2018 Southern Division Meeting Abstracts

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A genetic screen for pathogenicity genes in the fungus *Diaporthe longicolla* causing Phomopsis seed decay of soybean

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Phomopsis seed decay of soybean is an important economic disease in the United States. The disease is predominantly caused by *Diaporthe longicolla*. Currently, the molecular basis of Phomopsis seed decay is poorly understood. The objective of this study was to identify genes of *Diaporthe longicolla* involved in colonization of soybean seeds. Random insertional mutagenesis via *Agrobacterium tumefaciens* mediated transformation generated 1251 mutants of the pathogen. Two mutants with visually reduced seed colonization were selected for further study from a forward genetic screen. Target enrichment sequencing identified a single site of *Agrobacterium*-mediated T-DNA insertion in each mutant. In one mutant, a T-DNA insertion disrupted a putative serine threonine protein. In the other mutant, a T-DNA insertion was identified in the putative promoter region of a gene predicted to encode a cytochrome P450. Virulence assays on seeds and stems indicated that both mutants were impaired in seed colonization and the ability to induce necrotic lesions on stems. Additionally, neither mutant produced pycnidia on four different culture media. These results provide insight into genes that could have roles in virulence and asexual development in *Diaporthe longicolla*.

Evaluation of the impact of water-use efficient irrigation strategies on peanut disease management

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Soil moisture sensor or evapotranspiration (ET)-based irrigation scheduling and variable-rate equipment are technologies being promoted for water-use efficiency in peanut production. Irrigation frequency and variations in soil type and topography can result in spatiotemporal differences in soil moisture and canopy RH which are factors that affect pathogen growth. Reduced plant health caused by suboptimal irrigation and nutrient availability can further favor disease. This study aimed to investigate the impact of irrigation, fungicide use, and microclimate on peanut disease development. A split-plot randomized complete block design was used with five irrigation schedules (non-irrigated, standard, sensor-based with 30% or 50% maximum allowable depletion, and ET-based PeanutFarm) and three fungicide schedules including a non-treated control. Blocks were six zones defined by elevation, OM, and EC. Microclimate monitoring stations were installed in three broader-defined zones. Early (*Cercospora arachidicola*) and late (*Cercosporidium personatum*) leaf spot and stem rot (*Sclerotium rolfsii*) were rated over time, and vegetation indices were monitored using multispectral imagery. Heterogeneity in variance of leaf spot severity was observed across zones where variance generally increased with water applied depending on fungicide treatment. The results indicate that irrigation strategy as well as soil type and topography should be considered when managing peanut diseases.

Control of Botrytis blight of hydrangea with isofetamid, a new succinate dehydrogenase inhibitor fungicide

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The efficacy of isofetamid fungicide (Astun™), a new succinate dehydrogenase inhibitor (FRAC group 7) on Botrytis blight disease was investigated with whole hydrangea plants and fresh cut hydrangea flowers. Treatments (Astun™ SC at 10, 13.5 and 17 fl oz/100 gal and Decree 50WDG at 1.5 lb/100 gal) were applied to run-off using a backpack CO₂-pressurized sprayer at 40 psi on a 10-day interval. Hydrangea plants and fresh cut flowers (*Hydrangea macrophylla*) were inoculated by spraying with conidial suspension of *Botrytis cinerea* 24 h after treatment. Non-treated, inoculated and non-treated, non-inoculated plants or flowers served as controls. After inoculation, each plant or flower was enclosed in a clear plastic bag to increase the relative humidity for 24 hours. Severity of Botrytis blight was evaluated using a scale of 0–100% foliage or flower area affected. All of the treatments significantly reduced Botrytis blight severity and the area under the disease progress curve compared to the non-treated inoculated control for both experiments. Final disease severity rating in plants or flowers treated with Astun™ SC, regardless of rate, was comparable to those of plants or flowers treated with Decree 50WDG. The high and mid rate of Astun™ SC numerically reduced disease severity and progression of Botrytis blight compared to the low rate of Astun™ SC. Phytotoxicity was not observed in any of the treated hydrangea plants or fresh cut hydrangea flowers.

Development of fungicide rotation program for the control of powdery mildew of crapemyrtle

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Powdery mildew caused by *Erysiphe lagerstroemia* is one of the most common problems of crapemyrtle. Fungicide rotation at different application intervals was evaluated on crapemyrtle 'Muskogee' (*Lagerstroemia indica* × *L. fauriei*) and 'Whit I' (*L. indica* Raspberry Sundae™). The initial fungicide application was made after observing the first symptoms of powdery mildew disease. Treatments were applied in a 14 or 21-day rotation program. Treatment program contained Mural, Palladium, Concert II and Palladium. The severity of powdery mildew was evaluated using a scale of 0–100% foliage area affected. Plant quality/acceptability was evaluated using a scale of 1–9 where 1 is dead, 6 is commercially acceptable and 9 is a perfect plant. Powdery mildew infections occurred naturally and disease pressure was moderate. The final disease severity mean value was 37.1% and 53.5% in the non-treated control Muskogee and Whit I plants, respectively. Fungicide rotation program at both application intervals significantly reduced powdery mildew severity and disease progress compared to the non-treated control in both cultivars. The 14-day rotation program significantly reduced powdery mildew severity and disease progress compared to the 21-day rotation program in both cultivars. Non-treated control crapemyrtle plants for both cultivars were not commercially acceptable due to powdery mildew disease at the end of the experiment.

Influence of nitrogen rate and timing, application method, and simulated rainfall after fungicide application on brown patch severity in tall fescue

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In North Carolina, tall fescue (*Schedonorus arundinaceus* Schreb.) is the most commonly planted turfgrass species throughout the mountain and piedmont regions, particularly in home lawns and commercial landscapes. North Carolina is located in the transition zone, which is subject to hot, humid summers that predispose tall fescue to brown patch (*Rhizoctonia solani*). Field trials were conducted over a two-year period to evaluate the effect of nitrogen rate and timing, application method of a fungicide, and effect of rainfall following fungicide application on brown patch severity. Seven rates from 0 to 6 lb N 1000 ft⁻² yr⁻² using urea were initiated each year in March with repeat applications monthly at 1 lb N 1000 ft⁻². In a separate study, various timings of urea were conducted throughout the year for a total of 3 lb N 1000 ft⁻² yr⁻². No significant differences in disease severity or turfgrass quality were observed with regards to rate or timing in either study in both years. Azoxystrobin was applied with a ride-on spreader/sprayer (12 gal/acre), a commercial applicator gun (130 gal/acre), and a research spray boom (88 gal/acre). No differences were detected between the methods and all provided excellent control of brown patch. A rainfall event of 0.5 in. was simulated 30 minutes after application of various liquid and granular fungicides with overhead irrigation. No differences were detected between the treatments and all provided excellent control of brown patch.

Differences in fumonisin levels associated with commercial corn hybrids and advanced breeding lines

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Fusarium ear rot, caused by *Fusarium verticillioides*, commonly affects corn in the United States. The fungus is capable of producing fumonisin, a mycotoxin that can contaminate grain used to feed livestock. Extremely high levels of fumonisin occurred throughout much of the Texas High Plains in 2017, as a result of above average humidity and below average temperatures that occurred late in the season. A total of 79 entries were planted in four different trials to evaluate the performance of commercially available corn hybrids and advanced breeding lines. Entries were arranged in a randomized complete block design with three replications. Plots were two rows wide and 6.1 m long. Overall, signs of ear rot were low (<5%); however, symptoms associated with fumonisin were quite evident throughout all trials. Five ears were randomly collected from the middle of each plot, shelled and weighed. A 100-g sub-sample was ground and passed through a 20-mesh sieve. Fumonisin levels were estimated using QuickScan Fumonisin Test Kits (Envirologix,

Portland, ME). Fumonisin levels varied by trial. In trial 1, levels ranged from 0 to > 38 ppm (the upper limit of detection) averaging 2.4 ± 4.4 ppm. Fumonisin levels were considerably higher in the other trials averaging 15.9, 19.9 and 16.6 ppm with a standard deviation of approximately 14 ppm. Sampling for fumonisin is highly variable; however, these results suggest that differences in hybrid performance exist among the genotypes evaluated. Additional testing is needed to fully understand differences in resistance to Fusarium ear rot and fumonisin in this and other corn germplasm.

Variability of peanut spotted wilt severity based on location in Georgia

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Thrips-transmitted spotted wilt disease is a concern in peanut producing areas in the southeastern US. Here spotted wilt severity was documented in field trials at six geographic locations in Georgia. Based on Peanut Rx, a combination of production factors was chosen to create different levels of risk to spotted wilt. The low risk plots (50 – 65 risk points) had 1.25 - 25% end-of-season spotted wilt severity. The medium (70-110 points) and high (>115 points) risk plots ranged from 2 - 54.5%. Test plots in Midville and Reidsville (east Georgia), had higher spotted wilt severities of 54.5 and 33.25% as compared to Plains, Tifton, Attapulgus, and Stripling (west Georgia) with 14, 8.25, 10, and 5% respectively. Traps were used to assess thrips dispersal at each location. Higher counts of tobacco thrips were observed in traps at Midville and Reidsville as compared to other locations. This could explain the variability of spotted wilt severity at the test locations. Further, the pattern of thrips counts overtime corresponded with the predicted dispersal based on the TSWV and Thrips Risk Forecasting Tool. The magnitude of dispersing thrips was linked to the severity of spotted wilt at each location.

Flutianil: A new mode of action for powdery mildew control

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Gatten™ fungicide, a 5 EC formulation of flutianil, is a new mode of action (U13) for powdery mildew control. Results of replicated trial work across the United States have shown that Gatten is highly effective in preventing the development of powdery mildew. Although Gatten currently has an unknown mode of action, it is known to inhibit the formation of fungal haustoria and the extension of secondary hyphae. In addition it also causes malformation and agglutination of conidial chains. As a result, the product exhibits both preventative and curative activity against powdery mildew. Registration in the US is anticipated in early 2018. Crops on the initial label are expected to include summer squash, cucumber, cantaloupes, grape, cherry, apple and strawberry. Work on tolerances for additional crops including lettuce, fruiting vegetables, peach and hops are in-process. Flutianil was discovered by OAT Agrico Co., Ltd., Tokyo, and will be marketed in the United States by Nichino America, Inc., Wilmington, DE.

Phenotyping of stem rot and *Rhizoctonia* limb rot in an *Arachis hypogaea* RIL population

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Georgia peanut growers lose millions of dollars annually to stem rot (*Sclerotium rolfsii*) and *Rhizoctonia* limb rot (*Rhizoctonia solani*), and need more disease resistant cultivars. To better understand such resistance, we phenotyped the susceptibility to stem rot and limb rot of 126 lines from a RIL population and 10 checks in 2016 and 2017. The lines were planted in randomized complete blocks with two replicates in a fumigated and irrigated field. Eight plants per plot were inoculated with PDA plugs of *Sclerotium rolfsii*, and 1/3 of each plot was infested with oat seeds colonized by *Rhizoctonia* in August. In October the peanuts were inverted and rated. Between two years data, the coefficients of determination for stem rot and limb rot ratings were 0.398 and 0.194 respectively, which is an indication of potential resistance within these lines. We are mapping the resistance and comparing it to the from the other part of the same RIL population. To reduce the input of labor and space, we are testing inoculation methods to use in the lab or greenhouse. One of the best stem rot inoculation methods involves taping a 0.7-cm PDA plug with actively growing *S. rolfsii* to a detached peanut leaf. This method can separate very susceptible lines from more resistant lines, but cannot separate resistant lines from moderately susceptible lines. We are still working to improve these methods and hope to confirm the QTL we find with these methods.

Efficacy of fungicide-based management of blueberry rust in commercial production in southern Georgia for 2016 and 2017

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As part of a multi-year study focused at reducing grower costs, fungicides were evaluated for control of blueberry rust in a replicated trial within a row of mature (>10-yr-old) southern highbush blueberries (cv. Rebel) in commercial fields in three counties in southern Georgia in 2016 & 2017. Treatments were assigned using a RCBD and included an untreated control, Abound (azoxystrobin), Pristine (pyraclostrobin + boscalid), Indar (fenbuconazole), Orbit (propiconazole), Proline (prothioconazole), Quash (metconazole), Aprovia (benzovindiflupyr), Quilt Xcel (azoxystrobin + propiconazole), and a split schedule application of Abound (azoxystrobin) pre-harvest

followed by Bravo (chlorothalonil) until termination. Applications were made bi-weekly on 6 Apr, 21 Apr, 4 May (last prior to harvest), 18 May, 1 Jun, 15 Jun, and 29 Jun. Incidence and severity assessments were conducted five times over the 2016 season allowing for calculation of AUDPC for both measures. Record high winter month temperatures (2015–2016) ensured availability of primary rust inoculum on retained, previous-season leaves. Active urediniospore production was observed on overwintered leaves, symptoms were observed on new growth as early as 30 Mar 2016, and disease severity ratings on 15 Jun ranged from 0–70% on untreated control bushes. Except for Indar, the DMI fungicides (Proline, Quash, Orbit, Quilt Xcel) provided the best control overall, and Aprovia, a currently unlabeled SDHI fungicide, provided a level of control equal to the effective DMI fungicides. The 2017 follow-up study aimed at identifying optimal application periods (pre-harvest; mid-summer; early fall) and assessing impacts on yield produced no results due to low disease pressure.

Interaction of onion cultivar and growth stages on incidence of *Pantoea ananatis* bulb infection

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Center rot, caused by *Pantoea ananatis*, has been one of the most important bacterial diseases of onion leading to considerable economic losses. However, little is known regarding which growth stage the plant is most susceptible to bulb infection and if there are differences in susceptibility to bulb infection among sweet onion cultivars. In this study, five cultivars of sweet onion (Pirate, Sweet Harvest, 1518, Granex YPRR and 1407) were inoculated by clipping the tips of onion foliage and depositing 1 ml of 1×10^8 colony forming units/ml of *P. ananatis* suspension into the central leaf cavity. The inoculations were done at three growth stages (first leaf senescence, bulb initiation, and bulb swelling). Center rot incidence was assessed for pre-cured and cured onion bulbs. In addition, total bulb incidence of center rot for each cultivar inoculated at three growth stages were also calculated. Total bulb center rot incidence was significantly higher for Granex YPRR (84%) compared to other cultivars. Significant higher incidence of center rot was observed for bulbs whose foliage were inoculated during first leaf senescence stage (64%) compared to bulb initiation (55%) and bulb swelling (52%) stages ($P = 0.048$). Interactions between onion cultivar and inoculation stage on center rot bulb incidence was not significant ($P \geq 0.218$), when evaluated at different assessment periods. However, different cultivars displayed significant variability in susceptibility to bulb infection. The outcomes of this study may have implications in devising management strategies aimed at protecting most susceptible onion growth stages against *P. ananatis*.

Field performance of several maturity group IV and V soybean cultivars in a root-knot nematode infested field

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The southern root-knot nematode (*Meloidogyne incognita*) is one of the most important yield-limiting pathogens of soybean in Arkansas. Host plant resistance is an effective management tool; however, there is limited information on the susceptibility of available cultivars to *M. incognita*. The objective of this study was to evaluate several maturity group IV and V cultivars that were marketed with having resistance to the southern root-knot nematode. Forty-eight soybean cultivars were selected and grouped based on herbicide technology and maturity group. Soybean cultivars were planted in a field with a high population density of *M. incognita* (averaged 1,146 J2/100 cm³ of soil at harvest). Ten root systems from each of the four replication were rated based on percent of root system galled at R4-R5 growth stage. There was a strong negative correlation between galling and yield ($r = -0.84$, $= 0.00001$) across all experiments. Soybean cultivars with less than 10% root system galled were considered resistant compared to cultivar with the greatest percentage of root galling. Of the maturity group IV cultivars with tolerance to glyphosate and glufosinate five were identified as resistant with no resistance detected among those cultivars with tolerance to dicamba. Of the maturity group V cultivars, 12 cultivars with tolerance to glyphosate were resistant, 3 with tolerance to dicamba were resistant, while none of the cultivars with tolerance to glufosinate were resistant to the southern root-knot nematode. Though the many of these soybean cultivars were susceptible, a few were resistant, which would be a better option in fields with a damaging population density of root-knot nematode.

Race determination in *Cercospora sojina*: From phenotypic traits to genotypic patterns

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Frogeye leaf spot (FLS), caused by *Cercospora sojina*, is an important and recurrent disease of soybean in many production regions. Since the first report of FLS in the United States, new physiological races of *C. sojina* have emerged, which reflects the pathogen's ability to overcome genetic resistance conveyed by individual R-genes. The overarching goal of this study was to elucidate the genetic basis of race specificity in *C. sojina*. To this end, infection responses of 240 geographically diverse *C. sojina* isolates were determined in greenhouse assays on a set of six differential soybean cultivars: Davis, Tracy, Hood, Lincoln, Lee and Blackhawk. A draft genome sequence was obtained for 96 isolates, and single nucleotide polymorphisms (SNPs) were identified. A bulk segregation analysis was performed on two subpopulations defined by differential responses (resistance or susceptibility) on cultivars Blackhawk and Hood to identify SNPs associated with infection phenotypes. Molecular elucidation of the genetic structure underlying race determination in *C. sojina* will accelerate efforts to improve FLS genetic resistance in soybean through conventional and molecular breeding approaches.

Performance of a new fungicide premixture for managing soybeans infested with frogeye leaf spot

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Frogeye leaf spot (FLS) is a common foliar disease of soybeans, and strobilurin (FRAC Group 11) resistant FLS populations are widespread across the mid-south states (AL, AR, LA, MO, MS, and TN), corn belt (IL, IN, and OH), and mid-Atlantic region (NC and VA). Acropolis™ is a new fungicide premixture containing tetraconazole (FRAC Group 3) and thiophanate-methyl (FRAC Group 1). Regional studies consisting of replicated, small plot trials were initiated to examine the effect of Acropolis fungicide against FLS populations in soybeans. During 2016 and 2017, 26 field trials were conducted by academic and private scientists located in AR, IA, IN, KY, LA, MO, MS, OH, and TN. Acropolis, Domark®, Topsin®, Topguard®, Quadris Top® SBX, Priaxor® D (Components A+B), Headline®, and Affiance® were compared. Some locations did not reach adequate infestations of FLS; however, 5 (2016) and 13 (2017) locations reached at least 3% FLS severity. Acropolis applied once at R3 or as a sequential at R3 and 14 days later averaged equivalent or greater reductions in FLS severity and higher soybean yields compared with competitive fungicides. Results from 2016 and 2017 document that Acropolis is a very useful tool for managing FLS in soybeans. In addition, Acropolis offers two effective fungicidal modes of action that are different from Group 11 fungicides.

Identification of molecular biomarkers associated with reniform nematode (*Rotylenchulus reniformis*) resistance in soybean

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Reniform nematode (*Rotylenchulus reniformis*) is a yield-limiting pathogen of soybean in the Southeastern region of the United States. Several studies have identified soybean germplasm with resistance to reniform nematode and few studies have explored the soybean genome for quantitative trait loci (QTL) linked to reniform nematode resistance. Our objective for this study was to identify high resolution single-nucleotide polymorphism (SNP) biomarkers that correlate with reniform nematode resistance in soybean using genotyping-by-sequencing (GBS). A set of 250 recombinant inbred lines (RIL) developed from a cross between reniform nematode-resistant soybean cultivar, 'Forrest', and susceptible cultivar, 'Williams 82', was utilized to correlate reduced nematode reproduction to SNP markers, localizing specific QTL regions in the soybean genome. The phenotype of each RIL was determined by inoculating three replicates of each line with 2000 vermiform reniform nematodes. Nematode populations were quantified 8 weeks after inoculation. Leaf tissue was collected from each line for genotyping. DNA from each line was digested using specific restriction enzymes *MseI* and *PstI* to prepare gene libraries, then sequenced on the Illumina HiSeq platform and analyzed using several annotation tools. Genetic linkage maps were constructed using the R package, OneMap. We report SNP markers that correlate to the resistant phenotype observed in the developed lines. The characterized genetic markers can be used by soybean breeders in marker assisted selection to enhance their efforts in selecting and employing lines with known resistance to reniform nematode.

Use of single terminal spray applications to evaluate fungicide efficacy for control of pecan scab in commercial pecan orchards

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Georgia pecan growers lose millions of dollars annually to scab (*Venturia effusa*) and rely on fungicides for control. Evaluating fungicides is difficult and expensive as it requires replicated blocks of producing trees managed for that purpose. Also, many scab populations have reduced sensitivity to one or more classes of fungicide. This study was conducted with multiple fungicides, each at a full labeled rate and diluted to 950 L water/ha typical of commercial sprayers. They were hand-sprayed on individual terminals on nontreated trees in nine commercial orchards, each with a unique fungicide sensitivity profile. Light leaf scab developed and Quadris Top (difenoconazole + azoxystrobin) and Reliant (phosphite) were the most effective with 64% and 69% control, respectively, with Elast (dodine)/Super Tin (TPTH) giving only 16% control. Severe nut scab developed on nontreated fruit (65% severity), and Quadris Top and Elast/TPTH provided the best control (97% and 96%, respectively). TPTH alone gave 21% and 84% control, respectively of leaf and nut scab, and Abound (azoxystrobin) gave 37% and 71% control. Both Orius (tebuconazole) and Acropolis (tetraconazole + thiophanate methyl) substituted for TPTH early in the season improved leaf scab control but did not alter nut scab levels. Overall this method was a useful way to get relative efficacy data comparing various treatments on different scab populations with different levels of fungicide sensitivity.

In vitro fungicide sensitivity of *Magnaporthe poae* isolates collected from cool-season turfgrasses

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Summer patch, caused by *Magnaporthe poae*, is a destructive disease of cool-season turfgrasses, especially to *Poa* species. The pathogen also causes severe damage to creeping bentgrass (*Agrostis stolonifera*) in the transition zone. Chemical control of the disease on *Poa* species is well characterized in the Northeastern US, but little is known about chemical control of isolates infecting creeping bentgrass. An *in vitro* fungicide sensitivity assay was conducted to determine the effect of various fungicides on mycelial growth. There were six isolates tested. Of the six isolates, five of them were collected from creeping bentgrass in the SE and one collected from annual bluegrass in the NE. The fungicide sensitivity assay examined the effects of three succinate dehydrogenase inhibitors (SDHIs), four

demethylation inhibitors (DMIs), four strobilurins (QoIs), and four combination products containing multiple chemical classes. Fungicide sensitivity was measured by plating 5 mm potato dextrose agar (PDA) plugs infested with the fungus onto fungicide-amended media. Plates were incubated at 30°C and radial mycelial growth was measured 96 hours after plating. EC₅₀ values were determined using SAS statistical software. Isolates were most sensitive to the QoIs and the least sensitive to the SDHIs. These results provide a better understanding of the sensitivity of *M. poae* isolates from the Southeastern US to three common fungicide classes used in C3 turfgrass systems.

Dormant fungicide, oil, and growth regulator sprays affect populations of *Exobasidium maculosum* and development of *Exobasidium* leaf spot on blueberry

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The fungus *Exobasidium maculosum* causes *Exobasidium* leaf and fruit spot (ELFS) on blueberry in the southeastern U.S. Although the disease cycle is unknown, there is evidence that epiphytic yeast populations of *E. maculosum* serve as the primary inoculum for the disease each spring. Previous research has shown that dormant applications of lime sulfur (calcium polysulfide) and of the growth regulator hydrogen cyanamide reduce the disease, whereas dormant oil sprays increase disease intensity. This research was designed to elucidate the mechanism of this effect in the field. Dormant applications of the three compounds were made in a 'Premier' rabbiteye blueberry planting on 18 January 2017, and epiphytic populations of *E. maculosum* from twig samples were determined by dilution-plating at intervals before and after application. Results indicate that the late-dormant application of calcium polysulfide and, to a lesser extent, hydrogen cyanamide resulted in a decrease in surface populations, whereas dormant oil resulted in an increase compared with the untreated check. Preliminary data from potted 'Premier' trap plants exposed weekly indicated that pathogen population densities in the treated plots correlated with disease incidence in trap plants underneath the plots. This supports the hypothesis that the primary inoculum for ELFS occurs epiphytically and that by decreasing surface populations of *E. maculosum*, disease can be virtually eliminated at the single-bush level.

Relative susceptibility of commercial watermelon varieties to powdery mildew

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Powdery mildew (PM) of watermelon caused by *Podosphaera xanthii* has been occurring frequently in recent years and growers routinely apply fungicides to manage PM. The current study was conducted over three summers from 2014, to 2016 to determine the relative susceptibility of twenty eight watermelon varieties to *P. xanthii* populations prevailing in Charleston, South Carolina. USVL677-PMS, highly susceptible to PM and USVL531-MDR resistant to PM were included as controls in all three years. A randomized complete block design with three replications was used each year and plants were rated on a modified Horsfall-Barrett scale of 0-10 of increasing disease severity. During all three years USVL677-PMS was the most susceptible line with the highest AUDPC and abundant PM conidia on the lower leaves. In comparison USVL531-MDR was practically immune and resistant. The commercial pollenizers SP5, SP6 and Lion were all resistant to PM. Among the red fleshed varieties, Suprema a seedless watermelon was relatively resistant. Most of the seeded varieties evaluated (e.g. Malali, Black Mama, Mickey Lee) were highly susceptible to PM. Similar results were also obtained in growth chamber studies where the plants were inoculated with *P. xanthii* conidia (10⁵ conidia^{-ml}). Currently very few to no PM resistant varieties are available and there is a need to develop newer resistant varieties for use by watermelon growers.

Pathogenicity of *Leptographium terebrantis* to saplings of *Pinus taeda* L: Efficacy of the toothpick inoculation approach

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Leptographium terebrantis is root pathogen frequently associated with loblolly pine (*Pinus taeda* L.) stands that are undergoing a decline in the southeastern US. The fungus is vectored by root feeding bark beetles that inoculate stressed trees with *L. terebrantis* during their woody root feeding activities. The pathogenicity of *L. terebrantis* is commonly studied using agar plugs of fungal mycelia placed into stems or roots as a means of artificially vectoring the pathogen. However, in simulating the natural feeding habits of the beetles, an artificial inoculation approach involving wooden toothpicks was used to test the pathogenicity of *L. terebrantis* and assess the relationship between pathogenicity and radial inoculum density. Installed in naturally regenerating saplings of loblolly pine for eight weeks, *L. terebrantis* colonized toothpicks resulted in occlusions among the inoculated saplings. Sapwood occlusion increased with radial inoculum density and the volume of occluded tissue was significantly correlated with radial inoculum density. The fungus was re-isolated from the occluded tissue. Results indicate that the toothpick inoculation may be a practical alternative to the use of agar plugs for studying fungi associated with root feeding bark beetles.

A functional genomic screen for defense genes in *Glycine max* as it relates to parasitism by the plant parasitic nematode *Heterodera glycines*

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Roots perform a variety of functions, including water and nutrient uptake and support. Various pathogens impair these functions as a consequence of their pathogenic nature. The most important pathogen of soybean (*Glycine max*) is the parasitic soybean cyst nematode (SCN) *Heterodera glycines* which greatly impairs root functions and may lead to chlorosis of in shoots. *H. glycines* creates a multinucleate cell known as a syncytium from which it derives nutrients. The syncytium also serves as the site complex metabolic processes that lead to a resistant reaction that culminates in the death of the nematode. An analysis if gene expression within syncytia undergoing a resistant reaction has led to the identification of 1,787 genes that are expressed specifically during the defense process. Functional genomics analyses have identified a framework that can be experimentally induced by overexpressing these candidate resistance genes. In contrast, the defense process can be impaired by RNA interference (RNAi). The experiments have identified that a bacterial effector known as harpin can induce the expression of *NON-RACE SPECIFIC DISEASE RESISTANCE 1/HARPIN INDUCED1 (NDR1/HIN1)* coiled-coil nucleotide binding leucine rich repeat (CC-NB-LRR) signaling gene that functions in the defense process. Harpin also induced the expression of other proven defense genes, greatly increasing the knowledge base of how the defense process acts.

Fungicide sensitivity profile of *Colletotrichum gloeosporioides* from strawberry to seven different fungicides

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In the U.S. southern states, *Colletotrichum* crown rot (CCR) of strawberries is mainly caused by *Colletotrichum gloeosporioides*. In the beginning of the 2017–2018 Florida strawberry season, 25% of crown rot samples received in the GREC plant diagnostic clinic were affected by CCR. Management of this disease in Florida strawberry fields relies on the use of clean transplants and fungicides, such as azoxystrobin and thiophanate-methyl. Our objectives were to: i) monitor the fungicide sensitivity of *C. gloeosporioides* isolates to the currently registered fungicides azoxystrobin and thiophanate-methyl; and ii) screen *C. gloeosporioides* isolates for their sensitivity to the succinate dehydrogenase inhibitor (SDHI) fungicides. Forty-two *C. gloeosporioides* isolates from strawberry crowns were evaluated in PDA amended with azoxystrobin and thiophanate-methyl at 3 and 100 µg/ml, and fluopyram, isofetamid, penthiopyrad, fluxapyroxad, and benzovindiflupyr at 100 µg/ml. Thirty-one percent of the isolates (N = 13) were resistant to azoxystrobin, and seven percent (N = 3) were resistant to thiophanate-methyl. All *C. gloeosporioides* isolates from strawberry were insensitive to fluopyram, isofetamid and fluxapyroxad and sensitive to penthiopyrad and benzovindiflupyr. Results indicated that the SDHIs penthiopyrad and benzovindiflupyr could be used as an alternative to CCR management, but their use should be cautious to avoid resistance selection.

Use of spatial analysis to determine product efficacy and impact of foliar diseases on soybean

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Trials were completed near Hamburg, AR and Fresno, AR in 2017. Quilt Xcel (1535 mL/ha), Priaxor (584 mL/ha) and Trivapro (1462 mL/ha) were applied in Hamburg, Quadris Top SBX (548 mL/ha) and Trivapro (1462 mL/ha) were applied in Fresno and each trial had untreated controls. Treatments were arranged in a randomized complete block design, replicated three times, with application strips 10 rows wide extending the length of the field. GPS points were marked at approximately equal distances, 10 points per strip and foliar disease levels were rated in the top 1/3 of the canopy. Upon disease presence in the field, additional untreated strips were marked outside and adjacent to the test and rated. Yield data was collected and provided as georeferenced .shp files for each location. Spatial analysis of untreated points indicated yield distributions of both locations were significantly clustered across fungicide treatments and untreated controls (P = 0.006). At Fresno, little foliar disease occurred and yields were *NS* by treatments. At Hamburg, Asian soybean rust (SBR), caused by *Phakopsora pachyrhizi*, and Cercospora leaf blight (CLB), caused by *Cercospora kikuchii*, occurred at moderate to high levels. All fungicide treatments yielded significantly more than the untreated controls. Spatial analysis indicated SBR did not relate to yield (*NS*) while CLB was inversely related (P = 0.003) to yield and was likely the only yield limiting foliar disease present.

Integrated approaches to managing aphids and barley yellow dwarf in Tennessee wheat

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Wheat is the world's most widely cultivated crop. Over 220 million hectares are grown in the world, with 100,000–250,000 hectares normally grown in Tennessee. However, there are several aphid species (Hemiptera: Aphididae) that are found in wheat that can decrease yield and grain quality if not properly managed. The three most common species found in wheat include bird cherry-oat aphid (*Rhopalosiphum padi*), English grain aphid (*Sitobion avenae*), and greenbug (*Schizaphis graminum*). Although high numbers of aphids in wheat are needed to directly cause yield loss, relatively low numbers of aphids may reduce yield by the transmission of barley yellow dwarf (BYD). It is this transmission of BYD that typically has the most impact on yield. Cultural control such as delayed planting dates and chemical controls such as seed or foliar applied insecticides are common methods to manage aphid infestations and reduce BYD. Research is being performed in Tennessee to better understand the impact of insecticide seed treatments and foliar applied insecticides

on aphid control, the incidence of BYD, and wheat yield. This data highlights the importance of managing aphids on wheat. In addition, the use of enzyme-linked immunosorbent assays (ELISA) tests as well as qPCR testing is being performed to better quantify and qualify the severity of this BYD infestation. Additional tests are underway to evaluate how susceptible and resistant varieties respond to aphid management, including seed and foliar insecticide treatments.

The distribution of taproot decline in Mississippi soybean

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Taproot decline (TRD) is an emerging disease of soybean in the Mid-southern USA, caused by an undescribed species of *Xylaria*. The taproot of affected plants is dry and brittle to the touch resulting in the plant breaking at the soil line. Plants are typically stunted and exhibit interveinal chlorosis and necrosis. The primary diagnostic feature associated with TRD is black stroma observed on the taproot and lateral roots. In Mississippi, the first observations of TRD were in 2007. As an emerging disease in Mississippi, the distribution of TRD was determined in a two-year survey. Soybean plants displaying symptoms of TRD were collected from across Mississippi and gps coordinates recorded. The roots were cleaned and surface disinfested. Black stroma was removed from roots and plated onto water agar for 14 days. Hyphal tips from colonies characteristic of *Xylaria* were transferred to potato dextrose agar and incubated under continuous light at room temperature for 10 days. To confirm *Xylaria*, genomic DNA was extracted from fresh mycelium. PCR was performed using ITS4 and ITS5 primers. Amplicons were sequenced and compared to the ITS sequence of the *Xylaria* sp. isolate MSU_SB201401 (Accession no. KY433853). To date, TRD has been confirmed in 68 of 82 counties in MS demonstrating its widespread distribution. Awareness of TRD for Mississippi growers is important as the disease recurs and is most prevalent in no-till, continuous soybean field situations.

Crp1 drives pre-penetration infectious development via regulation of Frq1 in the maize pathogen *Cercospora zeae-maydis*

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Cercospora zeae-maydis causes gray leaf spot, one of the most important foliar diseases of maize. *C. zeae-maydis* enters leaves through stomata during pathogenesis. Pre-penetration infectious development, which includes spore germination, stomatal tropism, and appressorium formation, requires light and the photoreceptor/transcriptional regulator Crp1. The absence of light or disruption of Crp1 severely impairs stomatal tropism and appressorium formation, which suggests that Crp1 mediates light-dependent pre-penetration infectious development. However, the genetic network underlying Crp1 is unknown. Thus, the objective of this study was to elucidate how Crp1 regulates stomatal entry in *C. zeae-maydis*. To this end, Frq1, a conserved component of the fungal circadian clock, was identified as a regulatory target of Crp1. *FRQ1* expression was induced by light in a Crp1-dependent manner, and Crp1 was required for the circadian oscillation of *FRQ1* expression. Furthermore, deletion of *FRQ1* impaired pre-penetration infectious development and abolished lesion development. These findings suggest that *C. zeae-maydis* utilizes a circadian clock to regulate pre-penetration infectious development, a phenomenon that has not been described in fungal foliar pathogenesis.

Use of image analysis and photogrammetry as tools to quantify Tomato Spotted Wilt Virus symptom severity in peanuts

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Tomato Spotted Wilt Virus (TSWV) is an important pathogen of peanut in the Southeast United States. Phenotypic variation exists among peanut cultivars in their expression of TSWV symptoms. Evaluation of peanut varieties for their susceptibility to TSWV is a key step prior to release of new cultivars. Recently, image analysis in combination with machine learning has been explored as a tool to assist visual assessment of crop traits. The goal of this research was to investigate image analysis methods for their utility as assessment methods for spotted wilt severity. A full factorial design with peanut cultivar, plant population and insecticide as main effects was conducted in Quincy, FL in 2017. Six peanut cultivars, differing in resistance to TSWV, were planted in mid-April in order to increase the probability of TSWV infection. Visual and multispectral images were taken of the peanut plots and used to train a convolutional neural network (CNN) model for TSWV symptom recognition. Additionally, photogrammetry was used to generate 3D models to assess peanut canopy architecture and stunting of TSWV infected plants. Manual assessments using a visual rating scale for spotted wilt symptoms were compared to image analysis and photogrammetric methods. Preliminary results indicate that the CNN model and photogrammetry approaches have potential as tools to evaluate spotted wilt symptom severity.

Perennial ornamental enables virus spread across the United States

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Peonies have been plagued for a hundred years by a disease that causes reduced flowering, stunted growth, and galling of the roots. The biology of Lemoine's disease remains a mystery and the cause biotic or abiotic, has not been determined. *Cycas necrotic stunt* virus (CNSV), a member of the genus Nepovirus, has been found in 90% of 200 leaf samples taken from symptomatic plants from Alaska, Arkansas, Michigan and Oregon. Sequencing of the viral genome has revealed that the virus has undergone recombination with a

Grapevine Anatolian ringspot virus-like virus. The recombinant portion has been found in all sequenced isolates of the virus indicating that it occurred early in the evolution of the virus in peony or arose shortly after its introduction into the host. Other related nepoviruses are vectored by *Xiphinema* and *Longidorus* nematodes and their ability to transmit CNSV will be tested. To further explore how the virus moves in the environment, alternative ornamental hosts that are grown alongside peonies will be evaluated to determine whether they act as virus reservoirs have thus far escaped notice. The presence of CNSV across the United States makes it imperative that control methods be implemented to check the spread of the virus. The information generated from this project will be the first step in protecting ornamental crops from CNSV.

A forward genetic screen coupled with target-enrichment sequencing in *Cercospora zeae-maydis* identifies novel genes regulating cercosporin production

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Cercospora zeae-maydis causes gray leaf spot of maize (*Zea mays*), which impacts maize production worldwide. During pathogenesis, *C. zeae-maydis* produces cercosporin, a non-host-specific phytotoxin that is an important virulence factor for many *Cercospora* species. Although the gene cluster underlying cercosporin biosynthesis has been identified, the genetic regulation of cercosporin biosynthesis during pathogenicity has not been elucidated. In this study, a forward genetic screen for aberrant cercosporin production was performed to identify genes regulating cercosporin biosynthesis *in vitro*. Over 3000 genetically tagged mutants of *C. zeae-maydis* were created and screened for altered cercosporin production. A total of 75 mutants produced substantially higher or lower levels of cercosporin compared to the wild-type strain. To characterize the site(s) of insertion in each mutant, we developed a unique target-enrichment sequencing approach. Using this method, we identified 49 mutants carrying a single insertion of the mutagenesis cassette, and 26 mutants carrying multiple insertions. Novel genes potentially regulating cercosporin biosynthesis were identified, including genes involved in primary and secondary metabolism, signal transduction, and chromatin modification. The results from this screen have shed new light on cercosporin biosynthesis in *C. zeae-maydis*, and could help dissect the genetic regulation of cercosporin production during pathogenesis.

Screening of rose rosette virus PCR primers to identify the most effective and sensitive detection method and primer

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Since the Rose Rosette Virus (RRV) was identified and described in 2011, several PCR primers have been developed, targeting one of the RRV's seven-part viral genome. Because this virus is spread easily through the movement of its insect vector, *Phylloxera fructiphilus*, there is a need for a rapid and accurate detection method for quick diagnosis of the disease. The current management recommendation is removal of infected plants to reduce or slow the spread of this disease. In this study, we compared three primers that were developed for use on reverse transcription PCR (RT-PCR) and three primers optimized for use on TaqMan-quantitative reverse transcription PCR (RT-qPCR). The most widely used primers in diagnostics are RRV1 for RT-PCR (developed by Laney) and RRV2 for RT-qPCR (developed by Shefali). Our results show that for RT-qPCR detection, RRV2 is the most robust primer with CT values that were 3-5 cycles less than RRV2.1 and RRV2.2. For RT-PCR, the most robust primer is RRV3 when compared to RRV1 and RRV4. Results from this study help to provide information to allow diagnosticians to make appropriate selection of primers for Rose Rosette Disease (RRD) detection. It also shows that RRV primer optimization is mostly universal across the country, meaning that primers developed in one part of the country for RRD work as well as primers developed in a different area.

Establishing residual activity of current fungicides against downy mildew on cucumber

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In Florida managing cucurbit downy mildew (CDM), caused by *Pseudoperonospora cubensis*, is a weekly ordeal. Of the CDM fungicides available, many differ in the level and duration of activity. A true understanding of these differences will improve CDM fungicide program recommendations. Two replicated trials, established in Balm, FL February and September of 2017, assessed the residual activity of current fungicides against CDM on cucumber. Eleven fungicides and an untreated control were arranged in a randomized complete block design and included sub-plots for four application intervals. Fungicides were initially applied to each sub-plot and reapplied at increasing intervals of (1) weekly; (2) every two weeks; (3) every three weeks or (4) no reapplication over the 4-week trial. Plots were rated weekly for CDM severity. Residual activity for each fungicide was determined based on differences in CDM severity across each interval. In both trials, all fungicides statistically differed in residual activity based on comparisons of CDM severity across each interval; with eight of the eleven fungicides exhibiting significant differences between interval (1) and (4) in both trials. Oxathiapiprolin, cyazofamid, and fluazinam exhibited significant CDM control at intervals (1) and (2), compared to interval (4); whereas, CDM control for chlorothalonil and mancozeb dropped after interval (1). Results will be used to further improve spray recommendations for the management of CDM.

Current status of boxwood dieback caused by *Colletotrichum theobromicola* in the United States

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Boxwood (*Buxus* spp.) is a popular landscape shrub in the United States, and its wholesale market value was estimated to be \$103 million annually in 2010 by the USDA National Agricultural Statistics Service. Despite being deer resistant and drought tolerant, boxwoods are susceptible to several fungal diseases, including boxwood blight, *Macrophoma* leaf spot, *Phytophthora* root rot, and *Volutella* blight. In 2015, a new disease called boxwood dieback caused by *Colletotrichum theobromicola* **Delacr.**, was identified for the first time in the United States. Boxwood dieback has since been reported from Alabama, Georgia, North Carolina, South Carolina, and Virginia; with unofficial reports coming from several additional states. Most recently, boxwood dieback was confirmed in Texas. Boxwood dieback has a potential to rapidly spread in landscapes and nursery operations in the absence of effective management options. It can be easily introduced into propagative nursery operations, as well as commercial and home landscapes through the use of infected liners and potted plants. The similarity of symptoms between boxwood dieback and other diseases of boxwood, as well as a delay in the onset of symptoms, make it very difficult to identify and manage effectively. The lack of rapid detection tools, fungicide efficacy, and knowledge of host resistance present additional challenges for disease management. The current rate of boxwood dieback spread is alarming, and has the potential to devastate the boxwood industry in the United States, most likely via circulation of infected liners in the boxwood trade.

***Pantoea ananatis*: Genetic and biological analysis reveals plasmid localized accessory genes correlated with onion pathogenicity**

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Pantoea ananatis is an environmentally ubiquitous bacterium with strains exhibiting broad host ranges and variable host relationships. In Georgia and the eastern United States, *P. ananatis* is associated with leaf blight and center rot of onion (*Allium cepa* L); a recurring disease issue for onion growers. Our current understanding of virulence mechanism and pathogenicity factors in *P. ananatis* is limited. Comparative whole genome sequencing of ten *P. ananatis* strains (six foliar pathogenic and four non-pathogenic on onion), isolated over a period of 18 years, with varying pathogenicity phenotypes and isolation sources (asymptomatic weeds, thrips, symptomatic onion, and onion seedlings) revealed four genetic loci localized to a single contig present among foliar pathogenic strains. We named these pathogenicity-correlated regions the “Onion Virulence Regions (OVR) A-D”. The largest region, OVR-A is approximately 31 kbp and contains genes involved in redox regulation and plant cell wall degradation. The presence of plasmid partitioning proteins on OVR contigs and Eckhardt gel analysis revealed that OVR A-D are located on unique accessory plasmids ranging in size from 160-200 kbp. To further assess the presence of the OVR-A region in other *P. ananatis* strains (not included in whole genome sequencing study), primers specific to the phosphotransferase galacticol transporter system on OVR-A were designed and validated. These results indicate the role plasmids may play in determining the nature of host-pathogen interaction in the *P. ananatis*-onion pathosystem.

Touch-independent aflatoxin inhibition by atoxigenic *Aspergillus flavus* biocontrol strains

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Biocontrol atoxigenic strains competitively exclude aflatoxin (acutely toxic carcinogen in corn and oil-seed crops) accumulation by *A. flavus* through thigmoregulated “touch” inhibition. A growth rate study revealed the fastest growing atoxigenic strains inhibited aflatoxin production the most, supporting the requirement for touch within the first 24 hours. Except two slow-growing strains substantially inhibited aflatoxin production, revealing the possibility of an additional mechanism. Therefore, inhibition through a touch-independent mechanism was investigated. Several atoxigenic biocontrol strains were grown within 24-well plates separated from a common toxigenic strain (53) by 0.4 µm filter inserts. Additionally, 53 was grown in medium amended (1:1) with two and four day old culture filtrates of the atoxigenic strains. 53 produced low aflatoxin levels when separated from fastest-growing strain, 17, and slow-growing highly inhibitory strains K49 and Af36. The addition of four day old Af36, K49 and 17 filtrates to medium reduced 53's aflatoxin production. Filtrate from 17 resulted in >90% inhibition. Filtrate of 51 did not inhibit production, eliminating the possibility of a nutrient depletion effect. Aflatoxin reduction by filtrate and across inserts provides evidence of an extracellular substance(s) that inhibits aflatoxin production. Identification of this substance could lead to a novel biological chemical for suppression of aflatoxin production.

Multilocus analysis and fungicide sensitivity profiles of *Colletotrichum* spp. causing anthracnose on southern highbush blueberry in Florida

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Colletotrichum spp. within the *C. gloeosporioides* complex have been shown to cause anthracnose on blueberry fruit, stems and leaves. Cryptic species within the complex may differ in virulence, disease severity, host range and geographic distribution. Thus, identifying each species within a production area is critical to developing and maintaining efficient disease management strategies. During 2013–

2016, *Colletotrichum* spp. isolates were collected from north and central Florida farms experiencing difficulties controlling anthracnose using the QoI fungicide azoxystrobin. Morphological characterization and phylogenetic analyses of the internal transcriber spacer (ITS), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), chitin synthase (CHS-1), manganese-superoxide dismutase (SOD2), and cytochrome b (CYTB) gene sequences placed all isolates within the *C. gloeosporioides* complex and further identified isolates as *C. siamense*. Cloned segments of the CYTB gene were sequenced and fungicide resistant isolates had the G143A mutation commonly associated with resistance to QoI fungicides; a mutation that was not found in the sensitive isolates. The presence of this mutation indicates that the utility of QoI fungicides for anthracnose management will be reduced and producers will need to consider alternative integrated pest management strategies.

Liquid in-furrow fungicide, insecticide and fertilizer application combinations for disease prevention and yield enhancement in Mississippi dent corn

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One way to prevent increased insect root feeding and early-season disease pressure in dent corn is with the application of commercially available products in-furrow. Field trials were conducted during 2016 and 2017 in a Bosket very fine sandy loam soil to determine the role of fungicide (quinone outside inhibitor (QoI) (n = 3) and QoI plus SDHI (n = 1)), insecticide (pyrethroid), and liquid starter fertilizer to enhance corn plant growth and yield. In-furrow applications were made to regionally adapted corn hybrids that differed by year containing four fungicides, one insecticide, and a starter fertilizer for a total of 10 treatment combinations (alone and combined), replicated four times, with a non-treated control. Evaluations included chlorophyll content measurements using a SPAD meter, root weight and stem diameter evaluations, and yield. Whole plant samples (n = 5) were collected from each plot at approximately the V4 growth stage (4 collar corn) and separated into roots and shoots for evaluations. Significant increases in root weight and stem diameter were observed compared to the non-treated in 2016; however, not in 2017. Taken as a group of treatments (insecticide, fungicide, fertilizer) and regardless of year, fungicides alone increased stem diameter by 0.3%, starter fertilizer alone increased SPAD readings and yield by 0.5% and 11.2%, respectively, compared to the non-treated; however, none of the increases were determined to be statistically significant.

Prospecting for biological control agents against *Burkholderia glumae*, the causal agent of bacterial panicle blight of rice

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Bacterial panicle blight of rice caused by the bacterial pathogen *Burkholderia glumae* is an emerging disease with the potential to significantly affect rice production worldwide due to the increase in global temperature and the ability of the bacteria to grow at temperatures higher than 37°C. There are no resistant rice cultivars and chemical control methods are not available. Thus, identifying biological control agents is an important alternative control strategy. The objective for this project is to mine for bacteria that are able to inhibit the growth of *B. glumae* to be used as biological control agents. *In vitro* inhibition assays were conducted with twelve bacterial strains and three independent strains of *Pseudomonas* sp. were found to inhibit *B. glumae* growth. To evaluate whether *Pseudomonas* sp. have an effect on the pathogenicity of *B. glumae* in rice, eight-week old rice plants were inoculated with *B. glumae* or combinations of *B. glumae* with isolates of *Pseudomonas* sp. and it was found that co-inoculation with *Pseudomonas* sp. significantly reduce lesion length when compared to the plants inoculated with *B. glumae* alone. On the panicle, bacterial populations of *Pseudomonas* sp. were to higher than those of *B. glumae* suggesting that *Pseudomonas* sp. compete for resources with *B. glumae*. These results show the biological control potential of *Pseudomonas* sp. against *B. glumae*.

Cotton yield response to nematicide applications across spatially variable soil textures in NE Arkansas

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Crop protection tools including seed treatments and at-planting applications of insecticides/nematicides are available which, if effectively applied, can lessen pest-induced injury; however, the costs of these protectants may be prohibitively high. Expanded use of precision, site-specific approaches in spatially variable fields could allow reduced inputs of costly crop protection. A 2-year field trial was conducted in a spatially variable commercial field in NE Arkansas. This study investigated both plant and pest response to four at-planting treatments. Seed had a base treatment of the fungicide and insecticide combination, Aeris. The four treatments were 1) Aeris, 2) Aeris + COPeO, 3) Aeris + Velum Total (14 oz/A), and 4) Aeris + AgLogic (5 lb/A). Sample points for plant, insect pest, nematode, and soil monitoring activities were based on soil texture classes of loamy sand and coarse sand categorized using a soil electrical conductivity map generated using a Veris Soil Surveyor. The analysis was focused on the evaluation of plant and pest response in relationship to soil texture and the potential use of site-specific at-planting applications of insecticides/nematicides.

Finding a balance in the force: Meeting producer needs and promotion metrics through extension education efforts

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In order to ascend academic ranks, faculty are required to achieve distinction in their field. Campus based faculty are evaluated by their compilation of scholarly accomplishments related to teaching, funding for research, publications, service and outreach. Extension and

research faculty located off campus are evaluated on the same criteria; however, differences exist between the three appointments. For example, extension and research faculty not located on a main campus have difficulty demonstrating impact in teaching, due to limited formal interactions with students. In contrast, they can engage students informally through special projects, internships, summer employment and training of graduate students. Expectations in total funding or the type of grants received may also differ by appointment. One benefit of having an extension appointment is regularly interacting with commodity groups and industry partners. Development of long-term projects addressing current and emerging issues demonstrates stability in securing funds. Conducting pertinent research also provides ample information to generate extension publications, as well as peer-reviewed articles. Targeting journals that best reach clientele should not be dismissed when publications are evaluated, due to the economic impact they may have within an agricultural community. Extension faculty have an advantage when it comes to outreach due to the nature of the appointment. Opportunities to serve are available through committees within APS and other societies, participating in working groups or assuming local leadership roles. Overall, any extension program will benefit when there is overlap between some or all of the aforementioned areas.

Reproduction of *Rotylenchulus reniformis* on cotton cultivars in greenhouse and field studies

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The reniform nematode (*Rotylenchulus reniformis*) is an increasingly important pest of cotton in the Texas High Plains. Currently, management options for *R. reniformis* are limited to crop rotation and select seed treatment or in-furrow nematicides. Recent studies have shown that certain cultivars possessing dual gene resistance to the root-knot nematode (*Meloidogyne incognita*) negatively affect *R. reniformis* reproduction and provide a consistent yield advantage over susceptible cultivars in fields infested with *R. reniformis*. Reproduction of *R. reniformis* in a preliminary greenhouse study was 54 and 77% lower for Phytogen (PHY) 417WRF than PHY 499WRF under moderate and high nematode densities, respectively, whereas, reproduction for Stoneville (ST) 4946GLB2 was intermediate or greater than PHY 499WRF. Differences in reproduction were observed in field experiments that were conducted in fields with low, moderate or high nematode pressure, where populations at the end of the season were lower for PHY 417WRF than for PHY 499WRF and ST 4946GLB2. Differences in lint yield were observed among cultivars at three of seven locations. Yields were similar for ST 4946GLB2 and PHY 417WRF and were 406 and 505 kg/ha higher than PHY 499WRF in fields with high nematode pressure. Conversely, yields for PHY 417WRF were 449 and 413 kg/ha lower than ST 4946GLB2 and PHY 499WRF, respectively in a high yielding environment with no nematode pressure. These results suggest that ST 4946GLB2 is a robust cultivar that exhibits some level of tolerance to *R. reniformis*, whereas, PHY 417WRF possesses partial resistance to the nematode. Additional studies evaluating these and other commercially available cotton cultivars are needed.

Quantifying inoculum densities of *Verticillium dahliae* from cotton fields in the United States and Australia

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Quantifying populations of *Verticillium dahliae*, causal agent of Verticillium wilt, in soil is essential in estimating disease pressure and making management decisions in cotton. Studies were conducted in the United States and Australia to compare wet and dry isolation methods in conjunction with different selective media. Four fields with a history of moderate to severe Verticillium wilt, located near Lubbock, TX and Narrabri, NSW were selected and three replicate samples were collected from depths of 2-12 cm and 13-24 cm. Inoculum densities ranged from 0 to 90 microsclerotia per cc of soil and were consistently greater for the two Australian fields. Higher numbers of *V. dahliae* microsclerotia were obtained on Sorenson's NP-10 semi-selective media compared to other media evaluated. When combined across locations and depths, differences in isolation method, media and their interaction ($P \leq 0.001$) were observed. Lowering pH of Sorenson's NP-10 reduced germination of microsclerotia by 50 and 68% for the dry and wet method, respectively. Soil sampled from 2-12 cm had higher inoculum densities, accounting for 56% and 62% of the total inoculum recovered for the dry and wet method, respectively. These results support the advantage of Sorenson's NP-10 media in quantifying *V. dahliae* in soil. Dry plating yielded higher estimates of inoculum density. In estimating field populations, the top 12 cm of soil should be sampled. Additional sampling will be conducted to examine temporal changes during the growing season.

Rapid development of co-dominant markers for transgenic maize events

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New transgenic approaches to augment disease resistance, such as host-induced gene silencing (HIGS), show considerable promise for practical crop management. However, a major bottleneck associated with deploying transgenic resistance is the ability to rapidly introgress transgenes into advanced germplasm. In this project, a novel target-enrichment sequencing approach was created to rapidly identify genomic placement of transgene insertions, which subsequently enabled the creation of co-dominant, PCR-based markers to determine transgene presence and zygosity. Transgenic maize was created with a HIGS construct targeting a hexokinase of *Fusarium verticillioides*, a ubiquitous kernel pathogen. DNA extracted from T1 plants was subjected to target-enrichment sequencing for the border regions of the transgene. Bioinformatic analyses identified four distinct insertions across three transformation events. Co-dominant PCR markers were designed and successfully identified T3 plants that were heterozygous, homozygous, or lacking the

transgene. This technique will dramatically accelerate transgene introgression and pyramiding in advanced breeding lines of maize, and can be easily adapted to other agronomically important crops.

A new alternative host sustains systemic infection of Soybean vein necrosis virus

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Soybean vein necrosis virus (SVNV) is one of the most prevalent viruses present in all major soybean-producing states in the United States and Canada in recent years. It is urgent to understand factors that contribute to its epidemiology for the purpose of virus control and disease management. Several plant species, including members in *Convolvulaceae*, *Leguminosae* and *Solanaceae* families, were found to be hosts of SVNV. However, the virus infection is localized in most of these species, limiting their importance in virus epidemiology. To analyze the potential role of kudzu (*Pueraria montana*), an invasive legume plant covering millions of acres in Southeastern United States, foliar samples were collected in Mississippi and tested for SVNV infection. The results revealed that kudzu is a natural host of the virus, although at a low rate. A greenhouse-based experiment was set up to further study the interaction between SVNV and kudzu using viruliferous soybean thrips (*Neohydatothrips variabilis* Beach), the most efficient virus vector in nature. Both leaf and root tissues were tested positive for SVNV following thrips inoculation using multiple detection methods, which suggests kudzu is an alternative host that sustains systemic replication of SVNV.