2016 Southern Division Meeting Abstracts

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Dissemination of novel ectotrophic root-infecting fungi associated with bermudagrass via vegetative propagation from sod production in the Southeast

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Gaeumannomyces graminis var. *graminis* (Ggg) is an ectotrophic root-infecting (ERI) fungus characterized by presence of runner hyphae and hyphopodia on the outer surface of roots and stolons. Ggg is considered to be the primary causal agent of bermudagrass decline; however, six novel species of ERI fungi associated with bermudagrass decline have recently been identified. Of those, *G. paulograminis* was morphologically and molecularly distinct from Ggg. A concern for golf course superintendents is how these pathogens disseminate since vegetative propagation is the sole source of 'MiniVerde', 'TifEagle', and 'Champion' cultivars. Sod of these cultivars were obtained from sod farms in the southeastern U.S. Soil was washed from roots of sod samples which were shredded into sprigs and planted into sterile sand in 7.6 cm diameter containers. Each treatment (Cultivar/origin) had ten replicates maintained in a growth chamber at 30°C and 12 hr light cycle and watered to prevent desiccation. After 8 weeks, all plants were examined for signs of ERI fungi. Colonized plant material was surface disinfested and plated onto water agar. Hyphal tips were transferred to potato dextrose agar. Genomic DNA was extracted from colonies for identification based on the internal transcribed spacer region. The ERI fungus typically identified as Ggg based on hyphopodia was an identical match to *G. paulograminis* originating from MiniVerde and Champion cultivars from two different states.

Identification of quantitative trait loci and molecular markers for resistance to *Colletotrichum* crown rot in strawberry

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Colletotrichum crown rot (CCR) caused by *Colletotrichum gloeosporioides* is one of the most common and detrimental diseases on strawberry farms in subtropical regions, causing crown tissue necrosis and plant collapse, with no available fungicide with curative effects. Currently, strawberry cultivars grown in the U.S. have little resistance to CCR. In order to improve genetic resistance to CCR in the breeding germplasm at the University of Florida, it is critical to identify all genetic loci associated with CCR resistance. Genetic studies conducted during the 2013-2014 season evaluated a multi-family quantitative trait loci (QTL) discovery population for CCR resistance. Using whole-genome SNP genotyping (Affymetrix iStraw90 Axiom® SNP array) and pedigree-based marker-trait association analysis (FlexQTL™), two genomic regions (Cg1 and Cg2) conferring resistance to CCR were identified. To confirm and more precisely locate Cg1, a population was developed by crossing five resistant accessions predicted to be heterozygous at Cg1 with five susceptible accessions. A total of 248 clonally replicated individuals from the five full-sib families were planted in the experimental field at the Gulf Coast Research and Education Center (GCREC) in early October, 2015 and mortality is being rated weekly. The area under the disease progress curve (AUDPC) will be calculated for each individual at the conclusion of the fruiting season and utilized for the QTL detection/validation. DNA was extracted from each individual in the population and submitted for whole-genome SNP genotyping. We will further develop SNP-based high-resolution melting (HRM) and simple sequence repeat (SSR) markers in the Cg1 region. If successful, high-throughput markers will facilitate marker-assisted selection for CCR resistance in the UF strawberry breeding program.

Influence of ontogenic resistance, environment and timing of fungicide applications on development of powdery mildew on strawberries

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Powdery mildew, caused by *Podosphaera aphanis*, is an economically important disease of strawberry. Timing to start fungicide applications was evaluated in an experiment conducted in December and January under a high plastic tunnel in Wimauma, Florida. Alternate applications of Quintec and Torino following a grower-standard calendar or post-symptoms were effective in reducing powdery mildew severity. Sulphur was not effective. In another experiment, the number of susceptible and resistant leaves were counted in two plants per plot, for two cultivars, Festival and Sensation, under two environments, high tunnel and open field. Susceptible leaves were produced weekly on both cultivars throughout the whole season, however, Festival showed lower number of susceptible leaves and lower disease severity compared to Sensation. Disease severity was higher in the tunnel than in the open field. Rain events higher than 2.5mm reduced disease severity in the open field.

Monitoring and increasing awareness for Rose Rosette Disease in Texas

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Rose Rosette Disease has become an increasingly damaging problem for roses in the North Texas region (Dallas-Fort Worth metroplex). This disease is caused by the Rose Rosette Virus (RRV), an Emaravirus, which is transmitted by the eriophyid mite *Phyllocoptes fructiphilus*. This disease has become a major economic issue for the rose and landscape industry. In this survey, resulting observations suggest that disease symptomology varies with cultivar/variety. In 2015, 77 rose samples were tested for rose rosette at the Texas Plant Disease Diagnostic Laboratory in College Station, TX. Using a quantitative polymerase chain reaction (PCR) assay to detect the virus, 44 out of the 77 tested positive for RRV. Of these, 21 were new observations on cultivars that had not been previously detected in Texas. One of our efforts is to monitor the incidence and spread of Rose Rosette Disease in Texas. Certain criteria are used to allow for the differentiation of transmitted disease (by mite vector) versus translocated (by infected plants). Another effort to help alleviate the effects of Rose Rosette Disease is to promote awareness and education, and recruiting a cadre of volunteers to help monitor the extent, distribution and spread of this disease.

Determining whether fitness costs are associated with QoI-resistant isolates of the frogeye leaf spot pathogen

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Frogeye leaf spot, caused by *Cercospora sojina* Hara, is a foliar disease of soybean. Resistance to quinone outside inhibitor (QoI) fungicides was reported in Mississippi. The stability of fungicide resistance in fungal populations is dependent upon the fitness of the resistant members within the population. The objective of this study was to determine whether fitness costs are associated with QoI-resistant isolates of *C. sojina*. Fitness measurements of colony growth (CG), conidia production (CP), and conidia germination (CGerm) were determined for 24 *C. sojina* isolates, 13 QoI-resistant and 11 QoI-sensitive isolates, from MS. Cultures were grown in a growth chamber at 25°C with a 12-h photo-period or in an incubator at 17, 25, and 32°C in the dark. CG was measured for all isolates following a 14-day incubation on potato dextrose agar in the growth and incubation chambers. CP was determined for all isolates incubated 14 days on soybean stem-lima bean agar (SSLBA) or water agar (WA) in the growth chamber. Conidial suspensions of each isolate were deposited onto WA and incubated in the dark for 18 h before observing and quantifying CGerm. Fitness measurements were taken from the mother-plate and tenth subculture of each isolate. No differences in CG at 17 and 25°C (dark), CP on WA, or CGerm were observed. CG at 32°C of QoI-resistant isolates was significantly reduced compared to QoI-sensitive isolates; however, CP on SSLBA was significantly greater for QoI-resistant isolates.

Fungicides for improving the success of micropropagation of azaleas native to Alabama

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Micropropagation, often confused with 'tissue culture', is a technique for producing clones of desirable plants under sterile conditions. Unfortunately plants selected from landscapes for micropropagation are frequently infested with fungi. Our objective was to evaluate fungicides for eliminating this fungal infestation in order to improve the survival of shoot tip cuttings used for micropropagation. We used a modified woody plant medium (Economou and Read, 1984) for micropropagating azaleas (*Rhododendron* spp.) that are native to Alabama. This medium was amended with fungicides, including benomyl, tebuconazole, and propiconazole. At least four shoot tips from each of two azaleas ('PK Caly' and '1st Pink') were placed on fungicide- and non-amended media. After 19 days, the highest survival of plantlets (50%) was seen with benomyl-amended medium. The survival rate on propiconazole-amended medium was 22%, which is almost double the survival (13%) on non-amended medium. These results suggest that fungicides added to medium can increase the success rate for establishing plant cultures for micropropagation with native azaleas.

Influence of application technology on foliar fungicide efficacy in *Cercospora sojina* infected soybean

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Introduction of new herbicide tolerant crops require growers to use drift-reducing nozzle technology that produces very-coarse to ultra-coarse droplets. Due to the frequency of tank-mixed pesticide applications and the cost associated with utilizing drift-reduction technology, these changes could also affect other foliar pesticides. Soybean infected with *Cercospora sojina*, the causal agent of frogeye leaf spot (FLS), could be negatively impacted by reductions in spray coverage associated with coarser droplets. Field experiments were conducted in Jackson and Milan, Tennessee in 2014-2015 to evaluate the influence of droplet size on foliar fungicide efficacy in soybean infected with FLS. A premix of azoxystrobin and difenoconazole was applied through 3 spray nozzles with varying droplet size volume median diameters. Visual ratings were taken at 14 and 28 days after application (DAA). Leaf tissues samples were collected 0, 2, 4, 7 and 14 DAA for azoxystrobin quantification analyzed using HPLC-MS. FLS isolates were collected from each trial location and characterized as resistant or sensitive using RT qPCR. EC50 values were determined for FLS isolates to analyze levels of control at each leaf sampling date in comparison to azoxystrobin quantification. Results suggest that drift-reduction nozzle technology may not negatively affect fungicide efficacy on FLS in soybean.

Biocontrol of two *Streptomyces* spp. strains against lettuce basal drop caused by *Sclerotinia sclerotiorum*

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Relatively little is known about the activities and mechanisms of *Streptomyces* spp. as biological control agents (BCAs) on plants. Two *Streptomyces* isolates, *S. exfoliatus* FT05W and *S. cyaneus* ZEA17I, were found able to inhibit mycelial growth of *Sclerotinia sclerotiorum*, the causal agent of lettuce drop, up 75% *in vitro*. Colonization of host by potential BCAs plays a fundamental role in microbial assisted biocontrol. Therefore, we labeled them with the enhanced GFP (EGFP) marker to investigate their rhizosphere competence and ability to colonize the lettuce roots using confocal laser scanning microscopy (CLSM). The abundant colonization of young lettuce seedling root by both strains demonstrated *Streptomyces*' capability to interact with the host from early stages of seed germination and root development. Meanwhile, the two strains were detected also on two-week-old roots indicating their potential of long-term interactions with lettuce. Moreover, we observed their viability and persistence in the rhizosphere and in surface sterilized lettuce root tissues up to six weeks by quantifying their population dynamics. Finally, we studied the biocontrol activity of the two strains against *S. sclerotiorum* *in vivo*. When they were applied to *S. sclerotiorum* inoculated substrate in growth chamber, *S. exfoliatus* FT05W and *S. cyaneus* ZEA17I significantly reduced disease incidence by 40% and 50%, respectively, compared to the control. Interestingly, under field conditions, *S. exfoliatus* FT05W reduced disease incidence by 54%, but we did not observe protection of lettuce plants against *S. sclerotiorum* by *S. cyaneus* ZEA17I.

Distribution of *Candidatus Liberibacter asiaticus* within bark tissue of mature infected citrus trees

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Huanglongbing (HLB; syn. citrus greening) is a citrus disease caused by the vector-transmitted, phloem-limited bacterium *Candidatus Liberibacter asiaticus* (Las). HLB leads to a decrease in tree productivity; causing premature fruit drop, poor fruit quality, and shortened tree lifespan. With no known cure, HLB poses a great threat to citrus industries around the world. Much of current research is focused on treatments to eliminate or reduce Las populations in the tree. Previous research investigated Las distributions within younger greenhouse grown trees. To understand the effectiveness of treatments, it is essential to understand the distribution of infection in mature field trees and how populations of Las vary within the same tree. Bark tissue was used because the phloem in bark is more difficult to reach with bactericides or thermotherapy. Bark samples were collected at the graft union and at standard intervals in the canopy above and root system below. Soil DNA extraction kits were found to more reliably remove qPCR inhibitors from bark than plant kits. The highest populations of Las resided in the small diameter branches and canopy tissue of the sampled trees, while populations decreased by 2-3 logs in the larger diameter trunk, graft union, and upper root zone. There are several possible explanations for the distinct concentration pattern found in the infected trees that could assist in identifying and improving methods of control for HLB.

Characterization of the genetic diversity of *Puccinia emaculata* field isolates collected from switchgrass populations

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Switchgrass (*Panicum virgatum*) is a perennial C4 grass that was previously used for field coverage and forage. The Department of Energy (DOE) selected switchgrass as a model herbaceous bioenergy crop due to its high biomass yield potential and its ability to be cultivated on marginal lands with low nutrient and water inputs. Currently, switchgrass is not planted in monoculture. As a bioenergy crop, switchgrass will need to be grown on large acreages for many years. It is, therefore, important to utilize switchgrass varieties that are resistant to pathogen attack. *Puccinia emaculata* is one of the most widespread foliar pathogens found on switchgrass varieties, and the genetic variation of this pathogen is not well understood. Therefore, a comprehensive analysis of pathogen variation, pathogenicity, and genetic diversity is needed. This project has three major research objectives: 1) identify *P. emaculata* rust races within field isolates collected from cultivated switchgrass genotypes from across the US, 2) analyze the genetic diversity of *P. emaculata* rust present within and across field isolates, and 3) assess the virulence pattern of the set of diverse *P. emaculata* monospore isolates. *P. emaculata* field isolates were collected from symptomatic switchgrass genotypes from fields in eight states (Alabama, Georgia, North Carolina, Oklahoma, Tennessee, Texas, Virginia, and Wisconsin). To determine the general composition and diversity of *P. emaculata*, an internal transcribed spacer (ITS) primer pair was used to amplify DNA isolated from the *P. emaculata* field isolates collected from the eight states. The resulting 1.2 kb PCR product was cloned. Fifty-seven clones were sequenced and used for phylogenetic tree construction. Phylogenetic analysis indicated that there is low genetic diversity among the *P. emaculata* field isolates collected from cultivated switchgrass genotypes from the eight states.

***Xylella fastidiosa* in rabbiteye blueberry in Louisiana is genetically similar to a strain found in Southern highbush blueberry in Georgia**

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During the past ten years, *Xylella fastidiosa* has been confirmed as a pathogen of Southern highbush blueberry (*Vaccinium corymbosum* interspecific hybrids) in Georgia and Florida. Recent work in Louisiana has shown that it is also associated with reduced yield and altered fruit quality in 'Tifblue' rabbiteye blueberry (*Vaccinium ashei* = *V. virgatum*). Seven loci of the *X. fastidiosa* genome (*cysG*, *gltT*, *holC*, *leuA*, *malF*, *nuoL*, and *petC*) were sequenced from *X. fastidiosa*-infected rabbiteye blueberry leaf (petiole and midrib) tissue, in order to characterize the infecting bacteria using multilocus sequence typing (MLST). A comparison of sequences from rabbiteye blueberry tissue to allele sequences from an MLST database of *X. fastidiosa* isolates, along with published information about sequence types identified in various plant hosts, suggests that the strain associated with yield loss in a rabbiteye blueberry orchard in Louisiana is similar to isolates from blueberry in Georgia as well as isolates from both giant ragweed (*Ambrosia trifida*) and western soapberry (*Sapindus saponaria*) in Texas. This preliminary finding suggests that rabbiteye and Southern highbush blueberries and certain wild plants may act as alternative hosts of the same strain of *X. fastidiosa*. Additional work is being done to characterize *X. fastidiosa* found in wild plants surrounding a blueberry orchard, as well as in other rabbiteye blueberry plants.

Influence of interrupted wetness periods on anthracnose fruit rot of strawberry

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Anthracnose Fruit Rot (AFR), caused by *Colletotrichum acutatum*, is a major disease in Florida and the Southeastern of the United States. The Strawberry Advisory System (SAS), a web-based support system, was developed to provide recommendations on timing fungicide applications based on temperature and continuous leaf wetness duration. The purpose of this study was to evaluate the influence of interrupted wetness periods on AFR development. *C. acutatum* inoculated plants were subjected to continuous or interrupted wetness periods at 25°C. Continuous wetness periods consisted of 24h of wetness, whereas interrupted had initial wetness periods of 8 or 12h, followed by a dry period of 0, 2, 4, 6, or 8h (only for the 12h treatment). After the dry period, plants were exposed to additional wetness periods of 16 or 12h. Disease incidence was evaluated 9 days after inoculation. Initial wetness periods had significant impact on AFR development and disease incidence was lower in plants given an 8-h initial wet period than those exposed to 12h of wetness. Periods of 4h or more of interrupted wetness reduced fruit disease incidence when compared to 24h of continuous wetness.

Comparative transcriptome analyses of *Aspergillus flavus* isolates under different oxidative stresses and culture media

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Aspergillus flavus and aflatoxin contamination in the field are known to be influenced by numerous stress factors, particularly drought and heat stress. However, the purpose of aflatoxin production is unknown. Here, we report transcriptome analyses comprised of 282.6 Gb of sequencing data describing 11,144 of 13,487 (82.6%) annotated *A. flavus* genes which provides gene expression comparisons among different *A. flavus* isolates and between two culture media, aflatoxin conducive (sucrose) and non-conducive (peptone). We also identified genes that are differentially expressed (DEGs) in response to oxidative stress in media amended with H₂O₂. Isolates tolerating greater levels of oxidative stress exhibited fewer DEGs in comparison to those with less tolerance ($r \leq -0.6$). We found that proteolytic genes were more expressed in the non-conducive medium, while carbohydrate catabolic and glucose transporter genes (e.g. MFS transporters) were more expressed in the conducive medium. Among the observed DEGs, components of polyketide (aflatoxin) and isoprenoid (aflatem) secondary metabolite production along with kojic acid biosynthesis and monooxygenase genes were also prevalent. To our knowledge, this is the first study that explores the molecular responses of different *A. flavus* isolates to H₂O₂-induced stress in different culture media. Together, these results demonstrate a potential key role for secondary metabolite production in *A. flavus* oxidative stress responses.

Population dynamics of *Belonolaimus longicaudatus* in Central North Carolina

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The turfgrass industry in North Carolina is valued at an estimated \$4 billion dollars, and the grassy foundation it is built on is constantly under pathogen pressure. Sting nematode (*Belonolaimus longicaudatus*) is one of many damaging turf pathogens, but is problematic due to their high damage potential at very low numbers. Very little is known about sting nematode in North Carolina, nor how they handle the cold of the winter season. A better understanding of nematode population dynamics at cool climates will lead to more effective control. This study's objectives are to identify nematode population numbers over the year, and to understand the vertical distribution of the nematodes within a putting green soil column. Four golf courses in Central North Carolina were sampled monthly at three different depths. Nematode populations were consistent among the golf course as numbers ranged from 0-40 nematodes per 500cc soil during the winter and reached as high as 225 in the summer. Vertical distribution of the nematodes varied by golf course, with three out of four showing a majority of nematodes residing in the 0-10 cm depth. However, one golf course that uses unique cultural practices kept most of the nematode population between 10-20 cm, which is the extent of turfgrass rooting. This result suggests that cultural control can have a large impact on nematode location, and the potential for damage resulting from feeding.

Determination of a threshold for timing fungicide applications for control of postbloom fruit drop of citrus in Brazil

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Postbloom fruit drop (PFD) of citrus, caused by *Colletotrichum acutatum*, is controlled preventively in citrus orchards in Brazil, through calendar-based fungicide sprays during the flowering period. Although disease epidemics are frequent in citrus orchards, their intensity varies greatly each growing season, being extremely severe and causing significant yield losses when the flowering occurs during periods of frequent rainfall. Disease forecasting systems allow growers to time their sprays according to the most favorable periods for infection and avoid unnecessary sprays, thus reducing application costs and the selection pressure for resistant isolates of the pathogen. The objective of this study was to determine the action threshold for fungicide applications based on a model for conidial germination of *C. acutatum* that considers leaf wetness and temperature. Three action thresholds, 15%, 20% and 25% conidial germination, were compared to an untreated control and to a calendar-based application system in three experimental areas in the southwestern region of the state of São Paulo, in Brazil. According to our results, the best action threshold to trigger fungicide applications is at 20% conidial germination. A web-based forecasting system has been developed using this threshold and the number of sprays to control PFD was reduced by up to 66% when compared to the calendar-based application system, resulting in the same disease control.

An evaluation of peanut late leaf spot monocyclic components in the greenhouse

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Cultivated peanut (*Arachis hypogaea* L.) is an economically important crop that is produced in the United States and throughout the world. Cercosporidium personatum (Cp) causes late leaf spot (LLS) on cultivated peanut and can contribute to yield losses of up to 50% or even greater if LLS occurs with other diseases such as early leaf spot or rust. This study examined LLS monocyclic components of six lines (C1-6), including at least one genetically modified line that over-expresses chitinase. Plants were inoculated and lesions were evaluated on five leaves of each plant; lines were replicated five times. Few significant differences were noted. However, C2 tended to have the longest incubation period (IP, 13.8 days), while C4 had the shortest IP (9.0 days). At 42 days after inoculation, C3 had the fewest lesions (9.6), while C6 had the greatest number of lesions (30.4). Greatest defoliation was seen on both C5 and C6, while C1 had no defoliated leaflets. C6 had the largest lesions (1.16 mm diameter), while C3 had the smallest lesions (0.27 mm diameter). In order to maintain objectivity, tested lines were not identified, except for knowing that C6 is a commercially available cultivar.

***Pythium* species associated with root dysfunction of bermudagrass associated with sting nematode**

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Pythium root dysfunction is considered the major disease on bermudagrass in Florida based on the 2012 - 2015 data from the UF/IFAS Plant Diagnostic Center. According to previous research experience, bermudagrass infested with sting nematode (*Belonolaimus longicaudatus*) easily acquires *Pythium* root dysfunction. Root dysfunction of bermudagrass may be associated with both *Pythium* spp. and plant-parasitic nematodes. Bermudagrass samples from the UF/IFAS Nematode Assay Lab were used in our study. *Pythium* spp. were isolated from samples with high sting nematode population density (> 50 sting nematodes per 100 cm³ of soil). From these samples, *P. aristosporum* and *P. catenulatum* were identified using both morphological (oospores formation) and molecular methods (ITS1 and ITS4). Additional greenhouse experiments will be conducted to test the pathogenicity of these *Pythium* spp. on bermudagrass and their relationship with sting nematode on inducing bermudagrass root dysfunction.

Management of southern root-knot nematodes in soybeans using Telone® II soil fumigant

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Southern root-knot nematode (RKN), *Meloidogyne incognita*, can reduce soybean yields by 50% or more. Management strategies for this widespread pest include crop rotation, planting of resistant varieties where available and application of nematicides. Telone® II soil fumigant has played an important role in managing plant parasitic nematodes in a broad range of crops for over 50 years. Use rates are determined based on crop, soil types, application technology being employed, economics, and other variables. These studies were conducted to evaluate the use of Telone II to manage RKN when used in conjunction with soybean varieties with varying levels of RKN susceptibility in the mid-south. Results indicated that application of Telone II can increase yields 90% or more when applied prior to planting a RKN susceptible variety in infested fields. Telone II may also provide a benefit to growers planting moderately susceptible varieties, dependent largely on nematode populations, soil types and commodity prices.

Identification of genomic regions controlling resistance to aflatoxin contamination in a peanut recombinant inbred line population (Tifrunner × GT-C20)

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In peanut, limited genetic variation for disease resistance is available in breeding programs necessitating the identification of stable resistance sources for use in cultivar development. 'Tifrunner' is a runner cultivar while 'GT-C20' is a Spanish-type breeding line with resistance to aflatoxin contamination. We screened a RIL population generated from Tifrunner × GT-C20 for aflatoxin contamination resistance using a laboratory kernel screening assay. We scored visible fungal growth on kernels, and aflatoxin content using a fast methanol extraction method and a fluorometer (verified by TLC and ELISA). This phenotypic screening was repeated three times, each with three biological replicates. We found that surface sporulation ratings were normally distributed across the population. Aflatoxin levels varied among the RILs with a distribution skewed toward lower aflatoxin levels. Quantitative trait

locus (QTL) analysis for all replicates identified a total of 16 QTLs, five QTLs for aflatoxin contamination and eleven for fungal growth. Of these, five QTLs were major QTLs with more than 10% phenotypic variation explained (PVE). From these five major QTLs, one was found for aflatoxin contamination with 10.14% PVE, and three QTLs for the fungal growth (PVE = 13.23%, 11.21%, and 14.17%, respectively). These novel QTLs will be compared with recently released peanut diploid genome to identify putative resistance genes, and validated for potential applications in breeding.

Effect of planting date and peanut cultivar on leaf spot epidemics and pod yield with implications for organic production

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Choice of planting date can affect the risk of losses to early and late leaf spot caused by, *Cercospora arachidicola* and *Cercosporidium personatum*, respectively, of peanut, *Arachis hypogaea*, in both conventional and organic systems. The objective of this study was to characterize the effect of planting date on leaf spot epidemics and yield in new cultivars with moderate tolerance to these diseases. A field trial was conducted in 2015 in Tifton, GA. Treatments were six planting dates (24 and 27 April, 4, 11, 19, and May 26) arranged factorially with two cultivars, Georgia-06G and Georgia-12Y. Experimental design was a randomized complete block design with 4 replications. No foliar fungicides were applied. Late leaf spot was the predominant disease. Epidemics were severe in plots planted at the later dates. Final leaf spot ratings (Florida 1-10 scale) and AUDPC increased linearly with later planting date (Julian day) for both cultivars. Yield of Georgia-06G decreased linearly, and yield of Georgia-12Y decreased according to a quadratic function with later planting. For most planting dates, final leaf spot severity and AUDPC were lower and yield was higher for Georgia-12Y than for Georgia-06G. The combination of early planting with Georgia-12Y shows potential for minimizing risks of losses leaf spot and maximizing yield in situations such as organic production where fungicide would be minimal.

Application thresholds in controlling *Cercospora sojina*, the causal agent of frogeye leaf spot

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Soybean production has dramatically increased over the last decade throughout much of the Southeastern and Midwestern United States. Numerous diseases have impacted production, and many strategies have been implemented for their control. Foliar diseases have primarily been managed via variety selection and foliar fungicide applications. One such disease is frogeye leaf spot (FLS), caused by the fungus *Cercospora sojina*. Damage such as reduced photosynthetic area, loss of leaves, and pod necrosis has caused yield losses that have approached as much as 60%. Sequential fungicide applications of an azoxystrobin/difenoconazole premix were used to determine how best to manage FLS and determine if yields would be directly impacted by disease control. The field experiment was conducted during the cropping seasons of 2014-2015 at a total of 5 locations across West Tennessee. Two varieties were used, one susceptible and one resistant to FLS. A randomized complete block design was used with 10ft by 30ft 4 row plots and 4 replications. Applications were initiated at the beginning of reproduction and sequential applications were applied at 2-3 week intervals. Visual disease ratings were taken during the growing season using a percent area affected rating system. Yield was collected on the center two rows of each plot. Analyses indicate that variety selection and disease pressure dramatically influences the benefits of sequential applications in relationship to yield and disease control. Future management recommendations should consider variety response and on-site disease pressure. While sequential applications may not be warranted in all situations, they may be important in protecting and maintaining crop production goals.

Facilitation of innovation through technology

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Fungicide sensitivity assay on *Corynespora cassiicola* isolates from cotton

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Corynespora cassiicola, causal agent of target spot of cotton (*Gossypium hirsutum*), affects numerous crops and causes severe yield losses worldwide. Target spot is of increasing importance in cotton in the southeastern U.S. To manage target spot, growers rely on fungicide applications. Metconazole is a component of Twinline, one of the few fungicides labeled for management of target spot. Fungicide resistance is an important consideration where at-risk, site-specific fungicides such as metconazole are used to manage diseases caused by *C. cassiicola*. The objective of the research presented here was to determine the baseline sensitivity (EC_{50}) of isolates of *C. cassiicola* from cotton to metconazole. A total of 40 isolates were collected from cotton produced in five states (GA, AL, FL, LA, TN). Most isolates were collected from fields where metconazole had not been used previously. Sensitivity to metconazole of *C. cassiicola* isolates was determined under in vitro conditions using a mycelial growth assay. Isolates were tested to determine the effective fungicide concentration at which 50% of mycelial growth was inhibited (EC_{50}) for each of the 40 isolates. EC_{50} values of metconazole ranged from 0.016 to 0.20 with mean value of 0.05 $\pm$ 0.0. In comparison, EC_{50} values for isolates of *Fusarium graminearum* (wheat, New York) were 0.05 to 0.86 solat. Due to the increasing interest for management of target spot of cotton, sensitivity assays conducted now will be important to maintain effective management recommendation for growers. Establishment of baselines sensitivities is important to determine whether shifts to metconazole have occurred in the *C. cassiicola* pathogen population in the southeastern U.S.

Competition studies of QoI resistant and sensitive *Cercospora sojina* isolates, the causal agent of frogeye leaf spot

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Frogeye leaf spot (FLS), caused by *Cercospora sojina*, is a yearly foliar disease in Tennessee and causes substantial economic losses if not properly managed. Quinone outside inhibitor (QoI) fungicides are often used to manage FLS, but *C. sojina* isolates have developed resistance to this class of fungicides. Since the majority of soybean fields contain both QoI resistant and sensitive isolates, a better understanding of similarities and differences between such isolates in their biology and aggressiveness in causing FLS symptoms is needed. A greenhouse study was conducted at six different spore ratios of QoI resistant and sensitive isolates: 1:0, 9:1, 1:1, 1:9, 1:99, and 0:1. When the plants reached V2 growth stage, three treatments—non-fungicide-treated control (water), Quadris (azoxystrobin), and Quadris-Top (azoxystrobin plus difenoconazole) were applied to three replications, each replication consisted of four soybean plants (Blackhawk cultivar). Results of the greenhouse studies indicate that: 1) disease severity decreased as the ratios of the

inoculum source decreased in resistant conidia; 2) QoI resistant isolates were more aggressive, causing greater disease severity than QoI sensitive isolates on soybean 7 to 14 days after inoculation; 3) Quadris and Quadris–Top fungicides inhibited infection caused by QoI sensitive isolates, but only Quadris–Top provided effective disease control on FLS infection caused by the QoI resistant inoculum sources. This work will contribute to understanding differences in QoI resistant and sensitive *C. sojae* isolates and identifying any differences in effective control measures for FLS.

Strobilurin resistance of *Rhizoctonia solani* on rice in southwestern Louisiana appears to exclude trifloxystrobin based on in vitro assay

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Sheath blight is a major disease in Louisiana. In 2011, isolates of the sheath blight pathogen *Rhizoctonia solani*, anastomosis group 1-IA, from southwestern Louisiana were confirmed resistant to azoxystrobin. To assess the sensitivity to several strobilurin fungicides, 38 commercial rice fields in southwestern Louisiana were sampled. Sheath blight isolates were tested separately for azoxystrobin, pyraclostrobin, and trifloxystrobin sensitivity using an in vitro colony diameter assay on agar plates to determine the effective fungicide concentration (EC₅₀) that inhibits mycelial growth by 50% relative to maximum and minimum responses. Significant differences were found within both the azoxystrobin and pyraclostrobin EC₅₀ values, separating the fields into resistant, intermediate, and sensitive categories for these fungicides. In contrast, no significant differences were found within the trifloxystrobin EC₅₀ values. This could indicate that trifloxystrobin resistance has not developed. Across the different fungicides, there was no significant difference between mean azoxystrobin and pyraclostrobin EC₅₀ values, but both were significantly higher than the trifloxystrobin treatment mean. Trifloxystrobin could thus represent a potential management tool for azoxystrobin- and pyraclostrobin-resistant populations of *R. solani* in southwestern Louisiana.

Agricultural product combinations to reduce fungicide phytotoxicity in Mississippi soybean

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Recently frogeye leaf spot (FLS), caused by *Cercospora sojae* Hara, has re-emerged as an important foliar soybean disease. The continued interest in FLS is due in large part to the G143A substitution within the fungal population, which has resulted in widespread resistance to the quinone outside inhibitor (QoI) fungicides in Mississippi. At present, alternative fungicide modes of action (MOA) are suggested to manage QoI-resistant FLS. However, some fungicide products in the demethylation-inhibitor class effectively manage FLS, but their application results in a phytotoxicity to soybean leaves. Trials were conducted in 2015 to assess fungicide efficacy on QoI-resistant FLS and the resulting phytotoxicity on a FLS-susceptible variety. In addition to multiple fungicide MOAs, several foliar nutrient additives were evaluated in an attempt to reduce phytotoxicity. Fungicides were applied at the R3 growth stage. Visual assessments of FLS and phytotoxicity were made pre- and multiple times post-application. Certain MOAs significantly reduced FLS severity compared to the non-treated. In addition, prothioconazole (as Proline) applied at 21.92 ml/ha resulted in significantly greater phytotoxicity than the non-treated, a difference of 29.4%. In general, foliar nutrient additives did not significantly reduce observable phytotoxicity compared to the non-treated.

Evaluation of rice for bacterial panicle blight caused by *Burkholderia glumae* in Arkansas

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Bacterial panicle blight (BPB) nursery was established in the experimental field of Rice Research and Extension Center (RREC), Stuttgart, Arkansas. The major objective of this study was to evaluate the responses of rice varieties, cultivars and elite lines to bacterial panicle blight. Two hundred ninety rice entries were randomly arranged with two replications in hill plot planting. A suspension of bacterial panicle blight causing bacteria (*Burkholderia glumae*) were prepared using a 48 h old culture to inoculate each entry by spraying the bacterium approximately 108 bacteria/ml onto nearly emerged panicles. Inoculation was done twice within a four day interval. Severity of bacterial panicle blight was rated on a scale of 0-9, where 0 represented no symptoms, and 9 represented most severe in symptoms and damage. Disease assessments were made for all entries at or near maturity. All but several cultivars and lines were rated susceptible or very susceptible to bacterial panicle blight, with disease ratings from 5 to 9. Out of 290 entries screened only 12 scored the lowest rating signifying some level of resistant to moderately resistant both under natural and artificially inoculated plots. About Twenty-four entries were late in heading and show no symptom of BPB as the temperature declined during and after inoculation towards the end of the season. The possibility existed that they escaped disease infection due to unfavorable environment for the pathogen to multiply and cause infection. Repeated evaluation of the entries with resistance and moderately resistance reaction under different environmental conditions is recommended.

New grapefruit cybrids for potential citrus canker resistance in Florida

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Host resistance is the most desirable strategy for control of citrus canker caused by *Xanthomonas citri* subsp. *citri* (Xcc). A process called cybridization, the combination of cytoplasm and the nucleus from different species, is a useful somatic hybridization approach for *Citrus* improvement. Several putative cybrids were created through the fusion between nucellar callus cells of Meiwa kumquat (*Fortunella crassifolia*), a citrus canker resistant species, and mesophyll cells of grapefruit (*Citrus paradisi*), a citrus canker susceptible. To confirm the cybrids' genotype, 142 clones were screened with six EST-SSR markers and four CAPS markers for nuclear and organelle genotyping, respectively. For disease resistance screening, a syringe inoculation assay on attached leaves was performed to evaluate the response of 10 cybrids clones to Xcc. EST-SSR markers confirmed that all cybrid clones have a grapefruit nuclear genome; however, CAPS markers showed variation in cybrids' cytoplasmic genome. In 123 cybrids, kumquat mitochondria (mt) and chloroplast (cp) were identified, and in 19 cybrids, kumquat mt and grapefruit cp were present. Cybrid clones showed a range of citrus canker resistance, however all clones produced a significantly lower number of lesions than grapefruit plants. These cybrids have the potential to provide citrus canker resistance in commercial grapefruit varieties and contribute to study of cytoplasmic organelles in plant disease resistance.

Development and external validation of a model predicting within-season infection risk of cucumber by *Pseudoperonospora cubensis*

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Cucurbit downy mildew caused by *Pseudoperonospora cubensis* is the most damaging disease of cucurbits worldwide. Disease increase after initial infection depends on prevailing weather. Cucumber plants were exposed to field environmental conditions and naturally occurring inoculum over a 24- and 48-h period in Clayton, NC and Charleston, SC in multiple experiments from 2012 to 2014. Disease severity was assessed at 5 and 7 days after exposure, and weather variables during exposure were recorded. Using data collected in NC, 67 and 128 defined weather variables for the 24- and 48-h period, respectively, were examined and correlated with disease severity to identify variables that classified periods favorable for disease development. Binary logistic regression models with hours of relative humidity >80% and average daily temperature over the 24- and 48-h period had superior predictive ability. Based on a cut-off point of 0.5, final models had correct classification rates >80%, while sensitivity rates were >88%. Model specificity was high for the 24-h model with a rate of 65%. External model validation using data collected in SC resulted in correct classification rates

>70%, with sensitivity and specificity rates of 69% and 86%, respectively, for the 24-h model, and 84% and 100%, respectively, for the 48-h model. Cut-points that minimize costs associated with fungicide applications and crop loss due to overall error rates will be presented and discussed.

Monitoring shifts in fungicide resistance phenotypes for *Didymella bryoniae* in inoculated field plots

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Didymella bryoniae causes gummy stem blight on watermelon and can cause >50% yield losses. Fungicides are the main management option; but *D. bryoniae* resistance to three fungicide classes is known. To observe shifts in fungicide resistance over time when exposed to differing selection pressures, boscalid sensitive and resistant spores (1:1) were inoculated on watermelon in two field trials in Florida in 2015. Weekly treatments consisted of fungicides that would 1) select for resistant isolates (boscalid), 2) control in a non-selective manner (chlorothalonil), or 3) a rotation of these products. Weekly disease ratings were taken to record disease progression. Shifts in phenotype ratios were assessed by collecting infected tissue at 3 time points; 1) immediately prior to application, 2) after 3 applications, 3) when plots reached 90% severity. Isolates were cultured on media containing 0.068 and 0.170 mg/L of boscalid. Radial growth was measured to characterize isolates as sensitive or resistant based on percent inhibition. Phenotypes were analyzed by a chi-square test to determine significant shifts from the observed pre-spray ratios. Significant ($P < 0.05$) shifts in ratios were observed after 3 applications of boscalid resulting in a 24:1 and 1:0 at each trial location. Chlorothalonil only and rotation program did not significantly vary from each other. These results indicate resistant management guidelines are highly relevant to managing resistant field populations.

Application of high-throughput markers for *Phytophthora crown rot* resistance breeding in strawberry

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Phytophthora crown rot (PhCR) is the most common and a destructive disease in strawberry production in Florida. Mortality caused by this disease is commonly observed in warm temperature conditions during the plant establishment period, especially in October. Thus, this disease can significantly reduce fruit production when fruit prices are high and cause serious economic loss to Florida strawberry growers. At the moment, all major strawberry varieties grown in Florida are susceptible to PhCR. Also, soil fumigation before planting is ineffective in controlling this disease because the main inoculum source is infected nursery stock. Therefore, it is critical to develop new strawberry varieties for PhCR resistance. To identify genetic resistance to PhCR, we developed elite breeding populations, representing a total of more than 1,100 progeny from 122 full-sib families, and performed whole-genome single nucleotide polymorphism (SNP) genotyping (IStrow90 Axiom[®] SNP Array). Using a pedigree-based marker-trait association analysis (FlexQTL[™]) with 3,624 genetically mapped SNP markers, a large-effect QTL associated with PhCR resistance, Pc1 (LG 7D), was identified. For effective marker-assisted selection (MAS) for PhCR resistance, we have developed high-throughput markers tightly linked to the Pc1 resistance allele. The most informative markers will be implemented in MAS to increase genetic gains for this trait in the University of Florida strawberry breeding program. We will further discuss the application of high-throughput markers for marker-assisted strawberry breeding for PhCR resistance.

DNA-informed strawberry breeding: Development of a new high-throughput genotyping technology

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DNA tests have been widely used to develop new cultivars in many important crops. Strawberry breeding has recently been using molecular marker techniques to develop new flavorful and disease resistant cultivar development. Especially when a large number of samples need to be genotyped with limited resources, a rapid and cost effective high-throughput genotyping system is critically required. Thus, we developed a highly efficient genotyping method for strawberry breeding program in Florida. For a rapid and accurate genotyping, strawberry leaf tissues are directly used for identifying target traits. In addition, the high resolution melting analysis (HRM) was used to allow the processing of high sample numbers more accurately and efficiently with lower cost than traditional methods. Using this new high-throughput method, Total 8000 seedlings were successfully screened for peach aroma and perpetual flowering in strawberry breeding populations from the 2015 crossing cycle. Using this new method developed in this study is rapid, cost-effective and highly accurate; therefore, it enables the precision breeding for large number of samples and will provide great benefit to strawberry industry.

The resazurin-based assay as an alternative to evaluate *Botrytis cinerea* sensitivity to respiration-inhibitor fungicides

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Botrytis cinerea, a non-specific pathogen, can infect and cause disease in more than 400 hosts. The main control for *B. cinerea* diseases on cultivated crops relies on the use of fungicides. Fungicide-amended agar assays that evaluate mycelial growth and/or conidial germination are the most common methods to evaluate the sensitivity of this pathogen to the major fungicides used. The objective of this study was to adapt a resazurin-based assay to evaluate *B. cinerea* sensitivity to respiration-inhibitor fungicides and to compare it with the conidial germination assay. The sensitivity of eleven *B. cinerea* isolates to two fungicides (pyraclostrobin and boscalid) was tested at eight fungicide concentrations (0 to 10 µg/ml for boscalid, and 0 to 50 µg/ml for pyraclostrobin), two media (MEA or YBA for conidial germination assay and Complete Medium or HA at pH 6.5 for resazurin based assay), and evaluated at 24h after preparation of the plates. The EC50 value of the sensitive isolates varied from 0.001 to 0.799 µg/ml for both fungicides in the conidial germination assay and were highly correlated with the resazurin assay. Conidial germination required 4h 30 min more time, 5 times more space, and was US\$25 more expensive than the resazurin-based assay. In conclusion, the resazurin reduction methodology is a good alternative for screening sensitivity of *B. cinerea* isolates to respiration-inhibitor fungicides, especially when evaluating a large number of isolates.

Systemic infection of split roots by *Candidatus Liberibacter asiaticus* suggests rapid movement between phloem sieve tubes

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Huanglongbing (HLB; syn. citrus greening), caused by the phloem-limited bacteria *Candidatus Liberibacter asiaticus* (Las), poses one of the largest threats to citrus production. In ten years it has spread to most citrus trees in Florida. Citrus production in Florida is down 60% from the pre-HLB era. Las infects a tree when an infected *Diaphorina citri* (Asian Citrus Psyllid) feeds on phloem sap in a leaf. After infection of the leaf, Las rapidly colonizes the root system, but remains sequestered in the canopy. Canopy sectoring is thought to occur because of limited lateral connections of phloem sieve tubes. To investigate if lateral movement of Las between sieve tubes is distance or tissue specific, root systems of grafted and seedling trees were split to three different heights: below crown, above crown, and above graft union (or equivalent on seedlings). The trees were then graft inoculated above one side of the split root system. Infection in both halves of the root system was monitored weekly. The grafted and seedling trees displayed different patterns, suggesting graft unions play a role in lateral Las movement. The infection, spreading from the initial graft inoculation into each half of the root system of seedlings and grafted trees split to different heights, progressed with varying speeds. Phloem architecture in specific tissue types or active movement may play a larger role than source-sink relations in lateral movement of Las between sieve tubes.

Comparison of four RIL mapping populations of peanut for field response to late leaf spot

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Recombinant inbred line (RIL) populations of peanut (*Arachis hypogaea* L.) are being used to develop markers for resistance to several diseases, including late leaf spot (*Cercosporidium personatum*). Susceptibility to late leaf spot within populations has been characterized, but populations have not been compared within the same trial. In 2015, a field trial was conducted to determine the effect of 18 RILs from each of four mapping populations (S, T, 1799, and 1801). Based on ranked results from previous trials, the 6 RILs with the highest, 6 RILs with the lowest scores for leaf spot severity, and 6 RILs nearest the population mean were included from each population. Parental lines from all populations were included. Area under the disease progress curve (AUDPC) values for late leaf spot Florida 1-10 scale evaluations were highest for the S population. Mean AUDPC values were similar for T, 1799, and 1801 populations. AUDPC of SPT 06-06, a parental line for population 1801, was lower than for any other parent. However, four RILs from population 1799 were similar to that of SPT 06-06 and lower than that of cultivar Tifrunner, the resistant parent for population 1799. Results indicate the populations differ for leaf spot severity, but highest levels of leaf spot resistance in individual RILs may not come from the most resistant parent. Results also indicate that levels of resistance can be obtained in individual lines that are better than that of either parent.

Secretome analysis to identify potential effector genes of *Fusarium oxysporum* causing fusarium wilt in palms

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Fusarium oxysporum f. sp. *palmarum* [FOP] and *Fusarium oxysporum* f. sp. *canariensis* [FOC] cause lethal fusarium wilt on palms in Florida. Disease mechanism and management for both these pathogens are poorly understood. Studies on secretomes of *F. o. f. sp. lycopersici*, *F. o. f. sp. melonis*, and *F. o. f. sp. cubense* have indicated the presence of effector proteins, including members of the SIX protein family, extracellular enzymes, and toxins predicted to function in combating host defenses and infecting the plant. The focus of the current study is (i) to identify the potential effector genes and their role in pathogenicity, and (ii) to compare the FOC and FOP proteomes with various formae speciales of *F. oxysporum* to identify common and unique gene families. Insights about these formae speciales of *F. oxysporum* will enhance our understanding on host specific interactions leading to effective management strategies. To date, the FOP and FOC genomes were sequenced, assembled and annotated using multiple bioinformatics approaches for secretome analysis. Genome sizes for FOP and FOC are 46.9 Mbp and 46 Mbp, respectively, and SignalP predicted 1488 (FOC) and 1531(FOP) secretory proteins. Preliminary analysis of secretory proteins of both genomes indicate multiple copies of transporters and cell wall degrading enzymes such as cuticle degrading enzymes, chitinase, pectin lyase, lipases, and endoglucanase. Secretome analysis of FOP indicated the presence of HC-toxin synthetase, trichothecene biosynthesis, pisatin demethylase proteins indicating a possible role of toxins in pathogenicity. OrthoMCL was used to cluster related proteins within genomes, resulting in 396 (FOC) and 511(FOP) unique clusters. Further annotation is underway to identify putative functions of unique and common genes and develop hypotheses concerning differences in pathogenic specificities.

Effect of seed quality, seed treatment, and planting date on soybean emergence in Arkansas

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Seedling diseases cause stand loss in soybean whenever they are planted in Arkansas. The extent of loss depends on seed quality and seed treatment. For two years, high and low quality seed of the soybean cultivars Hutcheson and Osage, either treated with mefenoxam+fludioxonil or not treated, were planted every two weeks beginning in April and ending in September at the Vegetable Research Station, Kibler, AR. The tests were planted in a randomized complete block design with four replications. Stands were determined after two weeks. At the beginning, middle and end of each season, seed germination and accelerated aging were determined and soil was collected across the test. Seed and root pathogens were baited from the soil with untreated Hutcheson seed at 18, 25, or 32°C. Seed were assayed after three days and roots after seven days using modified corn meal agar and water agar, respectively. Resulting colonies were identified to species with PCR. *Rhizoctonia* spp. was also isolated from the soil using a toothpick method. Soybean stand was affected by both seed quality and seed treatment throughout the season with the highest stands coming with the treated seed. Seed treatment improved stands of both high and low quality seed at most planting dates. *Pythium* spp. were the only pathogens isolated from the seeds and *Fusarium* spp. were the main pathogens isolated from roots. Species determinations are underway.

The effect of oscillating temperatures on growth of *Fusarium oxysporum* f.sp *niveum* in-vitro

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Fusarium wilt of watermelon, caused by *Fusarium oxysporum* f.sp *niveum* (Fon), is a re-emerging disease in Florida causing significant commercial yield losses. Little is known regarding the growth response of the pathogen to daily soil temperature oscillations under production settings (raised beds, plastic mulch). A preliminary study measuring the soil temperature of watermelon beds found that temperature oscillated between 2-9°C around the mean. The purpose of this study was to examine the effects of oscillating temperatures on the mycelia growth of Fon in-vitro. Sixteen Fon isolates were incubated at mean temperatures of 12°C, 17°C, 22°C, 27°C and 32°C with daily oscillations around the mean of 0, 2 and 8°C. Colony growth was recorded at 48, 96 and 144 h. At 12°C a daily 2°C oscillation significantly ($P < 0.05$) reduced growth in comparison to the 8°C oscillation. The opposite effect was observed at 27°C and 32°C, where an 8°C oscillation significantly ($P < 0.05$) reduced mycelia growth compared to the 2°C. Growth rates differed among isolates, and for each isolate, growth at a constant 27°C was significantly ($P < 0.05$) greater than any other treatment. These results suggest that mycelia growth can be limited by temperature oscillations, and their effects are dependent on the magnitude and mean temperature. A better understanding of how daily soil temperature fluctuations affect Fon growth may be a starting point for modeling the risk of Fusarium wilt of watermelon.

Enhancing sporulation of *Corynespora cassiicola* to use for conducting research on epidemiology of the target spot of cotton

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Target spot of cotton, caused by *Corynespora cassiicola*, is an emerging disease of dryland and irrigated cotton which was first reported in 2011 in Alabama. In order to do research with this pathogen, it is first important to know conditions to optimize spore production. *Corynespora cassiicola* was isolated from a diseased cotton plant in Alabama and grown on V8 agar. Eight sets of conditions were investigated for optimizing spore production. Light exposure (continuous dark/ continuous light/ fluctuating light), temperature (ambient temperature and constant 23°C) and with or without scraping the mycelium were investigated. Spores were counted after 15 days growth. Results showed that *C. cassiicola* (isolate C1), when cultured under continuous light at ambient temperature or constant 23°C, without scraping, had the highest sporulation. Continuous dark at 23°C, with or without scraping, had intermediate sporulation, while cultures kept in fluctuating light conditions at 23°C, with or without scraping, had the lowest spore count. Based on these results, future studies will use *C. cassiicola* cultures incubated under continuous light at ambient temperatures.

Effect of anaerobic soil disinfestation on survival of *S. rolfii* sclerotia and soil populations of *Trichoderma*

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Anaerobic soil disinfestation (ASD), an alternative to chemical fumigation, effectively kills sclerotia of *Sclerotium rolfii*. However, its effect on the mycoparasite *Trichoderma* is not well-documented. We investigated the effect of ASD on *Trichoderma* population, and sclerotial germination and parasitism. Two mesh bags, each with 10 sclerotia, were buried in pots containing field soil and sand at 5- and 15-cm depths. Treatments were ASD, ASD+*Trichoderma*, and *Trichoderma* alone. Controls were unamended pots, covered and uncovered. The anaerobic conditions were maintained for 3 weeks by saturating pots and covering with polyethylene mulch. Sclerotial germination and *Trichoderma* parasitism were assessed on antibiotic-amended potato dextrose agar and *Trichoderma* selective medium at room temperature. Serial dilutions of soil on *Trichoderma* selective medium were used to determine *Trichoderma* populations. ASD and ASD+*Trichoderma* significantly suppressed *S. rolfii* at both depths (0 to 25%); sclerotial germination was highest in controls at 5 cm (49 to 87%). *Trichoderma* parasitism of sclerotia was greatest for ASD+*Trichoderma* (75 to 95%) and lowest for controls (45%). We observed high *Trichoderma* populations in ASD and ASD+*Trichoderma* pots; however, these populations were not significantly different from controls. This suggests that ASD, with or without *Trichoderma*, reduces sclerotial germination and enhances parasitism without reducing beneficial *Trichoderma* populations.

Population structure of *Cercospora sojina* collected from different soybean cultivars in Milan and Jackson, Tennessee

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Frogeye Leaf Spot (FLS) of soybean is caused by the fungal pathogen, *Cercospora sojina* Hara. FLS causes significant damage, mostly in the Southern U.S and was first reported in South Carolina in 1924. In 2013, the US produced 89 million metric tons of soybean worth \$ 23 billion. Symptoms appear as small light brown circular spots surrounded by a darkish brown to reddish circle. Lesions range from 1-5 mm in diameter with older lesions having a white center. As the disease progresses, lesions merge together and leaves fall prematurely. Several methods including fungicide treatment, crop rotation and host resistance are used for controlling FLS. Generally, quinone outside inhibitor (QoI) fungicides are used in controlling FLS but resistant isolates to QoI fungicides have developed. There have been limited studies of genetic diversity of *Cercospora sojina*. Currently, we are exploring variation in field populations using genome-wide single nucleotide polymorphism (SNP) markers. Candidate SNP markers were identified through de novo whole genome sequencing of three isolates. In 2015, 474 isolates were collected from 8 soybean cultivars (fungicide treated and untreated) from two counties in Tennessee. SNP genotypes will be assayed using targeted sequencing and the population structure of *C. sojina* discussed.

Two symptoms of *Cercospora* leaf blight of soybean: An indication of two diseases caused by the same pathogen

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Cercospora leaf blight (CLB), caused in soybean by *Cercospora kikuchii*, *C. flagellaris*, and *C. sigesbeckia*, is the most important soybean disease in Louisiana, where two symptoms are associated with this disease. Previous publications suggested that CLB starts with leaf purpling (thought to be caused by an accumulation of cercosporin), and then, as the disease progresses, leaves become blighted. Our observations in Louisiana suggested that these two symptoms are not correlated. The objective of this work was to examine the relationship between purple and blight symptoms as well as their relationship with fungal growth, cercosporin production by the pathogen and flavonoid production by the plant. To verify the relationship between the two CLB symptoms, soybeans were planted in two locations in 2013 and 2014. There was not a significant correlation between these two symptoms in Alexandria ($R^2 = 0.063$) or in Baton Rouge ($R^2 = 0.1383$). To verify the relationships among CLB symptoms, fungal biomass, cercosporin production and flavonoid concentrations in leaves, six soybean varieties were planted at three locations. The pathogen was detected in all leaves (including symptomless); however, blighted leaves had higher fungal biomass than purple leaves. Cercosporin was not detected in symptomless leaves but was detected in low and high concentrations in purple and blighted leaves, respectively. No anthocyanins were found in any leaves. Glyceollin was detected in higher concentration in the intermediate stages of blight symptoms. These results suggest two modes of pathogenesis, which indicates that the same pathogen causes two distinct diseases.

Spatial distribution of taproot decline of soybean

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A disease unique from other reported diseases of soybean has been observed in the southeastern Arkansas Delta. In fields where soybeans are R5, plants appear chlorotic, stunted, and when extracted from the soil, have black lateral roots and a malformed and necrotic taproot that is often black. The estimated yield loss from affected plants was approximately 30% in 2014 compared to non-affected plants. The impact to overall yield in fields was less than 1%. However, in 2015, disease was more severe in some fields. Additionally, in areas of symptomatic plants, gaps in stand were evident with dead plants between the chlorotic plants. When dead plants were extracted from the soil, the taproot was malformed and black if present. Two fields were chosen and 100 positions marked by GPS encompassing 0.70 and 0.67 ha in 2014 and 2015 respectively. Yellow plants were counted within 3 m of the GPS position in both years. In 2015, the number of dead plants and overall stand within 3 m was determined for each GPS position. Data were analyzed spatially using Moran's I in GeoDa. In both years, chlorotic plants were aggregated ($P=0.05$) indicative of a soilborne disease. The major ranges for yellow plants were 61.5 m and 128.4 m in 2014 and 2015 respectively. In 2015, the spatial distributions of yellow chlorotic plants and dead plants were related ($P=0.004$) and the relationship of yellow and dead plants was inversely related to overall healthy stand ($P<0.0001$).

Characterization of a partial cytochrome *b* fragment to determine the risk of QoI resistance in *Fusicladium effusum* from pecan

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Effective management of pecan scab, caused by *Fusicladium effusum* (Wint.), relies heavily on multiple fungicide applications per season. Several quinone outside inhibitor (QoI) fungicides are used to manage scab, but to date, resistance has not been reported. In other fungi, QoI resistance has been associated with amino acid substitutions in the cytochrome *b* (cyt *b*) gene at positions 129, 137, and 143. A substitution at position 143 (G143A) confers complete resistance, while the presence of an intron immediately downstream of this position prevents such a change from occurring. In this study, a partial fragment of the cyt *b* gene from *F. effusum* was sequenced and characterized to assess the risk of development of QoI resistance in this fungus. Sequence analysis of a 1,900-bp fragment revealed the presence of two introns, 360 and 1,400 bp in size, directly downstream of positions 135 and 143, respectively. No substitutions were identified at positions 129 or 143, but a substitution was found at position 137 in seven isolates. Both introns were present in all 125 isolates tested. Presence of the intron adjacent to position 143 in all isolates collected from Georgia provided strong evidence that this intron is ubiquitous in *F. effusum* populations and the risk of resistance associated with the G143A substitution is low. Understanding the potential for QoI resistance to develop in *F. effusum* greatly aids pecan growers in choosing effective fungicides for scab management.

***Aspergillus flavus* corn strains have higher inoculum potential than soil strains**

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Evidence indicates *Aspergillus flavus* strains differ in ability to infect crops. *Aspergillus flavus* isolated from soil and corn in 11 fields revealed only 6 of 16 vegetative compatibility groups (VCGs) infected corn. An infectivity titration experiment is underway to verify niche specificity. During inoculum production, two VCGs (1,4) predominant in corn produced substantially more conidia (28 and 33 mg conidia/gram corn grits) than the most predominant soil VCG 8 (2 mg/g) and a singleton soil isolate (6 mg/g). To determine if conidial production is higher for corn infecting strains, three isolates from each of the 6 corn and 3 predominant soil VCGs were grown on Czapek Dox solid medium. The four predominant corn VCGs (1,4,7,10) produced more conidia ($1.04 \times 10^7 \pm \text{S.D. } 0.697 \times 10^7$ conidia/colony area cm^2) than three VCGs (2,3,8) isolated strictly from soil ($9.04 \times 10^5 \pm 5.72 \times 10^5$ c/cm 2); VCG 1 which comprised 80% of the corn isolates produced the most conidia ($1.62 \times 10^7 \pm 0.454 \times 10^7$ c/cm 2). VCGs 5 and 9 were more frequently isolated from soil than corn. VCG 5 was comparable to the strictly soil VCGs whereas VCG 9 produced intermediate conidia ($6.96 \times 10^6 \pm 4.38 \times 10^6$ c/cm 2). Conidial production appears to correlate with infection of corn, but VCGs 9 and 10 produced abundant conidia without high infection frequency, indicating additional factors are important for establishing infection.

Phenotypic assessments of peanut nested association mapping (NAM) populations

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Nested association mapping (NAM) is a valuable innovation and multi-parental mapping population strategy in peanut genetics which increases the power to map quantitative trait loci and assists in extending the gene pool of elite peanut lines. In the peanut research community, two structured mapping populations were developed using a 2×8 (common by unique) factorial nested association mapping design, each with eight founders and a reference line. Here, we demonstrate its usefulness by assessing the phenotypic diversity of two assembled NAM populations (2×4). The common parents are Tifrunner and Florida-07 while the four unique parents are N08082oilc, C76-16, NC3033 and SPT06-06. We initially screened the phenotypic characteristics of the RILs including morphological and disease resistance traits. We found that leaf length and width, plant size, main stem height, and leaf spot resistance segregated within the assembled population and exhibited normal distributions. We also calculated the variance and heritability of each trait, and found that plant size had the lowest narrow sense heritability (0.06) while disease resistance had the highest (0.67) in the Tifrunner NAM population. In the Florida-07 population, main stem height had the lowest (0.27) and leaf width had the highest (0.73). Phenotyping of pod and kernel traits is underway along with further genotyping by sequencing. The NAM concept will promote the evaluation of the genetic diversity present in peanut gene pool.

Micronutrients may affect plant disease severity by interacting with components of the systemic acquired resistance pathway

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Host nutrition can affect plant disease severity, but the role it plays is not always understood. Previously, we reported regression models where micronutrients correlated with tomato spotted wilt severity in tobacco (*Nicotiana tabacum*) and sour skin severity in onion (*Allium cepa*). To test our hypothesis that cations may affect the salicylic acid (SA) pathway for disease resistance, field plots of tobacco and onions were established in a randomized complete block design with four replications. Treatments consisted of foliar-applications of Cu, Fe, Mn and Zn. Treatments were applied with or without acibenzolar-S-methyl, a SA analog and plots were rated for disease severity. Both tobacco leaves collected prior to harvest and onion bulbs harvested at optimum maturity were used for tissue analysis. In addition, whole transcriptome analysis was conducted on mRNA extracted from healthy onion bulbs representing opposite ends of the regression model. In tobacco, plants treated with Zn plus acibenzolar-S-methyl had significantly more disease than plants treated with the SA analog alone. Fe levels were lower in all leaves treated with the SA analog and were highest in Zn-treated tobacco leaves regardless of SA analog treatment. In onion, mRNA transcripts associated with the SA resistance pathway proteins, including B2, Grx-like, EDR1 and PR1, were expressed significantly greater (>500 fold increase) in bulbs from the low disease-high CU:Fe end of the regression model.

An update on newly launched fungicides in the South

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Oxathiapiprolin and Solatenol[®] are two new fungicide a.i.s which have recently received EPA registration. Orondis[®] (oxathiapiprolin) provides control of certain Oomycete diseases and is the first in a new class of fungicide (piperidinyl thiazole isoxazolines). The spectrum of activity includes the downy mildews and *Phytophthora* spp. (both soil and foliar). Labeled crops include fruiting, leafy, and bulb vegetables, cucurbits, brassicas, ginseng, succulent edible peas, potatoes, and tobacco. Initially, the products will be available in multi-packs: Orondis Opti[®] (with chlorothalonil), Orondis Ultra[®] (with mandipropamid) and Orondis Gold[®] (with mefenoxam). Solatenol[®] fungicide is a new broad spectrum fungicide. Four new products are currently labeled for use: Aprovia[®] (solo), Aprovia[®] Top (with difenoconazole), Elatus[®] (with azoxystrobin), and Trivapro[®] (with azoxystrobin and propiconazole). Elatus has shown excellent residual activity in peanuts on leaf spots, peanut rust, and southern blight. In potatoes Elatus has shown outstanding activity on *Rhizoctonia solani*. Aprovia Top will be available for use in vegetables where it has been shown to provide excellent control of foliar diseases such as powdery mildew and cucurbit gummy stem blight.

Reducing *Macrophomina phaseolina* colonization in soybean through secondary nutrition

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Charcoal rot (CR) of soybean, caused by *Macrophomina phaseolina* (Tassi) Goid (*Mp*), annually limits profitability. Throughout the southern United States, an estimated 11 million metric tons have been lost to charcoal rot over the past 20 years. The objective of this research was to reduce *M. phaseolina* colonization of field grown soybean by supplementing secondary nutrients, specifically calcium (Ca) and magnesium (Mg). In 2014 and 2015 non-irrigated, *Mp*-inoculated field trials were conducted in Stoneville, MS with a CR-susceptible and a CR-moderately resistant cultivar. Treatment applications consisted of 1,120 kg/ha rate of Ca and Mg alone and in combination at different growth stage timings including at plant, R1, and at plant followed by R1. Non-inoculated, non-treated plots served as the control. Root samples were taken at the R3, R5, R7, and R8 growth stages. Colony forming units (cfu) were used to quantify *Mp* colonization from ground root tissue and enumerating cfus in a *Mp* semi-selective medium. A steady increase in cfus occurred throughout the season with the CR-susceptible samples averaging 176 cfu/g at R5 to 21,088 cfu/g at R8 and the CR-moderately resistant samples averaging 47 cfu/g at R5 to 23,217 cfu/g at R8 regardless of treatment. In all cases, the greatest number of cfus were recovered from plants sampled at R8 than at prior growth stages. In some cases, applications of calcium and magnesium reduced colonization when compared to the control.

Response of root-knot nematode resistant cotton cultivars to Fusarium wilt

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Fusarium wilt, caused by the soilborne fungus *Fusarium oxysporum* f. sp. *vasinfectum* (Fov), is an increasingly important disease of cotton (*Gossypium hirsutum* L.). In Georgia and Texas, Fov causes little damage alone; however, losses are much more severe in the presence of the root-knot nematode (*Meloidogyne incognita*). The disease is most commonly managed through the planting of cultivars possessing partial resistance to *M. incognita*, as Fov resistant cultivars are lacking. Recent observations suggest that newly released cultivars with improved resistance to *M. incognita* are more susceptible to Fov. The objective of this research was to evaluate the performance of commercially available cotton cultivars in fields with a history of Fusarium wilt. Cotton cultivars possessing monogenic and polygenic resistance to *M. incognita* were planted in fields infested with Fov. In Texas, initial symptoms were observed by the fifth leaf stage and often resulted in mortality. Disease incidence for the cultivars 'Phytogen 367WRF' and 'Stoneville 4946GLB2' was less than 1%, whereas, 'Deltapine 1454NR B2RF' and 'Deltapine 1558NR B2RF' exhibited a 13-fold and 8-fold increase, respectively. Other cultivars including 'Phytogen 417WRF', 'Fibermax 2011GT' and 'Phytogen 427WRF' were intermediate averaging 2.9, 2.5 and 1.8%, respectively. Similarly, in Georgia, Fusarium wilt was more severe in Deltapine 1454NR B2RF than other cultivars evaluated. These results indicate that differences in the response to Fusarium wilt exists among commercially available *M. incognita* resistant cultivars. Additional efforts in characterizing the response to specific diseases prior to commercialization are needed.

Potential for seed transmission of 'Candidatus Liberibacter solanacearum' in jalapeno peppers

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Potato zebra chip has been causing widespread losses to potato production in the US since its first discovery in Texas in 2000. The disease is caused by the fastidious bacterial pathogen 'Candidatus Liberibacter solanacearum' (Lso), which is vectored by the potato psyllid (*Bactericera cockerelli*). The pathogen can infect all plants in the Solanaceae family including tomatoes and peppers. Experiments were conducted to determine whether seed from infected peppers can serve as a source of pathogen spread. Jalapeno pepper plants were planted in cages (1 plant/cage) in five replications under a center pivot irrigation system and infested with Lso-positive psyllids after fruit set (6 psyllids/plant). After harvest, peppers from each plant were tested by qPCR for Lso. Seeds were removed from fruits which tested positive for Lso and individually subjected to qPCR analysis. Seventy-five seeds from positive fruits were partially germinated, and the seed endosperms and embryos separately tested for Lso. Out of the 75 seeds tested, 100% of the seed endosperms tested positive for Lso but only 2.7% of the embryos tested positive. Finally, seeds from Lso-positive fruits were planted in the greenhouse and all tissue samples collected from emerged plants (64 total) tested negative for the pathogen. This suggests that Lso can be detected on pepper seeds; however, it is very unlikely that it can be transmitted to the next generation of plants through seeds.

The potential impact of anthracnose on sweet sorghum production

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Sweet sorghum (*Sorghum bicolor*) has been grown in the southeastern United States (US) for more than 150 years on a relatively limited scale, primarily for forage and the production of syrup. If sweet sorghum is cultivated on a commercial scale in the future for biofuels, diseases may become a significant limiting factor for production. Anthracnose is the most important disease of grain sorghum, causing losses of up to 50%. *C. sublineola* causes anthracnose on cultivated sorghum, including sweet sorghum, and also on the wild sorghum relative johnsongrass (*S. halapense*). Comparatively little is known about the occurrence or importance of anthracnose in sweet sorghum. The pathogenicity of *C. sublineola* isolates from sweet and grain sorghum, and from johnsongrass, was compared on the susceptible sweet sorghum inbred Sugar Drip in the field. The isolate from sweet sorghum was the most aggressive, while the johnsongrass isolates caused only minimal disease symptoms. There was no correlation between the levels of disease and sorghum biomass or juice yield or sugar content. The same fungal isolates were evaluated for aggressiveness in greenhouse assays and in detached leaf sheath assays. Results of these assays were similar to the field results, thus these protocols might be useful for screening sorghum germplasm for new sources of resistance or to characterize new isolates. Prior studies have suggested that removing the seed heads from sorghum plants increases the amount of sugar in the stalks, and others have suggested that increased levels of stalk sugar are correlated with decreased susceptibility of maize to anthracnose stalk rot. In the current study, seed head removal increased sugar levels in Sugar Drip some cases, but this had no effect on susceptibility to anthracnose.

Differential accumulation of reactive oxygen and nitrogen species in maize lines with contrasting drought tolerance and aflatoxin resistance

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Abiotic stresses such as drought stress can exacerbate aflatoxin contamination of maize kernels. Previous studies showed that maize lines resistance to aflatoxin contamination tend to exhibit enhanced drought tolerance and accumulate lower levels of reactive oxygen species (ROS) and nitrogen species (RNS) than those that are susceptible to both in leaves. In order to investigate whether ROS or RNS accumulation in kernel tissues along with relative humidity may potentially influence aflatoxin production, we performed an in vitro kernel screening assay to examine the accumulation of ROS and RNS over time in resistant (Lo964) and susceptible (B73 and an F1 of Lo964 x B73) lines with and without a 3 day pre-incubation in a 100% humidity environment. In the assay, kernels, with and without pre-incubation, were inoculated with *Aspergillus flavus* and examined daily for 7 days for ROS, RNS, and aflatoxin accumulation. Pre-incubation resulted in enhanced visible conidiation, however dramatically reduced aflatoxin production. Pre-incubation also resulted in increases in ROS and RNS levels at 2-3 days post inoculation while kernels without pre-incubation saw increases at 3-4 days after inoculation. In addition, Lo964 exhibited lower overall accumulation of ROS and RNS than B73 or the hybrid. This indicates that peaks in oxidative and nitrosative stress compounds later in infection and the accumulation of higher levels of said compounds are correlated with exacerbated aflatoxin production.

Draft genome sequence of *Stenocarpella maydis* as a resource for molecular genetics and functional genomics

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Stenocarpella maydis causes Diplodia ear rot, an increasingly problematic disease of maize. To date, little information is available regarding the molecular basis of pathogenesis in this organism, in part due to limited genomic resources. In this study, a reference genome was obtained and analyzed for *S. maydis*. The genome was assembled with a hybrid strategy that consisted of analyzing Illumina, Roche 454, and PacBio sequence data with the SPAdes assembler to produce a draft genome assembly. The draft assembly was improved with SSPACE for scaffolding, followed by GapFiller and PBJelly for gap filling. The final assembly consisted of 54.9 Mb, with a L50 of 49 and N50 of 305 Kb. Gene prediction was performed with the Maker pipeline that predicted 12599 genes, of which 7544 were functionally annotated with Blast2GO. A graphical visualization of the genome was created with JBrowse, where the gene distribution and its structure (exons and UTRs) can be seen. The draft genome will provide the maize pathology community a useful resource for molecular genetics, functional genomics, and analyses of population diversity.

A forward genetic screen in *Phomopsis longicolla* provides unique insights into pathogenesis

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Phomopsis longicolla (Hobbs) causes Phomopsis seed decay of soybean (*Glycine max*), and also causes lesions on soybean stems, pods, and petioles. *P. longicolla* can also exist endophytically within soybean stems, which has given rise to the hypothesis that pathogenesis occurs when the pathogen transitions from endophytic or hemibiotrophic growth to necrotrophy. In this study, a forward genetic screen was performed to elucidate genetic mechanisms underlying necrotrophy, and a RAD-seq approach was adapted to characterize genomic lesions in selected mutants. A collection of 1114 tagged, insertional mutants was created via *Agrobacterium*-mediated transformation, and mutants were evaluated individually in soybean stems for their ability to induce necrosis and form pycnidia. Six mutants induced significantly less necrosis in soybean stems than the wild-type strain, and four formed significantly fewer pycnidia. No gain-of-function mutations (increased necrosis) were observed. A modified RAD-seq protocol developed to identify the site of insertion was applied to a mutant significantly reduced in its ability to cause stem necrosis; a single copy of the disruption cassette integrated into the presumed promoter region of a cellobiohydrolase. This study describes new tools to dissect the interaction between *P. longicolla* and soybean, and provides new insight into conserved mechanisms underlying stem, pod, and seed necrosis caused by *P. longicolla*.

Sequencing and analyses of *Streptomyces* genomes reveal the emergence of new plant pathogenic species from mobilization of the pathogenicity island

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Potato scab is a globally common tuber disease caused by plant pathogenic *Streptomyces* species. About ten *Streptomyces* spp. are responsible for this disease; the most widely distributed and best studied of these is *Streptomyces scabiei*. The pathogenicity factor of scab-causing *Streptomyces* species is the phytotoxin thaxtomin A (TxtA) that inhibits plant cellulose synthesis. TxtA biosynthesis genes are localized on a mobile pathogenicity island (PAI). Here we sequenced genomes of ten plant pathogenic isolates from different geographically origins to study the evolution of plant pathogenicity in *Streptomyces*. Various versions of PAIs exist in different strains. We demonstrate that, *S. sp.* 96-12, originally isolated from potatoes in Egypt, was a novel pathogenic species; however, *S. sp.* 96-12 shared the same PAI with *S. scabiei*. We detected the mobilization of PAI during mating *S. scabiei* to non-pathogenic *S. diastatochromogenes* and site-specifically insertion into a putative GTP binding protein. Acquisition of *S. scabiei* PAI transferred *S. diastatochromogenes* to a pathogen, thus suggesting this PAI allows the emergence of novel pathogenic species. In addition, two strains (*S. europaeiscabiei* 96-14 and *S. sp.* 96-12) did not produce TxtA in oat bran broth (OBB). This was an unexpected result, as OBB has been widely used as an excellent TxtA-inducing medium. It is the first time that pathogenic *Streptomyces* strains that do not produce TxtA in OBB were isolated.

Management of Tomato chlorotic spot virus (TCSV): A predominant tospovirus severely infecting tomato in south Florida

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Tomato chlorotic spot virus (TCSV), a tospovirus transmitted by thrips, was first detected and reported in tomato plants from south Florida in 2012. In Miami-Dade County, severe outbreaks of TCSV during the 2014-2015 growing season and again in the fall of 2015 caused significant economic losses to tomato growers. TCSV has become established in south Florida, and the disease is showing up more widely with greater frequency across south Florida, bringing a great concern that TCSV may spread to other tomato production regions in the U.S.A. Field evaluations were conducted in Miami-Dade County in 2015 to develop strategies for management of this disease. Fourteen tomato varieties resistant to Tomato spotted wilt virus (TSWV) were evaluated in the spring 2015. All varieties tested showed varying levels of resistance to TCSV (10-40% vs. 100% infection in the susceptible cv. FL 47) 59 days after transplanting (DAP). Similar results from two repeated trials being carried out in the fall 2015 where all varieties had less than 4% disease incidence 53 DAP, whereas 34% plants of FL 47 showed TCSV symptoms. In an insecticide trial conducted in the spring 2015, only Radiant (spinetoram) and Exirel (cyantraniliprole) significantly reduced TCSV incidence compared to the untreated control. Other trials are underway to investigate the effect of metalized plastic mulch and plant activator acibenzolar-S-methyl (Actigard) on TCSV disease. Results from these trials will be reported.