclusion is that *Cercospora* species are developing resistance to fungicides, and this will cause issues when managing fungicide programs in the fields.

Reducing losses associated with poor grain quality using advanced soybean germplasm in Mississippi

J. FOMBA (1), M. Tomaso-Peterson (2), D. Cook (3), T. W. Allen (4), J. R. Smith (5), T. H. Wilkerson (6), (1) Mississippi State University, Stoneville, MS, USA; (2) Mississippi State University, Mississippi State, MS, USA; (3) Delta Research Center & Extension, Stoneville, MS, USA; (4) Mississippi State University, Stoneville, MS, USA; (5) USDA-ARS, Stoneville, MS, USA; (6) Mississippi State University-Delta Research and Extension Center, Stoneville, MS, USA

During years when environmental conditions post physiological maturity (R8) include extended periods of hot, wet weather, grain quality reductions can occur. Phomopsis seed decay, caused by *Phomopsis longicola* (PL), can cause economic losses associated with grain quality in soybean. The objective of this research was to determine differences in grain damage between soybean entries under environmental conditions conducive to reducing seed quality. During 2018–2020, field trials were established under rainout shelters ($n = 2$) consisting of greenhouse cold frames. Each shelter contained single row plots of each entry, replicated three times. All plots were inoculated with a PL spore suspension at the R5.5 growth stage. Shelter 1 remained fungicide non-treated. Shelter 2 received a 293 ml/ha fungicide application (Stratego YLD) at R7. Shelters were overhead irrigated for approximately 200 h each season. Plots were hand harvested at 2 weeks post R8 to determine plot weight and grain damage. Significant differences in damage, up to 74% between entries across years, were observed in the non-fungicide shelter. Progeny 4211 provided up to 75% greater plot weight compared to other entries. Numerical differences in damage and plot weight were observed across years between entries in the fungicide-treated shelter. Regardless of year, differences occurred between entries; however, additional research is needed to determine the potential of germplasm in reducing seed quality losses.

Using fungal endophytes of a wild relative to control *Fusarium oxysporum* in cultivated lettuce

N. COLON-CARRION, B. Pryor, E. Arnold, University of Arizona, Tucson, AZ, USA

Climate change is associated with increasing disease pressure in plants, affecting crop production and leading to economic losses in agricultural systems. Some fungal endophytes mitigate drought and thermal stress, and some may protect plants against disease. One strategy for promoting crop plant protection is to apply endophytes from their wild relatives, especially in areas that are dry, hot, or have high pathogen pressure. Here, we isolated endophytic fungi from *Lactuca serriola*, and investigated their utility to promote resistance of cultivated lettuce (*Lactuca sativa*) to *Fusarium oxysporum* f. sp. *lactucae* (FOL) under climate-change conditions. In phase 1 we are confirming the capacity of fungi from *L. serriola* to colonize cultivated lettuce and validating that they do not cause symptoms of disease. In phase 2 we will test whether these fungi inhibit the growth of FOL via in vitro bioassays. In phase 3 we will test how introduction of these fungi into cultivated lettuce decreases FOL disease severity under existing and elevated temperature regimes. To date we have observed that focal endophytes from *L. serriola* readily colonize *L. sativa*. None of the endophytes induces symptoms of disease. Bioassay results suggest potential inhibition of FOL, setting the stage for in vivo experiments. Overall this study sheds light on symbiont-mediated mechanisms of plant protection and develops a pipeline for translating endophytes of wild relatives of important crops.

Cover crop usage for the sustainable management of soilborne diseases in woody ornamental nursery production system

M. PARAJULI (1), F. Baysal-Gurel (1), M. Panth (2), (1) Tennessee State University, McMinnville, TN, USA; (2) Clemson University, Blackville, SC, USA

The fast-growing woody ornamental nursery industry in the United States has been greatly impacted by the soilborne diseases leading to the huge economic losses. The cover crop usage, extensively explored in fruits, vegetables and field crops, can be a potential tool in controlling soilborne diseases in woody ornamental nursery production. The objective of this study was to determine the impact of cover crops on soilborne disease suppressiveness in woody ornamental nursery production systems. Soils from red maple plantation grown with and without cover crop (crimson clover) were sampled following the complete senescence of the cover crop in 2020.

Greenhouse bioassays were conducted using red maple cuttings on inoculated (with *Rhizoctonia solani*, *Phytophthora vexans*, or *Phytophthora nicotianae*) and non-inoculated field soils. Plant height, total plant and root fresh weight were measured and plant roots were assessed for disease severity using a scale of 0 to 100% roots affected. Cover crop usage significantly reduced root rot severity caused by those pathogens in maple plants. Plants grown in cover crop used inoculated soil had numerically higher total plant and root fresh weight than the plants grown in non-cover crop used inoculated soil. There were no significant differences in plant height within the treatments. Implementation of cover crop usage may improve field woody ornamental production efficiency by reducing pressure from soilborne diseases.

Assessment of fungicide efficacy for hemp leaf spot and powdery mildew in Tennessee

R. AKINRINLOLA, Z. R. Hansen, University of Tennessee, Knoxville, TN, USA

With increased hemp acreage across Tennessee there has also been an increase in hemp diseases. Two of the most common diseases are hemp leaf spot (LS), caused primarily by *Curvularia* sp. and *Bipolaris* sp., and powdery mildew (PM), caused by *Golovinomyces* sp. A field trial was conducted to assess the efficacy of five fungicides against these diseases at the University of Tennessee Northeast Tennessee AgResearch and Education Center in Greenville, TN. Plots were arranged in a randomized complete block design with four replicates. The fungicides Stargus (*Bacillus amyloliquefaciens*), Defguard (*B. amyloliquefaciens* strain D747), Exile (potassium salts of fatty acids), Regalia (extract of *Reynoutria sachalinensis*), Quadris (azoxystrobin) (positive control), and one non-treated control were tested on the 'T1' hemp cultivar. Eight treatment applications were done between July 28 and October 8 at approximately 10-day intervals. Diseases were rated on September 28, October 8, and October 19. Exile, Regalia, and Quadris reduced both diseases. Stargus and Defguard reduced LS and PM, respectively. Quadris demonstrated excellent control of LS with a 98% reduction in disease index, while Exile and Regalia offered moderate control with a 44% and 41% reduction in disease index, respectively. Reduction of PM index by Quadris, Regalia, and Exile was also high, exhibiting 100%, 99%, and 91% reduction in disease index, respectively.

Development of a TaqMan assay for the detection of Groundnut bud necrosis orthotospovirus for quarantine screening

A. S. DERANIYAGALA (1), H. K. Sudini (2), S. Tallury (3), A. Roy (4), S. Bag (5), (1) Tifton, GA, USA; (2) ICRISAT, Patancheru, Telangana, INDIA; (3) USDA-ARS, Griffin, GA, USA; (4) USDA-APHIS-PPQ-S&T-CPHST, Beltsville, MD, USA; (5) University of Georgia, Tifton, GA, USA

Groundnut bud necrosis (GBNV) orthotospovirus is a thrips-transmitted virus prevalent in Asian countries. The major hosts include peanut, tomato, and potato, which happen to be major crops in the US. Therefore, it is crucial to prevent the introduction of GBNV into the US. The quarantine regulations established to prevent the entry of exotic pathogens rely on accurate detection of the pathogens. The goal of this study is to develop a rapid and reliable diagnostic tool to detect GBNV. Two different isolates of GBNV were received from India, under a USDA-APHIS permit. Specific primers and probe sets were designed to target conserved regions of the nucleocapsid (N) and movement protein (MP) genes. In addition, plant gene Actin-specific primers and a probe were used as an internal control. SYBR-Green based qRT-PCR and TaqMan qRT-PCR assays were developed to detect GBNV. The TaqMan assay has the efficiency of 91.3% and 91.4% for N and MP, respectively. The assays were sensitive enough to detect GBNV in a minimal of 0.05 ng/μl of total RNA. No cross-interaction was observed with closely related *Tomato spotted wilt orthotospovirus*, *Groundnut ringspot orthotospovirus*, and *Tomato chlorotic spot orthotospovirus*. TaqMan-based multiplex qRT-PCR was developed for rapid, specific, and sensitive detection of GBNV.

Exploring alternative management of plant pathogens of stevia in North Carolina, Mexico, and Paraguay

A. D. SANABRIA (1), G. Enciso (2), M. Maidana-Ojeda (2), J. F. Diaz-Najera (3), L. D. Thiessen (4), D. Shew (4), (1) North Carolina State University, Raleigh, NC, USA; (2) Centro de Desarrollo e Innovación Tecnológica, Hohenau, PARAGUAY; (3) Departamento de Fitotecnia, Colegio Superior Agropecuario del Estado de Guerrero, Guerrero, MEXICO; (4) North Carolina State University, Raleigh, NC, USA

Stevia is grown for the production of all-natural non-caloric sweeteners. As demand for stevia sweeteners is increasing worldwide, there is a desire for producing organic stevia in different countries; however, alternative disease management tools are lacking. We evaluated anaerobic soil disinfestation (ASD) for the management of stem rot caused by *Sclerotium rolfsii*. In 2019, experiments using carbon sources for ASD were carried out in microplots at Central Crops Research Station, Clayton, NC, USA. In 2020, field experiments were carried out at Colegio Superior Agropecuario del Estado de Guerrero, Mexico, and Centro de Desarrollo e Innovación Tecnológica, Paraguay, using a factorial arrangement 2x3, where factor A: soil disinfestation (soil amended with wheat bran and molasses vs non-amended) and factor B: foliar fungicide application (control vs azoxystrobin vs pyroligneous acid). In soils amended with wheat bran and molasses as carbon sources for ASD, the viability of sclerotia of *S. rolfsii* was significantly reduced. Soil disinfestation had a significant effect on fresh yield (P -value = 0.0443). The application of azoxystrobin (2,658.7 kg/ha) and pyroligneous acid (2,177.7 kg/ha) significantly increased the yield (P -value = 0.0007) compared to the nontreated control (1,411.7 kg/ha). These inexpensive organic amendments and botanical fungicides can be alternatives for the management of pathogens in stevia production systems.

Evaluating options for the control of *Rhizopus* soft rot on sweetpotato (*Ipomoea batatas*)

W. KALUWASHA, C. A. Clark, Louisiana State University, Baton Rouge, LA, USA

Rhizopus soft rot (RSR) is a postharvest disease of sweetpotato caused by the fungus *Rhizopus stolonifer*, which infects roots through wounds to cause a soft watery rot. Even though roots are cured following harvest to minimize the risk of RSR in storage, subsequent packing operations could create new wounds, thereby presenting more opportunities for infection to occur. Preventative applications are made, therefore, with the fungicide dicloran (Botran®) during packing. However, due to increasing concerns about fungicide residues on roots, there is a need for non-chemical options. This on-going two-year project seeks to explore the use of a biological product *Pseudomonas syringae* strain ESC-10 (Bio-Save 10LP), applied as a spray or as a dip to sweetpotato roots and/or re-curing of sweetpotato roots on the incidence of RSR in comparison to the fungicide dicloran. In the first year (2019), roots of five commercial cultivars were harvested, cured, and stored for either 120 days or 145 days. At each sampling time, roots were inoculated with a *R. stolonifer* spore suspension and subjected to the treatments either alone or as combinations. Roots were incubated under storage conditions (15°C, 85% RH) for 12 days, and RSR incidence data were recorded and analyzed. While cultivars responded differently to the various treatments, the first-year results collectively showed that the biological product Bio-Save 10LP was comparable to the fungicide dicloran in controlling RSR.

Evaluation of chemical and biocontrol products for the management of *Fusarium* root and crown rot of oakleaf hydrangea

S. NEUPANE, F. Baysal-Gurel, Tennessee State University, McMinnville, TN, USA

Fusarium root and crown rot caused by *Fusarium oxysporum* of hydrangea is not a common disease but has been an issue on some cultivars grown in Tennessee. An experiment was carried out to test the efficacy of different fungicides and biocontrol products for the management of *Fusarium* root and crown rot. Rooted cuttings of oak leaf hydrangea ‘Queen of Hearts’ were transplanted in no. 1 nursery containers. Plants were arranged in a complete randomized design in a shade house and inoculated by drenching 150 ml of 1×10^6 conidia/ml of suspension. Treatments were applied by the rate and interval according to IR-4 protocol. Plant height and width were recorded at the beginning and end of the experiment. Disease severity was assessed using a scale of 0–100% roots/crown affected. All treatments significantly reduced *Fusarium* root and crown rot severity compared to the non-treated, inoculated control. Treatments that most effectively reduced *Fusarium* root rot disease severity were BAS75002F, the low rate of MBI121, the low rate of Postiva, the low rate of SP2700, TXC2020 (applied 6 DAI), the low rate of Astun, Terraguard + the low rate of Astun and KleenGrow. *Fusarium* root rot disease severity percentages of those treatments were similar to the non-treated, non-inoculated control. Treatment that effectively reduced *Fusarium* crown rot disease severity was Empress and crown rot disease severity percentage of this treatment was similar to the non-treated, non-inoculated control.

Taken in plain sight: Fungal pathogens affecting watermelon production fields in Texas

B. MEYER (1,2), K. A. Cochran (3), K. Ong (1), (1) Texas A&M AgriLife Extension Service, College Station, TX, USA; (2) Texas A&M University, College Station, TX, USA; (3) Texas A&M University, Uvalde, TX, USA

Texas ranks 3rd in U.S. watermelon production, with watermelon being the largest annual horticultural crop grown throughout the state with over 40% of Texas counties growing watermelon annually. Two major fungal pathogens that affect watermelon production in Texas are gummy stem blight (GSB, *Stagonosporopsis cucurbitacearum*) and *Fusarium* wilt (FON, *Fusarium oxysporum* f. sp. *niveum*), which have the potential to result in millions of dollars of lost revenue. A survey was conducted to document fungal pathogens causing disease in Texas during the 2020 season. Symptomatic samples (30) were collected from each field from a total of 5 fields in 5 counties. Fungal pathogens were isolated and recovered using stem and/or root samples. Tissues were surface sterilized, plated on 25%PDA amended with antibiotics (10% cycloheximide), and grown for 1 week at 27°C. Pure culture isolates were recovered using hyphal tip isolation from resulting fungal growth. Isolates were morphologically identified and confirmed using PCR. The following fungi were identified: *Fusarium* spp., *Stagonosporopsis* spp., *Alternaria cucumerina*, *Colletotrichum orbiculare*, and *Chaetomium* spp. Pathogenicity tests were conducted using a representative isolate of fungi suspected to be of pathological importance. Evaluation of this survey may lead to a better understanding of pathogen community composition and prevalence, which has not been well documented to date.

Mango and avocado anthracnose: A major challenge for organic fruit production in south Florida

T. EGREJA (1), J. H. Crane (2), B. Schaffer (3), A. Sarkhosh (4), R. Gazis (2), (1) University of Florida, Doral, FL, USA; (2) University of Florida – Tropical Research and Education Center, Homestead, FL, USA; (3) University of Florida, Homestead, FL, USA; (4) University of Florida, FL, USA

South Florida’s subtropical climate is ideal for the commercial production of mango and avocado. However, the long periods of warm temperatures and high humidity are highly conducive to disease development. Losses due to disease limit profitability and present a major challenge for the organic production of mango and avocado fruit. Anthracnose, predominately caused by species in the *Colletotrichum gloeosporioides* species complex is the most common disease in mango and avocado. While foliage and branches are susceptible, the most damaging effects are to the flowers and fruits. In mango, losses occur early when fruit ripen on the tree, while in avocado losses mainly occur after harvest and during storage. Successful anthracnose control depends on the use of resistant cultivars, good cultural practices, proper fruit handling and storage, and the correct application of effective fungicides. Tools available to organic growers to prevent or control fungal diseases are limited. The goal of this project is to evaluate the potential of incorporating plant-

derived essential oils (EOs) into mango and avocado organic and conventional production. Different concentrations of EOs will be tested against specific populations of *Colletotrichum* spp. to determine dose-response effects of the EOs on pathogen growth and disease development. Knowledge generated in the first stage of the project, through in vitro and detached leaf assays, will inform further greenhouse and field trials.

Foliar symptoms of taproot decline are caused by systemic secondary metabolites produced by *Xylaria necrophora*

T. GARCIA-ARCA (1), P. Price (2), D. Galo (3), J. Solórzano (1), S. Sheffield (1), V. Doyle (1), (1) Department of Plant Pathology & Crop Physiology, Louisiana State University, Baton Rouge, LA, USA; (2) LSU AgCenter, Macon Ridge Research Station, Winnsboro, LA, USA; (3) Louisiana State University Agricultural Center, Baton Rouge, LA, USA

Taproot decline (TRD) is an emerging disease of soybean in the southern United States caused by *Xylaria necrophora*. While the first symptoms to become evident in the field are foliar interveinal chlorosis followed by necrosis, the pathogen is often isolated from necrotic roots and appears restricted to the root system. The foliar symptoms resemble those of sudden death syndrome (SDS) of soybean, a disease caused by the translocation of phytotoxic compounds from roots to leaves. We tested the hypothesis that secondary metabolites (SMs) released by *X. necrophora* are capable of producing chlorosis and necrosis on soybean leaves, similar to what is observed on plants diagnosed with TRD in the field. Stem cuttings of soybean (cultivars AG4632, P5414LLS, and Osage) and tomato were challenged with cell-free culture filtrates (CFCFs) from known pathogenic strains of *X. necrophora* and putative non-pathogenic species (*X. arbuscula* and *Colletotrichum siamense*). Chlorophyll content was estimated chemically and digitally, and root development was also used as a response variable. All cultivars exposed to diluted CFCFs from *X. necrophora* exhibited significantly reduced chlorophyll content, but no impact on tomato was observed. Osage exhibited potential resistance to TRD in greenhouse experiments, but our results suggest this resistance is unrelated to resistance to SMs. Chlorophyll content was not reduced by SMs of *X. arbuscula* or *C. siamense* in any hosts or cultivars.

Development and validation of *Peronospora belbahrii*-specific diagnostic markers

J. R. STANDISH (1), M. Bowman (2), K. L. Childs (3), M. Tian (4), L. M. Quesada (5), (1) North Carolina State University, Raleigh, NC, USA; (2) Ball Horticultural Company, West Chicago, IL, USA; (3) Department of Plant Biology, Michigan State University, East Lansing, MI, USA; (4) University of Hawaii at Manoa, Honolulu, HI, USA; (5) Department of Entomology and Plant Pathology, North Carolina State University, Raleigh, NC, USA

Basil downy mildew, caused by the oomycete *Peronospora belbahrii* (*Pbel*), is an important disease that affects basil production worldwide. Wind-dispersed sporangia and contaminated seed make disease management challenging. Identifying *Pbel* in seed-lots before sale or planting, or in field-grown basil before symptoms develop would allow for the timely deployment of disease management strategies. To address this need, an Illumina draft genome assembly and next generation sequencing reads for *Pbel*, as well as DNaseq and RNAseq reads publicly available for several downy mildew pathogens, were incorporated into a bioinformatics pipeline to predict *Pbel*-specific diagnostic markers. Based on these data, 114 putative single-copy marker candidates were present in *Pbel* only. The specificity of each candidate marker was validated using polymerase chain reactions against a diverse collection of *Pbel* isolates, basil, and other oomycetes, including many related downy mildew pathogens. Candidates that did not amplify in all *Pbel* isolates or that amplified in basil and/or in other oomycetes were removed; those remaining after validation were considered specific to *Pbel*. Overall, nine markers successfully amplified in all tested *Pbel* isolates but only two were determined to be *Pbel*-specific. These candidate markers are valuable for diagnostics, identifying *Pbel*-contaminated seed-lots, and detecting airborne sporangia, all of which may help to predict incoming basil downy mildew epidemics.

Management of huanglongbing-affected citrus root function by irrigation pH regulation

S. SHARMA, T. Vashisth, E. G. Johnson, University of Florida, Lake Alfred, FL, USA

Candidatus Liberibacter asiaticus (CLas) causes huanglongbing (HLB), a destructive disease of citrus. Though the psyllid vector feeds on leaves, reduced root health is the initial symptom. Past studies indicate a CLas–pH interaction alters root function. We conducted two experiments on the response of split root citrus in rhizotrons to high bicarbonate irrigation water acidified to pH 5.5, 6.5, and 7.5 with H₂SO₄. The first experiment tested the effects of differential pH from managed and unmanaged zones on HLB-affected tree health. The second experiment was set to determine if sensitivity to pH is a systemic or local effect of infection. Graft inoculation was done with healthy and CLas+ buds on ‘US-942’ (pH tolerant) and ‘Swingle’ (pH sensitive) rootstocks arranged in a RCBD of eight blocks, each with HLB and healthy rootstocks in 2:1 ratio. The results showed a slower infection rate in US942 and a lower established log CLas genomes per milligram of root (2.59) compared to Swingle (4.16), suggesting a partial resistance of US942 to CLas. Dry fibrous root mass of HLB-affected plants was lowest with pH 5.5 irrigation water in contrast to expectation. Significant reduction in leaf number over time supports HLB symptoms. Biweekly root tracing and preliminary physiological data indicated significant rootstock effects. The inconsistency in results compared to prior work with buffered irrigation water needs further study to recommend acidification treatments for HLB management.

Diversity and community structure of the Peruvian potato virome

R. I. ALCALÁ BRISEÑO (1,2,3), S. S. Fuentes (4), A. Perez (4), J. F. Kreuze (4), K. A. Garrett (1,2,3), (1) Emerging Pathogens Institute, University of Florida, Gainesville, FL, USA; (2) Food Systems Institute, University of Florida, Gainesville, FL, USA; (3) University of Florida, Gainesville, FL, USA; (4) International Potato Center, Lima, PERU

The Andean region is the center of origin and center of diversity for potato. We explore the diversity and community structure of viruses across altitude gradients in Peru. We surveyed the main potato production areas, collecting approximately 900 potato leaf samples from 11 departments and 100 fields across elevation gradients, from the coast of Lima to production concentrated at higher altitudes in the Cuzco region in the Andes. Applying machine learning and virome network analysis for virus classification, and network analysis across samples and geographic regions, we evaluated the virome composition of three regions of potato production in Peru. The Peruvian potato virome includes over 32 viruses, with the most common viruses causing important diseases being *Potato virus Y* (PVY, *Potyvirus*), *Potato virus X* (PVX, *Potexvirus*), and *Potato leafroll virus* (PLRV, *Polerovirus*). Novel viruses were also observed. We are evaluating the risk for virome dispersal and the implications of the virome structure for phytosanitary policies and for breeding for disease resistance.

Evaluation of in-furrow treatments to manage invasive root knot nematode (*Meloidogyne enterolobii*) in North Carolina cotton

Y. ROSADO RIVERA, A. Joyce, L. D. Thiessen, North Carolina State University, Raleigh, NC, USA

Cotton is one of the common rotational crops used in North Carolina in the coastal plain. Root knot nematode is the most economically important pathogen affecting this crop in the state, and the invasive species (*Meloidogyne enterolobii*) threatens the sustainability of the crop. The goal of this research was to evaluate two cotton varieties with varying levels of nematode resistance (PHY 340 susceptible, PX3D32 resistant), and four different in-furrow treatments to manage *M. enterolobii* in a naturally infested field in Johnston County, North Carolina. Treatments were applied in-furrow with a CO₂ backpack sprayer at 10 gal/acre, at planting or at planting followed by another application at 45 days after planting (DAP). Soil samples (500 cm³) were collected at planting, at midseason and at harvest per plot for nematode juvenile counts. PX3D32 and Propulse at planting followed by Velum either at planting or 45 DAP had higher stand than other treatments. PX3D32 with Propulse at planting had significantly fewer females per root weight than the PHY 340 with Propulse and Velum at transplant, but not significantly different from the other treatments. Based on our results in 2020, PX3D32 in combination with a Propulse in-furrow at planting reduced the female reproduction per weight and may be valuable for commercial farmers.

Variability in survival of grafted tomato plants exposed to the bacterial wilt pathogen in the field

J. SPAFFORD, E. Reeves, I. Meadows, North Carolina State University, Waynesville, NC, USA

Bacterial wilt (BW) of tomato is a devastating soilborne disease and is caused by *Ralstonia solanacearum*. One strategy to avoid this disease is the grafting of desirable cultivars, but BW-susceptible, onto BW-resistant rootstocks. We analyzed 37 rootstock-scion combinations composed of 11 rootstock and 6 scion varieties. Four plants of each rootstock-scion combination and one non-grafted scion variety were planted in a randomized block design with six replications in a field with a history of high BW disease pressure. BW was confirmed if bacterial streaming was observed. Non-grafted scion mortality ranged from 61 to 75%. Mean mortality was calculated as the percentage of plants that died in each treatment, disregarding the plots from which the adjacent susceptible scion variety did not wilt. Rootstocks Ganbarune Vect and Ganbarune No. 37 had the lowest mortality at 14%, while Parte had the highest mortality at 75%. When grafted, Cherokee Purple had the highest mortality at 42% across all rootstock varieties. The mean percentage of grafted BHN-589 plants that died from BW varied depending on the rootstock: 0% on Spike-K, High Power, Ganbarune Vect, and Ganbarune No. 37, but 50% on Survivor. Based on our results, rootstocks High Power, Ganbarune Vect, and Ganbarune No. 37 are recommended for fields with BW. The variability in mortality rates for grafted scions warrants further investigation into scion-rootstock interactions and disease resistance mechanisms.

Response of different cover crops against *Phytophthora nicotianae*

M. PANTH, A. Witcher, F. Baysal-Gurel, Tennessee State University, McMinnville, TN, USA

Phytophthora nicotianae is a soilborne oomycete pathogen that can infect more than 255 genera of plants in 90 families. Being one of the most devastating soilborne pathogens in the Southeastern United States, *P. nicotianae* can cause wilting; leaf chlorosis; and stem, crown, and root necrosis of plants. With the rising threat of pathogens in crop production coupled with increasing chemical resistance, many alternative management practices to contain the pathogens are being developed and put into use. The use of cover crops in a rotation plan is also being explored for the sustainable management of soilborne pathogens. However, a potential threat posed by these cover crops by acting as a secondary host to the pathogen is to be studied. A set of nine different cover crops—crimson clover, triticale, Austrian winter pea, annual ryegrass, red clover ‘Kenland’, buckwheat, tillage radish ‘Daikon’, cowpea ‘Iron & Clay’, and Japanese millet were selected and screened against *P. nicotianae*. Cover crop roots were assessed for *Phytophthora* root rot disease severity using a scale of 0–100% roots affected. At the end of two greenhouse trials, tillage radish ‘Daikon’, triticale, Japanese millet, annual ryegrass, cowpea ‘Iron & Clay’, and Austrian winter pea were consistently showing lower disease severity than other cover crops. These results can help growers successfully manage *Phytophthora* root rot.

Classical, molecular, and high-throughput sequencing techniques to screen new sweetpotato germplasm imported into the United States

M. E. MARKS (1), X. Hu (1), B. Atha III (2), J. A. Foster (3), R. D. French-Monar (4), (1) USDA, Beltsville, MD, USA; (2) USDA-APHIS Plant Germplasm Quarantine Program, Laurel, MD, USA; (3) USDA APHIS PPQ FO Plant Germplasm Quarantine Program, Beltsville, MD, USA; (4) USDA APHIS PPQ FO PGQP, Laurel, MD, USA

The USDA APHIS PPQ FO Plant Germplasm Quarantine Program (PGQP) protects U.S. agriculture against the entry, establishment, and spread of damaging plant pathogens in imported germplasm. Sweetpotato (*Ipomoea batatas*) is tested for a variety of viral pathogens of quarantine importance. Classical diagnostic techniques, such as grafting to the indicator *Ipomoea* spp. and ELISA are used in conjunction with PCR, RT-PCR, and high-throughput sequencing (HTS). Eight sweetpotato accessions were screened in 2020. Six accessions were positive for viruses such as SPLCV, SPVG, and/or SPVC in select tests conducted on the germplasm and were sent directly to therapy. The remaining two accessions tested negative for all plant pathogenic viruses by preliminary grafts, ELISAs, PCR, and HTS. However, one of these accessions had symptoms of vein clearing and leaf tip curling on a second set of grafts on *I. setosa*, and HTS on *I. setosa* tissue detected potyviruses. The remaining accession tested negative in all tests and was released. HTS confirmed the results obtained from the PCR, RT-PCR, and qPCR tests. Based on these and past findings, HTS has become an additional technique to incorporate into germplasm screening for pathogens of concern. These findings validated the importance of grafting, since viral symptoms may only occur on indicator plants due to increased virus titer. Testing confirmed the importance of using multiple diagnostic techniques for the same virus species or family.

Incorporating cropland connectivity as a new standard feature of geographic risk assessment and surveillance strategies

Y. XING (1,2,3), A. I. Plex Sulá (2,4,5), K. A. Garrett (1,2,3), (1) Emerging Pathogens Institute, University of Florida, Gainesville, FL, USA; (2) Food Systems Institute, University of Florida, Gainesville, FL, USA; (3) University of Florida, Gainesville, FL, USA; (4) Plant Pathology Department, University of Florida, Gainesville, FL, USA; (5) University of Florida, Gainesville, GUATEMALA

Cropland connectivity is a risk factor for invasion and saturation by crop-specific pathogens and pests. Cropland connectivity is a measure of the degree to which geographic patterns of cropland make it easy for pathogens to spread from one cropping area to another, through dispersal by wind or vectors, or movement with farming equipment or through local trade of plant materials. The importance of particular locations in geographic networks of cropland can be evaluated in terms of whether locations are likely to be hubs (connected to many other locations) or bridges (connecting parts of the network that might otherwise be separated). Network metrics that capture these traits have been combined in a cropland connectivity risk index (CCRI), described by Xing et al. (2020). Here we introduce tools in the R programming environment for making cropland connectivity easier to evaluate as part of a standard geographic risk assessment, potentially incorporating cropland connectivity with other risk factors, such as climate-based risk and trade-based risk. We present examples of cropland connectivity analysis for a range of crops key to nutrition security and tools for incorporating cropland connectivity in formal and informal pest risk assessments (PRAs).

Characterization of prothioconazole resistance in *Fusarium oxysporum* f. sp. *niveum* (FON) laboratory mutants

O. HUDSON, E. Ali, P. Ji, University of Georgia, Tifton, GA, USA

Fusarium wilt of watermelon is one of the greatest limiting factors for watermelon production worldwide. The causal agent, *Fusarium oxysporum* f. sp. *niveum* (FON), is difficult to control due to the presence of overwintering chlamydospores and the development of multiple races that can overcome the FON-resistant cultivars. In addition, only one fungicide is registered for control of FON, prothioconazole (Proline), which is a DMI fungicide with a moderate risk of developing fungicide resistance. There is no reported incidence of FON developing resistance to prothioconazole in the field to date, but the selection pressure is high due to the single chemistry being used. Herein, we report on the characterization of prothioconazole resistance in FON lab mutants. Wild-type isolates of FON were exposed to UV irradiation followed by a selection on an agar medium amended with different prothioconazole doses. In total, nine mutants were obtained and tested for sensitivity to prothioconazole using a mycelial growth inhibition assay to determine effective concentration to inhibit 50% growth or germination (EC₅₀ values). The EC₅₀ value for prothioconazole in resistant isolates was 109 µg/ml (PPM) and the resistance factor increased 20-fold compared to the wild-type isolates. The expression of FONCyp51 and presence of mutations were also investigated. Findings from this study will enable future resistance monitoring for prothioconazole resistance in *F. oxysporum* f. sp. *niveum* (FON).

Automated reporting of on-farm foliar fungicide trials in Arkansas with potential expansion to a regional project

T. N. SPURLOCK (1), R. Hoyle (2), (1) University of Arkansas System Division of Agriculture, Lonoke, AR, USA; (2) University of Arkansas System Division of Agriculture, Monticello, AR, USA

Eleven large block foliar fungicide trials were completed on soybean in Arkansas in 2020. Each trial contained two fungicide treatments and a nontreated control with three replications and treatments arranged in a randomized complete block design. Fungicides were applied at R2–R5 with a ground-driven sprayer. Five points were georeferenced approximately equidistant throughout each block, and disease incidence and severity were determined in a 1.5-m radius around each point, prior to fungicide treatment and again at R6. Grain was harvested with the local farmer's combine and yield monitor. All data were subjected to ANOVA followed by means separation of fixed effects using Tukey's honest significant difference test (HSD) at $P = 0.05$. All analyses and a report for each trial location were completed

in an automated model in ArcGIS Pro 2.4 using standard tools and custom script tools (developed using Python 3.6.8 or R 4.0.2). Weather and soils data, as well as high-resolution field images were included in the reports. Each farmer and county agent were presented with reports in less than five days from receiving yield data. By standardizing methods across locations and automating the analysis and reporting of each trials' results, this project could be more easily expanded regionally where reporting of on-farm foliar fungicide performance data would be valuable to soybean growers.

Identifying and evaluating vector competency of insect pests in North Carolina sweetpotato storage facilities for dispersal of *Ceratocystis fimbriata*

M. STAHR (1), A. Lytle (2), A. Huseth (2), M. Bertone (2), L. M. Quesada-Ocampo (3), (1) NCSU, Cary, NC, USA; (2) North Carolina State University, Raleigh, NC, USA; (3) Department of Entomology and Plant Pathology, North Carolina State University, Raleigh, NC, USA

Black rot, caused by *Ceratocystis fimbriata*, is a damaging sweetpotato post-harvest disease, yet no known insect vectors are present in North Carolina storage facilities. Thus, in this study we identified potential vectors in storage facilities and determined if they could harbor *C. fimbriata* inoculum. To identify potential vectors, sticky traps were placed in storage facilities for 1 week, and captured insects were visually identified. Overall, significantly more *Drosophila* species were detected, with *D. hydei* comprising 85% of samples. A population of *D. hydei* was reared in a controlled environment. Twenty cages with 50 adult flies and funnel traps containing healthy or *C. fimbriata*-infected sweetpotatoes were prepared. After 96 h, flies per trap were counted, and 20 flies each from the healthy and *C. fimbriata*-infected traps were randomly selected across all cages for further analysis. The selected flies were externally washed with a 5% Tween solution, surface sterilized, and then crushed in Tween for an internal wash. The wash solutions were plated onto carrot agar and checked for *C. fimbriata* growth over a 2-week period. After two temporal replications, *C. fimbriata* was isolated from 42% of flies from *C. fimbriata*-infected sweetpotatoes traps and 12% of flies from healthy sweetpotatoes traps. These findings suggest that *D. hydei* could be a vector of *C. fimbriata* in sweetpotato storage facilities, but further research is necessary to document transmission.

Mixtures of inpyrfluxam and elemental sulfur for management of late leaf spot of peanut

A. K. CULBREATH (1), T. B. Brennenman (1), R. Kemerait (1), H. Sanders (2), K. W. Seebold, Jr. (3), (1) University of Georgia, Tifton, GA, USA; (2) Valent USA, Tifton, GA, USA; (3) Valent USA LLC, Lexington, KY, USA

Inpyrfluxam is a new SDHI fungicide that has excellent activity against stem rot (*Athelia rolfsii*) of peanut (*Arachis hypogaea*) but does not provide adequate control of early leaf spot (*Passalora arachidicola*) or late leaf spot (*Nothopassalora personata*). A field experiment was conducted in Tifton, GA, to determine the mixtures of inpyrfluxam with elemental sulfur on leaf spot epidemics. Treatments included inpyrfluxam (Excalia 2.84 SC) (50 g a.i./ha) alone; elemental sulfur (Microthiol Disperss 80 W) (2,240 g a.i./ha) alone; mixtures of inpyrfluxam (50 g a.i./ha) and sulfur (2,240 g a.i./ha); chlorothalonil (Bravo WeatherStik 720 F) (1,260 g a.i./ha); and a nontreated control. Treatments were applied seven times at approximately 14-day intervals. Final leaf spot ratings (Florida 1–10 Scale) were 5.2, 8.5, and 2.6 for inpyrfluxam, alone, sulfur alone, and the combination of the two, respectively; 3.8 for the chlorothalonil standard; and 8.8 for the nontreated control (LSD = 0.8). Based on percent defoliation by leaf spot, percent control was 68% for inpyrfluxam, 3% for sulfur, and 98% for the combination. Observed efficacy of the mixture was greater ($P < 0.05$) than the expected (69% control), indicating synergistic effects of the two fungicides.

Spatial analysis of phony peach disease in commercial and research peach orchards in Georgia

K. JOHNSON (1), C. H. Bock (2), P. M. Brannen (1), (1) University of Georgia, Athens, GA, USA; (2) USDA ARS, Southeastern Fruit and Tree Nut Research Laboratory, Byron, GA, USA

Peach (*Prunus persica*) is one of the most economically important fruit crops in Georgia. Phony peach disease (PPD) is a reemerging disease threatening peach production throughout the central and southern regions of the state. PPD is caused by the phytochemical pathogen *Xylella fastidiosa* subspecies *multiplex* (Xfm) and is transmitted primarily by the glassy-winged sharpshooter, *Homalodisca vitripennis*. Nine peach orchards (five commercial and four research) were surveyed for PPD in the summer/fall of 2020, and a range of 153 to 691 trees were visually assessed in each orchard for PPD symptom expression. For each location, 10 symptomatic PPD trees were confirmed to be infected with Xfm using an Agdia AmplifyRP XRT+ for XF kit. Accuracy of visual detection was high (>93%). Spatial patterns of PPD-symptomatic trees were evaluated using doublet analysis and Ripley's K-function to better understand the pathogen's distribution within the orchards. Disease incidence among the surveyed orchards ranged from 12.1% to 30.5%. Differences were observed between the two analyses, with some locations showing aggregation. As both random and aggregated patterns of disease were observed in the orchards, various factors, including tree age, epidemic stage, and inoculum sources, could be associated with the spatial distribution of PPD.

In vitro sensitivity of *Aspergillus flavus* isolated from peanut seeds in Georgia in response to a quinone outside inhibitor fungicide azoxystrobin

M. GUNN, E. Ali, T. L. Stackhouse, S. Waliullah, A. K. Culbreath, T. B. Brenneman, University of Georgia, Tifton, GA, USA

Aspergillus flavus is an important pathogenic fungus affecting peanuts by production of aflatoxin, a potent human carcinogen. In infected peanuts, it can also cause seed rot and reduce seed viability and germination. In 2020, a total 105 *Aspergillus* isolates were collected from seven peanut seed lots in Georgia to determine the in vitro efficacy of QoI fungicide (azoxystrobin). Isolates identification were confirmed as *A. flavus* using their morphological characteristics on plate and nucleic acid-based PCR method with species-specific primers. In vitro experiments were conducted to characterize sensitivity distributions of these isolates of *A. flavus* to azoxystrobin. Mean EC50 values ranged from 0.12 to 297.22 µg/ml. Additional experiments were conducted to characterize the cytochrome b gene of these isolates for finding the mutation, if any, present that is associated with the resistance phenotype to QoIs. Our results showed that the majority of the mutations (65%) are Cyt B G143A, which confers complete immunity to the QoI's. We also observed Cyt B F129L mutation, which has been documented for QoI resistance, in another 20% of the isolates. These findings explained the cause of developing resistance in peanut seed lots so abruptly this year in GA. More detailed studies are being performed to assay the efficacy of other fungicides for controlling *A. flavus* populations in the colonized commercial peanut seed.

Survey of *Bipolaris* species causing foliar disease on weedy invasive grasses in Florida

A. ADHIKARI, B. R. Lane, P. Harmon, E. M. Goss, University of Florida, Gainesville, FL, USA

Non-native grasses that have been introduced for food, feed or forage have later become invasive weeds, defined as any unwanted plant species in a particular situation. Invasive weeds can experience a relatively disease-free period but accumulate pathogens over time. Invasive weedy grasses can have significant negative impacts on crops through direct competition. Indirect effects include serving as reservoirs for pathogens capable of causing disease on co-existing cultivated crops. Weedy plant populations tend to be more genetically diverse than cultivated crops and also may harbor more diverse and virulent pathogen populations. A study was conducted to identify *Bipolaris* spp. causing foliar lesions on common weedy and invasive grasses in Florida. Grass species included *Microstegium vimineum*, *Dicanthelium* spp., *Panicum* spp., *Cynodon* spp., *Sorghum* spp., *Stenotaphrum* spp., *Echinochloa* spp., and *Elymus* spp. from Alachua, Gadsden, and Polk counties. Symptomatic leaf tissues were plated onto water agar and incubated for a week. Resulting conidia characteristic of *Bipolaris* spp. were picked and transferred to PDA plates with sterile metal needle. Based on sequencing of the ITS region, the majority of isolates were identified as *B. yamadae*. *B. yamadae* was previously reported to be a pathogen of corn and sugarcane, which are also major crops in Florida, suggesting that populations of *B. yamadae* on weedy grasses could be a potential threat to agronomic crops in Florida.

Draft genomes and comparative analyses of binucleate *Rhizoctonia* isolates

J. GIL (1), M. Colle (2), T. D. Miles (2), A. Rojas (1), (1) University of Arkansas, Fayetteville, AR, USA; (2) Michigan State University, East Lansing, MI, USA

The *Rhizoctonia* species complex in the family Ceratobasidiaceae is commonly associated with its pathogenic lifestyle causing diseases in crops of economic importance. However, this family comprises saprobes and mycorrhizal symbionts associated with orchids. Based on hyphal recognition, anastomosis groups are distinguished within 2 major groups: multinucleate and binucleate, which differ in genome sizes, host specificity and number of secreted proteins, suggesting differences in pathogenesis or plant associations. While genomes of multinucleate anastomosis groups have been assembled and their pathogenicity mechanisms studied, binucleate isolates have not been equally described. Given this diversity and lack of information for binucleate isolates to date, studying the genome of multiple anastomosis groups remains necessary for a better understanding of the species. We present four draft genomes from binucleate *Rhizoctonia* isolates from Arkansas, Alabama, and Louisiana obtained with Nanopore sequences. Assemblies were 72.8 to 82 Mb long. Completeness of the genomes showed >75% complete ortholog genes based on BUSCO content. Between 17,223 to 19,452 genes with an average length of 2,108 nucleotides were annotated. Pairwise comparisons of read alignments were carried out to understand sequence similarities, and around 10,000 carbohydrate active enzymes (CAZs) were identified per sample. These preliminary genomic resources provide a framework for future comparative analyses.

Use of synthetic antifungal peptides to mitigate aflatoxin contamination

R. R. SWEANY (1), K. Rajasekaran (2), J. Cary (2), (1) U.S. Department of Agriculture-Southern Regional Research Center-New Orleans, New Orleans, LA, USA; (2) USDA-ARS, New Orleans, LA, USA

Aflatoxin contamination of corn, peanuts, and other oilseeds is a recurrent problem in the southern United States and other tropical and sub-tropical climates. Aflatoxin is a deadly, acute toxin and carcinogen produced by the fungus *Aspergillus flavus* after infection of seeds under both pre- and postharvest conditions. Synthetic antifungal peptide sequences derived from natural antimicrobial peptides found in *Cecropia* moths (D4E1) and horseshoe crabs (AGM182) were expressed in tobacco and cotton (D4E1) or corn (AGM182) via *Agrobacterium* transformation. A number of transgenic lines expressing these antifungal peptides were shown to have enhanced resistance to *A. flavus* growth and aflatoxin contamination. The cotyledons of D4E1-transformed cottonseeds demonstrated a significant reduction in the level of colonization by *A. flavus*, and similarly, there was limited fungal growth within the endosperm or embryo of AGM182 transformed corn kernels. Aflatoxin contamination was nearly eliminated when mature transgenic corn kernels expressing

AGM182 were inoculated with *A. flavus*. Incorporation of synthetic antifungal peptide genes into corn and cotton is a potential novel approach to enhance resistance to *A. flavus* infection and subsequent aflatoxin contamination both pre- and postharvest. Multi-location field trials are needed to evaluate the utility of incorporating these antifungal traits into elite lines.

A machine learning tool for smartphone-based rapid detection of tomato diseases

S. SENTIL, M. Choudhary, M. L. Paret, University of Florida, Quincy, FL, USA

Boasting a nutrition rich profile, tomatoes are a necessity for diets around the world. However, plant pathogens pose a significant threat to its sustainable production. Only tomatoes that satisfy strict industry criteria can be sold, which can be compromised by the untimely detection of such pathogens. This leads to the need for rapid detection mechanisms to maximize crop productivity and the timely implementation of disease control measures. Numerous deep learning approaches have been applied to detect diseased lesions on macroscopic images of tomato samples, that classify them based on observed features. Convolutional Neural Networks utilize fully connected networks, allowing for a lightweight model architecture. This study utilized two CNN approaches to distinguish 17 biotic and abiotic issues of tomatoes at the microscopic (30×) level using a smartphone attachable lens. Disease symptoms ($n = 100$), either on the upper or underside of the leaves, or on the surface of fruits, and diagnostically validated in the lab were extracted. Classifiers unique to the part of the plant the image is taken of, or a combined classifier consisting of all classes, were trained and tested. The combined architecture proved to be the optimal classifier, with an average precision of 93.2% and recall of 82.9%. This is expected to aid extension pathologists and farmers, especially in remote places of the world, to make reliable assessments regarding treatments for disease control.

Dollar spot disease detection: PCR-RFLP for rapid identification of *Clariireedia jacksonii* and *C. monteithiana*

T. L. STACKHOUSE (1), S. Waliullah (1), B. A. Bahri (2), A. D. Martinez-Espinoza (2), E. Ali (1), (1) University of Georgia, Tifton, GA, USA; (2) University of Georgia, Griffin, GA, USA

Turfgrass production is threatened throughout the world by dollar spot disease. This disease is caused by at least five recently reclassified pathogens within the *Clariireedia* genus, two of which are present in the United States (*C. jacksonii* and *C. monteithiana*). The symptoms include white to straw foliar lesions that can result in entire plants blighted and forming small, sunken spots on the turf, killing the grass to the soil surface. More money is spent annually on dollar spot control than any other disease on golf turf. There is a critical need for quick molecular dollar spot pathogen identification for rapid control measures. This research focuses on creating novel molecular assays for identification of dollar spot. The calmodulin gene region was targeted to produce *C. jacksonii* and *C. monteithiana* specific primers. While several primer sets were designed and tested for specificity and optimization, one was selected for RFLP differentiation potential based on single nucleotide polymorphisms between the two species. This assay produces two bands in one species and one band in the other. This method drastically reduces the time needed to identify dollar spot pathogens. The resulting assay can be used by growers or diagnosticians throughout the turfgrass industry for rapid and precise dollar spot pathogen identification. Future work includes direct PCR methods to eliminate the extraction step and LAMP protocol development to allow for field ready assays.

Approaching laurel wilt of avocado through different angles: From early and rapid diagnosis to building baseline knowledge for breeding programs

P. P. PARRA GIRALDO (1), J. H. Crane (2), B. Schaffer (1), R. Gazis (3), (1) University of Florida, Homestead, FL, USA; (2) University of Florida – Tropical Research and Education Center, Homestead, FL, USA; (3) University of Florida, IFAS, Department of Plant Pathology, TREC, Homestead, FL, USA

Laurel wilt (LW), a deadly vascular disease, caused by the fungus *R. lauricola* (RL), is spreading quickly across the US. The disease has killed 140,000 avocado trees in Florida and is rapidly spreading toward large avocado production regions in California and Mexico. While within-plant disease progress varies, all avocado cultivars tested have succumbed to the disease. Surviving trees have been documented in orchards with high disease incidence, encouraging screening for resistant/tolerant germplasm that includes outcrossed seedling material. The use of pesticides (propiconazole) and cultural practices (stumping and solarization) have not been successful in controlling outbreaks in commercial orchards. So far, the only cost-effective management strategy is the timely eradication of infected trees, which requires early detection of the pathogen. Building on knowledge generated over a decade of research, we are exploring novel approaches for LW management, including the prophylactic priming of the host's defense system and searching for resistance/tolerance through the high-throughput screening of numerous avocado genotypes. Also, we developed a PCR-based protocol for the detection of RL in 24 h that can be implemented in pathogen surveillance programs. By exploring multiple approaches, from detection to management, we aim to provide the industry with efficient strategies that can be integrated into a sustainable program to mitigate the impact of the disease.

Efficacy of fungicides, biofungicides, host plant defense inducers, and fertilizer to manage *Phytophthora* root rot of dogwood under flooding condition

K. NEUPANE, F. Baysal-Gurel, Tennessee State University, McMinnville, TN, USA

Phytophthora root rot caused by *Phytophthora cinnamomi* is one of the major diseases of flowering dogwood (*Cornus florida*). The pathogen causes plants to develop wilting, root rot, crown rot, and others, letting them die. Flooding is an important factor in the severity of the pathogen. In this study, the efficacy of different fungicides, biofungicides, host plant defense inducers, and fertilizer were studied to manage *Phytophthora* root rot in different flooding durations. Flowering dogwood seedlings were exposed to a simulated flooding of 1, 3, and 7 days. Treatments were applied preventatively 1 or 3 weeks before flooding and curatively 24 h after flooding. All treatments were drench applied to dogwood seedlings inoculated with *P. cinnamomi* 3 days before flooding. At the end of the trial, plant growth data were recorded and root systems were assessed for disease severity using a scale of 0–100%, and root subsamples were plated on PARPH-V8 medium to determine the percent recovery of *Phytophthora*. For both preventative applications, several treatments significantly suppressed the pathogen, but Alliete, Empress Intrinsic, Signature Xtra Stressgard, and Subdue MAXX were found to be the most effective. For curative application, all treatments significantly reduced root rot compared with the inoculated control at all flooding levels. This study will help growers to adopt preventative plans or to treat infected plants curatively against *P. cinnamomi* during flooding.

No trespassing! Barrier zone in the sweetpotato storage root prevents expansion of *Ceratocystis fimbriata* infections

C. H. PARADA ROJAS (1), A. Jansson (2), K. Pecota (3), C. Yencho (3), L. M. Quesada-Ocampo (1), (1) Department of Entomology and Plant Pathology, North Carolina State University, Raleigh, NC, USA; (2) Analytical Instrumentation Facility, North Carolina State University, Raleigh, NC, USA; (3) Department of Horticulture, North Carolina State University, Raleigh, NC, USA

Today, the soilborne pathogen *Ceratocystis fimbriata* remains a threat to sweetpotato production in the United States. Knowledge regarding the infection process of *C. fimbriata* in roots is still lacking. Here, we aimed to elucidate the mechanism controlling resistance at the storage root level. Previous research pointed to a case of age-related resistance with contrasting root inner core phenotypes for younger developing roots as compared to older roots. Thus, our objective was to investigate histopathological differences at the interface between *C. fimbriata* and canner (younger) and jumbo (older) storage roots using X-ray computed tomography (CT). Contrast enhanced micro-CT analysis of inoculated older and younger storage roots revealed structural differences in the primary cambium that potentially acts as a structural barrier against *C. fimbriata*. Microstructural parameters such as cell size, elongation, cell count, as well as porosity were quantified and analyzed in a 5 mm thick section of the barrier zone. Jumbo infected root cells reacted to *C. fimbriata* infection by accumulating cells in the interphase that appear to prevent expansion of hyphae to the inner core of the sweetpotato storage root. Our research highlights a potential pivotal role of a barrier zone in the age dependent defense mechanism of sweetpotato roots against infection by *C. fimbriata*.

Tools for evaluating and improving seed systems and seed health in roots, tubers and bananas

C. COX (1,2), E. Weinrich (1,2,3), J. L. Andrade-Piedra (4), M. McEwan (5), C. Almekinders (6), K. A. Garrett (2,3,7), (1) Plant Pathology Department, University of Florida, Gainesville, FL, USA; (2) Food Systems Institute, University of Florida, Gainesville, FL, USA; (3) Emerging Pathogens Institute, University of Florida, Gainesville, FL, USA; (4) International Potato Center (CIP), Lima, PERU; (5) International Potato Center, Nairobi, KENYA; (6) Wageningen University & Research, Wageningen, NETHERLANDS; (7) University of Florida, Gainesville, FL, USA

Roots, tubers, and bananas (RTB) are important food security crops around the world. Small-scale farmers in developing countries typically acquire RTB seed informally where quality control is largely unregulated. Pathogens and pests can accumulate in planting material through successive cycles of vegetative propagation, reducing yield and market value. The CGIAR RTB Seed System Toolbox was created through a cross-disciplinary, collaborative approach in response to seed degeneration and other bottlenecks in seed systems. Designed for stakeholders working to increase food and seed security outcomes, the toolbox houses 11 tools to diagnose, evaluate, and improve seed systems. The seed health package, for example, combines three key seed health management components: clean seed, disease resistant varieties, and on-farm management. Results support training and decision making by researchers, policy makers, and practitioners and allow for evaluation of seed degeneration, disease, and yield outcomes for specific systems and user groups (e.g., gender and youth). In addition, we present a landscape analysis of seed system stakeholders and interventions in Sub-Saharan Africa across all major crops, while highlighting RTB seed health challenges. This work is designed to scale seed system research and development where access to good, quality seed is in high demand but in chronically short supply.

Determining the efficacy of fungicides in the control of dragon fruit stem and fruit canker

T. DE PAULA LELIS (1), J. H. Crane (2), S. Zhang (1), R. Gazis (3), (1) University of Florida, Homestead, FL, USA; (2) University of Florida – Tropical Research and Education Center, Homestead, FL, USA; (3) University of Florida, IFAS, Department of Plant Pathology, TREC, Homestead, FL, USA

Stem and fruit canker, caused by *Neoscytalidium dimidiatum*, is the most important disease affecting dragon fruit production in south Florida. Field incidence could reach 70%, causing significant economic losses. Currently, there are few fungicides registered for disease control in dragon fruit, and none of these are labeled for *N. dimidiatum*. Due to the extended length of the crop's harvest season, these

formulations are used too often and not as part of a rotation regime, thus increasing the pathogen population's chances of developing resistance. To provide additional chemical tools to growers, the sensitivity of *N. dimidiatum* toward Abound (azoxystrobin), Switch (cyprodinil and fludioxonil), Tilt (propiconazole), and Luna Sensation (fluopyram and trifloxystrobin) was assessed through in vitro assays and field trials. The effective concentration to inhibit mycelium growth by 50% (EC₅₀) was estimated at different concentrations: 0.01, 0.1, 1, 10, and 100 µg/ml. The EC₅₀ value was 0.076, 0.206, and 6.378 µg/mL for Switch, Tilt, and Luna Sensation, respectively. None of the concentrations tested for Abound were sufficient to inhibit *N. dimidiatum* mycelium growth. Field trials supported in vitro findings, with treated plants showing fewer disease symptoms than untreated plants. This study highlights the efficacy of current labeled products and the potential of additional available fungicides in reducing disease pressure by stem and fruit canker.

Quantifying phloem callose formation in CTV-infected *Citrus macrophylla* trees

M. KHALILZADEH (1), S. Welker (2), A. Levy (3), (1) University of Florida, Lake Alfred, FL, USA; (2) University of Florida, Plant Pathology Department, Auburndale, FL, USA; (3) University of Florida-CREC, Lake Alfred, FL, USA

Callose is a helical polymer of β-1,3-glucan that has various functions during viral infection in plants. Callose deposition at the plasmodesmata (PD) regulates the cell-to-cell movement of macromolecules by changing the size exclusion limit (SEL) of PDs. After virus infection, callose is deposited at PD to inhibit virus spread, but it was shown that virus movement proteins reduce callose levels to open PD to enable viral movement. *Citrus tristeza virus* (CTV) infects and multiplies in the cells of the phloem exclusively and has limited cell-to-cell movement. Despite the rapid progress in CTV research, involvement of callose deposition in CTV cell-to-cell and vascular movement is not clear and there is a lack of information in this aspect. The objective of this study was to investigate the differences in callose deposition among healthy and CTV-infected *Citrus macrophylla* trees. We collected comprehensive images from phloem tissues of healthy and infected plants stained with aniline blue. We used ImageJ to perform quantitative measurements of callose deposition from fluorescence images followed by statistical analysis of data using the ANOVA function in R. Our results show that CTV-infected trees have a higher number of callose deposits in phloem tissues. Lack of callose breakdown in CTV-infected trees may be responsible for restricting the virus to the phloem.

Identification and expression profiling of effectors in the hop downy mildew pathogen *Pseudoperonospora humuli*

S. PURAYANNUR (1), L. M. Cano (1,2), M. Bowman (3,4), K. L. Childs (4), D. H. Gent (5), L. M. Quesada-Ocampo (1), (1) Department of Entomology and Plant Pathology, North Carolina State University, Raleigh, NC, USA; (2) University of Florida – Fort Pierce, FL, USA; (3) Ball Horticultural Company, West Chicago, IL, USA; (4) Department of Plant Biology, Michigan State University, East Lansing, MI, USA; (5) U.S. Department of Agriculture, Agricultural Research Service, Corvallis, OR, USA

Downy mildew caused by the obligate biotrophic oomycete *Pseudoperonospora humuli* is one of the most devastating diseases that affect commercial hop (*Humulus lupulus*). Although host resistance is an effective management strategy, sources of resistance are scarce. In this study, we predicted the secretome and effectorome from the published genome of the *P. humuli* isolate OR502AA. We identified 321 apoplastic effectors and 296 RXLR/RXLR-like effectors in the *P. humuli* secretome comprising 1,250 proteins. The identified RXLRs also included WY domain-containing proteins that lacked canonical RXLR domains. RNA-seq analysis in 12 isolates of *P. humuli* revealed conserved transcript evidence for 171 apoplastic effector genes and 201 RXLR-encoding genes. Expression profiling of the effector-encoding genes by RNA-seq conducted on infected hop leaves collected at various time-points revealed elevated expression of some apoplastic and cytoplasmic effectors. The expression patterns of selected effectors were confirmed through quantitative RT-PCR. We report here a set of 75 in planta expressed core effectors that are conserved among 12 *P. humuli* isolates. These genes are ideal candidates for effector-assisted breeding to develop new downy mildew resistant hop varieties.

Isolation of three strains of *Slafractonia leguminicola* and attempts at pathogenicity tests on red clover (*Trifolium pratense* L.)

I. KAGAN, U.S. Department of Agriculture, Agricultural Research Service, Lexington, KY, USA

Slafractonia leguminicola (Gough and E.S. Elliott) Alhawatem, Baucom, Sanogo, and Creamer (formerly *Rhizoctonia leguminicola*) is the causal agent of blackpatch disease of red clover (*Trifolium pratense* L.) and other legumes. Consumption of infected legumes by livestock can lead to profuse salivation ("slobbers syndrome") due to the production of slaframine (an alkaloid) by *S. leguminicola*. Finding other sources of feed for slobbering livestock can be an economic hardship. Clover cultivars resistant to *S. leguminicola* could help to mitigate disease progress caused by the fungus in pastures, but no resistant cultivars are known. *S. leguminicola* was isolated from three sources in Kentucky: red and white clover collected from a pasture in which horses had been observed to slobber and red clover hay associated with slobbering cattle. The three isolates were identified as *S. leguminicola* by microscopy and by PCR amplification of a fragment of the ITS region. Red clover (cultivar "Kenland") was inoculated with either of the pasture isolates by spraying with a homogenate of mycelium grown on liquid red clover media. Inoculation with the white clover isolate resulted in small lesions in one experiment. Reproducible induction of symptoms is a future goal. Pathogenicity tests may lead to identification of resistant cultivars, which could then be utilized by producers to decrease the risk of slobbers syndrome in livestock.

LAMP assay as a robust, field deployable diagnostic tool for detection of *Cucurbit leaf crumple virus*

S. WALIULLAH (1), K. S. Ling (2), E. Cieniewicz (3), J. E. Oliver (1), P. Ji (1), E. Ali (1), (1) University of Georgia, Tifton, GA, USA; (2) USDA-ARS, Charleston, SC, USA; (3) Clemson University, Clemson, SC, USA

Cucurbit leaf crumple virus (CuLCrV) is one of the most important begomoviruses that infects cucurbits worldwide. To diagnose this pathogen rapidly and efficiently from infected leaf tissues, a loop-mediated isothermal amplification (LAMP) assay was developed. A set of six specific LAMP primers were designed and synthesized, targeting a total 240 nt sequence regions in the DNA A of CuLCrV for the detection of the virus from various infected leaf tissues. Real-time LAMP amplification with the Genie® III system was executed, which was further confirmed by gel electrophoresis and SYBR™ Green I DNA staining for visual observation. The reaction conditions, including optimum reaction temperature and time, were determined. No cross-reactivity was seen with other begomoviruses in single virus-infected and mixed virus-infected assays. The sensitivity assay demonstrated that the LAMP reaction was more sensitive than conventional PCR, but less sensitive than qPCR. However, it was simpler and faster than the other assays evaluated. The LAMP assay also amplified from CuLCrV-infected symptomatic and asymptomatic samples more efficiently than PCR. Successful LAMP amplification was observed in mixed virus-infected field samples. This simple, rapid, and sensitive method has the capacity to detect CuLCrV in samples collected in the field and, therefore, is suitable for early detection of the disease to reduce the risk of epidemics.

Stevia, in the quest of sweetness...Plant diseases appear! Identifying priority diseases limiting stevia production in Paraguay

A. D. SANABRIA (1), J. E. Barua (2), A. A. Cubilla-Rios (3), G. Enciso (4), M. Maidana-Ojeda (4), D. Shew (5), L. D. Thiessen (5), (1) North Carolina State University, Raleigh, NC, USA; (2) Universidad Nacional de Asuncion, Central, PARAGUAY; (3) Facultad de Ciencias Químicas, Universidad Nacional de Asunción, Central, PARAGUAY; (4) Centro de Desarrollo e Innovación Tecnológica, Hohenau, PARAGUAY; (5) North Carolina State University, Raleigh, NC, USA

Stevia (*Stevia rebaudiana*) is an important specialty crop for Paraguayan farmers, generating income for more than 30% of rural families. The main constraints of stevia production are yield losses caused by plant diseases, their inappropriate identification, and the incorrect use of pesticides to control them. The objective of this work was to train researchers, extensionists, and growers on disease diagnostic and to identify priority diseases limiting stevia production. Two workshops were conducted, one in Facultad de Ciencias Químicas, Universidad Nacional de Asunción, Paraguay, and the other in Facultad de Agronomía “Universidad Católica Nuestra Señora de la Asunción,” Itapúa, Paraguay. In addition, we conducted a survey about the higher priority research areas needed for stevia in Paraguay. We provided a list of diseases of stevia and asked participants to rank them from 1 (a high priority) to 10 (low priority). A total of 40 participants attended, including extension agents, faculty, public investigators, stevia producers, private consultants, and graduate students with experience in stevia research or production. The survey results show that stem rot (*Sclerotium rolfsii*), and damping-off ranked as high-priority diseases for stevia growers, followed by Septoria leaf spot, Sclerotinia rot, and charcoal rot. In contrast, nematodes, bacterial diseases, Alternaria leaf spot, and TSWV (Tomato spotted wilt virus) were ranked as lower priority diseases for stevia growers.

Huanglongbing infection in sweet orange is associated with abnormal phloem callose deposition and carbohydrate transport dysfunction

S. Welker (1), M. Dutt (2), A. LEVY (3), C. Vincent (2), (1) University of Florida, Plant Pathology Department, Auburndale, FL, USA; (2) University of Florida, Lake Alfred, FL, USA; (3) University of Florida-CREC, Lake Alfred, FL, USA

Huanglongbing (HLB) is a disease of citrus that is caused by the bacteria *Candidatus* ‘Liberibacter asiaticus’ (CLAs). This disease causes substantial loss of yield for citrus growers. HLB-infected plants appear to experience dysfunction in the normal transport of carbon from the source leaves to the sink tissues. To explore this phenomenon, we incorporated a ¹⁴C tracer into the normal photosynthetic reactions of HLB-positive and -negative ‘Hamlin’ sweet orange trees on two rootstocks. This allowed the non-invasive measurement of the translocation speed of carbon compounds through the phloem of the trees. In the same phloem tissue, we measured the amount of callose formations and the quantity of CLAs genetic material. We also quantified the amounts of sucrose, starch, and ¹⁴C-containing compounds in the stem phloem, leaf, and root tissue. We found that the interaction between CLAs status and rootstock type had a significant effect on phloem translocation speed, leaf carbohydrate export, and structural root sucrose concentration. Statistical testing revealed that the quantity of callose deposits and CLAs genetic material in the phloem have a significant negative effect on translocation speed. These findings demonstrate that CLAs infection greatly impacts the tree’s ability to transport and store carbohydrate compounds, and that this effect may vary with the host rootstock. This information can be used to guide citrus cultivar selection in the future.

Evaluation of potential biological control agents in reducing the impact of *Rhizoctonia solani* and *Fusarium graminearum* in controlled environments

S. A. SHARFADINE, C. M. Rojas, A. Rojas, University of Arkansas, Fayetteville, AR, USA

Rhizoctonia solani, a soilborne fungal pathogen, is the causal agent of sheath blight, which is one of the most devastating diseases in rice production systems globally. Rice is an important agronomic crop highly consumed all around the world. Currently, sheath blight is managed primarily by fungicide application, use of tolerant rice varieties, and cultural practices. Sheath blight has the potential to cause up to 50% yield losses in fields where very susceptible cultivars are planted. *Fusarium graminearum* is the causal agent of Fusarium head blight (FHB), a devastating disease in wheat, barley, and other cereal crops that causes significant yield losses around the world.

Bacterial strains of *Burkholderia cepacia* and *Pseudomonas fluorescens* were used as biological agents to evaluate their antagonistic effects against three isolates of *R. solani* and one isolate of *F. graminearum* in controlled environments. Two *Pseudomonas* strains: PBL3 (*P. protegens*) and PBL 18 (*B. cepacia*) and two strains of *Burkholderia*: PBL 18 (*B. cepacia*) and PBL 33 (*Burkholderia* sp.) were used in this experiment. PBL 24 and PBL 18 show promising antagonistic effect against both *R. solani* and *F. graminearum* isolates in both dual-culture and seed-plate assay methods in controlled environments.

In vitro and in field application efficacy of local *Trichoderma* strains against Fusarium wilt of tomato

J. D. CARRILLO (1), L. Yang (2), G. E. Vallad (1), (1) Gulf Coast Research and Education Center, University of Florida, Wimauma, FL, USA; (2) China Agricultural University, Beijing, Haidian, CHINA

Commercial and locally derived strains of *Trichoderma* are applied as biological control agents to control many plant pathogens in diverse agricultural settings. However, their efficacy against Fusarium wilt of tomato caused by *Fusarium oxysporum* f. sp. *lycopersici* (*FOL*) in sandy soil is limited. Therefore, we conducted dual culture assays on PDA to evaluate the antagonistic ability of locally recovered *Trichoderma* against 3 strains of *FOL*. This was followed by field trials comparing the efficacy of 10 local *Trichoderma* species, a commercial product, and an untreated control in fall of 2020. Conidial suspensions were applied at a rate of 1×10^{11} spores/acre 2 weeks before planting through drip tape followed by drenching at planting, 2- and 4-weeks post planting. All tomato seedlings were inoculated with 3×10^6 *FOL* spores 1 day before planting. Plant height and disease incidence (DI) were recorded every 2 weeks, while disease severity (DS) and yield were recorded at the end point. In vitro results indicated two species (*Trichoderma* sp.(I) and *T. longibrachiatum*) significantly reduced the growth ($P < 0.05$) of all strains of *FOL* after 7 days. In the field, *T. longibrachiatum* showed lower DI and DS ($P < 0.05$) followed by *T. parareesei* and *Trichoderma* sp. (IV) compared to other treatments. There were no significant differences in plant height and yield. This study suggests local *Trichoderma* strains may provide enhanced control of *FOL* compared to commercial products in Florida

Examining interactions between Thimet® and early and late leaf spot on peanut, a surprising finding

M. J. NEWARK (1), S. Ludwig (2), P. Porpiglia (3), (1) AMVAC, Gainesville, FL, USA; (2) AMVAC, Arp, TX, USA; (3) AMVAC, Newport Beach, CA, USA

Thimet® (Phorate) is an organophosphate insecticide applied in-furrow to peanuts for control of thrips and suppression of Tomato spotted wilt virus (TSWV). In 2018, Dan Anco and Ian Small noted that plots treated with phorate had delayed onset of leaf spot symptoms. In 2019 and 2020, AMVAC commissioned 12 trials to explore and confirm indications that phorate delayed leaf spot symptoms in peanut. Locations included academic sites in Georgia, Florida, North Carolina, South Carolina, and Alabama. Five treatments were evaluated, including Thimet (6 lb/A), Velum Total (18 fl oz/A), Admire Pro (10 fl oz/A), and AgLogic (7 lb/A), all applied at plant in a randomized complete block design. Plots were evaluated for leaf spot incidence, leaf spot severity, defoliation, and yields. In 2019, multiple trials had a significant reduction in defoliation caused by early and late leaf spot. In Florida, defoliation was significantly reduced at 98 and 133 DAP. In South Carolina, a significant reduction in leaf spot incidence was observed in Thimet-treated plots for 106 days after planting compared to the check. In 2020, disease pressure was lighter at several locations. However, a 7-day delay in leaf spot was observed in one site in Florida with a significant reduction in defoliation observed up to 111 days after planting.

Utilizing a population genetics approach to facilitate crop-specific management of the cucurbit downy mildew pathogen, *Pseudoperonospora cubensis*

K. D'ARCANGELO (1), A. Rahman (2), T. D. Miles (3), L. M. Quesada-Ocampo (4), (1) North Carolina State University, Raleigh, NC, USA; (2) Corteva Agrisciences, Indianapolis, IN, USA; (3) Michigan State University, East Lansing, MI, USA; (4) Department of Entomology and Plant Pathology, North Carolina State University, Raleigh, NC, USA

Pseudoperonospora cubensis is an oomycete pathogen that causes downy mildew on many crops within the *Cucurbitaceae*. Following a population shift in 2004, cucurbit downy mildew has become the most devastating disease of cucurbits in the eastern United States due to a failure of previously effective cucumber host resistance and reduced efficacy of some commercial fungicides. Using microsatellites and isolates from a wide range of hosts, it was determined that two host-adapted *P. cubensis* clades exist. Using next generation sequencing and bioinformatics, species-specific and host-preference diagnostic markers were identified, and a qPCR assay was developed. TaqMan® qPCR assays for detection of single nucleotide polymorphisms (SNPs) known to confer resistance to FRAC 11 and FRAC 40 fungicides were also developed. When isolates were genotyped, it was revealed that SNPs conferring resistance to FRAC 40 fungicides were more prevalent in Clade 2 isolates, and wild hosts were capable of harboring resistant *P. cubensis* isolates. Additionally, the clade assay was implemented into user-friendly, impaction-type spore-trapping systems in sentinel plots for validation. Upon successful application in the field, our findings will significantly improve *P. cubensis* biosurveillance by monitoring inoculum levels, delivering refined information about cucurbit infection risk, distribution of fungicide resistance in fields and ultimately guide population-informed management practices.

Development of race specific primers to molecularly distinguish between Race 0 and Race 1 of *Phytophthora nicotianae*

S. M. COCHRAN (1), T. Schappe (1), S. Purayannur (2), L. M. Quesada-Ocampo (2), L. D. Thiessen (1), (1) North Carolina State University, Raleigh, NC, USA; (2) Department of Entomology and Plant Pathology, North Carolina State University, Raleigh, NC, USA

Phytophthora nicotianae is a polycyclic hemibiotroph and is the causal agent of black shank disease in tobacco. It is not possible to distinguish between races of *P. nicotianae* in situ, and current diagnostic methods for race determination are time-consuming and require greenhouse screening assays with varieties of tobacco containing known resistance genes. The goal of this research is to develop a race-specific molecular assay to save researchers and growers time, money, and resources. The genomes of representative *P. nicotianae* isolates from Race 0 and Race 1 populations were sequenced, annotated, and aligned. RNA for five representative isolates of each race were sequenced to aid in genome alignment and annotation. Diagnostic PCR primers will be designed from the annotated genomes and transcriptomes to distinguish between Race 0 and Race 1 by utilizing differential SNPs. Primers will be tested from known Race 0 and Race 1 isolates from North Carolina. An updated survey of race structure in North Carolina will be conducted utilizing the developed primer sets.

In-season survey of soybean taproot decline incidence and severity on selected Mississippi Delta farms

W. KINGERY, Starkville, MS, USA

Soybean (*Glycine max* (L.) Merr.) taproot decline (TRD) was first reported in Mississippi over 12 years ago and has been established to be caused by a species of *Xylaria*. Its progression in Mississippi has led to significant yield losses in fields with severe infestations. Mechanisms of *Xylaria* spp. pathogenesis are largely unknown. In order to document the incidence and severity of TRD, the expression and impact of TRD along with farming system characteristics on selected Mississippi Delta farms were documented in 2019 (18 fields) and 2020 (20 fields) through the utilization of a widely applied field survey instrument. Surveyed fields were divided into quadrants and TRD occurrence within observation areas (approximately 15 m radius) was characterized via a rating protocol. TRD intensity was determined by the percentage of infected plants along 3 m of crop row; these measurements were replicated in each quadrant. The survey was made at the R5 soybean developmental stage. Since numerous species of *Xylaria* are known to exist as saprophytes, crop residues are a key component of TRD assessment. Surface residue was visually rated as percent ground cover. Buried residue was assessed through root zone excavation of two infected plants per 3-m sampling transect. The infection incidence and severity were not strongly correlated with surface residue, but a very high percentage (>95%) of infected plants had buried residue within the top 15 cm of the rooting zone.