2013 Southern Division Meeting Abstracts

Abstracts presented at the APS Southern Division meeting in Baton Rouge, Louisiana, February 8–10, 2013. 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: Albers, C. R., and Woodward, J. E. 2013. Effect of soil nitrate levels and *Verticillium dahliae* populations on cotton production in West Texas. (Abstr.) *Phytopathology* 103(Suppl. 1):S1.1. <http://dx.doi.org/10.1094/PHYTO-103-5-S1.1>

Effect of soil nitrate levels and *Verticillium dahliae* populations on cotton production in West Texas

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Phytopathology 103(Suppl. 1):S1.1

Verticillium wilt, caused by the soilborne fungus *Verticillium dahliae*, is an economically important disease of cotton (*Gossypium hirsutum* L.). The fungus survives long periods of time as microsclerotia (ms) and previous studies have shown a positive correlation between disease incidence and ms. Currently, the disease is managed using an integrated approach, which includes cultivar selection, crop rotation, irrigation amount and high seeding rates. Field studies were conducted in 2011 and 2012 to investigate the influence of nitrogen on disease development. Six rates of nitrogen (0–280 kg ha⁻¹) were applied prior to bloom to the cultivars Deltapine (DP) 0912B2RF, DP104B2RF, DP1032B2RF and Fibermax (FM) 9160B2F, which were selected based on differences in susceptibility to *Verticillium* wilt and relative maturity. Initial nitrate levels ranged from 5.0 to 123.5 and 2.8 to 15.2 kg ha⁻¹ at soil depths of 0–15 and 46–61 cm, respectively. Microsclerotia were found throughout the soil profile and were most abundant at 46–61 cm. Baseline populations of *V. dahliae* were similar in three fields with drip irrigation (1.4 ms/cm³) and lower (0.7 ms/cm³) in fields utilizing pivot irrigation, all of which are well below levels where damage is observed. Disease incidence was low (<5%) and nitrogen had little effect on cotton yield or disease incidence. Differences were observed among cultivars where the susceptible cultivars (DP0912B2RF and DP1032B2RF) tended to exhibit more vascular discoloration and foliar symptoms than the partially resistant cultivars (DP104B2RF and FM9160B2F). Under such low disease pressure, yields were greatest for the earlier maturing susceptible cultivar DP0912B2RF. Similarly, yields for the susceptible mid-maturing DP1032B2RF were higher than the partially resistant cultivars in 2012. Drought conditions experienced throughout the duration of this study had an adverse effect on disease development; therefore, additional studies are needed to fully understand the influence of nitrogen on *Verticillium* wilt in cotton.

Impact of tassel fungicide applications on the *Aspergillus* and *Fusarium* spp. mycoflora of harvested field corn in Mississippi

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Phytopathology 103(Suppl. 1):S1.1

Since 2006, fungicide applications in field corn production at important growth stages (tassel; VT) have increased exponentially. In principal,

marketed fungicide strategies suggest a fungicide applied in the absence of disease will provide an automatic yield enhancement. However, as a whole, the greater set of data from unbiased sources suggests timed fungicide applications in the absence of disease are not economically beneficial. A three year research effort was conducted in Mississippi to consider the response of field corn to fungicides applied at VT (azoxystrobin + propiconazole, propiconazole, pyraclostrobin) at labeled rates (14, 4, and 6 fl oz/A, respectively) including an untreated control. In addition to observing field variables and collecting yield, harvested grain was plated on defined salts, semi-selective medium and colonies of *Aspergillus* and *Fusarium* were enumerated from ten replicate plates containing 13 corn kernels each. Data were analyzed to determine the effect of field parameters including previous crop history and fungicide treatment on enumerated fungi by genus from either irrigated or non-irrigated field sites. Yield was significantly greater in irrigated fields where corn followed cotton than where corn followed soybean, by 8.5%. In non-irrigated fields, yield was significantly greater in situations where corn followed soybean, by 8.3%. Fungicide alone did not influence the recovery of *Aspergillus* or *Fusarium*; however, when *Fusarium* was the dependent variable, a significant previous crop by treatment interaction occurred where corn was the previous crop in irrigated and non-irrigated situations.

Field evaluation of southern corn rust epidemics in Georgia and Florida

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Phytopathology 103(Suppl. 1):S1.1

Southern rust caused by *Puccinia polysora* is a destructive foliar disease of corn in the southern United States. Effect of hybrid, fungicide and timing of application on southern rust epidemics and corn yield was investigated. Field studies were established in Georgia (Tift Co. and Decatur Co.) and Florida (Marion Co.) in 2012. A total of four field trials were planted to both rust-susceptible Pioneer 33M57 (*Rpp9-*) and rust-resistant Pioneer 33M52 (*Rpp9+*). Treatments in each location included pyraclostrobin and pyraclostrobin + metconazole applied at seven different timings: (i) V5 (five leaf stage), (ii) R1 (silk emergence), (iii) R2 (blister development), (iv) V5 + R1, (v) V5 + R2, (vi) R1 + R2 and (vii) V5 + R1 + R2. Final severities of southern rust in trials planted in April in Tift and Decatur counties were less than 1% and 9% leaf area coverage, respectively; use of fungicides did not significantly increase yield over the untreated control. Final disease severities in late-planted trials at Tift and Marion counties were less than 46% and 28%, respectively. In these late-planted trials, disease severity was significantly reduced in plots planted to P33M57 when fungicide was applied at silking stage. Use of fungicides increased yields by as much as 27% over the untreated control in Tift co. and by as much as 41% in Marion Co. Rust severity and yields in plots planted to P33M52 were significantly different from those planted to P33M57. Two other diseases, northern leaf blight and southern leaf blight, were present in this field trials and may have also impacted yield.

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

<http://dx.doi.org/10.1094/PHYTO-103-5-S1.1>

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Pecan truffles: Cultivating a new commodity

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Phytopathology 103(Suppl. 1):S1.2

Pecan truffles (*Tuber lyonii*) were first found in Texas in 1957, and subsequently in Georgia in 1987 in commercial pecan (*Carya illinoensis*) orchards. They have since been found in many pecan orchards, and in association with other tree species such as hickories (*Carya* spp.) and oaks (*Quercus* spp.). With the growing demand for truffles for culinary purposes, there is considerable interest in this species, but supplies have been very limited since the ascocarps are hypogaeal and not uniformly distributed. Truffle dogs are becoming available which greatly enhance harvest efficiency, and cultivation efforts are expanding. Artificial inoculations of pecan and oak seedlings have succeeded in synthesizing *T. lyonii* ectomycorrhiza under axenic conditions, but the trees have not yet produced ascocarps. Pecan seed and seedlings were inoculated with a spore slurry of *T. lyonii* in 2001 in field plots in Tifton, GA. The first ascocarps were harvested in the fall of 2012, demonstrating that this species can be successfully grown from artificially inoculated trees.

Aflatoxin accumulation in IITA-ARS maize lines tested in the southern U.S.

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Phytopathology 103(Suppl. 1):S1.2

Six tropical maize (*Zea mays* L.) germplasm lines, TZAR101 through TZAR106, with resistance to aflatoxin contamination were developed in Nigeria by the International Institute of Tropical Agriculture through a collaborative breeding project with Southern Regional Research Center of the USDA-ARS. These lines, registered and released in 2008, were derived from biparental crosses and backcross populations involving African tropical elite inbred lines with some aflatoxin-resistance and temperate inbred lines from the U.S. with proven resistance as parents. The TZAR lines also have good agronomic traits and resistance to important diseases in the lowlands, including southern corn leaf blight, southern corn rust, and ear rot. These lines were developed for potential use in national programs of Central and West Africa and for breeding programs in the U.S. In 2010, the first year of availability of the TZAR lines for U.S. trials, they were grown and tested as inbreds at Mississippi State, MS. In 2011, they were grown and tested as single cross hybrids at Mississippi State and at Lubbock and College Station, Texas; and in 2012, again at Mississippi State. Inbred trials were also conducted at Baton Rouge, LA in 2011 and 2012. TZAR105 has yet to be tested. Results of resistance trials show variation in the performance among TZAR lines, but overall, TZAR103 and TZAR106 have demonstrated the highest levels of resistance, and compared favorably with entries from other resistance sources tested during trials. Results are discussed in the presentation.

Analysis of microorganisms in aerosols collected at altitudes between 1.5 and 38 km: Lessons for long distance transport of plant pathogens

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Phytopathology 103(Suppl. 1):S1.2

Microorganisms (i.e., bacteria, fungi, and viruses) aerosolized from surfaces and transported in the high atmosphere must tolerate low relative humidity, a high fluence of ultraviolet (UV) radiation, and low temperatures. Concentrations of cells collected at select altitudes in the troposphere range from 104 to 106 cells m⁻³, however little work has been done to quantify the number of cells present at higher altitudes (up to 38 km). Recent studies have shown that microorganisms in the troposphere are capable of intercontinental transport, influence precipitation, and metabolize carbon compounds in cloud droplets. Determining the concentration of cells in the stratosphere will be the first step towards understanding if significant environmental contributions are being made at higher altitudes. During September 2012, we launched two separate sampling missions to determine how the numbers of total of cells and viable microorganisms vary with altitude. The first mission was a prototype of new microbiological sampler with multiple chambers designed to collect from three separate target altitudes. Each sampling chamber holds forty plastic rods covered with silicon grease. A rod has a sampling area of 3.5 × 10⁻⁵ m² and

serves as an impact sampler when the chamber doors open at the pre-defined altitudes. The second payload was integrated with the High Altitude Student Platform (HASP) during flights in 2011 and 2012. This payload also measured important environmental parameters that microorganisms encounter from 1.5 to 38 km: a temperature range of 34°C to -45°C, 2% RH, and a pressure of 1 mbar. The recovery of viable microorganisms from the atmosphere will allow for controlled laboratory simulations to determine the levels of resistance to multiple environmental stressors. A microorganism that is desiccation tolerant, psychrotolerant, and radiation resistant or capable of forming endospores would be well equipped to survive atmospheric transport.

A transcriptome analysis to identify the regulon of the TofI/TofR quorum sensing system implies the presence of DSF-mediated signaling system in *Burkholderia glumae*

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Phytopathology 103(Suppl. 1):S1.2

Burkholderia glumae is the major pathogen causing bacterial panicle blight on rice, which is one of the most severe rice diseases in the southern United States. Most of the known virulence factors of *B. glumae* are regulated by the quorum sensing (QS) system composed of the LuxI homolog, TofI, and the LuxR homolog, TofR. The only known quorum sensing signal generated by the TofI/TofR QS system has been identified as *N*-octanoylhomoserine lactone (C8-HSL). To better understand the role of the quorum sensing system in *B. glumae*, a transcriptome analysis was performed using RNA-sequencing approach with the virulent *B. glumae* strain, 336gr-1, and its TofI/TofR QS-deficient derivative. Through the comparison of the two expression profiles, one putative non-coding small RNA located downstream of genes encoding thioesterase superfamily protein and (3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase was found to be significantly suppressed in its transcription in the mutant deficient in the TofI/TofR QS system. A previous study revealed that the dehydratase and thioesterase activities were required for the synthesis of another type of QS signal, diffusible signal factor (DSF), in *Burkholderia cenocepacia*, implying that *B. glumae* may also produce DSF for unknown signaling function. To determine the presence and function of DSF in *B. glumae* as well as the role for the small RNA dependent on the TofI/TofR QS system, mutational analyses of the putative genes for DSF biosynthesis and the downstream region encoding the small RNA are being performed.

Effects of fungicide and cultivar selection on seed quality with delayed harvest

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Phytopathology 103(Suppl. 1):S1.2

Soybean seed quality and vigor are important aspects of seed performance. Quality and vigor are affected by foliar fungicide application and vary according to cultivar. The objective of this study was to test effects of azoxystrobin, cultivar selection, and delayed harvest in a typical field environment in Arkansas. Seven cultivars were selected for their resistance to *Phomopsis longicolla* and *Cercospora kikuchii*, both of which are problematic pathogens of soybean at the University of Arkansas Vegetable Research Station in Kibler, AR. Fields were planted in 2008, 2009, and 2010 with seven cultivars, including resistant and susceptible genotypes. Azoxystrobin was applied at a rate of 438 ml/ha at R5 growth stage. Plots were harvested 3 weeks after first reaching harvest maturity. Seed were tested for quality and vigor using standard germination, accelerated aging, Seed Vigor Imaging System (SVIS), electrical conductivity, and microflora assays. Overall, seed germ and vigor was highest and seed infection lowest in 2008. The cultivar MO/PSD-0259 had high quality and vigor scores in 2008 and 2010, but not in 2009 when environmental conditions were the most favorable for *P. longicolla* infection. The cultivar Osage had high standard germination, accelerated aging, SVIS ratings over the three years, and low electrical conductivity in 2009 and 2010. The cultivar Sween97 had the lowest values in the SVIS, accelerated aging, and standard germination testing in 2009 and 2010, high levels of *P. longicolla* infection. Sween97 also statistically had the lowest values for vigor testing in 2008. Fungicide application increased seed quality and vigor, and reduced seed fungal infection in 2009 and 2010, but not in 2008.

Silver nanoparticles as a novel nematicide in turfgrass

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Phytopathology 103(Suppl. 1):S1.2

One of the most prevalent turfgrass pests in the United States is the root-knot nematode (*Meloidogyne* spp.). Treatments for root-knot nematodes in

turfgrass are limited. Novel nematicides are required to treat this pest. In this study, silver nanoparticles were tested as a potential nematicide. Silver nanoparticles were synthesized by the reaction of silver nitrate with sodium borohydride using a 0.2% starch solution as the stabilizer. For laboratory tests, soil was collected from a field infested with root-knot nematodes divided into samples of 100 cm³ each, and then were treated with silver nanoparticles at 150, 30, 15, 3, and 1.5 mg/L, and water as a control. Treatment times were 1, 2, 4, and 8 days. After treatment, samples were placed in Baermann funnels for 48–72 hours to extract the nematodes from the soil. Extracted nematodes were counted. Results showed that only 5–10% of the original population of nematodes remained after 4 days of treatment with 150 mg/L. In a field trial (16-ft² plot, 4 replicates per treatment) established in April 2012, nematode control with silver nanoparticles (sprayed biweekly followed by irrigation until complete saturation) was compared to a conventional treatment, Nortica (Bayer CropScience; treated at 87.5 g/120 ft² monthly), and to an untreated plot. Turf quality of plots were rated biweekly using a 1–6 scale with 1–5 being poor and ≥6 being acceptable. Once per month, 100 cm³ soil samples were collected from each plot, placed in a Baermann funnel for 48–72 hours and extracted nematodes were counted. Neither treatment reduced nematode population significantly in the field, while an increase in turf quality by these treatments was observed between April and June. In vitro tests of silver nanoparticles as a potential nematicide were promising. Future studies are necessary to evaluate their field efficacy due to inconsistency between nematode population and turf quality.

Biology and management of spinach anthracnose

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Phytopathology 103(Suppl. 1):S1.3

Anthracnose, caused by *Colletotrichum dematium*, is an emerging foliar disease on spinach. Fungicide programs that include strobilurin fungicides for white rust (*Albugo occidentalis*) have not been effective on anthracnose. In fungicide efficacy trials, a pre-mixture of cymoxanil+fludioxanil has provided 60 to 75% disease control compared to no treatment ($P = 0.05$). Azoxystrobin, pyraclostrobin, and thiophanate-methyl, which are effective against anthracnose diseases on other vegetable crops, have not reduced levels of spinach anthracnose. Registration of cymoxanil+fludioxanil on spinach is pending. In order to better understand factors affecting anthracnose development, the combined effects of temperature and leaf wetness period on disease development were evaluated in dew chambers. Plants were inoculated with 9.5×10^5 conidia/ml and exposed to interrupted (12-hr/d) wetness periods that totaled 0, 3, 6, 9, 12, 24, 48, 72, and 96 hr at each temperature from 10 to 32°C on 2.78°C intervals. The effects of wetness period, temperature, and their interaction were significant ($P < 0.01$) on disease severity (percentage of leaf area with disease). Orthogonal polynomial contrasts of temperature effects were quadratic ($P < 0.01$) with a maximum disease severity observed between 18.3 and 26.7°C. However, temperature responses were variable and a specific optimum temperature was not identified. The effects of wetness duration on disease severity were cubic and increased from 2% at 3 hr to a maximum of about 50% at 96 hr. Disease severity exceeded 5% at 6 hr wetness and 10% at 12 hr wetness, indicating that economically important levels of disease can develop following relatively brief wetting periods.

Aphid feeding behavior and virus resistance in somatic fusions and crosses of *Solanum bulbocastanum* and *Solanum tuberosum*

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Phytopathology 103(Suppl. 1):S1.3

Potato virus Y (PVY) and Potato leafroll virus (PLRV) are the most important aphid-transmitted viruses in potato, *Solanum tuberosum*. Removing either the virus or the vector will eliminate disease, increase yields and reduce losses due to quality issues. Unfortunately North American seed potato producers have experienced an unprecedented and now decade-long PVY epidemic even with seed potato certification programs focusing on reducing virus inoculum. Research efforts have focused on reduction of either vector numbers or virus transmission through host plant resistance. *Solanum tuberosum* + *S. bulbocastanum* somatic fusions created for introgression of late blight resistance and subsequently backcrossed to cultivated potato were screened to determine if aphid resistance, virus resistance, and late blight resistance could be concurrently incorporated. Several lines pyramided *Myzus persicae*, *Macrosiphum euphorbiae*, and PVY resistance. Virus resistance field screenings over four years indicated 29 lines were resistant to PVY. However, this research did not address aphid probing behavior. Differences in probing behavior can influence virus transmission as aphids determine host suitability with brief intracellular probes (potential drops) which can result in virus acquisition and transmission. Electrical penetration graphs were used to record feeding behavior on resistant and susceptible plants. Parameters scored (per

probe) were pre-probe duration, number of potential drops, egestion duration, ingestion duration, and number of ingestion pulses. With these techniques, we ascertained whether the resistance(s) expressed in these potato lines was due to antixenosis or antibiosis and if this could be used to reduce virus transmission.

Rose rosette virus is the causal agent of Rose rosette disease

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Rose rosette disease (RRD) was discovered in the 1930s causing witches'-broom on roses in North America. In 2011, a new virus, provisionally named Rose rosette virus (RRV) was identified and perfectly correlated with typical RRD symptoms. Previous research has shown that RRD is transmitted by the eriophyid mite *Phyllocoptes fructiphilus*. Koch's postulates have not been completed for RRD/RRV since no RRV local lesion host has been identified, nor has it been feasible to purify the virus. *P. fructiphilus* mites were collected from *Rosa multiflora* affected by RRD. Mites were individually transferred to roses, which previously tested negative for RRV. Two months post inoculation; material tested positive for RRV. Mosaic and mottling patterns developed on the leaves, followed by distorted leaves, and proliferation of shoots; all of which are described as RRD symptoms. This is the first time *P. fructiphilus* has been proven to transmit RRV and the subsequent development of typical RRD provides evidence that RRV is the causal agent of RRD.

Epiphytic survival of *Pseudomonas* sp. (causal agent of Yellow bud in onions) on *Lolium multiflorum* L. and *Rumex crispus* L. in Georgia, U.S.A.

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Phytopathology 103(Suppl. 1):S1.3

Yellow bud is an emerging bacterial disease of onion. The causal agent is an ice-nucleating and non-fluorescent *Pseudomonas* sp. A survey of potential weed hosts was carried out in the Vidalia onion-growing zone (VOZ) in 2012. Italian ryegrass (*Lolium multiflorum*) and curly dock (*Rumex crispus*) were identified as asymptomatic hosts supporting epiphytic populations of *Pseudomonas* sp. These weeds are widespread in Georgia, thus presenting an opportunity to assess their role in yellow bud epidemiology. Samples of the two weed species were collected from sites along the perimeter of and within the VOZ ($n = 5$ sites) during late June, August and October of 2012, thus representing the onion non-growing season. Samples ($n = 10$ / weed species/site) were collected and shaken overnight in 25 ml of phosphate-buffered saline at 24°C. After incubation, total genomic DNA was extracted and SYBR green-based, real-time PCR was used to amplify the coronafacate ligase (cfl) gene. Also, suspect bacteria were recovered from weed washes by spread-plating aliquants of 0.1 ml on nutrient agar supplemented with 0.5% yeast extract. Identity of *Pseudomonas* sp. was confirmed by LOPAT tests, pathogenicity on onions and sequencing of 16S rRNA and cfl genes. In June, *Pseudomonas* sp. was detected from Italian ryegrass and curly dock in 100 and 40% of the sample sites, respectively. During the months of August and October, the bacterium was recovered from Italian ryegrass in 60 and 10% of the sample sites. In contrast, during the same period, the bacteria were recovered from curly dock in 40 and 80% of the sample sites. These data demonstrate that the *Pseudomonas* sp. responsible for yellow bud can survive as epiphytes on Italian ryegrass and curly dock between onion crops and act as a potential source of initial inoculum for onions seeded in early September.

Detection and characterization of *Xanthomonas campestris* pv. *vitians* strains

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Phytopathology 103(Suppl. 1):S1.3

Three semi-selective media, - Tween B, MMG (maltose, methyl green and antibiotics) and MMY (mannitol-glutamate yeast extract agar)-, which were previously published for the isolation of *Xanthomonas* spp., were evaluated for use in ecological studies for isolation of *Xanthomonas campestris* pv. *vitians* (Xcv), causal agent of bacterial leaf spot of lettuce. In vitro assays showed that MMY allows the highest recovery percentage in comparison to nutrient agar, ranging from 70 to 90% recovery of Xcv strains. MMY inhibited growth of most contaminating bacteria and allowed reliable identification of Xcv strains from weeds, and irrigation water. Xcv strains were detected in a number of weeds, including *Chenopodium album*, *Solanum americanum*, *Amaranthus spinosus*, *Amaranthus blitoides*, and *Portulaca oleracea*. Putative *Xanthomonas* colonies, from weeds and irrigation water, were selected for pathogenicity tests and molecular characterization. Two sets of primers were used to amplify and sequence putative *X. vitians*. These

include the hrp-specific primers set, which targets the detection and identification of phytopathogenic xanthomonads; and a set which targets a glycosyl hydrolase that appears to be unique to *X. campestris* pv. *vitiensis* and *X. gardneri*. Preliminary results indicate that Xcv was frequently recovered during fall and springs crops.

Comparative sensitivity of conidial germination and mycelial growth of *Didymella bryoniae* to azoxystrobin

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Phytopathology 103(Suppl. 1):S1.4

The sensitivity of conidial germination and mycelial growth of the gummy stem blight (GSB) pathogen, *Didymella bryoniae*, to the QoI fungicide azoxystrobin (AZO) was compared in vitro to determine if mycelial growth assays can be used as an alternative to conidial germination assays for AZO resistance screening. Twenty four isolates of *D. bryoniae* previously collected in 2009 and 2010 from GSB-infected watermelon were used in this study. Eleven of the isolates were characterized as AZO-sensitive (AZO-S) and 13 of the isolates were characterized as AZO-resistant (AZO-R). The effective concentration of AZO at which conidial germination (C-EC₅₀) or mycelial growth (M-EC₅₀) was inhibited by 50% was estimated for each isolate. For AZO-S isolates, M-EC₅₀ values were significantly higher than C-EC₅₀ values in both trials. For AZO-R isolates, M-EC₅₀ and C-EC₅₀ values were greater than 10 µg/ml, the highest concentration tested. Relative growth of AZO-S isolates was significantly lower than relative germination at AZO concentrations ≤0.3 µg/ml; however, at concentrations ≥1.0, relative growth was significantly higher than relative germination. At 10 µg/ml, relative growth was 0.44 and 0.42 in trials 1 and 2, respectively, but conidial germination of AZO-S isolates was completely inhibited. Mycelial growth and spore germination of AZO-R isolates were only slightly inhibited at AZO concentrations ≤0.1 µg/ml and there were no significant differences between relative growth and relative germination. Relative growth of AZO-R isolates was significantly lower than relative germination at AZO concentrations ≥0.3 µg/ml in trial 1 and ≥3.0 µg/ml in trial 2. Although complete inhibition of mycelial growth was not observed at any AZO concentration tested, there was a clear distinction between AZO-S and AZO-R isolates at 1.0 µg/ml. At 1.0 µg/ml, isolates with relative growth values ≥0.90 can be considered AZO-R and isolates with relative growth values ≤0.70 can be considered AZO-S.

Maize WRKY transcription factors and their potential roles in regulating defense gene expression during *Aspergillus flavus* infection

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Phytopathology 103(Suppl. 1):S1.4

Infection of maize (*Zea mays* L.) kernels by *Aspergillus flavus* and their subsequent contamination with aflatoxin, a carcinogenic mycotoxin, results in significant crop loss and negative effects on human and animal health. Resistance to such fungal pathogens is affected by defense signal transduction pathways under the regulation of various macromolecules, including WRKY transcription factors (WRKY TFs). This study examined the responses of seven WRKY TFs: *ZmWRKY21*, *ZmWRKY53* (two homologs), *ZmWRKY67*, *ZmWRKY68*, and two putative WRKY TFs. The responses of these WRKY TFs to infection were examined over a time course in maize lines B73 (susceptible) and TZAR-101 (resistant) using real-time quantitative PCR. The expression of three defense genes, Nonexpressor of Pathogenesis-Related Protein 1 (*npr-1*), Pathogenesis-Related Protein 1 (*pr-1*), and Ethylene Responsive Factor 1 (*erf-1*) were also examined. One homolog of *ZmWRKY53* displayed the highest degree of differential expression in response to infection with expression levels approx.100x higher in the susceptible line in all treatments and at most time points. This WRKY TF is homologous to *Arabidopsis thaliana* WRKY33, a key regulator of salicylic acid (SA) and jasmonic acid (JA) defense pathways. The expression of the SA defense pathway gene, *npr-1*, showed some induction in response to infection in the resistant line while the downstream *pr-1* gene showed no induction in response to infection in the resistant line, and elevated early expression in the susceptible line. The JA and ethylene responsive gene, *erf-1*, displayed induction in the resistant line only. These results indicate that maize resistance to *A. flavus* may be JA-dependent and possibly regulated by *ZmWRKY53*.

Characterizing the differences between early and late leaf spot epidemics in response to prescription fungicide programs

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Phytopathology 103(Suppl. 1):S1.4

Previous research has demonstrated the efficacy of prescription fungicide programs to reduce combined effects of early (ELS) and late leaf spot (LLS), caused by *Cercospora arachidicola* and *Cercosporidium personatum*, respectively. ELS continues to be predominant in GA, but LLS has experienced resurgence in recent years. Field trials were conducted at two locations at the Coastal Plain Experiment Station in Tifton, GA, in 2011 and 2012, to assess the impact of this disease shift on the efficacy of prescription programs. Two market types ('Georgia-06G' and 'New Mexico Valencia' or 'Georgia Valencia') were planted in May of both years. Fungicides included azoxystrobin, tebuconazole, propiconazole, and chlorothalonil applied at rates and timings appropriate for high, moderate, and low risk programs, (7, 5 and 4 applications, respectively). Five stems were destructively sampled from each plot on a bi-weekly basis and the number of sporulating ELS and LLS lesions were counted. From these results fields were described as predominantly ELS or LLS. Over two years, severity of the predominant disease tended to increase with decreasing fungicide applications; however where the second disease was of minor occurrence, severity among treatments did not differ from the untreated check. Where ELS was predominant, onset of ELS was several weeks prior to that of LLS; if LLS was predominant, onset of both diseases coincided. For both locations, disease intensity across treatments was statistically higher in the runner compared to the Valencia cultivar. Compared to the untreated check, yields were numerically and often significantly greater across fungicide programs, but did not differ statistically between treatments.

VIGS study of proteins identified in soybean and *Phakopsora pachyrhizi* interaction

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Phytopathology 103(Suppl. 1):S1.4

Phakopsora pachyrhizi is the causal agent of Asian Soybean Rust (ASR) disease. This pathogen has the potential to cause severe yield losses as all U.S. commercial soybean varieties are susceptible. In order to understand the compatible and incompatible host-pathogen interactions at the molecular level, we conducted a time-course study of *P. pachyrhizi* infection of an immune and a susceptible Recombinant Inbred Line (RIL) derived sister lines using DIGE proteomics and compared their protein profile differences. Based on the gel analysis, we identified approximately 70 differentially expressed proteins between the two lines with and without *P. pachyrhizi* inoculation and these protein spots were sequenced using mass spectrometry. Several of the rust infection induced proteins were further studied using virus-induced gene silencing (VIGS) strategy to determine their importance in soybean resistance to rust infection. These genes were cloned in the *Bean pod mottle virus* (BPMV) vector and inoculated into the soybean plants through particle bombardment. After four weeks of particle bombardment, the soybean plants were inoculated with ASR in the greenhouse. After inoculation, leaf samples were collected at different time points from 0 h to 14 d and are currently being analyzed using qPCR. Preliminary results showed successful silencing of candidate genes and as well as changes in ASR disease development on virus treated soybean leaves.

Pathogenicity of fungi isolated from giant miscanthus (*Miscanthus x giganteus*) in Mississippi

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Phytopathology 103(Suppl. 1):S1.4

The production of giant miscanthus (*Miscanthus x giganteus* Greef et Deu, Mxg) as a biofeedstock crop has dramatically increased with the expansion of the alternative energy industry in the United States. Plant disease issues may be detrimental to establishment success and biomass yields; both necessary for the economic practicability of producing this crop. In 2011 a two-year study was initiated to monitor "Freedom", "Illinois", and "Nagara" Mxg for foliar disease symptoms on a monthly basis throughout the growing season. Fungi were isolated from symptomatic tissue, identified, and those known as pathogens of graminaceous hosts were selected for pathogenicity evaluations. Foliar lesions were excised from mature leaves, segmented, and surface disinfested prior to plating on water agar. Emerging fungi were isolated after 21 days of incubation then identified by fungal morphology and comparative analysis of ITS rDNA to entries present in the GenBank database. Thirty-one fungal genera were identified from 4,400 samples and eight genera were selected for pathogenicity screening; *Alternaria*, *Ascochyta*, five species of *Bipolaris*, *Colletotrichum*, *Curvularia*, *Phoma*, *Pithomyces* and *Septoria*. Whole plant inoculations were conducted in growth chambers to evaluate the pathogenicity of selected fungal isolates. Healthy Mxg plants were inoculated with a spore or macerated mycelium solution and held in a mist chamber for 24 hours, incubated under humid conditions for 14 days, then placed in a greenhouse for symptom development. To date, successful

completion of Koch's postulates has been achieved with *Colletotrichum navitas*, *Bipolaris oryzae*, and *B. sorokiniana*.

The complex regulatory and signaling network for the virulence of the rice pathogenic bacterium *Burkholderia glumae* revealed by various molecular genetic and genomic studies

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Phytopathology 103(Suppl. 1):S1.5

Burkholderia glumae is the primary causal agent of the rice disease, bacterial panicle blight, which causes serious damages in rice production in the southern United States and other rice-growing areas worldwide. The bacterial quorum-sensing (QS) system mediated by the LuxI and LuxR family proteins, TofI and TofR respectively, are known to be the key regulatory/signaling component essential for the production of important virulence factors, including toxoflavin, flagella and lipase. Several regulatory factors controlling the production of individual virulence factors have also been studied. Nevertheless, our knowledge of the global regulatory/signaling system for the coordinated expression of virulence genes is still very limited. In our recent studies, several important regulatory/signaling factors were newly identified and their functions in the bacterial pathogenesis by *B. glumae* were characterized. The PidS/PidR two-component regulatory system was shown to be required for the functional type III secretion system and toxoflavin production. TofM encoded by the conserved gene located between *tofI* and *tofR* were identified as a modulator of the TofI/TofR QS system. In addition, NtpR and TepR, a LysR-family protein and a sigma 54-dependent response regulator respectively, were confirmed to be novel negative regulators for the production of toxoflavin. These newly found regulatory/signaling factors of *B. glumae* would help to augment our understanding of the virulence mechanism conferring this globally emerging rice disease.

Impact of *Brassica juncea* cover cropping on rice sheath blight disease incidence, severity and rice yield

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Phytopathology 103(Suppl. 1):S1.5

Sheath blight, caused by *Rhizoctonia solani* AG 1-1A, is one of the major rice diseases in the southern rice production areas in the U. S. One of the effective and recommended management options for rice sheath blight is a 2-year rotation. However, this option is often not economically viable and practical for rice farmers. The objective of the study was to evaluate the efficacy of integrating biofumigation cover cropping, fungicide, and partial resistant cultivar to control sheath blight in the field. A field experiment was laid in a split-split plot design with cover cropping (winter *Brassica juncea* cover crop and winter fallow), rice cultivars (Cocodrie and Presidio) fungicide rates (azoxystrobin) as the main plot, sub plot and sub-sub plot factors respectively. Brassica cover cropping, rice cultivars and fungicide application rates did not significantly interact with each other. Brassica cover cropping resulted in lower disease incidence and severity but no significant yield increase compared to fallow plots. The partial resistant rice cultivar (Presidio) outperformed the susceptible cultivar (Cocodrie) with respect to yield, disease incidence and severity. The fungicide applied at the full recommended rate (9 fl oz/acre) similarly reduced sheath blight severity as the half of the recommended rate (4.5 fl oz/acre) but significantly reduced disease incidence compared with the half of the recommended rate. Brassica cover cropping can reduce disease incidence and severity in rice, but more research is needed to evaluate its impact on rice yield under high disease pressure.

Effective use of soil management zones for application of Telone® II in cotton in 2012

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Phytopathology 103(Suppl. 1):S1.5

Control recommendations for root-knot nematodes (*Meloidogyne incognita*) and reniform nematodes (*Rotylenchulus reniformis*) in cotton are based on species present, soil types, nematicide efficacy, economics, and other variables. Research results show that the use of soil maps and ECa data can be used effectively to identify low and high risk, or "responsive" zones. As a result, input costs can often be reduced by 30–40% by using this technological approach to assist in nematode management. This study was initiated to further evaluate cotton yield responses when Telone® II was applied in four soil management zones. Yield monitor data from this trial demonstrated the positive effects and value of the Telone II applications in soil management zones.

Yellow vein of some ornamental plants: Viral or genetic?

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Phytopathology 103(Suppl. 1):S1.5

Selections of many ornamental plants exhibiting green leaves with vein discolorations have been propagated and commercialized as distinct cultivars. Some of them are of genetic nature; however, others are caused by plant viruses. This is the case of the yellow-veined Japanese honeysuckle, infected with the begomovirus *Honeysuckle yellow vein mosaic virus*. There are other ornamental plants with unique foliar phenotypes in the form of yellow vein for which the nature of the symptom is not known. To determine whether the phenotype is of viral or genetic origin, we selected Crocodile geranium (*Pelargonium peltatum*), Golden Net Bush (*Pseuderanthemum carruthersii*), and Gold Veined Oxalis (*Oxalis corymbosa*). These plants are available through nursery catalogs and at garden centers across the United States. Successful graft transmission of the putative virus was obtained with Crocodile geranium and Golden Net Bush. Similarly, successful whitefly transmission was obtained with the putative yellow vein causing virus of Gold Veined Oxalis. Due to the nature of the symptoms shown by these three ornamental plants, we suspected that a begomovirus may be the causal agent. Therefore, rolling circle amplification of viral DNA and PCR amplifications using degenerate primers for the genus Begomovirus were performed. Obtained data supports that plant viruses are the cause of the yellow vein of these ornamental plants.

Demography and disease of Gray's lily *Lilium grayi* on Roan Mountain, TN/NC

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Phytopathology 103(Suppl. 1):S1.5

A previously unreported leaf spotting disease has been observed on *Lilium grayi*, (Gray's lily), on Roan Mountain, TN/NC. The fungal pathogen *Pseudocercospora inconspua* (G. Winter) U. Braun was shown to be the disease agent. The purpose of this study was to analyze the effects of disease on the population of Gray's lilies. Observations across three growing seasons showed disease clusters that were relatively stable in location between seasons but that grew in magnitude within seasons. Clusters of healthy plants were detected that also were stable in location but whose sizes decreased as the growing seasons progressed. These patterns are consistent with an infectious process influenced by the environment. Further spatial analyses using autocorrelation, showed that plants spaced at increasing distances decreased in the similarity of their health status. Morphological characteristics did not show clustering or spatial autocorrelation, an observation that suggests size and vigor metrics were not risk factors for disease. The impact of disease on plant survival proved to be severe as, of those infected, there was 100% mortality in seedlings and >80% above ground mortality in mature plants. The pathogen, *P. inconspua* is responsible for the lily leaf spotting disease that occurs with a high incidence rate throughout the Gray's lily population and where occurring, this disease leads to above ground plant collapse, often before seed maturation.

The effects of fungicides on the latent stage of pecan anthracnose

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Phytopathology 103(Suppl. 1):S1.5

Anthrachnose, caused by *Colletotrichum gloeosporioides*, is a common disease of pecans (*Carya illinoensis*) in Georgia, especially during wet years. There can be an extended latent period between infection and symptom development. In 2011, trees in the field sprayed with Absolute (5.0 fl oz), Quadris Top (10 fl oz), ProPhyt (32 fl oz), Sovran (3.2 oz) + Orius (4.0 fl oz), and Super tin (6 fl oz) + Elast (25 fl oz) had 70, 70, 86, 57 and 37% fewer latent infections per leaf than nontreated leaves in 2011, and 43, 85, 55, 40 and 41% fewer than the nontreated in 2012, respectively. To evaluate protectant activity, pecan seedlings were sprayed with Super Tin, Quadris Top, or ProPhyt at similar rates to the field as the field study, one day prior to inoculation with *C. gloeosporioides*. Only the ProPhyt did not reduce the average number of latent infections formed per leaf. To test eradicant activity, the same treatments were applied to infected, asymptomatic pecan seedlings and the number of latent infections was measured over time. At day 10 and day 20 post inoculation (PI), none of the treatments reduced levels of latent infections compared to controls. However, at 35 days PI, all three treatments had fewer latent infections. Reductions in field infections may result from either protectant activity, or possibly long term eradicant activity of latent infections.

Virulence deficiencies associated with the mutation of *aroA* and *aroB* genes of *Burkholderia glumae* strain 411gr-6

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Phytopathology 103(Suppl. 1):S1.6

The rice pathogenic bacterium *Burkholderia glumae* is the primary causal agent of bacterial panicle blight (BPB) of rice, and also causes wilting symptoms in some field crops. Along with the known virulence factors (i.e. toxoflavin, lipase and flagella-dependent motility), high night temperature and humidity is equally important for outbreaks of BPB, which causes up to 70% yield reductions. Previously, we reported that some strains of *B. glumae* produce dark pigments which are under the control of the *PidS/PidR* two component regulatory system. In an attempt to figure out the role of these pigments in pathogenicity of *B. glumae*, a pigment-producing virulent strain, 411gr-6, was randomly mutagenized with mini-Tn5gus and several non-pigmented mutant derivatives were screened and characterized in this study. Among the pigment-deficient mutants screened, two mutant strains, LSUPB114 and LSUPB116, were characterized to have transposon insertions in *aroA* encoding 3-phosphoshikimate 1-carboxyvinyltransferase and *aroB* encoding 3-dehydroquinate synthase, respectively. Interestingly both of the enzymes encoded by *aroA* and *aroB* are involved in the shikimic acid pathway, which is responsible for the synthesis of aromatic amino acids. We demonstrate here that the dark pigments are important for the tolerance of *B. glumae* cells to UV radiation, and that the genes involved in the shikimic acid pathway are required for the growth of *B. glumae* in minimal media. Moreover, the shikimic acid pathway mutants, LSUPB114 and LSUPB116, were unable to produce visible symptoms on rice panicles and showed reduced toxoflavin production phenotypes, indicating the importance of the shikimic acid pathway in bacterial pathogenesis.

Role of amino acids, vitamins and inorganic salts in the development of *Cercospora janseana* L. Miyake

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Phytopathology 103(Suppl. 1):S1.6

Cercospora janseana L. Miyake causes the fungal rice disease narrow brown leaf spot. During the last few years, this disease has been causing significant yield losses (10–40%) in rice growing states of United States and worldwide. Recent and frequent outbreaks of this disease are serious concerns for researchers and growers. Due to sparse information available related to this pathogen and disease, studies have been conducted to explore the factors affecting growth and development of *C. janseana* in the Crop Loss Assessment Laboratory of Department of Plant Pathology and Crop Physiology, Louisiana State University, Baton Rouge. To do so, it is necessary to know about the pathogen's nutritional and environmental requirements to study its biology and host-pathogenic interactions. *Cercospora* is one of the fungal species which is difficult to grow and sporulate in vitro. In this study, different kinds of media were tested: PDA, ½ PDA, ¼ PDA, water agar, corn meal agar, yeast agar, rice leaf extract, V8 (10%) and V8 (20%). Among the media, maximum mycelial growth and sporulation of the fungus was observed on V8 (20%). Using V8 (20%) as a base media, further amendments were done with L-amino acids, vitamins and inorganic salts. Amino acids used were: adenine, alanine, arginine, histidine, threonine, tryptophan, phenylalanine, leucine, isoleucine, methionine, glutamine, glutamic acid, valine, lysine, proline, tryptophan, cystine, glycine, nicotinic acid and aminobenzoic acid. Vitamins used were: thiamine, ascorbic acid, riboflavin and pyridoxine. Inorganic salts used were: potassium monophosphate, potassium chloride, calcium chloride, manganese chloride, magnesium sulphate, iron sulphate, copper sulphate, zinc sulphate, and boric acid. Of the media amended with leucine, isoleucine, methionine, glutamic acid, thiamine has shown significant increased growth and sporulation of *C. janseana* as compared to unamended V8(20%).

Incidence of blackberry viruses in the United States

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Phytopathology 103(Suppl. 1):S1.6

Blackberry production has increased in the southern U.S.A. in the past ten years. Along with the increase in production, there has also been an increase in virus disease incidence, a fact this study aims to address. Blackberry yellow vein associated virus (BYVaV), Beet pseudo-yellow virus (BPYV), Blackberry chlorotic necrotic virus (BCRV), Strawberry necrotic shock virus (SNSV), Tobacco streak virus (TSV) and Blackberry leaf mottle associated virus (BLMaV) are some of the viruses speculated to affect yield and plant longevity. To examine the presence of these viruses in the southern U.S.A., field samples, collected from six states and sentinel plants, collected from Arkansas and North Carolina, were tested by reverse transcription-PCR (RT-

PCR). This survey revealed the presence of the majority of the viruses in many areas whereas viruses were also detected in sentinel plants that were grown in the field for only one month.

Endornaviruses in common bean of Mesoamerican origin

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Phytopathology 103(Suppl. 1):S1.6

Endornaviruses are dsRNA viruses that range from 9.8 to 17.6 kbp; infect plants, fungi, and oomycetes; lack cell-to-cell movement; are present in every cell; are transmitted only via gametes; and do not cause apparent symptoms. They infect economically important crops (e.g., avocado, barley, broad bean, common bean, cucurbits, and pepper), some plant pathogenic fungi, and the oomycete *Phytophthora* sp. Recently, it has been reported that many common bean cultivars are infected with two distinct endornaviruses designated *Phaseolus vulgaris* endornavirus 1 and *Phaseolus vulgaris* endornavirus 2. Results from testing selected common bean cultivars from the two major centers of domestication (Mesoamerica and the Andes) indicate that these two endornaviruses are common in cultivars of Mesoamerican origin but not in those of Andean origin. In this investigation, we tested a variety of common bean genotypes from both centers of domestication and belonging to the various market types currently used in the United States. We also tested 25 wild *P. vulgaris* collections and 18 *Phaseolus* spp., including four domesticated species. Our results suggest that in Mesoamerica, these viruses were introduced during domestication and that plants infected with these two viruses were selected. We can only speculate that their presence is beneficial. The effect that these viruses have in common bean is not known.

Managing pre- and post-harvest *Phytophthora* fruit rot of watermelon in the Southeast

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Phytopathology 103(Suppl. 1):S1.6

Fruit rot, caused by *Phytophthora capsici*, is an emerging disease in most watermelon producing regions in Southeastern U.S. Between 2003 and 2010 we observed many watermelon farms in GA, SC, and NC where growers did not harvest the crop due to severe fruit rot. Experiments were conducted from 2008–2012 in a *P. capsici* infested field to identify fungicides effective for managing pre- and post-harvest development of *Phytophthora* fruit rot. Weekly treatments of Forum, Zampro, Prophyt + Kocide 2000, Revus rotated with Prophyt + Kocide, V-10208, and rotation of Revus with Presidio significantly reduced pre-harvest fruit rot compared to non-treated controls. Application of Actigard (1.0 oz/A) every week reduced pre-harvest fruit rot in some years. Rotations of Actigard with Revus or Presidio also reduced pre-harvest fruit rot. Post-harvest development of fruit rot was evaluated by inoculating symptomless fruit harvested four days after the last spray. Each fruit was inoculated with a 7-mm agar plug from an actively growing *P. capsici* colony and maintained in a humid chamber (>95% RH, 25 ± 2°C) for five days. Post-harvest development of fruit rot was less on fruit treated with Zampro, Forum, V-10208, Presidio rotated with Revus, Actigard rotated with Revus or Presidio compared to non-treated control. Weekly application (4–5 sprays) of Actigard did not affect the number of fruits per plot than on non-treated control or fungicide treatments. Fungicide applications should be part of an overall management strategy that also includes the use of well drained fields and proper irrigation practices.

The interactive effects of soybean mosaic virus infection and salt stress on soybean cultivars that vary in chloride uptake

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Phytopathology 103(Suppl. 1):S1.6

With increased irrigation and agricultural expansion into marginal lands, saline soils are increasingly problematic for farmers worldwide. Cultivars of soybean *Glycine max* (L.) Merr., an important agronomic crop, can differ widely in their reaction to salt stress. Soybean lines that accumulate chloride in the leaves are typically salt sensitive and are referred to as inclusions. Those that sequester chloride in the roots are generally more tolerant and are called excluders. Because plants in the field are also challenged with pathogens, we set out to examine the interactions of a viral infection and salt stress and their effects on molecular and physiological responses in soybean. We infected two soybean cultivars that differ in chloride uptake, cv. Clark (an inclusion) and cv. Manokin (an excluder), with *Soybean mosaic virus* (SMV), an important pathogen of soybean. Two different salts, NaCl and CaCl₂, in three concentrations of equal amounts of chloride (25, 50 and 100 mM chloride) were

applied to soybeans inoculated with SMV. The soybeans were flooded daily. Chlorophyll levels were measured daily using a SPAD meter, and photosynthesis rates were measured via CO₂ gas exchange. After 14 days the soybeans were visually rated for salt damage and SMV severity, and plant height was measured. Soybeans infected with SMV were severely stunted and developed viral symptoms regardless of salt treatment. Infection with SMV did not decrease salt tolerance in Manokin; however, infected Clark and Manokin soybeans treated with the highest levels of chloride died earlier than SMV-free soybeans. Photosynthesis was reduced in both Clark and Manokin with salt stress regardless of SMV infection. However, at the lowest chloride levels photosynthesis was significantly lower in SMV-infected plants compared to uninfected soybeans. The preliminary results suggest in some cases there are additive negative effects on plant performance by salt and SMV infection.

Environmental factors affecting oospore germination and infection of plant roots by the sorghum downy mildew fungus, *Peronosclerospora sorghi*

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Phytopathology 103(Suppl. 1):S1.7

Sorghum downy mildew, caused by *Peronosclerospora sorghi*, is an economically important disease of sorghum and corn in the tropics and subtropics. Oospore infection of seedling roots leads to systemic infection, resulting in yield loss, but environmental conditions in soil that affect oospore germination and infection of plants are not well understood. The specific objective of this study was to evaluate the effect of soil type and soil matric potential on oospore germination on roots of host and non-host plants (soybean, wheat, rice, corn, cotton, and hairy vetch). Oospores were obtained from the leaves of greenhouse-grown sorghum plants by harvesting leaves with necrotic lesions. Leaves were air dried at room temp (25C) for 4 days, cut into pieces approximately 4–5 cm long and pulverized in a Waring blender. The resulting powder was vortexed in water for several seconds. The mixture was filtered through double-ply cheese cloth and oospores that settled after 10 minutes were washed on a 37 micron sieve. The oospores were air dried at room temperature overnight and were stored at room temperature. To measure germination, oospores were placed on polycarbonate membranes under seedling roots. After 4, 5, 6, and 7 days, the membranes were removed and stained in phenolic rose bengal. Oospore germination on sorghum roots ranged from 5–20% during these time periods, with most germ tubes dead by day 7. This oospore assay technique can be useful in evaluating factors affecting oospore germination.

Understanding the impact of *Pythium* on floriculture crops in North Carolina

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Phytopathology 103(Suppl. 1):S1.7

Herbaceous ornamentals exhibiting symptoms of *Pythium* root rot were collected from 26 greenhouses in 21 counties in NC. Symptoms ranged from mild stunting to severe wilting, root rot, and death. Roots were assayed on selective media and 369 isolates of *Pythium* were recovered from 36 host species. Selected isolates were identified by sequencing of the ITS rDNA region. Twelve species were identified, with *P. aphanidermatum*, *P. irregulare*, and *P. myriotylum* comprising 81% of the 173 isolates sequenced. *P. aphanidermatum* was recovered at 10 locations, *P. myriotylum* at 5, and *P. irregulare* at 13. Eleven greenhouses had more than one species present. To assay sensitivity to mefenoxam, all 369 isolates were grown in wells of 48-well micro-titer plates containing clarified V8 agar amended with 100 ppm mefenoxam. Colonization was scored after 24 to 48 h on a scale of 0 (no growth) to 5 (entire well colonized). Fifty-three percent of the isolates were resistant to mefenoxam (mean score > 4). All 24 isolates of *P. myriotylum* were sensitive, whereas sensitivity varied among isolates of *P. aphanidermatum* and *P. irregulare*. Resistant and sensitive isolates of the same species were found within the same greenhouse. The aggressiveness of *P. aphanidermatum* and *P. irregulare* was evaluated on poinsettia, gerbera daisy, and petunia. Both *Pythium* species caused more severe disease on poinsettia than on gerbera daisy. Severity on petunia was low in initial collections and inoculation trials. *P. aphanidermatum* was more aggressive than *P. irregulare* on all hosts. Sensitivity to mefenoxam was not related to aggressiveness. We will use the results of this study to evaluate the need for and the feasibility of offering mefenoxam resistance screening as a diagnostic service at the Plant Disease and Insect Clinic.

Plant health risk associated with irrigating nursery crops with *Phytophthora*-infested water

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Phytopathology 103(Suppl. 1):S1.7

Phytophthora species are water-borne plant pathogens that can be disseminated in streams and rivers, as well as in reclaimed irrigation water, and may pose a risk in ornamental nurseries if used for irrigation. *Rhododendron* and *Pieris* plants at two commercial nurseries were irrigated with water naturally infested with *Phytophthora* during the 2011 and 2012 growing seasons to assess the risk of disease. *Phytophthora* was consistently recovered from water samples at every collection time, but was only detected on two of the 384 ‘trap’ plants during the two years (i.e. <1% of plants). Pathogenicity assays proved that *P. hydropathica* and *P. taxon PgChalmydo*, the most commonly recovered taxa in the irrigation water at both nurseries along with *P. pini* (*P. citricola* complex), were foliar pathogens of *Rhododendron* and *Pieris*. However, no species was able to cause root rot on these hosts. Overall, the disease risk associated with irrigating the *Rhododendron* and *Pieris* ‘trap’ plants with *Phytophthora*-infested water was low.

Field trials for control of *Phymatotricopsis omnivora* in grapevines in Texas

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Phytopathology 103(Suppl. 1):S1.7

Texas is currently the 5th largest wine producing state in the nation with 263 wineries and an economic impact of 1.7 billion dollars. There is a growing concern for the threat of Texas (cotton) root rot (TRR), caused by *Phymatotricopsis omnivora*, to this relatively young, rapidly expanding winegrape industry. A recent survey of 40 grape growers revealed the disease is a serious problem, with some notable exceptions, in most of the American Viticultural Areas (AVA) in Texas. Two field trials were initiated in the summer of 2012 to test four different classes of fungicides at varying rates in an attempt to suppress the disease. One trial is in a commercial vineyard and the other is in an experimental vineyard where the soils are naturally infested with *P. omnivora*. Flutriafol, one of the fungicides being tested, is currently used to control TRR on cotton. The active ingredients of the other fungicides include cyprodinil, pyraclostrobin/boscalid, and fluazinam. These are labeled to control root rot diseases in row crops or are already used in vineyards for other grape diseases. In the experimental vineyard, after one growing season, vines treated with flutriafol at ten times the labeled rate for cotton exhibited significantly reduced periderm formation, delayed leaf senescence, and decreased incidence of late season powdery mildew when compared to the other treatments. Similar results in periderm formation were observed in the commercial vineyard. There has been insufficient time to determine how the fungicides will influence the incidence or severity of TRR or the long term impact on vine health.

Genetic analyses of *ntpR* encoding a LysR-family transcriptional factor for its negative regulatory function for the virulence of the rice pathogenic bacterium *Burkholderia glumae*

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Phytopathology 103(Suppl. 1):S1.7

Burkholderia glumae is the major causal agent of bacterial panicle blight of rice, a disease that can cause severe yield losses, and is becoming an increasingly important pathogen worldwide. The phytoxin, toxoflavin, is the most important virulence factor of *B. glumae* and is required for full virulence. The currently known regulatory cascade of toxoflavin production involves *tofl*, *tofR*, *toxJ*, *toxR*, and the *toxABCDE* and *toxFGHI* operons that encode the TofI/TofR quorum-sensing system, the transcriptional activators ToxJ and ToxR, and the components of the toxoflavin biosynthesis pathway and toxoflavin transport system, respectively. Transposon mutagenesis of a virulent strain of *B. glumae* isolated from diseased rice panicles in Louisiana yielded a number of mutant derivatives with increased toxoflavin production. Two mutant derivatives were found to be disrupted in a putative open reading frame (ORF) encoding a LysR-type transcriptional regulatory protein. This putative ORF was named *ntpR* for negative regulator of toxoflavin production LysR. Additional independent mutations of *ntpR* created via homologous recombination reproduced the phenotype of the original mutant derivatives. Complementation of the *ntpR* mutant derivatives with a plasmid-borne clone of *ntpR* resulted in a substantial reduction in toxoflavin production, indicating that *ntpR* is a negative regulatory gene for toxoflavin production. In order to develop a better picture of the regulatory functions of *ntpR* in *B. glumae*, transcriptome profiles and virulence gene expression associated with *ntpR* are currently being analyzed. Increased knowledge of *B. glumae* virulence factors and their regulatory mechanisms will contribute to a greater understanding of bacterial pathogenesis by this pathogen and will help to develop effective disease control strategies.

Evaluating different application methods of fluensulfone for control of *Meloidogyne incognita* in cucumber

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Fluensulfone is a new nematicide that is member of the flouroalkenyl chemical group. Two field trials were conducted in the spring and fall of 2012 to evaluate the efficacy of different application methods of fluensulfone for control of southern root-knot nematode (*Meloidogyne incognita*) in cucumber (*Cucumis sativus*). Treatments of fluensulfone were applied either pre-plant incorporated (PPI) or via 3 different drip applications with all fluensulfone treatments being applied at a rate of 3 kg/ha. All drip treatments were applied at the same time, but were separated by using different pulse irrigation methods. Drip treatment 1 received no pulse irrigation, treatment 2 received pulse irrigation 1h after treatment, and treatment 3 received pulse irrigation at treatment. A PPI treatment of oxamyl was used in the trial as an industry standard at a rate of 2 gal/a. Plant vigor, harvest data, and root gall ratings were recorded. All drip treatments significantly improved vigor when compared to the oxamyl treatment and the untreated check during the spring trial. Drip treatments significantly improved yield when compared to the untreated check during the spring and all drip treatments significantly reduced root galling severity compared to the oxamyl treatment and the untreated check. Stand counts were recorded during the fall trial because of high seedling mortality caused by *Pythium* spp. All nematicide treatments had significantly higher stand counts compared to the untreated check. Fluensulfone PPI and drip treatment 3 yielded significantly better than either oxamyl or the untreated check during the fall. Although a numerical reduction in gall ratings was noted with drip treatments 1 and 2 versus the untreated check in the fall trial, differences were not significantly different. These data suggest that control of root-knot nematode may be obtained with a pre-plant drip injection of fluensulfone.

Visual assessments and canopy reflectance for monitoring disease progress of leaf spot diseases of peanut

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Early and late leaf spot caused by *Cercospora arachidicola* and *Cercosporidium personatum*, respectively, can cause severe losses on susceptible peanut (*Arachis hypogaea*) cultivars. Visual estimates of leaf spot severity are typically used for monitoring disease progress. Measurements of canopy reflectance have shown promise for providing more objective evaluations of disease severity and readings that could be linked with GPS systems. The purpose of these experiments was to evaluate the utility of a canopy reflectance meter for measuring leaf spot severity and monitoring disease progress. Field experiments were conducted in which two cultivars Georgia-06G and Tifguard, were combined in split-plot arrangement with treatments of varying numbers of fungicide applications, including non-treated plots, to allow different levels of disease development. Multiple visual leaf spot ratings (Florida 1-10 scale) and remote sensing assessments were made for each plot to monitor the epidemics. On each evaluation date, canopy reflectance in the visible and infrared light spectrum was measured using a Crop Circle Crop Scanner with an ACS-210 active sensor. Normalized difference vegetative index (NDVI) was calculated from those measurements. Late leaf spot was the predominant foliar disease in 2011, and early leaf spot was predominant in 2012. Leaf spot epidemics began earlier and were much more severe in 2012 than in 2011. Epidemics typically were less severe for Tifguard than for Georgia-06G. NDVI values correlated more closely with visual disease severity estimates than either visual spectrum or near-infrared reflectance. NDVI values appear to be a better indicator of varying levels of defoliation and varying levels of incidence before defoliation occurs.

Large patch activity in 'Palisades' zoysiagrass in response to irrigation, nitrogen and Civitas applications

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The use of zoysiagrass (*Zoysia japonica* and *Z. matrella*) on golf courses and in the landscape is increasing across the southern United States due to its aesthetic appeal as well as excellent heat, drought, shade and cold tolerance. Despite these desirable characteristics, a primary limitation of zoysiagrass is its susceptibility to large patch, caused by the soilborne fungus *Rhizoctonia solani*. Knowledge is lacking concerning the relationship between summer-

time cultural management programs, specifically irrigation and nitrogen level, and large patch activity during subsequent fall and spring periods. Field trials were initiated in May 2012 at the Texas A&M University Turfgrass Ecology Field Laboratory in College Station. Goals of this study are to 1) evaluate the performance of 'Palisades' zoysiagrass, as influenced by irrigation [100, 60, 45 or 36% ETo (reference evapotranspiration)], nitrogen (0, 49, 98 or 196 kg N ha⁻¹) and application of a biofungicide (Civitas) during the summer, 2) determine the relationship between summertime treatments and large patch activity in the fall and spring, and 3) characterize seasonal dynamics of *R. solani* and other *Rhizoctonia* spp. present and active in the turfgrass during rapid summer growth, spring and fall transition, and dormancy. Turfgrass performance evaluations indicated acceptable density and quality were achieved at irrigation levels of 36% x ETo throughout the summer. Increasing irrigation above 60% x ETo was not beneficial. Both nitrogen and Civitas applications resulted in short-term greening, but neither significantly improved density in this low-input species. Surprisingly, *Rhizoctonia* spp. other than *R. solani* were prevalent in soil and thatch during the summer. *R. solani* strains became prevalent as soil and air temperatures declined during the fall. Simultaneously with the drop in temperatures, large patch developed, regardless of summertime cultural management. Interestingly, subplots receiving the most irrigation and nitrogen had few to no symptoms.

Effect of sexual recombination on population diversity in aflatoxin production by *Aspergillus flavus*

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Aspergillus flavus is the major producer of carcinogenic aflatoxins (AFs) in crops worldwide. Recent efforts to reduce AF concentrations in crops have focused on the use of two non-aflatoxigenic *A. flavus* strains, AF36 and NRRL 21882 (Afla-Guard), as biological control agents. These products are applied at high densities to agricultural fields, where they competitively exclude native aflatoxigenic strains and thereby reduce AF contamination. Natural populations of *A. flavus* show tremendous variation in AF production, some of which can be attributed to environmental conditions, differential regulation of the AF biosynthetic pathway, and deletions or loss-of-function mutations in the AF gene cluster. Understanding the evolutionary processes that generate genetic diversity in *A. flavus* may also explain quantitative differences in aflatoxigenicity. Several population studies using multilocus genealogical approaches provide indirect evidence of recombination in the genome and specifically in the AF gene cluster. More recently *A. flavus* has been shown to be functionally heterothallic and capable of sexual reproduction in laboratory crosses. In the present study, we characterize the progeny from nine *A. flavus* crosses using toxin phenotype assays, DNA sequence-based markers and array comparative genome hybridization. We show high AF heritability linked to genetic variation in the AF gene cluster, as well as recombination through the independent assortment of chromosomes and through crossing over within the AF cluster that coincides with inferred recombination blocks and hotspots in natural populations. Moreover, the vertical transmission of cryptic alleles indicates that while an *A. flavus* deletion strain is predominantly homokaryotic, it may harbor AF cluster genes at a low copy number. Results from experimental matings indicate that sexual recombination is driving genetic and functional hyperdiversity in *A. flavus*. The results of this study have significant implications for managing AF contamination of crops and for improving biocontrol strategies using non-aflatoxigenic strains of *A. flavus*.

The novel regulator, *tepR*, influences toxoflavin production and virulence in the rice pathogenic bacterium *Burkholderia glumae*

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Burkholderia glumae is an important rice pathogenic bacterium that causes bacterial panicle blight. Toxoflavin, lipase and flagella are known to be important virulence determinants of *B. glumae*. Mutants deficient in one of these virulence factors were shown to be almost non-pathogenic. All of these major virulence factors are produced under the control of quorum sensing system. In our previous study to search for the genetic elements underlying toxoflavin production by *B. glumae*, *tepR* encoding a sigma 54 dependent response regulators was identified as a putative negative regulator for

toxoflavin production, virulence in rice, and elicitation of hypersensitive response on tobacco leaves. In this study, a marker-less *tepR* deletion derivative of *B. glumae* 336gr-1, LSUPB397, was created by using the newly developed suicide vector system, pKKSacB, and this mutant was complemented with a plasmid-borne *tepR*. Virulence-related phenotypes including toxoflavin production of the *tepR* deletion mutant and complemented strains were examined along with the wild type strain *B. glumae* 336-gr1. Our quantification assay for toxoflavin production confirmed the negative regulatory function of *tepR* in toxoflavin production of *B. glumae*. Along with this, roles for *tepR* in other virulence-related phenotypes of *B. glumae*, including lipase production, flagella-dependent motility, and maceration of onion bulb are also being investigated.

Molecular diversity of the peanut rust pathogen and its host

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Phytopathology 103(Suppl. 1):S1.9

Puccinia arachidis Speg is the causal agent of peanut rust, an important foliar disease of peanut in mainly low input peanut (*Arachis hypogaea*) producing countries with warm, tropical climates. Management of this disease in these countries is best realized through host resistance. Knowledge on the variability of the *P. arachidis* populations and the genetics of resistance to peanut rust should help us to effectively breed for stable resistance and thus effectively manage the peanut rust disease on the long run. Our objective was to determine the genetic polymorphism of *P. arachidis* and its peanut host. We evaluated sequences of the 5.8S-ITS2-28S region of *P. arachidis* isolates, collected from different regions in North America, South America, Central America and Asia, over different growing seasons. Preliminary results from the sequenced ITS region of the *P. arachidis* isolates do not indicate high genetic variability among the populations studied. To our knowledge, no information on the population structure of *P. arachidis* has been published. We furthermore characterized a selection of cultivated peanut genotypes, consisting of newly developed CRSP breeding lines, plant introductions and commonly grown cultivars, using SSR markers, previously identified as being able to detect high levels of polymorphism in peanut genotypes. The SSR markers used detected polymorphisms, however, none were able to distinguish resistant from susceptible peanut genotypes. These results will be presented and discussed.

Sensitivity of *Cercospora kikuchii* populations to quinone outside inhibitor, demethylation inhibitor, and methyl benzamidazole carbamate fungicides

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Phytopathology 103(Suppl. 1):S1.9

Purple seed stain and *Cercospora* leaf blight, caused by *Cercospora kikuchii*, are major diseases of soybean worldwide and have become increasingly difficult to manage in Louisiana. Therefore, to determine if resistance to fungicides has occurred in *C. kikuchii*, evaluations were conducted using Louisiana populations from 2000, 2011, and 2012. Baseline fungicide sensitivities, as determined by calculating EC50 values from radial growth assays, of *C. kikuchii* isolates from 2000 were determined for quinone outside inhibitor (QoI) and demethylation inhibitor (DMI) fungicides. This population had not been exposed to QoI and DMI fungicides. Fungicide sensitivities were then calculated to monitor sensitivity shifts in 2011 and 2012 populations. Because isolates were either sensitive or resistant to thiophanate-methyl, a MBC fungicide, a discriminatory dose of 5 µg/ml was used to determine the percentages of resistant isolates for 2000, 2011, and 2012. Baseline sensitivities to the QoI fungicides: azoxystrobin, pyraclostrobin, and trifloxystrobin averaged 0.10, 0.02, and 0.02 µg/ml, respectively. Mean EC50 values for the 2011 population subjected to QoI fungicides were significantly higher at 70.49, 10.06, and 22.72 µg/ml, respectively. Baseline sensitivities to the DMI fungicides: flutriafol, tetraconazole, and propiconazole averaged 0.45, 1.66, and 0.18 µg/ml, respectively. DMI sensitivities for isolates from 2011 were essentially unchanged at 0.40, 0.96, and 0.41 µg/ml, respectively. For thiophanate-methyl, the frequencies of resistant isolates from the years 2000 and 2011 were 23.3 and 44.8 percent, respectively. Results for QoI, DMI, and MBC sensitivities for 2012 are being summarized. Based on these results, fungicide resistance has occurred in *C. kikuchii* since 2000.

Disease progression in response to the necrotrophic fungal pathogen, *Phoma medicaginis* on *Medicago truncatula* accessions differing in levels of triterpene saponins

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Phytopathology 103(Suppl. 1):S1.9

Plants produce multiple secondary metabolites that can negatively impact invading pathogens or other pests. Saponins are amphipathic glycosides found in many plant species and have been associated with a number of activities including protection from pathogen and herbivore pests. Though saponins are found in numerous plant species, triterpene saponins are found primarily in dicotyledons, including legumes. The objective of this research was to determine if accessions of *Medicago truncatula* Gaertn. with dissimilar levels of saponins differ in susceptibility to the necrotrophic fungal pathogen *Phoma medicaginis*. Four accessions of *M. truncatula* (A17, GRC43, ESP105, and PRT178) were inoculated with *P. medicaginis* and subsequently rated for disease susceptibility. Accessions A17 and GRC43 each have relatively high levels of foliar saponins, whereas accessions ESP105 and PRT178 have low levels. To date, it appears that susceptibility to *P. medicaginis* in the *M. truncatula* accessions that were tested does not correlate strictly with saponin concentrations; this is possibly due to additional differences in the genetic backgrounds of these plant accessions. To further evaluate the interaction of *M. truncatula* and the pathogen, *P. medicaginis* was transformed via *Agrobacterium*-mediated transformation to overexpress a gene encoding green fluorescent protein (GFP). Transgenic isolates will be used to visually assess the infection process on leaves and how it differs between plant lines. In addition, we are evaluating plant susceptibility to both aphids and nematodes on these same accessions. More refined tests using plants of similar backgrounds will be necessary to definitively determine the role of saponins in this host-pathogen system; however, the current approach will provide a valuable preliminary description of the interaction among these plant accessions and multiple plant pests.

Efficacy of seed treatments on soybean stand and yield across environments in Arkansas

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Phytopathology 103(Suppl. 1):S1.9

The effects of seed treatments and planting dates on soybean stand and yield were determined at three locations in Arkansas from 2009 to 2011. Nine fungicide seed treatments, some including an insecticide, and an untreated check were evaluated in a total of 25 trials. Plots were established in April, May and June with a planting density of 170,000 to 215,000 seed/ha and a row spacing of 76 to 91 cm in four row plots. All of the emerged plants in the center two rows of each plot were counted two and four weeks after planting and yields were taken. Seed treatments had significantly higher stands than the control in 32% of the trials with positive responses occurring across locations and planting dates. Significant increases in yield with seed treatments compared to the control occurred in 16% of the trials across locations and planting dates. Metalaxyl alone, specific for *Pythium* spp., significantly increased stands over the control in two tests. Fludioxonil alone improved stands in six tests and yields in two tests. Fludioxonil plus mefenoxyim with or without azoxystrobin or thiamethoxam significantly improved stands over the control in seven trials and yields in four trials. Trifloxystrobin plus metalaxyl with or without imidacloprid resulted in significantly greater stands than the control in six tests and greater yields in four tests. PCNB plus carboxin, specific for *Rhizoctonia solani*, improved stands over the control in four trials and yields in two trials. When significant, yields were 12 to 86% greater than the control.

Suppression of sheath blight development in rice and sclerotia germination of *Rhizoctonia solani* by rice-associated strains of *Bacillus* spp.

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Phytopathology 103(Suppl. 1):S1.9

Sheath blight of rice, caused by the fungus *Rhizoctonia solani*, is an economically important rice disease that is occurring throughout the rice-producing areas in the world, including the southern United States. Significant losses in grain quality and yield may occur in severely infected rice fields. Despite its economic importance, there are no completely resistant rice cultivars against this fungal rice disease and control methods for sheath blight are limited to heavy usage of fungicides. Only a few fungicides can effectively control this disease and heavy usage may cause negative impacts on agroecosystems. The use of biological agents may provide an alternative control method for sheath blight in rice. In our previous study, some rice-associated bacteria isolated from various rice cultivars in the field were found

to have antifungal activities against *R. solani* *in vitro*. All of these rice-associated bacteria were identified as *Bacillus* spp. based on 16S rDNA sequence analyses. In this study, the antifungal strains of rice-associated *Bacillus* spp. tested effectively suppressed sheath blight symptom development under both greenhouse and field conditions when they were applied 24 hours prior to a challenge inoculation with *R. solani*. These strains also suppressed sheath blight lesion development and sclerotia germination in a detached leaf assay and a sclerotia germination assay, respectively. These results suggest that these rice-associated bacteria have potential as a future biological control agent against sheath blight.

***Rhizoctonia solani* AG11: Spatial analyses reveal strategies of a successful parasite**

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Phytopathology 103(Suppl. 1):S1.10

Rhizoctonia solani AG11 is the most populous *Rhizoctonia* spp. in fields undergoing rice and soybean rotations in Arkansas. Evidence suggests it is weakly pathogenic on rice and soybean and the fungus is isolated frequently from plant material. The objective of this work was to determine the spatial distribution of *Rhizoctonia* spp. in fields undergoing rice and soybean rotations. A modified toothpick baiting procedure was used to isolate *Rhizoctonia* spp. from soil samples, 5 samples per position, from three fields with 98, 97, and 96 positions intermittent of the rice levee system. Soybean plants were sampled, 10 plants per position, from each of the three fields at V3. *Rhizoctonia* spp. were isolated using selective media and grouped according to like morphology and quantified by position. In three fields near Hazen, AR, populations of *R. solani* AG11 demonstrated spatial aggregation. Isolates recovered from soybean plants correlated spatially to the driest areas of the fields ($P = 0.002$, $P = 0.077$, $P = 0.011$) demonstrating soil environment influenced colonization. The distribution of higher soil populations in one field were at lower elevation ($P = 0.002$) and higher eluted organic matter ($P = 0.073$) about the GPS positions. In 2012, stands were reduced in the lower areas of the fields. A soybean stand assay using the soil samples from GPS positions of one field indicated *Pythium* spp. caused seedling disease and higher populations of *R. solani* AG11 correlated spatially to less seedling disease and improved stand ($P = 0.0007$). Spatial studies will aid in understanding the complexity of factors determining populations of microflora and disease development in ecosystems. This potentially leads to management that favors naturally occurring suppressive soils and serves to lower inputs by the farmer.

The effects of salinity on *Pythium* seed and root rots of soybean

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Phytopathology 103(Suppl. 1):S1.10

Increasing salinity is an important factor limiting agricultural productivity worldwide. In addition to direct effects on plant growth and yield, plants grown under saline conditions may become more susceptible to biotic and other environmental stresses. *Pythium* species are important soilborne seedling pathogens of soybean. Studies have suggested that salinity increases severity of *Pythium* damping-off and root rots. The objective of this study was to determine the effects of salinity on virulence of selected *Pythium* spp. on soybean cultivars which differ in chloride tolerance. Plants were grown from seed for 21 days in controlled environments. Soil was treated with a calcium chloride solution to create a range of electrical conductivity levels in noninfested soil and soil infested with *Pythium* species which differ in virulence and reproductive strategies. The goal of this research was to establish and characterize the impact of increasing salinity levels on diseases associated with *Pythium* spp. Plant stand and weight decreased with increasing salinity. Stands and plant weight reductions were generally additive with increasing salinity and the presence of *Pythium*. However for some isolates, disease increased more at moderate relative to low salinity levels. Experiments are being conducted to determine whether this effect is due to soybean plant response to infection or effects on the pathogen. There was no apparent difference between chloride includers and excluders for seedlings.

Diversity of fungal and bacterial communities in tip/end rot diseased sweetpotatoes

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Phytopathology 103(Suppl. 1):S1.10

The microbial community present in tip/end rot diseased sweetpotatoes is comprised of several dominant species, with a diverse group of less-frequently occurring microorganisms. Species richness and diversity values across sampling dates or growth stages (including storage) varied for both bacteria and fungi. Diversity, evenness and community coefficient values will also be discussed for the overall data. *Bacillus* spp., *Lysobacter enzymogenes*, and *Paenibacillus lentimorbus* accounted for more than 50% of total bacteria identifications. Average densities for the three most dominant species had twice the population values than all other bacterial isolates. Some of these species could be used as biological controls, such as *Bacillus cereus*, used in the control of fungal diseases in crops and nematode control, or *P. lentimorbus* which may help manage early blight of tomato by inhibiting *Alternaria solani*. The most commonly occurring potentially pathogenic fungi were *Macrophomina phaseolina*, four species of *Aspergillus*, and three species of *Trichoderma*. Over 10 species of *Fusarium* were identified but two potentially pathogenic isolates were identified as *F. oxysporum* and *F. solani*. The latter species accounted for nearly 70% of the isolates from early season samples originating from seed stock and bedding plants. Post-harvest samples showed differences in relative abundance of the dominant species, with *M. phaseolina* increasing to an average of 6.5% in samples originating from storage, and important *Fusarium* spp. decreasing to an average of 27% between 60 and 90 days post-harvest. Select species collected were evaluated for their pathogenicity potential during the current investigation.

Reaction of selected rice cultivars to infection by *Ustilaginoidea virens*

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Phytopathology 103(Suppl. 1):S1.10

False smut, caused by *Ustilaginoidea virens*, was discovered in Arkansas in 1997. The disease is normally identified by the presence of orange and black sori (= spore balls, pseudomorphs) that appear on panicles. The fungus is both seed borne and soil borne and the erratic nature of the disease on many cultivars has hampered development of effective management strategies for this disease. We conducted two field experiments at research stations near Newport and Pine Tree, Arkansas in which 12 selected cultivars were planted in replicated plots to investigate the reaction of selected cultivars to infection by *U. virens*. We determined the number of infected panicles per sq. meter (incidence) and the number of sori per panicle (severity) at harvest for each cultivar. We then compared the severity and incidence of sori on panicles of all 12 cultivars at each location and across locations. The comparisons show that false smut appeared to be significantly less severe on 'Katy', 'Kaybonnet', 'Jes' and 'Jupiter' than on the other cultivars in these tests. Furthermore, disease severity was greater on most cultivars at Newport than at Pine Tree. With additional study, the statistically significant differences in reaction to infection by *Ustilaginoidea virens* among the cultivars across locations may offer another strategy to help manage this emerging disease of rice in Arkansas.

Optimum temperatures for mycelial growth, sclerotial germination, and colonization of peanut leaves by *Sclerotium rolfsii*

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Phytopathology 103(Suppl. 1):S1.10

The effects of temperature on growth and development of *S. rolfsii* were explored relative to recent unusual occurrences of peanut (*Arachis hypogaea*) stem rot early in the season. Experiments were established on thermogradient tables with 24 temperatures between 14 and 34 C. The optimal temperature for mycelial growth of 3 isolates from peanut was 29 to 30 C. The optimal temperatures for sclerotial germination were from 31 to 33C for 2 isolates, and slightly lower for the third. Colonization of excised leaves by *S. rolfsii* was also evaluated on three peanut cultivars (GA-06G, Bailey and GA-09B) with different levels of susceptibility to stem rot in the field. The optimal temperature for colonization was 25 to 30 C with little difference among cultivars.

Identification of ectotrophic root-infecting fungi in association with ultradwarf bermudagrass (*Cynodon dactylon* × *C. transvaalensis*)

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Phytopathology 103(Suppl. 1):S1.10

The growth and quality of bermudagrass putting greens decline during the summer and early fall months in the Deep South. Root systems appear blackened, rotted, or stunted and are frequently colonized with dark, runner hyphae that are characteristic of ectotrophic root-infecting (ERI) fungi. The focus of this study was to isolate and identify ERI fungi from ultradwarf bermudagrass roots. Colonized roots were cut into 1-cm sections, surface

disinfested with a 0.6% NaOCl solution, rinsed three consecutive times with sterile-distilled water, plated on modified potato dextrose agar (PDA), and incubated for 7 days at room temperature under 24 hour fluorescent light. Hyphal tips were transferred to PDA. Genomic DNA was extracted from sterile, pure cultures of isolated fungi. The internal transcribed spacer (ITS) regions of rDNA were amplified by PCR using ITS1 and ITS4 primers. The Basic Local Alignment Search Tool (BLAST) was utilized to compare ITS regions of the unknown Mississippi State University (MSU) isolates to known ITS sequences retrieved from the National Center for Biotechnology Information (NCBI) GenBank. Evolutionary analyses of rDNA-ITS regions were performed with Molecular Evolutionary Genetics Analysis (MEGA5) software. Phylogenetic relationships suggest MSU isolates are closely related to turfgrass root pathogens of the genera *Ophiosphaerella* and *Gaeumannomyces*, but share greatest lineage with *Magnaporthe* spp.

Effects of minor element nutrition on *Cercospora* leaf blight of soybean

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Phytopathology 103(Suppl. 1):S1.11

Cercospora kikuchii is the causal agent of both *Cercospora* leaf blight (CLB) and purple seed stain in soybean. CLB is considered to be the most serious disease of soybean in Louisiana. CLB appears late in the season and is currently managed through early planting and fungicides. Several minor elements at different rates were tested as foliar sprays on field grown soybeans and evaluated based on visual disease ratings. Elements also were tested *in vitro* for their effects on radial growth and pigment production by multiple isolates of *C. kikuchii*. The concentrations of elements used in these tests were chosen based on published tissue analyses and on recommended rates of application for correcting minor element deficiencies in soybean. The isolates were grown under conditions conducive for synthesis of cercosporin; the photoactivated toxin produced by *C. kikuchii*. Growth rates and pigment production of the isolates were recorded at 7 and 14 days after plating. Of particular interest were the elements aluminum and iron for their inhibitory effects on fungal growth and cercosporin production and manganese for its exacerbation of disease in the field.

Evaluation of flutriafol for efficacy towards cotton and peanut diseases in Texas

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Phytopathology 103(Suppl. 1):S1.11

Cotton (*Gossypium hirsutum* L.) and peanut (*Arachis hypogaea* L.) are economically important crops in west Texas. Various diseases pose challenges to producers throughout the region. While several fungicides are registered in peanut for management of peanut diseases, few products are available in

cotton. Field studies were conducted from 2008–2010 to evaluate the efficacy of the fungicide flutriafol (0.063 to 0.252 kg a.i. ha⁻¹) for management of early leaf spot (*Cercospora arachidicola*) and late leaf spot (*Cercosporidium personatum*) in peanut. All rates reduced leaf spot incidence compared to the non-treated control with the 0.126 and 0.252 kg a.i. ha⁻¹ rates performing similarly to tebuconazole (0.022 kg a.i. ha⁻¹) the commercial standard. Yields were similar among all treatments in 2008 and 2009; however, use of flutriafol at the two higher rates increased yields by 623 and 121 kg ha⁻¹ over the non-treated control and tebuconazole standard, respectively. Additional studies were conducted in 2012 to evaluate the effect of at plant in-furrow applications of flutriafol on Fusarium wilt (*Fusarium oxysporum* f. sp. *vasinfectum*), root rot (*Phymatotrichopsis omnivora*) and Verticillium wilt (*Verticillium dahliae*) in cotton. Flutriafol had no effect on incidence of Fusarium wilt or yield. No differences in disease incidence were observed among treatments for Verticillium wilt under low pressure; however, cotton yields were higher (~84 kg ha⁻¹) in plots treated with flutriafol at 0.144 or 0.216 kg a.i. ha⁻¹. Applications of flutriafol at 0.144, 0.216 and 0.288 kg a.i. ha⁻¹ reduced incidence of cotton root rot by 71.4, 79.6 and 85.7%, respectively, when compared to the non-treated control. Corresponding yield increases of 269, 374 and 432 kg ha⁻¹ were observed. Based upon these studies, applications of flutriafol can be used in the management of early and late leaf spot of peanut, as well as root rot in cotton; however, additional studies are needed regarding Fusarium and Verticillium wilt.

Understanding soybean vein necrosis disease: Implications of vectors and alternative hosts

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Phytopathology 103(Suppl. 1):S1.11

Soybean vein necrosis associated virus (SVNaV) has been found widely spread in North America. SVNaV has typical tospovirus genome organization and shares minimal similarity with members of the genus, making it a distinct member of the group. Transmission experiments with the soybean thrips (*Sericothrips variabilis*) provided evidence that SVNaV is the causal agent of soybean vein necrosis disease (SVND) and was thus renamed to soybean vein necrosis virus (SVNV). The identification of soybean thrips as the natural vector of SVNV provides for the first time experimental evidence that this common pest in agriculture is capable of transmitting a virus. The high SVNV transmission efficiency with soybean thrips signifies the critical role of this species in disease epidemics. Given that two legume species other than soybean can sustain virus replication and soybean thrips are one of the major species infesting legume fields in the South Central U.S., it is highly possible the virus can be spread further away through the vector and consequently cause more diseases in other legumes. A proper control strategy of soybean thrips is therefore needed to reduce the SVND pressure.