2015 Southern Division Meeting Abstracts

Abstracts presented at the APS Southern Division meeting in Atlanta, Georgia, February 1–2, 2015. The abstracts are arranged alphabetically by the first author's name. Recommended format for citing division meeting abstracts, using the first abstract below as an example, is as follows: Appel, D. N., and Ong, K. L. 2015. The results of survey for citrus greening on the Upper Gulf Coast of Texas. (Abstr.) *Phytopathology* 105(Suppl. 2):S2.1. <http://dx.doi.org/10.1094/PHYTO-105-4-S2.1>

The results of survey for citrus greening on the Upper Gulf Coast of Texas

D. N. APPEL (1), K. L. Ong (1)

(1) Texas A&M AgriLife Extension Service, College Station, TX, U.S.A.
Phytopathology 105(Suppl. 2):S2.1

Annual citrus surveys have been conducted for *Diophorina citri*, the Asian Citrus Psyllid (ACP) and citrus greening disease, along the Texas Upper Gulf Coast since 2010. The objective is to determine whether any ACPs carry the citrus greening pathogen, *Candidatus Liberibacter asiaticus*. The focus is largely on dooryard citrus throughout 8 counties in Southeast Texas. Through 2013, 1839 samples were collected, consisting of adults ($n = 657$), nymphs (367), eggs (4), and citrus foliage (811). No samples were positive for the pathogen, as tested with a multiplex, quantitative real-time PCR assay by the Texas Plant Disease Diagnostic Laboratory (TPDDL) in College Station, TX. Two Potential Actionable Suspect Samples (PASS) were forwarded to the USDA-APHIS-PPQ-CPHST Laboratory in Beltsville, MD. The 2012 sample tested inconclusive and the 2013 sample confirmed negative. Although the surveys were not conducted to investigate population dynamics of the ACP, some seasonal trends in psyllid numbers were observed. In contrast, contaminated ACPs and diseased trees have been detected by others in the commercial citrus growing region in the Rio Grande Valley (RGV) of South Texas. Contaminated nursery stock from the RGV was suspected to have been delivered to nurseries within the survey area. As of November, 2014, the TPDDL has confirmed the presence of infected nursery stock in 10 nurseries in 3 counties. Quarantines and other regulatory actions are in place to contain the disease. These events reinforce the need for continuing survey for pathogen encroachment into the Upper Gulf Coast landscape.

The effect of oscillating temperatures on the growth rate of *Sclerotium rolfsii*

R. L. BAROCCO (1), N. S. Dufault (1)

(1) University of Florida, Gainesville, FL, U.S.A.
Phytopathology 105(Suppl. 2):S2.1

Sclerotium rolfsii is a soil-borne fungal pathogen that causes significant diseases on a wide variety of crop hosts. Weather-based models for site-specific management of plant diseases typically use microbial growth curves based on studies with constant mean temperatures. However, daily changes in temperatures under natural conditions fluctuate over time with variable minimum to maximum ranges. For this study, the growth rates of 23 Florida *S. rolfsii* isolates from peanut, tomato, and pepper were measured under 15, 20, 25, 30, and 35°C mean temperatures that oscillate along a sine wave curve

with a 24-hour cycle and amplitudes of 0, 4, or 8°C. Plugs of hyphae were plated on 2.5% acidified potato dextrose agar, and growth was measured every 12 hours for a duration of 48 hours. Mycelial growth decreased with increasing amplitudes for the mean temperatures of 25, 30, and 35°C. When the amplitudes were 0 or 4°C, optimum mycelial growth rates for all isolates were observed at the 30°C mean temperature. However, optimal mean temperatures for mycelial growth differed among isolates when the amplitude was 8°C. At this amplitude some isolates grew optimally at a mean of 25°C and others at a mean of 30°C. This study indicates that the growth response of *S. rolfsii* to temperature will vary depending on the isolate and range of temperatures which the pathogen is exposed to during a day. The information from this study can be used to improve risk models for diseases caused by this devastating pathogen.

In furrow applications of azoxystrobin for peanut seed and seedling disease management

T. BRENNEMAN (1), R. Kemerait (1), A. Culbreath (1)

(1) UGA, Tifton, GA, U.S.A.

Phytopathology 105(Suppl. 2):S2.1

Azoxystrobin (Abound 2.08F) was evaluated as an in furrow (IF) spray at three different rates with peanut (Cv. Tifguard) seed either nontreated or treated with Dynasty PD (250 g/kg of seed). Two tests were conducted in 2014, each with 5 replications in a split plot design, with seed treatment as whole plots and IF sprays a sub plots. When Dynasty PD was used, the IF sprays had no effect on plant stands, growth, diseases or yield in either test. With no seed treatment applied, all three rates of azoxystrobin (0.5, 0.11 and 0.22 kg/ha) IF more than doubled final plant stand in both tests, and also increased plant growth. These treatments had no effect on stem rot (*Sclerotium rolfsii*) at harvest, but pod yield was increased significantly by all IF treatments in both trials by an average of 1383 and 1783 kg/ha, respectively. There were few differences among the three rates of IF sprays. While seed treatments alone are usually adequate for a good plant stand and pod yield, an IF spray of azoxystrobin at 0.05–0.11 kg/ha can help protect young plants under more severe disease pressure.

Evaluation of systemic fungicides in pecans and implications for disease management

K. A. BROWN (1), T. B. Brenneman (1)

(1) University of Georgia, Tifton, GA, U.S.A.

Phytopathology 105(Suppl. 2):S2.1

Scab (*Fusicladium effusum*) is a common disease of pecans, especially during wet years, and frequent fungicide sprays are needed to prevent serious losses. Some fungicides used on pecans are known to move systemically in other crops, but little is known about this phenomenon in pecan tissues. The movement of tebuconazole (TEB = Orius 3.6), azoxystrobin (AZO = Abound 2.08), a phosphite (PHO = Rampart), and TPTH (Super Tin 4L), a protectant, was studied by treating lower leaves on a terminal, then sampling nontreated leaves above those on the same stem. Samples were taken 1, 3, 5 and 7 days after fungicide application and bioassayed with *Sclerotium rolfsii*. TEB, AZO

The abstracts are published as submitted. They were formatted but not edited at the APS headquarters office.

<http://dx.doi.org/10.1094/PHYTO-105-4-S2.1>

© 2015 The American Phytopathological Society

and PHO all reduced the diseased area versus the protectant (Super Tin). AZO showed the best control 1 day after spray application, whereas PHO had better control at 7 days. AZO and PHO exhibited faster movement and better residual control 7 days after application than other treatments. Results indicate that systemic fungicides can help protect foliage that was not uniformly sprayed, or that developed after the previous application.

Influence of application technology on foliar fungicide efficacy in *Cercospora soja* infected soybeans

S. A. BUTLER (1), H. Young-Kelly (1), G. Kruger (2)
(1) University of Tennessee, Jackson, TN, U.S.A.; (2) University of Nebraska, North Platte, NE, U.S.A.
Phytopathology 105(Suppl. 2):S2.2

Use of new herbicide tolerant crops will require growers to use drift-reducing nozzle technology that produces very-coarse to ultra-coarse droplets. Pesticides that have contact or locally systemic activity are typically not as effective when applied with large spray droplets. Due to the frequency of tank-mixed pesticide applications and the cost associated with utilizing drift-reduction technology, these changes will also affect other foliar pesticides. Soybean crops infected with *Cercospora soja*, the causal agent of frogeye leaf spot (FLS) in soybean, could be negatively impacted by reductions in spray coverage. Field experiments were conducted in Jackson and Milan, Tennessee in 2014 to evaluate the influence of application technology on foliar fungicide efficacy in soybean infected with FLS. Quadris Top (azoxystrobin and difenoconazole) was applied through 9 nozzle arrangements. Nozzle treatments included 3 angles of 0°, 30°, and a combination of 10° and 50°, 2 fan arrangements of single and twin, and 3 droplet size ranges of >medium (200–250 microns), >ultra-coarse (400–850 microns), and a combination of medium and ultra-coarse (575 microns). Disease index ratings were taken at 14 and 28 days after application (DAA). Leaf samples were collected 0, 2, 4, 7, and 14 DAA for dosage quantification to be analyzed using high-performance liquid chromatography/mass spectrometry. In 2014 between 2 locations, no significant differences have been found between treatments of spray angle, fan arrangement, or droplet size based on disease control and yield comparisons. Results suggest that drift-reduction nozzle technology may not negatively affect fungicide efficacy on FLS in soybean.

Effects of an experimental seed treatment supplement and potash fertilization on seedling diseases of snap bean and soybean and on crop yield

C. CANADAY (1), S. D. Stewart (1), A. McClure (1)
(1) University of Tennessee, Jackson, TN, U.S.A.
Phytopathology 105(Suppl. 2):S2.2

Seedling diseases cause damping-off, root rot, stunting, and yield loss on many crops. Losses can be exacerbated with application of muriate of potash (KCl). The effect of experimental seed treatment supplements on seedling diseases of snap bean and soybean, with and without potash fertilization, were evaluated in a series of field experiments in 2013 and 2014. A split-plot design was used in all tests with potash rates as whole plots and seed treatment supplements as subplots. In 2013, adding an experimental seed treatment supplement (Supplement A) to the standard snap bean seed treatment increased snap bean emergence, reduced seedling disease incidence, increased the stand of healthy plants, and increased yield by over 65%. Potash applied 3 days after planting (and after 1.3 inch of rain) had no effect on any variable. In 2014, twelve soybean seed treatment supplements were evaluated. None of the supplements had an effect on seedling emergence or disease incidence. Adding Supplement A to the standard seed treatment increased soybean yield by over 6.0 bu/A. Soybean yield with no potash was nearly identical to an application of 50 lb K₂O/A applied 11 days before planting. Application of muriate of potash at 100 and 150 lb K₂O/A reduced soybean yield by 5.8 and 9.9 bu/A, respectively, compared to the 50 lb K₂O/A rate. The disease control benefits of Supplement A appear to vary with the crop. A yield increase with Supplement A appears more consistent.

Fungal colonization and cercosporin and flavonoid concentrations for two different symptoms of *Cercospora* leaf blight in soybean

E. CHAGAS FERREIRA DA SILVA (1), T. G. Garcia Aroca (1), A. V. Lygin (2), A. K. Chanda (3), C. L. Robertson (1), B. M. Ward (1), R. W. Schneider (1)
(1) Louisiana State University AgCenter, Baton Rouge, LA, U.S.A.; (2) University of Illinois, Urbana, IL, U.S.A.; (3) University of Minnesota, Crookston, MN, U.S.A.
Phytopathology 105(Suppl. 2):S2.2

Cercospora leaf blight (CLB), caused by *Cercospora kikuchii*, is the most important soybean disease in Louisiana. Two different symptoms are

associated with CLB: purple leaves (believed to be due to cercosporin accumulation) and blight. Previous publications suggested that CLB starts with leaf purpling and leaves become blighted as the disease progresses. Our findings showed that there was not a significant correlation between these two symptoms, which suggests that they may be a result of two diseases caused by the same pathogen. We investigated the possibility that the purple symptom is a plant reaction, and the blight is the actual disease. The objectives of this work were: 1) to determine the relationships among fungal biomass in leaves, cercosporin concentration and the two symptoms, and 2) to determine the concentrations of flavonoids in symptomatic leaves. Four soybean cultivars were planted at two locations. Leaves showing different severities of the two symptoms were collected for quantification of anthocyanins, flavonoids and cercosporin, using HPLC, and fungal colonization, using qPCR. In general, *C. kikuchii* was detected in all leaves (including symptomless); however, blighted leaves had higher fungal biomass than purple leaves. Cercosporin concentrations also were higher in blighted leaves. No anthocyanins were found in any leaves. Coefficients of determination ranged from 0.09 to 0.24 for glyceollin and other variables.

Complete genome sequences of nine isolates of *Canna yellow streak virus* reveal its relationship to *Sugarcane mosaic virus* subgroup of potyviruses, intraspecific genetic diversity and expands the natural host range of *SCMV* subgroup of potyviruses

R. P. CHAUHAN (1), P. Rajakaruna (1), J. Verchot (1)
(1) Department of Entomology and Plant Pathology, Oklahoma State University, Stillwater, OK, U.S.A.
Phytopathology 105(Suppl. 2):S2.2

Canna yellow streak virus (CaYSV) was first reported in Europe and the full genome sequence was reported in 2010 from UK. CaYSV has been recently reported in USA but there is no information about the genetic variation or possible origin of CaYSV in the country. Given the popularity and global trade of cannas a clear picture of disease incidence and genetic diversity of CaYSV is critical to disease management. In this project, eight RT-PCR reactions were carried out to amplify the entire genome of one CaYSV-OK, three CaYSV-BZ and five CaYSV-NC isolates which were obtained locally in Oklahoma. These PCR products were either cloned or directly sequenced. Contigs were prepared and assembled using CAP3 DNA sequence assembly program. The maximum likelihood tree using MUSCLE algorithm with 1000 bootstrap replications determined that CaYSV belongs to *Sugarcane mosaic virus* (SCMV) subgroup of potyviruses. It was intriguing to see that the BZ isolates clustered with the European and Israeli isolates and OK isolate clustered with the Thai isolates reported in GenBank. Multiple sequence alignment of amino acid sequences among CaYSV isolates showed greatest sequence diversity in N-terminal region of the coat protein suggests that this might be the most suitable region for discriminating CaYSV isolates. Further biological characterization identified *N. benthamiana*, *C. quinoa* and *P. vulgaris* as experimental hosts that support systemic infection. Studying the molecular variability, genetic structure and biological characters of CaYSV will provide new insight into molecular history, dispersion and emergence of these viruses which is critical to disease management.

Impact of outer membrane protein MopB on the biofilm formation of *Xylella fastidiosa*

H. CHEN (1), P. P. Kandel (1), J. Parker (1), L. Cruz (1), L. De La Fuente (1)
(1) Auburn University, Auburn, AL, U.S.A.
Phytopathology 105(Suppl. 2):S2.2

Xylella fastidiosa is the causal agent of many economically important plant diseases. This bacterium is limited to surviving inside the xylem vessels of host plants, where mineral nutrients are transported from roots to leaves. The virulence of this pathogen is significantly correlated with the available concentrations of mineral elements. Previous research showed that Ca²⁺ increases the virulence traits of this bacterium, including twitching motility and biofilm formation. The mechanisms of these effects are not well understood. In this work, we focus on the role of the outer membrane protein MopB in the biofilm formation of *Xylella fastidiosa*. A *mopB* gene knockout mutant was constructed. Experiments to assess the effects of Ca²⁺ supplementation on biofilm formation showed that the *mopB* mutant has decreased biofilm formation compared to the wild-type strain. Furthermore, the *mopB* mutant shows no increase in biofilm formation in response to Ca²⁺ supplementation, in contrast to the wild-type strain. In addition, two different calcium-binding motifs were identified based on the analysis of the amino acid sequence of MopB. Currently the virulence of this mutant is being assessed in greenhouse experiments. We hypothesize that MopB is important for the biofilm formation inside xylem vessels of the host plant, and in particular this protein has a role in the increased virulence mediated by Ca²⁺.

Frogeye leaf spot response to solo and combination fungicides

A. M. COCHRAN (1), H. M. Kelly (2), K. Lamour (1), W. J. Jordan (2), B. P. Vega (2)

(1) The University of Tennessee, Knoxville, TN, U.S.A.; (2) The University of Tennessee, Jackson, TN, U.S.A.

Phytopathology 105(Suppl. 2):S2.3

In 2010 frogeye leaf spot (FLS) demonstrated resistance to the quinone outside inhibitor (QoI) fungicides. In an effort to understand the efficacy of different fungicides in light of QoI fungicide resistance, field trials were conducted in a randomized complete block design in five locations in Tennessee and one in Illinois during the 2013–2014 soybean growing seasons. A minimum of six foliar fungicides with different solo or combination modes of actions were evaluated on Asgrow 4832 soybean using an R3 application time. FLS disease severity and yield were obtained from the center two rows of each plot. *C. sojae* spores from test plots were evaluated for QoI resistance by plating on fungicide amended and unamended media. The negative correlation between yield (bu/a) and increasing FLS disease severity (%) was demonstrated during both growing seasons. The three-way combination treatment (Priaxor+Domark) was the highest yielding in half of the 2014 trials. Dual combination treatments were generally within the top three highest yielding of each trial, while the lowest yielding were the solo QoI and DMI treatments which were ranked similarly to the untreated controls. FLS severity did not differ significantly between the untreated and the solo strobilurin treatment. Future research will focus on analyzing FLS lesion DNA to assess the pressure exerted by the various fungicides on selection for G143A mutation conferring QoI-fungicide resistance using qPCR and to evaluate the overall population diversity of *C. sojae* using 48 designed SNP markers.

Experiences with fungicide resistance in Florida citrus

M. M. DEWDNEY (1)

(1) University of Florida, Lake Alfred, FL, U.S.A.

Phytopathology 105(Suppl. 2):S2.3

Foliar fungal diseases of citrus are historically production limiting for fresh fruit and processing cultivars in Florida because of cosmetic defects, defoliation, and premature abscission. Few fungicide classes have been registered for use in citrus limiting rotation options. The primary fungicide class used for the last decade, aside from copper, are the quinone-outside inhibitors (QoI) but recently 57.6% of the *Alternaria alternata* isolates, causal agent of Alternaria brown spot, were found to be resistant to QoI fungicides in a statewide survey of tangerine blocks. The proportion of resistant isolates differed significantly ($P < 0.0001$) with cultivar susceptibility and application frequency. All resistant isolates carried the G143A point mutation in the cytochrome *b* gene (*cytb*). The resistance was stable and isolate fitness was not affected by the resistance trait. Since QoIs are fundamental to the control of the emerging disease citrus black spot, a baseline study was done on the Florida population of *Guignardia citricarpa*. All isolates were found to be sensitive to QoIs and an intron was found in *cytb* immediately post G143 potentially blocking resistance conferring mutations. In addition, the *G. citricarpa* population was screened for sensitivity to five demethylation inhibitor (DMI) fungicides to be potentially field tested. All isolates were sensitive and difenoconazole and fenbuconazole had greater efficacy than the other tested DMI's ($P < 0.0001$).

Screening winter canola for seedling resistance to black leg

C. I. DIAZ (1), J. Damicone (1)

(1) Oklahoma State University, Stillwater, OK, U.S.A.

Phytopathology 105(Suppl. 2):S2.3

Black leg disease, caused by the fungus *Leptosphaeria maculans*, is a common disease of winter canola (*Brassica napus*) in Oklahoma. Major resistance genes (*Rlm*) are expressed in seedlings and interact with avirulence genes in *L. maculans* (*AvrLm*). The presence of avirulence alleles in the local pathogen population was determined by inoculating differential cultivars harboring *Rlm1* and *Rlm2,3* and PCR amplification of avirulence alleles *AvrLm1*, *AvrLm4-7*, *AvrLm6*. Avirulence alleles *AvrLm6* (90%) and *AvrLm4-7* (96%) were prevalent in the local population ($n = 94$), whereas *AvrLm1* and *AvrLm2-3* presence was only 27% and 10%, respectively. Five races (*AvrLm6*, *AvrLm4-7*, *AvrLm6,4-7*, *AvrLm1,6,4-7* and *avrLm1,2,3,6,4-7*) were identified and used to characterize seedling resistance in 25 commercial cultivars and breeding lines. Most (64%) commercial cultivars and breeding lines were susceptible to all five races and lack specific resistance genes. Some entries (12%) presented race non-specific resistance, while other (24%) had heterogeneous resistance to one, more than one, or all races. The study showed that commercial Roundup-Ready cultivars currently grown in the region generally lacked seedling resistance genes, except for DKW46-15 which seemed to be resistant to *AvrLm4*. Most conventional cultivars and hybrids appeared to have heterogeneous resistance to one or more races with

the exception of Dimension, Visby and Rossini which were resistant to all races. Several breeding lines had heterogeneous resistance to all races, except for KSUR21 which was susceptible to all races.

Severity of bacterial leaf spot in pepper is affected by cation concentrations in pepper tissues

B. DUTTA (1), D. Langston (2), H. Sanders (1), S. Smith (1), R. Gitaitis (1)

(1) University of Georgia, Tifton, GA, U.S.A.; (2) Tidewater Agricultural Research and Extension Center, Suffolk, VA, U.S.A.

Phytopathology 105(Suppl. 2):S2.3

Regression models based on cation concentrations in plant tissues were developed for predicting bacterial leaf spot (BLS) severity in pepper (*Capsicum annuum* L.) caused by *Xanthomonas euvesicatoria*. Models from two consecutive years of field study (2012–2013) consisted mainly of combinations of Cu^{2+} , Fe^{2+} , Zn^{2+} and Mn^{2+} . Among other roles, these cations act as co-factors for superoxide-dismutase (SOD) enzymes, namely *Cu-ZnSOD*, *FeSOD*, and *MnSOD*. SODs detoxify reactive oxygen species forming salicylic acid (SA, a component of systemic acquired resistance (SAR)). The BLS-cation model was also a good fit for relative expression of the genes *Cu-ZnSOD* ($P = 0.05$; adj. $R^2 = 0.92$) and *MnSOD* ($P = 0.009$; adj. $R^2 = 0.98$). Relative expression of the *NPR1* gene (non-expresser pathogenesis-related protein, another component of SAR) fit a model consisting of *Cu-ZnSOD*, *FeSOD*, and *MnSOD* values ($P \leq 0.0001$; adj. $R^2 = 0.93$). In addition, SA levels and *MnSOD* expression were related to BLS severity in two commercial pepper fields. Learning how cation concentrations and their relative ratios affect SODs, SA and SAR could lead to improved disease risk predictions and prescribed fertilization practices using precision agricultural techniques.

Management of daylily rust with different fungicide combinations and spray intervals

R. S. EMMITT (1), K. L. Stevenson (2), T. B. Brennenman (2), J. W. Buck (1)

(1) University of Georgia, Griffin, GA, U.S.A.; (2) University of Georgia, Tifton, GA, U.S.A.

Phytopathology 105(Suppl. 2):S2.3

Daylily (*Heemerocallis* spp.) is an herbaceous perennial that is used extensively in the American landscape. Daylilies remained relatively pest-free until the introduction of daylily rust caused by the fungus *Puccinia hemerocallidis*, in 2000. Fungicides across several chemical classes are currently registered for daylily rust and growers rely heavily on these for the management of this disease. The objectives of this study were to determine the most cost effective fungicide combinations and application intervals for managing daylily rust in the field. Foliar spray combinations and spray intervals were evaluated in field experiments, under high disease pressure, in Griffin, GA in 2014. Foliar spray combinations of azoxystrobin + propiconazole, azoxystrobin + chlorothalonil, and azoxystrobin alone at 21 days provided comparable protection to azoxystrobin alone at 14 days. The combinations of propiconazole + chlorothalonil and thiophanate-methyl + chlorothalonil at 21 or 28 days did not differ from the untreated control. Elimination of less efficacious active ingredients and unnecessary applications from spray regimes can help growers maximize profitability by reducing expenses and simplifying inventory and storage.

Aflatoxin production and oxidative stress in *Aspergillus flavus*

J. C. FOUNTAIN (1), L. Yang (1), P. Khera (2), R. C. Kemerait (1), R. D. Lee (1), B. T. Scully (3), R. K. Varshney (2), B. Guo (4)

(1) University of Georgia, Tifton, GA, U.S.A.; (2) International Crops Research Institute for the Semi-Arid Tropics, Hyderabad, India; (3) USDA-ARS, Fort Pierce, FL, U.S.A.; (4) USDA-ARS, Tifton, GA, U.S.A.

Phytopathology 105(Suppl. 2):S2.3

The colonization of crops by *Aspergillus flavus* results in the production of aflatoxins. Aflatoxin production is also exacerbated by abiotic stresses in the field. Here, we investigated the role of reactive oxygen species (ROS), which accumulate in plant tissues in response to drought and heat stress, and aflatoxin production in different isolates of *A. flavus* and *A. parasiticus*. Ten isolates were used, including nine *A. flavus* toxigenic (+) and atoxigenic (-) isolates: NRRL3357(+), A9(+), AF13(+), Tox4(+), A1(-), K49(-), K54(-), AF36(-), and Aflaguard(-), and one *A. parasiticus* isolate, NRRL2999(+). The isolates were cultured in toxin-conductive yeast extract-sucrose (YES) media supplemented with hydrogen peroxide (H_2O_2) with a concentration gradient from 0 to 45mM in 5mM increments for 7 days at 32°C. The different isolates responded to the H_2O_2 gradient differently in terms of biomass and survivability. Aflatoxin production was also found to be enhanced by increasing $[\text{H}_2\text{O}_2]$. However, growth in the toxin-inconductive media, yeast extract-peptone (YEP), all isolates survived at a higher $[\text{H}_2\text{O}_2]$. Therefore, additional studies will seek to understand why different isolates behave

differently in YES and YEP media in response to H₂O₂ stress in order to examine the potential functional roles of aflatoxin production and ROS in *Aspergillus spp.* The activity levels of antioxidant enzymes and the expression of stress responsive genes will also be examined.

Nematodes associated with edamame, *Glycine max* L. (Merr.), and their effect on yield and quality in Arkansas

J. E. FULTZ (1), T. Kirkpatrick (2)

(1) University of Arkansas, Fayetteville, AR, U.S.A.; (2) University of Arkansas, Hope, AR, U.S.A.

Phytopathology 105(Suppl. 2):S2.4

Edamame, also known as vegetable soybean, *Glycine max*, has been growing in popularity in the US as a high-fiber, low-sugar snack in recent years. In 2012, American Vegetable Soybean and Edamame, Inc. established the first commercial processing plant in the United States near Mulberry, Arkansas. Since edamame is harvested as an immature bean, management practices vary from those used for conventional soybean. Plant-parasitic nematodes, particularly *Meloidogyne incognita* (root-knot) and *Heterodera glycines* (soybean cyst) known to be wide-spread in Arkansas, are pests of concern. The objective of this study was to 1) determine the nematodes associated with edamame in Arkansas edamame fields 2) evaluate new breeding lines for resistance to *M. incognita* and *H. glycines* 3) determine the effect of root-knot and soybean cyst nematode infection on edamame quality and yield. Production fields were surveyed in 2013 and 2014 immediately following harvest to determine the presence, identity, and relative population density of parasitic nematodes. Edamame lines developed by the Arkansas soybean breeding program were evaluated for host suitability to *M. incognita* and *H. glycines* in greenhouse trials. Moderate resistance to root-knot was identified in one studied line. Yield was notably reduced by both *Heterodera* and *Meloidogyne*. However, quality analysis of infected crops did not show significant alteration of components of lipid, starch, protein, and sugar. This work will aid producers and crop advisors in developing nematode management strategies for edamame production and provide insight on the potential risk of root-knot and soybean cyst nematodes to this emerging crop.

An evaluation of *Cercospora arachidicola* epidemic subprocesses as confirmation of field observations

L. GONG (1), K. Bowen (1)

(1) Auburn University, Auburn, AL, U.S.A.

Phytopathology 105(Suppl. 2):S2.4

Cultivated peanut (*Arachis hypogaea* L.) is an economically important crop that is produced in the United States and throughout the world. *Cercospora arachidicola* (Ca) causes early leaf spot on cultivated peanut and can contribute to yield losses of up to 50%. Recently released peanut cultivars, such as Georgia-06G, Georgia-09B, and Georgia-12Y, have shown varying levels of resistance to Ca in field observations. This study examines incubation period, number and size of lesions, and proportion of sporulating lesions of these three cultivars using whole peanut plants in a growth chamber. Lesions were evaluated on five leaves of each plant; cultivars were replicated three times. Incubation periods for GA-09B, GA-06G, and GA-12Y were 9.06, 20.50, and 26.00 days, respectively. At 17 days after inoculation (DAI), lesion counts for GA-09B, GA-06G, and GA-12Y were 10.20, 5.55, and 0.33, respectively. At 42 DAI, GA-09B had the largest lesions at 5.03 mm diameter, while GA-06B and GA-12Y had 3.36 and 2.53 mm diameter lesions, respectively. At 42 DAI, the proportion of lesions with conidia were 22.79%, 10.99%, and 7.67% on GA-09B, GA-06G, and GA-12Y, respectively. GA-12Y has a longer incubation period, lower lesion count, smaller lesion size, and lower proportion of sporulating lesions than other cultivars, which suggests this is the most resistant cultivar of these three. Conversely, GA-09B has a shorter incubation period, higher lesion count, larger lesion size, and higher proportion of sporulating lesions than other cultivars, which suggests greater susceptibility.

Effect of fungicides on chlorophyll content, yield, and test weight of winter wheat in the absence of foliar disease

N. GRAF GRACHET (1), R. M. Hunger (1), M. E. Payton (1), J. T. Edwards (1)

(1) Oklahoma State University, Stillwater, OK, U.S.A.

Phytopathology 105(Suppl. 2):S2.4

Fungicides can alleviate losses caused by diseases in susceptible cultivars of wheat. Some of these fungicides are labeled as plant health promoters with associated claims of increased greenness, improved drought tolerance, and increased yield. This study measured changes in chlorophyll content, yield and test weight associated with fungicide application in hard red winter wheat in the absence of foliar disease. Near Stillwater, OK, two field trials (a dryland

and an irrigated trial) were planted with 'Duster' (resistant to most foliar diseases) and 'OK Bullet' (susceptible) cultivars. At Feekes 10.3, the commercial fungicides Headline (pyraclostrobin), Caramba (metconazole), and Twinline (pyraclostrobin plus metconazole) (BASF Corporation, Florham Park, NJ) were applied at labeled rates. Chlorophyll content of leaves was determined using a SPAD (Soil and Plant Analyzer Development) 502 Plus Chlorophyll Meter (Spectrum Technologies, Inc., Aurora, IL) before and after fungicide application. Disease incidence in both experiments was absent due to an extended dry winter and spring. None of the fungicides increased chlorophyll content, yield or test weight in either trial compared to the not sprayed control. Hence, these results do not support claims of plant health benefits afforded by application of fungicide in the absence of disease.

Relationship between target spot intensity and seed cotton yield

A. HAGAN (1), K. Bowen (1), M. Pegues (2), J. Jones (1)

(1) Auburn University, Auburn, AL, U.S.A.; (2) Auburn University, Fairhope, AL, U.S.A.

Phytopathology 105(Suppl. 2):S2.4

Impact of target spot on cotton yield was evaluated in southwest Alabama. The experimental design was a factorial with variety as the main plot and Headline application number as the split plot treatment. While DPL (Deltapine) 1050 and DPL 1252 were sown in 2012 and 2013, respectively, PhytoGen 499 was planted in both years. A total of 1 to 5 and 1 to 4 applications of Headline 2.09SC at 9 fl oz/A were made in 2012 and 2013, respectively, every 2-wk starting at first bloom. Disease intensity ratings began 3 wk after the start of bloom and were repeated at 2-wk intervals into mid-September. Ratings were made using a 1 to 10 scale, and transformed into % defoliation values. Target spot intensity was lower on DPL 1050 and DPL 1252 than PhytoGen 499, while mean yields were similar. Target spot intensity on all varieties declined as Headline application numbers increased. While Headline application number did not impact DPL 1050 yield, significant yield gains were obtained with PhytoGen 499 with two compared with three applications on DPL 1252. Estimated yield loss is up to 250 and 400 lb lint/A for DPL 1252 and PhytoGen 499, respectively. The equations Y (yield) = $3544 - 1.6$ (% defoliation) [$R^2 = 0.012$ NS] and $Y = 4068 - 8.85$ (% defoliation) [$R^2 = 0.34^{**}$] describe the relationship between disease and yield for DPL 1050 and PhytoGen 499, respectively in 2012, and $Y = 3771.9 - 17.1$ (% defoliation) [$R^2 = 0.29^{**}$] and $Y = 3675.3 - 10.2$ (% defoliation) [$R^2 = 0.34^{**}$] for DPL 1252 and PhytoGen 499 in 2013.

Fungicide selection and application timing impact southern rust control in corn

A. HAGAN (1), H. L. Campbell (1), M. Pegues (1), J. Jones (1), B. Miller (1)

(1) Auburn University, Auburn, AL, U.S.A.

Phytopathology 105(Suppl. 2):S2.4

Damaging southern rust (*Puccinia polysora*) outbreaks are periodically observed in Alabama corn (*Zea mays* L.). Single and two application registered fungicide programs were evaluated for southern rust control and yield response at two irrigated sites in southwest Alabama. The corn varieties Pioneer 2023 BVT and Pioneer 2023YHR were established on March 27 and May 7 at study site 1 and 2, respectively. Fungicides were applied with a 'high-boy' sprayer at 15 gpa to 4-row plots in a randomized complete block. At site 1, single applications were made at growth stage (GS) V6 and VT, while two application program treatments were made at either V6 or VT, each followed by (fb) an R2 application; all treatments were applied at GS VT fb R2 at site 2. The VT fb R2 Priaxor, Quilt Xcel, Stratego YLD, Headline AMP, and Aproach fb Aproach Prima programs gave effective rust control at site 1. While some rust control was obtained some single VT application programs, rust ratings for the V6 Stratego YLD and the non-treated control were similar. When compared with the non-treated control, higher yields were obtained with all VT fb R2 well as the V6 4 fl oz/A Stratego YLD programs. At site 2, VT fb R2 Headline 2.09SC and Quilt Xcel gave the best rust control, while the Headline AMP and Priaxor also performed well. Tilt 3.6E and Muscle 3.6F (tebuconazole) programs were ineffective. Highest yield gains were obtained at site 2 with those programs that provided superior southern rust control.

Management of nematodes in cotton fields with variable soil types using Telone II soil fumigant and root-knot nematode resistant varieties

R. HAYGOOD (1), D. Burns (2), E. Burris (3), C. Overstreet (4), S. Blanche (1), C. O'Hara (1)

(1) Dow AgroSciences, Indianapolis, IN, U.S.A.; (2) LSU AgCenter, St. Joseph, LA, U.S.A.; (3) Burris Consulting, St. Joseph, LA, U.S.A.; (4) Louisiana State University, Baton Rouge, LA, U.S.A.

Phytopathology 105(Suppl. 2):S2.4

Application of Telone® II soil fumigant has played an important role in managing plant parasitic nematodes in vegetables, strawberries, potatoes, corn, cotton and other crops for over 50 years. Use rates are determined based on crop, soil types, application technology being employed, economics, and other variables. Cotton yields can be greatly impacted by root-knot nematodes (*Meloidogyne incognita*) which thrive in sandier soils as well as by reniform nematodes (*Rotylenchulus reniformis*) which can cause serious yield losses in soils with higher clay content. Site specific applications of Telone II are based on the use of soil maps and apparent soil electrical conductivity (EC_a) data to identify low and high risk areas, or “responsive” zones, with root-knot nematodes. Identifying these responsive zones has enabled cotton growers to increase return on investment by applying the soil fumigant in those areas where it is most needed. However, the variability in the distribution of soil types and nematode species as well as the introduction of new root-knot nematode resistant varieties increases the complexity of nematode management decisions. These studies were conducted to evaluate the use of site specific applications of Telone II and root-knot nematode resistant varieties in fields with variable soil types and nematode populations in the mid-south. ®Trademark of Dow AgroSciences LLC. Telone® II is a Restricted Use Pesticide. Always read and follow label directions.

Watermelon root rot in southwest Florida

K. E. HENDRICKS (1), P. D. Roberts (1)
(1) University of Florida, Immokalee, FL, U.S.A.
Phytopathology 105(Suppl. 2):S2.5

Watermelon grown in southwest Florida accounted for 20% of the states watermelon sales in 2012 season. Dieback of watermelon vines can have severe impacts on watermelon production. In 2014 dieback on watermelon was noted in multiple commercial fields in Hendry County, FL within 1 to 2 weeks of fruit set. Field symptoms included die-back from vine tips towards the crown, dead leaves and discoloration and rotted roots. Symptoms were not consistent with Squash vein yellowing virus. Examination of the vascular tissue within the crown and root was negative for the symptomatic browning associated with *Fusarium* wilt. Fungal and bacterial isolations were made from crown and root tissues on potato dextrose agar and nutrient agar, respectively. A number of bacteria, fungi and oomycetes were isolated. Pathogenicity testing is ongoing.

Discovery of different carlaviruses infecting elderberry

T. HO (1), I. E. Tzanetakis (1)
(1) University of Arkansas, Fayetteville, AR, U.S.A.
Phytopathology 105(Suppl. 2):S2.5

Elderberry (genus *Sambucus*) belongs to the family Adoxaceae. Fruit is often used to make syrup, wine, or even medicine. Double stranded RNA was extracted from elderberry plants with virus-like symptoms collected from the National Clonal Germplasm Repository, Corvallis, OR, in 2011. Degenerate oligonucleotide reverse transcription PCR amplification was performed and the resulting products were multiplexed for 454 junior sequencing. VirFind online bioinformatics tool (<http://virfind.org>) assembled and revealed the presence of new carlaviruses. After various sequence mapping and subtraction steps, at least 5 different novel carlavirus species were discovered based on the similarities of their RdRp and CP genes to known carlaviruses. Four full length carlavirus genome sequences were subsequently completed using RACE (Rapid Amplification of cDNA Ends) and additional Sanger sequencing. Currently, *Carlavirus* genus has 52 species recognized by the ICTV. The presence of several carlaviruses in a small number of plants suggests that there may be additional undiscovered viruses in elderberry. The use of VirFind together with specialized bioinformatics steps involved for novel virus discovery study are also discussed.

RNA-seq analysis of soybean near-isogenic line carrying Asian soybean rust-resistant and -susceptible alleles

D. HU (1), D. H. Oh (2), M. Dassanayake (2), D. Walker (3), Z. Chen (1)
(1) Department of Plant Pathology and Crop Physiology, Louisiana State University Agricultural Center, Baton Rouge, LA, U.S.A.; (2) Department of Biological Science, Louisiana State University, Baton Rouge, LA, U.S.A.; (3) USDA-ARS Soybean/Maize Germplasm, Pathology, and Genetics Research Unit, Urbana, IL, U.S.A.
Phytopathology 105(Suppl. 2):S2.5

Asian soybean rust (ASR) caused by *Phakopsora pachyrhizi*, was first reported in Louisiana in 2004. Currently, all U.S. commercial soybean cultivars are susceptible to *P. pachyrhizi*, and the only available method to control this disease is through fungicide application. Therefore, there is an urgent need to develop varieties that are resistant or tolerant to ASR to reduce its potential to cause yield losses in the U.S. To investigate the soybean basal

and inducible defense mechanisms in response to *P. pachyrhizi*, differential gene expression in near-isogenic lines (NILs) of ASR-susceptible and ASR-resistant soybean was analyzed by RNA-Seq. 24 RNA samples were sequenced from two time points after inoculation with three replications, yielding average 24 million reads (100bp paired) per sample using the Illumina HiSeq 2500 platform and sequencing by-synthesis technology. Sequence reads were aligned to the soybean reference genome sequence (Glyma1.01, <http://www.phytozome.net/soybean>) using RNA-seq Unified Mapper (<http://www.cbil.upenn.edu/RUM/>). Genes showing significantly different expression in ASR-susceptible and ASR-resistant NILs were identified using the DESeq package (<http://www-huber.embl.de/users/anders/DESeq/>) based on a model using negative binomial distribution. More than 97% reads were unambiguously aligned to the soybean genome. Of a total of 54181 annotated soybean genes, 755 and 586 were up- and down-regulated, respectively, in the ASR-resistant NIL relative to the ASR-susceptible NIL at 12, and 72h after inoculation (hai). Gene ontology (GO) analysis showed that 34 GO categories, such as 0016706 and 0044260, were significantly enriched among up- or down-regulated gene groups.

Reproduction of *Meloidogyne incognita* and *M. graminis* on several grain sorghum hybrids

K. M. HURD (1), T. R. Faske (1)
(1) University of Arkansas, Division of Agriculture, Cooperative Extension Service, Lonoke, AR, U.S.A.
Phytopathology 105(Suppl. 2):S2.5

Grain sorghum production has increased for the past few years across the Mid-South and hybrids are often selected as a rotational crop with the assumption that all grain sorghum hybrids are equal in susceptibility to root-knot nematodes. Currently, there is little information on the reproduction of *Meloidogyne incognita* and no information on the reproduction of *M. graminis* on commercially available grain sorghum hybrids. The susceptibility of 27 grain sorghum hybrids to *M. incognita* and *M. graminis* were examined in several greenhouse experiments. In each host test the inoculum density was 2000 nematode eggs/pot. Reproduction of *M. incognita* was lower ($P \leq 0.05$) on sorghum hybrids REV RV9782, REV RV9803, REV RV9823, Pioneer 93P99, and REV RV9794 compared to Golden Acres 5556 and Dyna-Gro 765B. Numerically, all sorghum hybrids supported a lower level of *M. incognita* reproduction than cotton cv. DP 0912 B2RF, but a similar level to that of a corn hybrid, Pioneer 31G71. Reproduction of *M. incognita* was higher ($P \leq 0.05$) on more than half of the grain sorghum lines evaluated compared to *M. graminis*, suggesting grain sorghum is a better host for *M. incognita* than *M. graminis*. Overall, the majority of the grain sorghum hybrids were relatively similar in susceptibility to *M. incognita*; however a few hybrids were more susceptible than others, which emphasize the importance of selecting the least susceptible hybrids as a rotational crop to reduce populations of root-knot nematodes.

Assessment of fluopyram for management of *Meloidogyne incognita* on soybean

C. S. JACKSON (1), T. R. Faske (2), M. Emerson (2)
(1) University of Arkansas, Department of Plant Pathology, Fayetteville, AR, U.S.A.; (2) University of Arkansas, Division of Agriculture, Cooperative Extension Service, Lonoke, AR, U.S.A.
Phytopathology 105(Suppl. 2):S2.5

The southern root-knot nematode, *Meloidogyne incognita*, is an important plant-parasitic nematode affecting soybean production. Fluopyram is an SDHI fungicide that was recently confirmed to be nematostatic to *M. incognita*. Currently, few studies have investigated the suppression of root-knot nematodes (RKN) by fluopyram on soybean. Thus, the objective of this study was to evaluate fluopyram as a seed treatment (ST) and in-furrow (IF) application for suppression of *M. incognita* compared to other commercially available seed treatment nematicides, *Bacillus firmus* (I-1582) and abamectin. This trial was conducted in a commercial soybean field with a low population of RKN at planting. Numerically, nematode eggs per gram of root at 30 DAP was lower for fluopyram, abamectin, *B. firmus* treated seed, and fluopyram applied IF than the non-treated control. Further, a numeric reduction in galls per root system was observed 30 DAP on abamectin treated seed compared to fluopyram applied as a ST and IF. Alternately, the percentage of root galling at 60 DAP was lower ($P = 0.05$) on fluopyram applied as a ST and IF than seed treated with a combination of fluopyram + abamectin. All fluopyram treatments had a numerically higher yield than the non-treated control. Fluopyram applied as an IF application was more associated with numeric reduction in root-gall ratings, nematode reproduction, and increased yield than fluopyram as a seed treatment. Further, the suppression of RKN reproduction by fluopyram applied IF on soybean appeared to be somewhat similar to that of abamectin and *B. firmus* applied as a seed treatment.

On-farm application of supplemental chloropicrin to improve Fusarium wilt control in tomato

T. P. JACOBY (1), G. Vallad (1), N. Boyd (1)
(1) University of Florida, Wimauma, FL, U.S.A.
Phytopathology 105(Suppl. 2):S2.6

Fusarium wilt (caused by *Fusarium oxysporum* f. sp. *lycopersici*; FOL) has reemerged as a challenging disease for Florida tomato growers since the adoption of methyl bromide alternative fumigant systems. Based on the recovery of total *F. oxysporum* from throughout the soil profile, previous studies identified non-fumigated row middles and under-fumigated regions within the raised bed as a likely source of inoculum for migrating roots. A series of large scale field trials were initiated in December 2013 at a grower site with a history of Fusarium wilt. The objective was to test the benefit of applying chloropicrin along the edges of raised beds in addition to the standard Pic-Clor60 fumigation within the raised bed. Two weeks after fumigation, soil samples collected from 14 locations throughout the soil profile showed that the supplemental chloropicrin application significantly reduced total *F. oxysporum* levels, resulting in an increase in total root biomass extending from the edges of the bed into the row middle by the end of the season. The supplemental application of chloropicrin statistically decreased the incidence of Fusarium wilt over the grower standard, leading to a 23% increase in tomato yields. The differences observed in the field combined with supporting data leads us to believe that this supplemental fumigation strategy will be a vital tool for the management of Fusarium wilt in tomato.

Effect of new peanut genotypes on leaf spot severity and yield when grown without fungicides

B. S. JORDAN (1), A. K. Culbreath (1), W. D. Branch (2)
(1) University of Georgia, Dept. of Plant Pathology, Tifton, GA, U.S.A.; (2) University of Georgia, Dept. of Crop and Soil Sciences, Tifton, GA, U.S.A.
Phytopathology 105(Suppl. 2):S2.6

Control of early and late leafspot diseases caused by *Cercospora arachidicola* and *Cercosporidium personatum*, respectively, are critical for peanut *Arachis hypogaea* production in both conventional and organic situations. Cultivars with resistance and/or tolerance to one or both pathogens could reduce direct losses to these diseases when effective fungicides are not available, and indirect losses in cost of control when fungicides are available. A field trial was conducted in Tifton, GA in 2014 in which eleven breeding lines and three cultivars, Georgia-04S, Georgia-06G, and Georgia-12Y were grown without foliar fungicide applications. Experimental design was a randomized complete block with five replications. Late leaf spot was the predominant foliar disease, and epidemics were severe by the end of the season. Final leaf spot ratings (Florida 1-10 Scale) ranged from 8.3 in Georgia-06G to 5.0 in GA072523-11 (LSD = 0.8). Nine of the breeding lines had final leaf spot ratings lower than those of Georgia-06G. Yields ranged from 5219 kg/ha in Georgia-04S to 7465 kg/ha in GA072523-9. Yields were 7136, 7465, 7147, and 7143 kg/ha for genotypes GA072523-1, GA072523-9, and GA072523-10, and the cultivar Georgia-12Y, respectively, all of which were higher than the 6329 kg/ha for Georgia-06G (LSD = 807). Several of the breeding lines show potential for use in production regimes with reduced or no fungicide applications for leaf spot control.

Genetic recombination of *Xylella fastidiosa* cultured in microfluidic chambers with grapevine sap

P. P. KANDEL (1)
(1) Auburn University, Auburn, AL, U.S.A.
Phytopathology 105(Suppl. 2):S2.6

Xylella fastidiosa (Xf) is a bacterial plant pathogen causing incurable diseases in grape, citrus, and other crops. There is growing evidence of Xf shifting to new host plants and to new geographic regions, and the isolates obtained from these infections are found to be genetically different. This genetic difference causing new emerging diseases of Xf is hypothesized to be due to genetic recombination caused by horizontal gene transfer (HGT). Interestingly, natural competence (NC), a mode of HGT in which bacterial cells take up and recombine free DNA from the environment, is described in Xf. Studies show that NC occurs readily in Xf in vitro, but its occurrence in planta is not reported mainly because of the complexities associated with its study in nature. To more closely approximate in planta conditions, we used a microfluidic chamber setting (MC) that resembles the plant xylem vessels that Xf naturally inhabits and culture medium supplemented with different concentrations of grapevine sap to create a natural environment mimic system (NEMS). Using combinations of live and dead antibiotic marker-tagged Xf mutant cells, we demonstrated that NC occurs in the NEMS and the recombination frequency is comparable to that obtained from experiments conducted on agar plates and in MC containing only artificial media. These

results suggest that NC can occur in nature and might be responsible for the recently described host and geographical shifts in Xf.

Pomegranate (*Punica granatum* L.) in Florida: A disease snapshot

A. N. KC (1), G. E. Vallad (1)
(1) University of Florida, Wimauma, FL, U.S.A.
Phytopathology 105(Suppl. 2):S2.6

Pomegranate production in Florida has gained considerable attention due to its nutritional value and as a possible alternative crop for citrus. As small scale production was initiated, losses to disease were identified as a major limiting factor to increased production. To address these problems, surveys were conducted in four different locations in Central Florida. Diseased samples from leaf, stem, pedicel, flower, and fruits were collected. Isolations from symptomatic tissues were made following standard laboratory protocols. The isolated fungal species were identified based on morphological characters and amplification of genomic DNA from 30 fungal species with ITS1 and ITS4 primers. The resulting sequences were compared with subsequent database in NCBI and pathogen was identified based on % identity. Attached and detached leaf assays and a detached fruit assay were conducted to determine pathogenicity. Among thirteen different fungal species isolated from symptomatic tissues, eight fungal species including *Colletotrichum* sp., *Neofusicoccum parvum*, *Amphilogia* sp., *Piliella granati*, *Lasioidiplodia* sp., *Alternaria* sp., *Nigrospora sphaerica*, and *Corynespora cassicola* were pathogenic on leaves showing a range of leaf spot and decay symptoms. Five fungal species including *Colletotrichum* sp., *Neofusicoccum parvum*, *Amphilogia* sp., *Piliella granati*, and *Lasioidiplodia* sp., were also highly pathogenic on fruit. *Pestalotiopsis clavispora*, *Phyllosticta elongata*, *Nigrospora sphaerica*, and *Epicoccum nigrum* were frequently isolated from the samples but were not pathogenic in any of the assays. This study provides a snapshot of fungal diseases prevalent on pomegranate in Florida and provides numerous gateways for future studies on pomegranate diseases.

Seasonal dynamics and the impacts of fungicide use on the diversity of pathogens causing brown patch of tall fescue

A. KOEHLER (1), H. D. Shew (1)
(1) NCSU Plant Pathology, Raleigh, NC, U.S.A.
Phytopathology 105(Suppl. 2):S2.6

Brown patch, caused by the *Rhizoctonia solani* complex, is the most severe disease of tall fescue in home lawns across the southeast US. Multiple studies have reported a diverse group of species and anastomosis groups associated with symptoms of the disease. Understanding the genetically distinct populations of pathogens present is an important consideration for the management of this disease. Early (May) and late (July-August) season isolates were collected to better understand seasonal pathogen distribution, and to identify if pathogen diversity has changed following continued use of strobilurin fungicides by comparing isolates to those of a previous survey. *Rhizoctonia* species were isolated from individual brown patch lesions on tall fescue leaf blades in the summers of 2013 and 2014 in managed (fungicides applied) and unmanaged yards. Isolates were identified to species and anastomosis group by sequencing the ITS region. *Ceratobasidium* sp., *R. solani* from anastomosis groups 2-IIIB and 1-IB, and *R. zae*, were found. *Ceratobasidium* sp. were the most prominent in early season sampling with *R. solani* and *R. zae* dominating late season sampling. One hundred twenty four isolates, including 6 historic isolates from untreated yards, were assayed for sensitivity to the fungicides azoxystrobin, flutolanil, fluxapyroxad, and propiconazole. Mean EC₅₀ values varied across fungicides and species, but no resistance was observed.

Oxathiapiprolin: A new fungicide for control of Oomycete diseases

P. Kuhn (1), A. Tally (2), M. D. WIGLESWORTH (2)
(1) Syngenta, Greensboro, NC, U.S.A.; (2) Syngenta Crop Protection, Greensboro, NC, U.S.A.
Phytopathology 105(Suppl. 2):S2.6

Oxathiapiprolin is a new fungicide developed for control of certain Oomycete diseases. This active ingredient is the first in a new class of chemistry (piperidinyl thiazole isoxazolines). The mode of action is novel and indications are that the chemistry binds to an oxysterol binding protein. The spectrum of activity includes the downy mildews, *Phytophthora* (both soil and foliar), and *Pythium ultimum* (other Pythiaceae are unaffected as are *Albugo* spp.). Use rates as low as 12 g ai/ha have shown excellent activity against foliar Oomycetes, with rates slightly higher (70 g ai/ha or higher) for soil-borne Oomycete diseases. Oxathiapiprolin has shown activity on all stages of the fungal life cycle. Application of the product will be permitted as both soil and foliar; via ground, chemigation, aerial, or drip. Oxathiapiprolin moves in the xylem, exhibiting translaminal and acropetal movement. Studies have shown that after deposition on the leaf surface, oxathiapiprolin becomes

rainfast within 20–30 minutes. All trials have shown excellent crop tolerance alone or in mixture with other active ingredients. EPA registration is expected in the 3Q of 2015 on Fruiting Vegetables, Leafy Vegetables (Leafy Greens sub group), Cucurbit Vegetables, Brassica Vegetables (Head and Stem), Bulb Vegetables, Ginseng, Succulent Edible Peas, Tuberous or Corm (foliar only), and Tobacco. To minimize buildup of resistance, specific guidelines will be proposed for use in each crop as well as tank-mix partners. Premixes will be available in the future. To help prevent resistance, Syngenta does not support straight oxathiapiprolin programs in experimental or commercial use.

Evaluation of cotton (*Gossypium hirsutum*) cultivars and their responses to nematode seed treatments and its physiology

C. LAND (1), K. S. Lawrence (1), P. Cobine (1)

(1) Auburn University, Auburn, AL, U.S.A.

Phytopathology 105(Suppl. 2):S2.7

Our objectives were to evaluate the response of selected cotton cultivars in the presence and absence of the reniform nematode (*Rotylenchulus reniformis*) with and without seed treatment nematicides. Symptomatic leaves were also collected to determine the nutrient content in the presence and absence of the reniform. Field plots were arranged in a replicated paired plot design with seeds untreated or treated with Thiodicarb and Abamectin. Nematodes were collected for analysis from 3 random plants per plot at 42 days after planting. Leaves showing reniform symptoms of interveinal chlorosis and distinct greening veins were taken for analyzed by inductively coupled plasma machine (ICP) to measure nutrient content and compared to leaves without reniform pressure. The data was analyzed with SAS 9.3 and means compared using Tukey's HSD ($\alpha \leq .10$). The presence of the reniform nematode reduced yield by 63% across all varieties compared to cotton without nematode pressure. The nematicides increased yield 23% or an average of \$127/ha with \$0.65 cotton. They also reduced reniform population densities by 30%. DP1454NRB2RF supported the lowest density of reniform eggs, 1552 eggs/gr root, among cultivars without seed treatment nematicide; however, with seed treatment PHY375WRF supported the lowest number of eggs at 1163 eggs per gram of root. Results from the ICP analysis indicated cotton leaves with reniform nematode symptoms had statically lower amounts of Calcium, Boron and Iron. The minerals Zinc, Manganese, and Magnesium were present in higher levels in the reniform nematode symptomatic leaves than in leaves without reniform from Alabama.

Induction of systemic resistance in Chinese cabbage against black rot by plant growth-promoting rhizobacteria

K. LIU (1), C. Garrett (1), J. W. Kloepper (1), J. A. McInroy (1)

(1) Auburn University, Auburn, AL, U.S.A.

Phytopathology 105(Suppl. 2):S2.7

Black rot, caused by *Xanthomonas campestris* pv. *campestris*, is the most important and potentially destructive disease in cabbage. The objective of this study was to select plant growth-promoting rhizobacteria (PGPR) strains and to form strain mixtures with the capacity to elicit induced systemic resistance in Chinese cabbage. Components of this study included testing individual PGPR strains in greenhouse assays, and testing mixtures of PGPR in greenhouse and field tests. Twelve PGPR strains were selected for individual PGPR greenhouse assay. Ten individual PGPR strains reduced the number of foliar lesions, and five individual PGPR strains increased the fresh shoot weight, dry shoot weight and fresh root weight. Four individual strains (AP136, AP209, AP282 and AP305) were combined in mixture-1, and mixture-2 added three additional strains (AP7, AP18 and AP218). Both mixtures and three individual strains significantly reduced black rot, and mixture-2 increased the dry shoot weight and dry root weight. In the field test, all the tested treatments significantly reduced the disease incidence at three weeks after transplanting, the head disease severity at the harvest time, and increased the market yield compared to the nonbacterized control.

The control of cotton root rot in Texas winegrapes with the fungicide flutriafol

S. A. MCBRIDE (1), D. N. Appel (1)

(1) Texas A&M University Department of Plant Pathology and Microbiology, College Station, TX, U.S.A.

Phytopathology 105(Suppl. 2):S2.7

Among the challenges facing the Texas winegrape industry is *Phymatotrichopsis omnivora*, the cotton root rot (CRR) pathogen. Concern from grape growers is becoming significant because there are no recommendations for disease control. Two experimental control trials were initiated in vineyards in the spring of 2012 to test flutriafol, a fungicide being used successfully to control CRR on cotton. Flutriafol was applied at 0.26 lbs/a.i./acre (1X), 2.6 lbs/a.i./acre (10X), and 5.2 lbs/a.i./acre (20X) through a manually applied soil drench. At one of the vineyards, Flat Creek, there was a significantly lower

level of disease development in the 10X plots, as compared to untreated controls. In 2014, two new field trials were established using chemigation at Flat Creek and a new vineyard, Hoover Valley. The experimental block at Hoover Valley consists of 30 rows of Petite Syrah on 5BB rootstock with 118 vines/row. Two rates of flutriafol at 0.26 lbs/a.i./acre (1X) and 0.52 lbs/a.i./acre (2X) were applied through the irrigation system with 10 plots (rows)/treatment. In the untreated plots disease increased from 0–5.5% over a 12 week period following treatments. No disease was observed until week 11 in any of the treated plots. However, by week 12, disease incidence had increased to 2.5% and 1.4% in the 1X and 2X plots, respectively. All remaining trials in the vineyards continue to be monitored for disease development. Based on these and similar studies a Section 18 emergency registration may be requested for use by the grape growers to control this devastating disease.

Evaluating fungicide sensitivity of regional *Blumeria graminis* f. sp. *tritici* populations in the United States

E. MEYERS (1), R. Parks (1), C. Arellano (1), C. Cowger (1)

(1) North Carolina State University, Raleigh, NC, U.S.A.

Phytopathology 105(Suppl. 2):S2.7

Blumeria graminis f. sp. *tritici* (*Bgt*), cause of wheat powdery mildew, has a high likelihood of developing fungicide resistance because of the large quantity of spores produced along with the mixed mode of reproduction. Additionally, once reduced sensitivity appears in a population it can influence nearby populations because spores are dispersed aerially. This study seeks to determine if fungicide sensitivity in *Bgt* populations differs regionally in the United States. In 2013, wheat powdery mildew samples were collected from 11 unsprayed wheat fields in eight states grouped into four regions (Deep South, Mid-Atlantic, Great Lakes, and Plains). The sensitivity of over 150 single-spored isolates was evaluated by inoculating them individually on susceptible detached wheat leaves previously sprayed with fungicides and floated on benzimidazole-amended agar. Five fungicides (tebuconazole, prothioconazole, pyraclostrobin, picoxystrobin, and fluxapyroxad) were evaluated at 11 rates each, in ranges chosen based on initial experiments with a small subset of isolates. EC₅₀ values were determined for each field, state, and region using regression and compared using ANOVA. Preliminary partial results indicate significant regional differences for tebuconazole and prothioconazole with *Bgt* isolates from the Deep South being the least sensitive, Mid-Atlantic and Great Lakes isolates moderately sensitive, and Plains isolates the most sensitive. Interestingly, Plains isolates were least sensitive to pyraclostrobin and fluxapyroxad, Great Lakes and Deep South isolates moderately sensitive, and Mid-Atlantic isolates the most sensitive. The sensitivity to picoxystrobin was not significantly different among regions.

Investigation of the potential disease complex concerning *Pythium aphanidermatum* and *Meloidogyne incognita* on cucumber

K. A. MORRIS (1), D. B. Langston (2)

(1) University of Georgia, Tifton, GA, U.S.A.; (2) Virginia Tech, Suffolk, VA, U.S.A.

Phytopathology 105(Suppl. 2):S2.7

A growth chamber trial on cucumber in 2011 demonstrated a possible disease complex between *Pythium aphanidermatum* (PA) and *Meloidogyne incognita* (RKN) on cucumber. Two growth chamber trials were conducted in 2014 to investigate this potential disease complex. Treatments included cucumber seedlings inoculated with: PA alone, RKN alone, PA + RKN, and an untreated control. Each pathogen was inoculated to 14 day old cucumber seedlings that were planted into 7.5 × 25 cm cone-tainers containing a soil mixture of 3 parts sand, 3 parts sterilized field soil, and 1 part germinating mix. Inoculated pots received 1500 J2 stage RKN juveniles or 3000 g of sand-corn meal PA inoculum. Once inoculated, cucumbers were placed in a growth chamber at 28 C, 12 h photoperiod, and 75% humidity. Plants were monitored daily for 3 weeks for symptoms of PA infection. The presence of PA was determined on symptomatic plants by isolating hypocotyl sections onto PDA and observing colony morphology and microscopic characteristics of PA. In each trial, plants inoculated with both pathogens demonstrated significantly greater plant death than pots inoculated with either pathogen alone. These results indicate that a disease complex between RKN and PA exists in cucumber.

Characterization of *Colletotrichum* species causing bitter rot of apple in Kentucky orchards

M. MUNIR (1), E. Dixon (1), B. Amsden (1), L. J. Vaillancourt (1), N. W. Gauthier (1)

(1) Department of Plant Pathology, University of Kentucky, Lexington, KY, U.S.A.

Phytopathology 105(Suppl. 2):S2.7

Multiple species of *Colletotrichum* cause bitter rot of apple. Characteristics such as pathogenicity, spore production, and fungicide sensitivity can vary

with species. Total of 585 isolates were collected from 25 counties and characterized morphologically and by various molecular approaches. Three morphotypes corresponded to reported descriptions. Morphotype 1, distinguished by pink color on media, orange conidial masses and fusiform-shaped spores, was consistent with *C. acutatum*. Morphotype 2 contained gray or white mycelial colonies with or without orange conidial masses and spores that were either fusiform or rounded; these were similar to both *C. acutatum* and *C. gloeosporioides* and difficult to distinguish. Morphotype 3 produced ascospores and resembled *Glomerella cingulata*. Morphotype 2 amplified with primers specific to *C. acutatum* or *C. gloeosporioides*, while morphotype 1 was consistent with *C. acutatum*, and morphotype 3 consistent with *C. gloeosporioides* (anamorph of *G. cingulata*). Multigene sequence analyses suggested that sample isolates belong to newly erected species. Morphotype 1 was identified as *C. fioriniae*, which resides within the *C. acutatum* species complex, and morphotype 3 was categorized as *C. siamense*, which is grouped within the *C. gloeosporioides* species complex. Morphotype 2 contained isolates of both *C. fioriniae* and *C. siamense*. Molecular fingerprinting suggested that isolates within *C. fioriniae* belong to a single clone. Isolates within *C. gloeosporioides* were more diverse. Pathogenicity was not consistent with species. Isolates of *C. fioriniae* produced more spores within apple lesions compared to *C. siamense*. These findings indicate that two distinct species of *Colletotrichum* cause bitter rot of apple in Kentucky.

Development of 5' nuclease probes for detection and quantification of *Pseudoperonospora cubensis* sporangia

K. N. NEUFELD (1), L. M. Quesada-Ocampo (1), P. S. Ojiambo (1)
(1) North Carolina State University, Raleigh, NC, U.S.A.
Phytopathology 105(Suppl. 2):S2.8

Pseudoperonospora cubensis, the causal agent of cucurbit downy mildew (CDM), is considered the most damaging disease of cucurbitaceous crops worldwide. Sporangia produced by the pathogen are disseminated by wind currents and deposited on the canopy during rain events. Simulation of sporangia transport from the CDM ipm pest information platform for extension and education (CDM ipmPIPE) are used to establish the risk of disease outbreak but the system has not yet been validated. Primers were developed to identify and quantify the amounts of sporangia in rainwater samples to facilitate comparison of observation of *P. cubensis* sporangia in rain water collections with simulations of wet deposition of sporangia from the CDM ipmPIPE forecasting system. Quantitative real-time polymerase chain reaction (qPCR) assays utilizing 5' nuclease probes were developed and evaluated for sensitivity, specificity and quantification of sporangia of the pathogen. Single copy gene primers from housekeeping regions of *P. cubensis* were selected and tested for sensitivity and specificity. The final product from these primers was then sequenced and assays developed using IDT primer-quest. Specificity tests showed that the assay did not amplify DNA of closely related oomycete pathogens such as *Peronospora tabacina*, *Peronospora belbahrii* or *Phytophthora infestans*. The assay was validated with a set of seven isolates collected over multiple years and host types in the eastern U.S.

A preliminary study examining fitness cost associated with maintaining fungicide resistance in the absence of selection for *Didymella bryoniae* epidemics in Florida watermelon production

M. J. NEWARK (1), N. S. Dufault (1), M. L. Paret (1)
(1) University of Florida, Gainesville, FL, U.S.A.
Phytopathology 105(Suppl. 2):S2.8

Didymella bryoniae, the causal agent of gummy stem blight, is a major watermelon pathogen that is primarily managed using fungicides. *D. bryoniae* has developed resistance to major single mode of action fungicides, such as boscalid. The objective of this study was to determine if there are visible shifts in populations of *D. bryoniae* in-vivo with different fungicide selection pressures. Two isolates of *D. bryoniae*, one sensitive and one resistant to boscalid, were inoculated onto watermelons at equal proportions. Treatments were applied to either select for resistance or to control *D. bryoniae* in a nonselective manner. Samples were collected three times in the trial to assess populations at different selection periods. Disease ratings were also taken in order to observe any contrasts in disease control. Isolates were obtained from symptomatic leaf or stem tissue and were cultured on quarter strength potato dextrose agar (QPDA). Pure cultures were replated onto QPDA media amended with two rates of boscalid (0.0068 and 0.017mg/l). This represented two and five times the EC₅₀ baseline sensitivity for boscalid. Radial growth was measured at two perpendicular points 48, 72, and 96 hours post-culturing and were compared to the control to determine percent inhibition. Phenotypes were characterized by being either sensitive or resistant and proportions were analyzed for ratio shifts compared to the inoculated ratio. Differences were observed between treatments in disease severity. Based on fungicides sprayed, evident shifts in populations were observed.

Characterization of *Pseudomonas syringae* associated with watermelon and squash disease outbreaks in Florida and Georgia

E. A. NEWBERRY (1), M. L. Paret (1), J. B. Jones (2), L. Ritchie (1), J. H. Freeman (1), N. S. Dufault (2), B. Babu (1), E. M. Goss (2), G. E. Vallad (3), P. D. Roberts (4), B. Hochmuth (5), A. Drew (6), K. Beckham (2)
(1) North Florida Research and Education Center, University of Florida, Quincy, FL, U.S.A.; (2) University of Florida, Gainesville, FL, U.S.A.; (3) Gulf Coast Research and Education Center, University of Florida, Balm, FL, U.S.A.; (4) South West Florida Research and Education Center, University of Florida, Immokalee, FL, U.S.A.; (5) Suwannee Valley Agricultural Extension Center, University of Florida, Live Oak, FL, U.S.A.; (6) Levy County Extension, University of Florida, Bronson, FL, U.S.A.
Phytopathology 105(Suppl. 2):S2.8

In 2013 and 2014, a new disease of watermelon (*Citrullus lanatus*) and squash (*Cucurbita pepo*) was observed throughout Florida and Georgia. In Florida, there was an estimated 5–15% yield loss due to severe infection at the early stages of the crop, leading to leaf blighting, transplant losses, and delayed fruiting of infected plants affecting marketability. Bacteria were consistently isolated from foliar lesions and tested for fluorescence on King's Medium B (KMB) agar. Isolates were identified as *Pseudomonas syringae* based on biochemical tests (LOPAT) and sequence analysis of the 16S+23S rRNA region. Similar *P. syringae* isolates recovered from cucurbits prior to 2013 were collected for comparison. Multi Locus Sequence Analysis (MLSA) of bacterial isolates and pathotype sequences from the Plant Associated Microbes Database indicated that two genetically different groups of *P. syringae* are associated with recent disease outbreaks, and are members of genomospecies 1. These two groups are distinct from other pseudomonads pathogenic on cucurbits and display different levels of fluorescence on KMB. Further investigation into copper resistance, seed transmission, and host range is needed in order to aid in the development of an Integrated Pest Management protocol.

Assessment of biological and chemical fungicides for control of downy mildew of basil

J. S. PATEL (1), S. Zhang (1)
(1) University of Florida, Homestead, FL, U.S.A.
Phytopathology 105(Suppl. 2):S2.8

Downy mildew of basil, caused by *Peronospora belbahrii*, has become an economically important disease in the USA. Only few effective fungicides are registered and available for management of downy mildew of basil. Therefore, a field study was conducted to evaluate biological fungicides Double Nickle at 1qt/A, Timorex Gold at 1.5%, Zonix at 76 fl. oz/A, Organocide at 2 fl. oz/gal, Taegro at 4 fl. oz/ A, Cueva at 1 gal/A, a chemical compounds A20641A (oxathiaprolin) at 0.25 fl. oz/A, Double Nickle + Cueva, Double Nickle + Organocide, Zonix + Organocide, Taegro + Organocide, Cueva + Organocide, and alternating applications of A20641A with Organocide for control of downy mildew of basil. Seeds of basil var. "Genovese" were planted on raised beds in a randomized complete block design. Basil plants were naturally infected with *P. belbahrii* in the field. Foliar sprays were made weekly after first indication of disease symptoms. Among the treatments, Quadris + Prophyt (the standard chemical control), A20641A, Cueva, and alternating applications of A20641A with Organocide and Cueva with Organocide significantly ($P < 0.05$) reduced disease severity of downy mildew 68 days after planting. A20641A alone and Quadris + Prophyt had the least AUDPC values. The highest yield was received from treatments A20641A and Quadris + Prophyt which were significantly ($P < 0.05$) greater than the non-treated basil. Data from this study indicate that the new chemistry A20641A can be applied alone and in alternation with other effective fungicides for integrated management of downy mildew of basil.

Effect of thiophanate-methyl and prothioconazole fungicides on asexual life stages of *Fusarium oxysporum* f. sp. *niveum* from watermelon

A. PETKAR (1), D. Langston (2), K. Stevenson (1), J. Buck (3), P. Ji (1)
(1) University of Georgia, Tifton, GA, U.S.A.; (2) Virginia Tech, Suffolk, VA, U.S.A.; (3) University of Georgia, Griffin, GA, U.S.A.
Phytopathology 105(Suppl. 2):S2.8

Fusarium wilt of watermelon, caused by *Fusarium oxysporum* f. sp. *niveum* (FON), is a serious threat to watermelon production in the United States. Little information is available regarding fungicides effective for suppressing the pathogen. In this study, we assessed the effect of thiophanate-methyl and prothioconazole on asexual life stages of FON isolates from watermelon in Georgia. Based on a mycelial growth assay on fungicide amended agar, 4, 84, and 12% of the 100 isolates tested were resistant, intermediately sensitive, or sensitive to thiophanate-methyl at 100 µg/ml, respectively. All isolates were sensitive to prothioconazole at 10 µg/ml, and EC₅₀ value of prothioconazole that inhibited mycelial growth of the isolates averaged 1.7 µg/ml. Of 18

isolates evaluated in a microconidial production assay, 28, 11 and 61% were resistant, intermediately sensitive, or sensitive to prothioconazole at 10 µg/ml. Microconidial germination assays showed that all isolates were resistant to prothioconazole at 10 µg/ml, while 64 and 36% of the isolates were intermediately sensitive or sensitive to prothioconazole at 100 µg/ml. The results indicated that different asexual life stages of FON were differentially affected by the fungicides and the isolates were more sensitive to prothioconazole than thiophanate-methyl. The study provides useful information for identifying effective fungicides to manage Fusarium wilt of watermelon.

Prevalence of fungicide resistance in Louisiana soybean and rice

P. PRICE (1), M. Purvis (1), H. Pruitt (1), C. Hollier (2), R. Schneider (2), D. Groth (3), B. Padgett (4)
(1) LSU AgCenter, Winnsboro, LA, U.S.A.; (2) LSU AgCenter, Baton Rouge, LA, U.S.A.; (3) LSU AgCenter, Crowley, LA, U.S.A.; (4) LSU AgCenter, Alexandria, LA, U.S.A.
Phytopathology 105(Suppl. 2):S2.9

From 2000 to 2012, fungicide use in soybean has increased from 5 to 71% of planted acres. In Louisiana, producers typically apply prophylactic treatments of strobilurin, triazole, benzimidazole, and/or carboxamide fungicides at R3 (pod initiation). *Cercospora* leaf blight (*C. kikuchii*) and frogeye leaf spot (*C. sojina*) have been the most prevalent soybean diseases in recent years. Control failures with strobilurins and benzimidazoles used for *Cercospora* leaf blight have been commonplace for many years throughout the state. Results from field experiments over the past 5 years failed to identify any commercially available products that are consistently efficacious against *Cercospora* leaf blight. Additionally, resistance of *C. kikuchii* to benzimidazole and strobilurin fungicides has been confirmed, is widespread, and is estimated to occur in 33 and 85% of the pathogen population, respectively. In 2014, failures involving strobilurin fungicides for management of frogeye leaf spot were noted in northern Louisiana. Several products containing triazoles were identified that are effective on frogeye leaf spot and may preserve yield. Resistance of *C. sojina* to strobilurins appears to be widespread and has been confirmed in 11 parishes. *Rhizoctonia solani* isolates from rice and soybean samples collected from south central Louisiana fields with failed control were tested for sensitivity to azoxystrobin and found to be 10 times more tolerant than isolates where strobilurin fungicides remain effective. These isolates were found to be cross resistant to all strobilurins used in the area. More research is needed to further define resistance distributions, prevalence, and sensitivities to other chemistry types.

Effect of fungicide and application timing on target spot (*Corynespora cassiicola*) in Louisiana cotton

P. PRICE (1), M. Purvis (1), H. Pruitt (1)
(1) LSU AgCenter, Winnsboro, LA, U.S.A.
Phytopathology 105(Suppl. 2):S2.9

Target spot, caused by the fungus *Corynespora cassiicola*, is an emerging issue in cotton (*Gossypium hirsutum*) in the Mid-South. In 2014, target spot was widespread in cotton producing areas of central and northeast Louisiana. In some cases cotton fields were two-thirds defoliated as a result of the disease. Two trials were conducted at the Dean Lee Research Station (DLRS) in Alexandria, LA, and one at the Macon Ridge Research Station (MRRS) near Winnsboro, LA. Treatments consisted of Headline, Priaxor, Quadris, and Topguard applied during the first and/or third week of bloom. At DLRS in D&PL 1133, plots treated with Priaxor during the third week of bloom had significantly lower disease incidence than the non-treated control. At DLRS in Phytogen 499, plots treated with Headline or Priaxor during the third week of bloom had significantly less disease incidence than the non-treated control. Plots treated with Priaxor during the third week of bloom had significantly less defoliation than the non-treated control. At MRRS in Phytogen 499, plots treated with Priaxor during the first week of bloom had significantly lower disease incidence and defoliation than the non-treated control. Priaxor or Headline applied during the third week of bloom had significantly lower disease incidence and defoliation than the non-treated control. Additionally, plots treated with Headline at first bloom followed by Priaxor during the third week of bloom or *vice versa* had significantly lower disease incidence and defoliation. None of the fungicide treatments resulted in significant yield preservation in any of the trials.

The efficacy of biological fungicide foliar treatments to control basil downy mildew in the greenhouse

S. C. RHODES (1), K. L. Ong (1)
(1) Texas A&M AgriLife Extension Service, College Station, TX, U.S.A.
Phytopathology 105(Suppl. 2):S2.9

Basil downy mildew, caused by *Peronospora belbahrii*, was first reported in the United States in Florida in 2007. In Texas, the first recorded incident

occurred in 2009 when infected basil was sent by local nurseries to the Texas Plant Disease Diagnostic Laboratory. This disease is a major issue for greenhouse hydroponic growers in producing a quality crop for fresh market sale; buyers will not pay for a diseased crop, which will lead to major economic losses. Although there are management programs that can be followed to manage this disease, growers have seen increases in operational costs due to fungicide applications and, primarily, labor. Each plant must be individually cleaned to ensure that the best quality product is brought to market. We conducted a trial to evaluate two biological fungicides applied as foliar treatments against basil downy mildew. This experiment was conducted on 6-inch (~ 5–6 week old) plants obtained from a hydroponic producer. These plants were treated with Actinovate AG, RootShield Plus WP or a combination of Actinovate AG and RootShield Plus WP. Twelve days after foliar treatment, plants were inoculated with *P. belbahrii* sporangia (1.5×10^3 sporangia/ml). When symptoms appeared, plants were rated on a 1 to 10 scale for disease severity. Subsequently, plants were evaluated every two to three days to monitor disease progression.

Role of minor nutrients on tomato spotted wilt of tobacco (*Nicotiana tabacum*) and superoxide-dismutase and NPR1 genes

S. A. ROOKS (1), A. K. Watson-Selph (1), B. Dutta (1), R. D. Gitaitis (1), C. Nischwitz (2), S. W. Mullis (3), A. K. Culbreath (1), A. S. Csinos (1)
(1) University of Georgia, Tifton, GA, U.S.A.; (2) Utah State University, Logan, UT, U.S.A.; (3) University of Georgia, Blairsville, GA, U.S.A.
Phytopathology 105(Suppl. 2):S2.9

In previous studies, levels of tomato spotted wilt (TSW) of tobacco (*Nicotiana tabacum*), caused by *Tomato spotted wilt virus* (TSWV), had a linear relationship to certain cations in the soil. In multi-year studies, predictive equations from soil analyses were developed that consisted of concentrations of Cu, Fe, Zn, and the Fe:Mn and Cu:Fe ratios as variables. Interestingly, the Cu:Fe ratio was the highest contributing factor in all years. In year 1 the spatial distribution of TSWV-infected plants exhibited a gradient of TSW severity that matched with the gradient of the Cu:Fe ratio in the soil. In 2014, we surveyed multiple sites at the UGA Bowen Farm near Tifton, GA and analyzed soil cation concentrations for elements, which were used as independent variables in the predictive TSW models. Based on model predictions, two sites (approximately 100 m apart) were selected as high- and low-TSW risk areas prior to tobacco planting. When plants were rated for TSW prior to harvesting, plants at the low-risk sites had 4.5% TSW severity compared to 33.1% disease severity at the high-risk site. Low-risk site plants had a 5.5-fold, 2.3-fold, and 625-fold increase in the expression of *MnSOD*, *FeSOD*, and *NPR1* genes, respectively, when compared to plants in the high-risk site. These results support our hypothesis that these cations affect genes regulating systemic acquired resistance pathways and the detoxification of reactive oxygen species. Eventually soil profiles of fields used in conjunction with TSW predictive models could be part of a management strategy to control TSW of tobacco.

Resistance to fungicides in pathogens of stone and small fruits

G. SCHNABEL (1)
(1) Clemson University, Clemson, SC, U.S.A.
Phytopathology 105(Suppl. 2):S2.9

Fungicides with single-site inhibitory effects are more favorable in their toxicity profiles and are generally more effective than multisite fungicides. But usage over time will lead to resistance development in the target pathogen and sometimes secondary pathogens that used to be of little importance. In this presentation, an overview is provided of widespread resistance to FRAC 1 and 3 fungicides in the primary pathogen of stone fruits *Monilinia fructicola* and emerging resistance to FRAC 1, 7, and 11 fungicides in the secondary, non-target pathogens such as *Colletotrichum* species and *Alternaria alternata*. While these organisms are just now starting to accumulate resistances to multiple fungicides, examples exist where pathogens of small fruits have accumulated resistance to up to seven different FRAC codes. Resistance to multiple fungicides in individual isolates of field populations challenge current recommendations for resistance management in that mixtures and alternations may continue to select for these individuals. Strategies to manage multifungicide resistance in *Botrytis cinerea* from strawberry are discussed.

Evaluation of sodium selenate as a seed disinfectant to eradicate *Xanthomonas vesicatoria*, *X. euvesicatoria* and *X. perforans* on pepper and tomato seeds

M. SHAHRTASH (1), M. L. Lewis Ivey (2)
(1) Louisiana State University, Baton Rouge, LA, U.S.A.; (2) LSU AgCenter, Baton Rouge, LA, U.S.A.
Phytopathology 105(Suppl. 2):S2.9

Bacterial leaf spot is caused by three species of *Xanthomonas* (*X. vesicatoria* (Xv), *X. euvesicatoria*, (Xeu), and *X. perforans* (Xp)) in Louisiana. Bacterial leaf spot is seedborne and very difficult to manage once it becomes established in the field. Experiments were performed to determine the effect of sodium selenate, a non-essential element that is toxic to many organisms at excessive levels, in eliminating Xv, Xeu, and Xp on pepper and tomato seed. Bacterial populations were significantly reduced when grown on yeast dextrose carbonate medium amended with 38, 77, or 382 mg/l sodium selenate compared to the non-treated control. Tomato and pepper seed artificially infested with a mixture of Xv, Xeu, and Xp ($\sim 10^4$ CFU/ml) were treated with hot water (pepper seeds-30 minutes, 51°C; tomato seeds-25 minutes, 50°C) or chlorine (20%, one minute), which represent industry standards for disinfecting seed, or sodium selenate (765 mg/l, 30 minutes). All three treatments significantly reduced the incidence of infested pepper and tomato seed compared to the non-treated infested control. The incidence of infested pepper seeds following treatment with sodium selenate was significantly higher compared to chlorine and hot water treated seed. There was no difference in the incidence of infested seed between chlorine treated and sodium selenate treated tomato seed. Hot water treatment of pepper and tomato seed was the most effective at reducing *Xanthomonas* spp. on seed. The presence of *Xanthomonas* spp. was confirmed using colony-pick PCR with *Xanthomonas*-specific PCR primers. None of the treatments significantly reduced or delayed germination.

Spatial distributions of *Meloidogyne incognita*, *Rotylenchulus reniformis*, and *Thielaviopsis basicola* during a 10 year cotton monoculture and implications for site-specific management

T. N. SPURLOCK (1), T. L. Kirkpatrick (2), C. S. Rothrock (3), S. Monfort (4), A. C. Tolbert (1)

(1) University of Arkansas, Monticello, AR, U.S.A.; (2) University of Arkansas, Hope, AR, U.S.A.; (3) University of Arkansas, Fayetteville, AR, U.S.A.; (4) University of Georgia, Tifton, GA, U.S.A.

Phytopathology 105(Suppl. 2):S2.10

Meloidogyne incognita and *Rotylenchulus reniformis* are economically important plant pathogenic nematode species in cotton production. *Thielaviopsis basicola* causes black root rot of cotton, a seedling disease that can stunt seedlings and reduce vigor in cool wet soils. Losses increase dramatically as a result of a synergistic interaction between *T. basicola* and either nematode species. Evidence from 2001–2003 in a texturally diverse cotton field near Portland, Arkansas, USA suggested that populations of *M. incognita* had the greatest effect on yield in soils with greater sand content. Nematode samples from 512 grids (4×30 m) in the field indicated *R. reniformis* increased in population density and distribution in the field during the 2001–2003 periods. The field was monocultured to cotton until 2013 when soybean was grown and nematode and *T. basicola* population densities were again measured from the original 512 plots. Over the 10-year period, incidence and distribution of *M. incognita* decreased while incidence and distribution of *R. reniformis* increased. *Thielaviopsis basicola* population levels and distribution were consistent with those seen in 2003. Pathogen populations were largely aggregated and correlated with soil texture. Bivariate spatial analysis and spatial regression indicated a significantly dispersed distribution and inverse relationship in 3 of 4 years and 2 of 4 years respectively confirming competition and displacement of *M. incognita* by *R. reniformis*. Pathogen populations were not related to yield loss across soil textures. The greatest yield consequence occurred in the sandier areas of the field indicating these three pathogens can be managed site-specifically by textural zone.

An investigation into QoI resistance in isolates of *Cercospora sojae* throughout Mississippi soybean production fields

J. R. STANDISH (1), M. Tomaso-Peterson (1), T. W. Allen (2), S. Sabanadzovic (1), N. Aboughanem-Sabanadzovic (1)

(1) Mississippi State University, Mississippi State, MS, U.S.A.; (2) Mississippi State University, Stoneville, MS, U.S.A.

Phytopathology 105(Suppl. 2):S2.10

A survey of Mississippi soybean fields was conducted during the 2013 and 2014 growing seasons to collect frogeye leaf spot (FLS), *Cercospora sojae* Hara, infected leaf samples. Quinone outside inhibitor (QoI) fungicides have been widely used to manage FLS in MS. However, resistance to this fungicide class has been confirmed in *C. sojae* isolates from several soybean producing states. Resistance to QoIs is generally associated with the presence of a nucleotide point mutation resulting in an amino acid substitution within the cytochrome *b* (*cyt b*) gene. A glycine to alanine substitution at position 143 (G143A) confers complete resistance to the QoI fungicides. The objective of this study was to screen *C. sojae* isolates from MS for resistance to the QoIs by identifying *cyt b* point mutations. Genomic DNA was extracted from the

collected fungal isolates (n>500) as well as a baseline isolate collected prior to the release of the QoIs. Primers were developed to amplify a 250-bp *cyt b* gene fragment, and the resulting nucleotide sequences were analyzed and compared to identify point mutations. A PCR-RFLP method using the *AluI* restriction enzyme was adopted for screening purposes. Greater than 90% of the isolates screened were confirmed to carry the G143A amino acid substitution. Understanding the distribution of QoI resistant *C. sojae* isolates in MS will greatly aid soybean farmers in choosing effective fungicide product chemistries to manage FLS in the future.

Evidence for volatile aflatoxin stimulatory and inhibitory chemicals produced by *Aspergillus flavus*

R. R. SWEANY (1), K. E. Damann Jr. (1)

(1) LSU AgCenter, Baton Rouge, LA, U.S.A.

Phytopathology 105(Suppl. 2):S2.10

The fungal pathogen *Aspergillus flavus* produces toxic and carcinogenic aflatoxins which contaminate corn, peanuts, cotton and tree nuts. Aflatoxin production is highly variable between strains, growing conditions, replicates and experiments. This study investigated whether culture density or number, and volatiles produced by the fungus regulate aflatoxin production. Two closed systems employing 48-well plates (glucose salts liquid medium) or eight open small Petri dishes (glucose salts solid medium) inside a closed large Petri dish were used. Aflatoxin was extracted after four days (liquid medium) or five days (solid medium) of growth at 25°C and quantified by HPLC. Increasing the number of inoculated wells with isolate 53 (12, 24, 36, or 48) in 48-well plates increased mean aflatoxin production indicating a stimulatory effect. Perimeter wells had substantially more aflatoxin production than interior wells indicating a location effect. Increasing the number (1, 4, or 8) of small dishes inoculated with isolate 53, 4, or 70s inside a closed larger dish decreased aflatoxin production indicating an inhibitory effect, except 53 inoculated on a single dish. This effect was most apparent when the volatile adsorbent activated charcoal was added to the large dish bottoms. Activated charcoal increased aflatoxin production in all treatments except 70s inoculated on a single dish. Results indicate aflatoxin production is modulated upward by a volatile production in liquid culture and downward by volatile production on solid medium. Volatiles and culture density should be considered in design and interpretations of aflatoxin experimental data and as a potential regulator of aflatoxin production in crops.

Characterization of soybean and its wild relatives host resistance and Asian soybean rust (ASR) pathogen variability for durable resistance

P. TIAN (1), S. M. Smith (1)

(1) University of Georgia, Athens, GA, U.S.A.

Phytopathology 105(Suppl. 2):S2.10

Asian soybean rust (ASR) is caused by *Phakopsora pachyrhizi* and is one of the most aggressive soybean diseases. Resistance to ASR is controlled by six resistance genes (*Rpp1-6*) that are ineffective when challenged with different ASR isolates. Knowledge of the genetics of host resistance to ASR and the variability of ASR populations are essential in dissecting the relationship between the host and pathogen, and developing effective breeding strategies for resistance. This project has three major research components: 1) characterization of soybean and its wild relatives host resistance, 2) analysis of ASR pathogen variability, and 3) integration of host and pathogen datasets to identify durable resistance. Eight ASR field isolates were collected from 5 different locations in Georgia from 2011–2013. Based on phenotype, the 8 field isolates represent 3 different field isolates. Population genetic analysis of the internal transcribed spacer region (ITS) and ADP-ribosylation factor (ARF) genes suggested that over 115 ITS and 111 ARF genotypes are present in the current Georgia ASR population. Additionally, the resistance of 16 released Georgia cultivars and 8 soybean relatives were tested by inoculation with ASR Georgia field isolates. Soybean cultivar Hyuuga and all of the tested wild relatives demonstrated a high level of resistance. Conversely, all of the released soybean cultivars were susceptible. By using RNA sequencing, candidate core effector genes in the ASR isolates and the corresponding host resistance genes will be identified and can potentially be used to develop durable broad-spectrum disease resistance strategies for soybean cultivars grown in Georgia.

Characterization of *Pseudomonas viridiflava* causing bacterial speck-like symptoms on tomato in Florida

S. TIMILSINA (1), H. Adkison (1), J. B. Jones (2), G. E. Vallad (1)

(1) Gulf Coast Research and Education Center, University of Florida, Wimauma, FL, U.S.A.; (2) University of Florida, Gainesville, FL, U.S.A.

Phytopathology 105(Suppl. 2):S2.10

Pathogenic strains of *P. viridiflava* have been isolated from bacterial speck-like symptoms on tomato foliage and fruits in Florida. Four housekeeping

genes (*gapA*, *gyrB*, *rpoD* and *gltA*) along with 16S rRNA gene sequence were used to phylogenetically characterize *Pseudomonas* strains along with their type strains. All strains were identified as *P. viridiflava* based on MLSA, but formed two groups distinct from the type strain. Interestingly, these two groups of *P. viridiflava* also varied in the LOPAT test based on their ability to produce levan on nutrient media amended with 5% sucrose. One phylogenetic group behaved typically for *P. viridiflava* by not producing levan, while the second group produced a distinct yellow-colored domed colony suggesting possible levan sucrase activity. Levan production by the second group of *P. viridiflava* strains was confirmed using concanavalin-A; a lectin compound that specifically binds to levan forming a precipitate.

Fungicide resistance in turfgrass systems: A case study in benzimidazole and QoI resistance

M. TOMASO-PETERSON (1)

(1) Mississippi State, MS, U.S.A.

Phytopathology 105(Suppl. 2):S2.11

Golf course putting greens may receive more than 30 fungicides applications per growing season. The golfer's expectation to maintain pristine putting green surfaces requires the reliance on fungicides for disease control. The benzimidazoles were the first single-site penetrant fungicides applied for turfgrass disease control. Within three years of use, fungicide resistance was reported in the dollar spot pathogen. After 25 years, *Colletotrichum cereale*, causal organism of turfgrass anthracnose, was reported to be resistant to the benzimidazole, thiophanate-methyl. Shortly after the introduction of the QoI fungicide, azoxystrobin, control failures for anthracnose were also noted. Both the benzimidazole and QoI fungicides have single-site modes of action increasing the risk of fungicide resistance among turfgrass pathogen populations with qualitative sensitivity distributions. A survey of creeping bentgrass putting greens was conducted in southern states to determine the occurrence of benzimidazole and QoI resistance in populations of *C. cereale*. Fungicide sensitivity assays were determined for isolates collected from putting greens with a history of thiophanate-methyl and azoxystrobin applications. All *C. cereale* isolates showed a lack of sensitivity to both fungicides. Molecular confirmation at the benzimidazole and QoI target sites, tubulin and cytochrome b proteins, respectively, supported results of multiple resistance.

Fungicides for controlling sugar beet diseases in Georgia

T. N. TORRANCE (1), T. B. Breneman (1), T. M. Webster (2)

(1) University of Georgia, Tifton, GA, U.S.A.; (2) USDA, Tifton, GA, U.S.A.

Phytopathology 105(Suppl. 2):S2.11

Southern blight (*Sclerotium rolfsii*) and *Cercospora* leaf spot (*Cercospora beticola*) are two devastating diseases of sugar beets (*Beta vulgaris*). Sugar beets are not traditionally grown in Georgia, but have potential as a winter crop for biofuel. However, effective fungicides will be essential for consistent production. A replicated trial in 2013–2014 evaluated 12 fungicide programs, each with four sprays on about a 21-day interval starting on 17 April on cultivar ECR306. Frequent spring rain lead to severe *Cercospora* leaf spot in the trial. Six fungicide treatments including azoxystrobin, pyraclostrobin, triphenyltin hydroxide, and prothioconazole reduced leaf spot severity. Other triazoles, phosphites and thiophanate methyl were not effective on leaf spot. Effective treatments usually doubled crop yield, and seven treatments had higher yields than the control. Southern blight incidence was very low, presumably because this was the first year of sugar beet production.

Evaluating novel ectotrophic root-infecting fungi as possible etiological agents for summer decline of ultradwarf bermudagrass

P. L. VINES (1), M. Tomaso-Peterson (2), T. Allen (2)

(1) Mississippi State University, Starkville, MS, U.S.A.; (2) Mississippi State University, Mississippi State, MS, U.S.A.

Phytopathology 105(Suppl. 2):S2.11

Roots of ultradwarf bermudagrasses expressing symptoms of summer decline are typically brown to black in color, diminutive in size, and frequently colonized with dark runner hyphae, growth cessation structures, and simple hyphopodia, which are characteristic signs of ectotrophic root-infecting (ERI) fungi. Research at Mississippi State University led to the identification of six novel fungal species (*Gaeumannomyces paulograminis*, *Magnaportheiopsis hawaiiensis*, *M. cynodontis*, *M. taurocanis*, *Candidacolonium cynodontis*, and *Pseudophialophora cynodontis*) and two previously recognized species (*G. graminis* var. *graminis* and *M. incrustans*) from colonized roots. The objective of this study was to screen the ERI fungal species for pathogenicity on 'Champion' and 'MiniVerde' ultradwarf bermudagrasses. Representative isolates from each of the eight fungal species were selected and grown on potato dextrose agar (PDA) under 24 hour fluorescent light until complete colonization of PDA occurred. The experiment was conducted in a randomized complete block split-plot design with three replications.

Ultradwarf bermudagrass cultivars (n = 2) were whole plots and fungal isolates (n = 10) were split-plots. *In vivo* inoculations were performed in three inch diameter pots and placed in light- and temperature-controlled growth chambers for eight weeks. Pathogenicity was assessed through a series of evaluation parameters and Koch's postulates were confirmed by reisolation of the fungus from roots within each pot. Results from this study will be discussed in detail.

QTL analysis of disease resistance to leaf spots and TSWV in peanut (*Arachis hypogaea*)

H. WANG (1), P. Khera (2), A. K. Culbreath (1), M. K. Pandey (2), C. Holbrook (3), R. K. Varshney (2), B. Guo (3)

(1) University of Georgia, Tifton, GA, U.S.A.; (2) International Crops Research Institute for the Semi-Arid Tropics, Patancheru, INDIA; (3) USDA-ARS, Tifton, GA, U.S.A.

Phytopathology 105(Suppl. 2):S2.11

Early leaf spot (ELS), caused by *Cercospora arachidicola*, late leaf spot (LLS), caused by *Cercosporidium personatum*, and Tomato spotted wilt virus (TSWV) result in great losses in yield in peanut (*Arachis hypogaea* L.). In order to identify quantitative trait loci (QTL) for resistance to these diseases, and also identify markers linked to these traits, a genetic linkage map was constructed using a population of 162 recombinant inbred lines (RILs) from a cross between 'Tifrunner' and 'GT-C20'. The map consisted of 426 SSR markers arranged into 24 linkage groups (LGs) with a total map length of 1980.78cM and an average distance of 4.6cM between adjacent loci. These RILs were evaluated for resistance to ELS, LLS, and TSWV in the field from 2009 to 2013. A total of 49 QTL were identified on 16 LGs for these disease resistance traits with phenotypic variance explained (PVE) ranged from 6.26% to 15.54%. Of these QTL, 16 were for ELS, 22 for LLS, and 11 for TSWV, respectively. Among the 49 QTL, 13 QTL were found to be major QTLs (PVE >10%), including 7 for ELS, 5 for LLS and 1 for TSWV. Four consistently expressed QTL regions were identified in more than two environments for ELS (LGA05, LGA06), LLS (LGA05) and TSWV (LGA04) with PVE of up to 13.20%, 12.35% and 14.40%, respectively. Interestingly, LGA05 was identified as a "resistance gene rich" LG for both ELS and LLS. Further study is needed to identify the potential resistance gene(s) through fine-mapping approach.

Foliar applications of minor elements suppress *Cercospora* leaf blight and rust in soybeans

B. M. WARD (1), C. L. Robertson (1), R. W. Schneider (1), E. Chagas Ferreira da Silva (1), T. G. Garcia Aroca (1)

(1) LSU AgCenter, Baton Rouge, LA, U.S.A.

Phytopathology 105(Suppl. 2):S2.11

Both *Cercospora* leaf blight (*Cercospora kikuchii*) and rust (*Phakopsora pachyrhizi*) of soybean are serious diseases in the southern U.S. where yield losses approaching 40% have been recorded. More sustainable methods of disease management are always being sought particularly since widespread fungicide resistance in *C. kikuchii* has been documented in Louisiana. Minor elements were applied by foliar sprays during the R5-6 growth stage to field-grown soybeans during in 2011, 2012, and 2013 in Louisiana in order to determine their effects on disease severity. Rates of minor element applications were based on concentrations commonly applied in foliar fertilization where literature was available. After application, quantitative disease severity assessments for both diseases were made. Aluminum, boron, iron, and zinc had varying degrees of efficacy for both diseases; however, not all elements were consistently beneficial across all rates applied. Manganese consistently exacerbated CLB. While these effects were not sufficiently efficacious to be used as stand-alone treatments, they could be used to augment existing management strategies. Furthermore, we need to investigate combinations of minor elements and relate application rates to tissue concentrations, which may vary across locations.

Solatenol™ fungicide – a new SDHI fungicide from Syngenta

M. D. WIGLESWORTH (1), A. H. Tally (1)

(1) Syngenta Crop Protection, Greensboro, NC, U.S.A.

Phytopathology 105(Suppl. 2):S2.11

Solatenol™ fungicide is a new broad spectrum foliar fungicide discovered and developed by Syngenta. It is currently registered in Brazil and Paraguay. In the US, Solatenol fungicide (ISO name benzovindiflupyr) registration is expected first quarter 2015. Four products will be launched: Aprovia™ (solo), Aprovia™ Top (plus difenoconazole), Elatus™ (plus azoxystrobin), and Trivapro™ (and co-pack with azoxystrobin and propiconazole). Solatenol is in FRAC Group 7. The very high affinity for succinate dehydrogenase results in its high intrinsic activity. Solatenol's high intrinsic activity combined with strong binding to the plant's wax layer from where it slowly penetrates into

the plant tissue, results in long lasting disease control. Key strengths of Solatenol fungicide include activity on Asian soybean rust (*Phakopsora pachyrhizi*), *Septoria tritici* on wheat, and apple scab (*Venturia inaequalis*). Use rates as low as 30 g ai/ha are extremely efficacious on soybean rust. It also has excellent activity on many leafspots, rusts, powdery mildews, *Rhizoctonia* spp., and *Sclerotium rolfsii*. Elatus will be positioned in peanut where it has shown excellent residual activity of early leafspot (*Cercospora arachidicola*), late leafspot (*Cercosporidium personatum*), peanut rust (*Puccinia arachidis*), and Southern Blight (*Sclerotium rolfsii*). Peanut fungicide programs including Solatenol Fungicide have shown excellent seasonal control of peanut diseases and resulted in improved yield compared to the best disease control programs currently available. Aprovia Top provided excellent powdery mildew and gummy stem blight control in cucurbits. Baseline sensitivity studies are underway to determine specific cross-resistance with other SDHIs currently on the market.

Sequencing and characterization of Canna yellow mottle virus

D. S. WIJAYASEKARA (1), P. R. Hoyt (1), J. Verchot-Lubicz (1), M. A. Webb (1)

(1) Oklahoma State University, Stillwater, OK, U.S.A.
Phytopathology 105(Suppl. 2):S2.12

Canna yellow mottle virus (CaYMV) belongs to the family *Caulimoviridae* under genus of *Badnavirus*. Badnaviruses are recently reported as emerging pathogens in many agricultural crops and have circular double stranded DNA that can sometimes integrate into the host genome. CaYMV was first reported in Japan in 1979, and later in USA and most recently in Italy. CaYMV causes symptoms such as mottling with yellowing, venial chlorosis and at severe stages indicate necrosis in leaves. PCR diagnostic tests on 150 symptomatic canna plants indicates the correlation between disease symptoms and the presence of the virus. Southern analysis was carried out using CaYMV infected cannas and we identified the genomic DNA to be two bands of approximately 7.5 and 8.0 kb in length. Electron microscopy of purified virus confirmed the presence of typical bacilliform particles. In spite of its prevalence, the total genome length sequence is still not reported. To discover the total genome of this novel badnavirus, next generation sequencing was done and 2500 bp part of the virus was revealed which belong to the open reading frame three of the virus. PCR primers were designed to reveal the remaining 5000 bp of the viral genome. At this time we cloned and sequenced 3500 bp of the genome. Blasting search shows this virus close to gene bank reported canna yellow mottle virus with 99% identity and phylogenetic analysis revealed that this virus is closely related to gene bank reported genome fragments of isolate AKCanna10 (Accession: KC880352.1 GI: 527179248).

Suppression of charcoal rot in soybean caused by *Macrophomina phaseolina* using secondary nutrients

T. WILKERSON (1), M. Tomaso-Peterson (2), B. Golden (1), S. Lu (2), A. B. Johnson (2), T. W. Allen (1)

(1) Mississippi State University, Delta Research and Extension Center, Stoneville, MS, U.S.A.; (2) Mississippi State University, Starkville, MS, U.S.A.
Phytopathology 105(Suppl. 2):S2.12

Charcoal rot (CR) of soybean, caused by *Macrophomina phaseolina* (Tassi) Goid (*Mp*), is a ubiquitous soilborne disease that affects over 500 hosts and can limit profitable soybean production in some years. The disease is typically more devastating in hot dry years in non-irrigated situations, but over the last ten years CR has been reported from irrigated soybean fields in the Mississippi Delta. The objective of this research is to evaluate the effects of secondary nutrients, specifically calcium (Ca) and magnesium (Mg), on the suppression of CR. An inoculated greenhouse rate response trial using a CR-susceptible variety evaluated seven rates, 0, 25, 100, 250, 500, 750, and 1,000 lb/A, of Ca and Mg applied alone and in combination at three timings: at plant, R1, and at plant followed by (fb) R1. A significant increase in seed weight was observed with the 1,000 lb/A rate of Ca + Mg at planting compared to the non-treated. Two field trials, one each with a susceptible and moderately resistant cultivar, were conducted in 2014. Treatment applications consisted of Ca and Mg alone and in combination at plant, R1, and at plant fb R1 at 1,000 lb/A compared with a non-treated. Field plots were inoculated with *Mp* in-furrow at planting in addition to a non-inoculated set of plots. Mg applied at R1 provided the greatest yield benefit, albeit not significant, over the inoculated non-treated in both trials. Some treatment combinations may have negatively affected yield.

Impact of current production practices in peanut on the development of tomato spotted wilt virus in southeast United States

B. W. WILLIAMS (1), R. Kemeraït (1), A. Culbreath (1), R. S. Tubbs (2)

(1) Department of Plant Pathology, University of Georgia, Tifton, GA, U.S.A.; (2) Department of Crop and Soil Sciences, University of Georgia, Tifton, GA, U.S.A.

Phytopathology 105(Suppl. 2):S2.12

Spotted wilt, caused by thrips-vectored *Tomato spotted wilt virus* (TSWV), is a viral disease affecting peanut production in the United States. In 1996, a risk assessment method (eventually known as Peanut Rx) was introduced whereby production practices, host resistance and at-plant insecticide usage were assessed to predict risk to TSWV. Even with current increases in host resistance, incorporation of these factors is integral to TSWV management programs. The objective of this study was to assess continued impact of the Peanut Rx management tool on development of TSWV. Trials were conducted in Tifton, GA in 2013 and 2014 to compare resistant and susceptible cultivars, at-plant insecticides, tillage systems, and row pattern on incidence of TSWV. In a trial repeated in 2013 and 2014, incidence of TSWV was 53.9% and 54.7% lower, respectively, in runner-type peanut cultivars as compared to Virginia-type cultivars. In 2013, all at-plant insecticides provided a significant reduction in TSWV incidence when compared to the untreated control. In 2014, phorate, but not thiomethoxam seed-treatment, significantly reduced incidence of TSWV. Reduced tillage systems and twin row pattern significantly reduced incidence of TSWV as compared conventional tillage and single row patterns. In 2013 and 2014, reduced tillage resulted in a 65.8% and 40.1% reduction in TSWV incidence, respectively, as compared to conventional tillage. Twin-row patterns resulted in a 31.2% and 16.3% reduction in TSWV incidence, respectively. This study documents the continued importance of Peanut Rx for management of TSWV in peanut even with the use of more resistant cultivars.

Evaluation of flutriafol for management of cotton root rot in Texas

J. WOODWARD (1), J. H. Ramirez (2), G. D. Morgan (3)

(1) Texas AgriLife Extension Service, Lubbock, TN, U.S.A.; (2) Texas A&M AgriLife Extension, Vernon, TX, U.S.A.; (3) Dept. of Soil & Crop Sciences, College Station, TX, U.S.A.

Phytopathology 105(Suppl. 2):S2.12

Cotton root rot, caused by *Phymatotrichopsis omnivorum* (Duggar) Hennebert, is responsible for significant losses in lint yield throughout cotton production regions in Texas. Historically, chemical management options have been ineffective, or cost prohibitive. Recent studies evaluating in-furrow applications of the fungicide flutriafol have resulted in excellent control of the disease; however, significant stand loss has been observed. Field trials evaluating different application methods including T-band and Y-split applicators were conducted during the 2013 and 2014 growing seasons. Disease incidence in non-treated control plots ranged from 15 to 54%; whereas, plots treated with flutriafol in either a T-band or with a Y-split exhibited similar levels of disease ranging from 0 to 6%. Stand establishment was negatively affected when flutriafol was applied using a Y-split applicator with damage increasing at higher use rates. When averaged across use rates, yield increases of 6 to 42% were observed with flutriafol applied with T-band. Despite the impact on stand establishment flutriafol applied via a Y-split applicator resulted in a 14 to 24%. These results corroborate previous findings regarding the efficacy of flutriafol towards cotton root rot. Additional studies investigating methods to alleviate the potential for phytotoxicity are warranted.

Biological potential of *Bacillus* spp. to reduce the populations of *Heterodera glycines* and promote plant growth in soybean

N. XIANG (1), K. S. Lawrence (1)

(1) Auburn University, Auburn, AL, U.S.A.

Phytopathology 105(Suppl. 2):S2.12

Heterodera glycines (SCN), is one of the most damage pathogens to soybean production. The objective of this study is to select the effective *Bacillus* spp. strains to reduce the population of SCN. In order to achieve the goal, *in vitro* assays were conducted in 96-well plates to evaluate the effectiveness of 19 *Bacillus* spp. strains on paralysis of SCN J2s and inhibition of SCN eggs hatch. Greenhouse trials were conducted to determine population density development of SCN when exposed to the *Bacillus* spp. strains. Data were analyzed in SAS 9.2 using PROC GLIMMIX. *In vitro* results indicated that 14 strains including *B. amyloliquefaciens*, *B. mojavensis*, *B. pumilus*, *B. safensis*, *B. solisalsi*, *B. subtilis* subsp. *subtilis* significantly reduced live numbers of SCN J2s compared with water control ($P < 0.05$). Five strains of *B. safensis*, AP-280, AP-3, AP-7, AP-281, and *B. subtilis* subsp. *subtilis* AP-279 significantly inhibited SCN eggs hatch ($p < 0.05$). The greenhouse trial indicated that strains AP-301 (*B. amyloliquefaciens* subsp. *plantarum*) and AP-52 (*B. subtilis* subsp. *subtilis*) reduced ($P < 0.10$) the numbers of soybean cysts at 60 days after planting (DAP). Strains AP-153 (*B. megaterium*) and AP-280 (*B. safensis*), reduced ($P < 0.10$) the number SCN juveniles. Soybean

plant height was increased by strain AP-18 (*B. pumilus*); however, plant fresh and dry weights were statistically similar. Strains AP-301(*B. amyloliquefaciens* subsp. *plantarum*), AP-52 (*B. subtilis* subsp. *subtilis*), AP-153(*B. megaterium*), AP-280 (*B. safensis*), and AP-18 (*B. pumilus*) will be tested in the microplot and the field for biological control and yield production on soybean in 2015.

Isolation and assessment of P-solubilizing bacteria from switchgrass (*Panicum virgatum* L.) for plant growth promotion and nutrient uptake

J. XU (1), J. W. Kloepper (1)

(1) Auburn University, Auburn, AL, U.S.A.

Phytopathology 105(Suppl. 2):S2.13

Switchgrass is widely evaluated as a model energy crop because it grows rapidly in temperate climate zones, can reach heights of 2–3 m on marginal lands and requires low levels of fertilization. This rapid plant growth with little fertilization suggests a possible involvement of microorganisms that can be used as biofertilizers. The objective of this project was to isolate and characterize P-solubilizing bacteria from rhizosphere soil and endophytically from inside roots and stems of switchgrass. Putative P-solubilizing bacteria were isolated using different isolation media with various phosphate sources. The P-solubilizing activity was confirmed by the molybdenum-blue method. IAA and siderophore production were evaluated *in vitro*. 16S rDNA sequencing was used for the bacterial identification. Selected P-solubilizing strains were tested on corn as microbial inoculants under greenhouse condition. The results showed that the selected P-solubilizing strains promote corn growth by increasing fresh root, dry shoot, dry root weight, chlorophyll content and height. Some bacterial strains significantly increased plant nutrient uptake without significantly promoting plant growth.

Maize sensitivity to drought stress is associated with differential responses to reactive oxygen species

L. YANG (1), J. C. Fountain (1), X. Ni (2), P. Ji (1), R. D. Lee (1), B. T. Scully (3), R. C. Kemerait (1), B. Guo (1)

(1) University of Georgia, Tifton, GA, U.S.A.; (2) USDA-ARS, Tifton, GA, U.S.A.; (3) USDA-ARS, Fort Pierce, FL, U.S.A.

Phytopathology 105(Suppl. 2):S2.13

Aflatoxin contamination of crops is exacerbated by preharvest drought stress. Previously, we identified maize drought responsive proteins in lines with differing drought sensitivities, and proposed a model for drought responses. The sensitive line, B73, exhibited a vigorous induced response to stress while the tolerant line, Lo964, exhibited stable, constitutive expression of defense proteins. In order to verify the proposed model, we examined the metabolic responses of tolerant (A638, Grace E-5, Va35, Lo964), and susceptible (B73 and Lo1016) maize lines to drought stress focusing on reactive oxygen species (ROS) metabolism including catalase and superoxide dismutase activity. The lines were cultivated in the greenhouse with controlled irrigation for 30 days (V3-V4 stage). Drought was then induced by withholding water for 9 days followed by a recovery period of normal irrigation for 3 days. Leaf and root tissue samples were collected every 3 days for both drought and normally irrigated samples. Overall, the observed enzyme activities were constitutively higher in tolerant lines than in susceptible ones which showed a rapid induction following drought induction. Lo964 tissues were also found to accumulate less ROS than B73. This is in agreement with the proposed model, and suggests that tolerant lines may be able to better sequester ROS than susceptible lines. Continuing studies will examine this in additional lines and explore the roles of additional metabolites.