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Proceedings of the 46th Annual Meeting of the Southern Soybean Disease Workers (March 6-7, 2019, Pensacola Beach, Florida)

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Abstracts for presented posters

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Agenda for the 46th Annual Meeting of the Southern Soybean Disease Workers, March 6-7, 2019, Hilton Hotel, Pensacola Beach, FL

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Evaluating Phytotoxicity in Response to Fungicide by Adjuvant Combinations

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Over the past decade an increased number of field-related observations associated with injury to soybean foliage following fungicide applications have been made. Injury to soybean foliage, or phytotoxicity, can occur as a result of the application of fungicide products that contain specific chemical classes. The symptoms that generally occur as a result of phytotoxicity can include interveinal chlorosis that presents as yellowing and necrosis between the veins typically in the upper canopy 14-28 days post-application. Moreover, phytotoxicity will progress over time and appears to get worse between 21 and 28 days post-application. Diseases that produce interveinal chlorosis and can be mistaken for fungicide phytotoxicity include: charcoal rot, Phytophthora root and crown rot, red crown rot, stem canker, sudden death syndrome, and taproot decline. In general, fungicides in the demethylation inhibitor class (DMI; triazole) can all produce phytotoxicity that ranges from extremely minor (much less than 1% of the foliage presenting symptoms) to severe (greater than 50% of the canopy presenting interveinal chlorosis). In addition, products that contain mixed mods of action that include a DMI class fungicide are much more frequently associated with phytotoxicity events than stand-alone DMI fungicides.

A fungicide which has previously been observed to produce a moderate level of phytotoxicity, prothioconazole (as Proline, 3 fl oz/A), was applied with and without several adjuvants over a four-year period in Stoneville, MS (2015-2018). The adjuvants represented several commonly used products in the MS soybean production system and included: crop oil concentrate (COC), methylated seed oil (MSO), Penetrator Plus, DyneAmic, non-ionic surfactant (NIS), soysurf, and SilWet L-77, were applied at 0.125 and 0.250% (v/v). Applications were made between R3 and R4.5 depending on year of application. Different cultivars were used in 2018 as compared to the other study years, but in general cultivars tended to be frogeye leaf spot-susceptible save for one FLS-resistant cultivar in 2018. Disease evaluations depending on the specific disease present and location within the canopy were made both pre and multiple times post-application using a 0-9 scale where 0=no disease, 5=moderate disease and 9=severe foliar disease. However, diseases such as Septoria brown spot and target spot were evaluated based on presence within the canopy by using a modified 0-9 scale based on the location of the disease in the canopy with 0=not present, 5=mid-canopy and 9=upper-canopy. All fungicide applications were made in 15 gallons of water/Acre. Yield was also collected at R8 and standardized to 13% moisture.

In general, significant differences were observed in the level of phytotoxicity as a result of each adjuvant combination. However, a greater degree of phytotoxicity was observed in treatment combinations with the greater, 0.250% v/v application rate. Strangely, combinations that included COC visually appeared to produce less severe phytotoxicity which goes against the conventional wisdom that a NIS would generally be considered to be the less harsh adjuvant choice. Future suggestions for adjuvant combinations would suggest that if an adjuvant were needed, for the purposes of aerial application, an adjuvant rate should not exceed 0.125% to decrease the potential for phytotoxicity as a result of DMI fungicides.

Effect of delayed harvest on the seed quality of commercial soybean cultivars

Rupe, J.C. [1], Rojas, J.A. [1], Holland, R. [1], Segalin, S.R. [1,] Bond, R.D. [2], Still J.A. [2], [1]Department of Plant Pathology, Corp, Soil, and Environmental Sciences[2], University of Arkansas, Fayetteville, AR, USA.

Fall of 2018 was exceptionally rainy across much of the South and Midwest delaying harvest by weeks. This led to high levels of visibly damaged seed due to high levels of seed infection by various fungi and bacteria. Two different trials were conducted, one using commercial varieties and the second using varieties from a United Soybean Board sponsored regional cultivar test. For both tests, seeds were collected and rated for visual quality and seed infection in 2018. The commercial cultivar test planted at Vegetable Research Station, (Kibler, AR) consisted of 212 cultivars from mid maturity group (MG) III to late MG V. There were 15, 35, 38, 53, 53, and 18 cultivars in MG 3.5-4.2, 4.3-4.5, 4.6-4.7, 4.8-4.9, 5.0-5.4, and 5.5-5.9, respectively. These were planted in a randomized block design with three replications. The regional cultivar test was planted at the Lon Mann Research Station (Marianna, AR). In this test, 8, 16, and 21 cultivars were in MG 4-4.5, 4.6-5.0, and 5.1-5.8 respectively. At Kibler, harvest of the commercial cultivar test should have begun on late September, but it was delayed until mid to late October 2018. From each plot at both trials, 140 seed were randomly selected and the number of seed with purple seed stain (PSS), that were brown in color or chalky in color were determined as well as the total number discolored seed. To establish seed infection, four replicates of 50 seed from each plot were surface disinfested and plated on acidified PDA and incubated at room temperature. The resulting fungi were classified and recorded based on morphotype. Data were transformed to proportions and analyzed with PROC GLIMMIX using the beta transformation. In most maturity groups, there were significant (P<0.05) cultivar differences in the proportion of seed that were PSS, brown, chalky or the total proportion of discolored seed. Across MGs in both trials, the proportion of seed with PSS ranged from 0.001 to 0.16, with brown seed from 0.001 to 0.10, with chalky seed from 0.0 to 0.14 and total seed discoloration ranged from 0.01 to 0.24. There were similar ranges of discolored seed from the regional cultivar test at Marianna. Seed from this test were plated on PDA. The two primary fungi recovered were *Phomopsis longicolla* with proportions ranging from 0.08 to 0.76, and *Cercospora kikutchii* with proportions ranging from 0.01 to 0.47. There were significant cultivar differences in fungal seed infection with both these fungi. We will be reporting on our current studies using select cultivars from each maturity group in which we will be identifying the pathogens infecting the seed as determined by plating and molecular methods and assessing seed vigor. From our findings, there are significant differences between cultivars in their response to delayed harvest due to wet weather.

Virome of *Macrophomina phaseolina* isolates collected from soybean fields in Mississippi

Nina Aboughanem-Sabanadzovic, Tessie Wilkerson, Tom Allen & Sead Sabanadzovic

Thirty five isolates of *Macrophomina phaseolina* (Mp), an important and polyphagous phytopathogenic fungus, collected from soybean fields in Mississippi were isolated in pure culture and submitted to dsRNA extraction and subsequent custom-based pair-end Illumina sequencing. Results of this study revealed presence of complex patterns of high molecular weight dsRNA molecules in majority of examined isolate. Presence of viruses was confirmed by observation of negatively-stained purified preparations from dsRNA-containing fungal isolates under transmission electron microscope. Computer-based assembly of Illumina-generated raw sequence data resulted in numerous virus-specific contigs varying in size from several hundred to nearly twenty thousand nucleotides. Analyses revealed presence of numerous recently reported mycoviruses from this host and of dozens of new viruses belonging to recognized genera and/or families of mycoviruses with dsRNA and ssRNA genomes of both polarity. Several viruses discovered in this work appear to belong to completely new taxa, while significant number of ORF-containing sequences (ORFans) did not match currently available data in GenBank. These results further the knowledge about mycovirus diversity. Possible effects of these viruses on fungal host is yet to be fully understood.

Genomic evidence for interspecific hybridization in *Cercospora* cf. *flagellaris* strains associated with Cercospora leaf blight of soybean

Alex Zaccaron[1], Kona Swift[1], Ahmad Fakhoury[2] and Burt Bluhm[1]

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Cercospora leaf blight (CLB) is a resurgent disease of soybean worldwide. For many years, *Cercospora kikuchii* was considered to be the sole causal agent of CLB. However, recent studies indicated that additional *Cercospora* species, particularly *Cercospora* cf. *flagellaris,* are associated with CLB in the U.S. and other countries. Little is known about the genetic basis of pathogenesis in *C*. cf. *flagellaris*, and genetic resistance is broadly lacking in commercial soybean cultivars. The goal of this study was to define population structure and potential mechanisms of pathogenesis in *C*. cf. *flagellaris* through comparative genomics. During the 2017 growing season, 685 strains of *C*. cf. *flagellaris* were collected from symptomatic soybean leaves from thirty locations within eight U.S. states. Additionally, 25 strains were isolated from cotton, basil, watermelon, and mint leaves. Whole-genome resequencing was performed for 26 *C*. cf. *flagellaris* strains from diverse locations and plant hosts. Draft genome assemblies ranged in size from 32.8 to 35.7 Mb, with an average size of 33.7 Mb. Phylogenetic analyses identified 25 of the 26 isolates as *C*. cf. *flagellaris*, and the final isolate as *C.* cf. *sigesbeckiae*. In addition, phylogenetic analyses organized the 25 *C*. cf. *flagellaris* isolates into four lineages that do not corroborate with their geographical location of origin. Pairwise whole genome alignments indicated high levels of variability, and revealed non-conserved genomic regions that suggests the analyzed isolates underwent interspecific hybridization. These results will serve to comprehend the spreading and host adaptation of *C*. cf. *flagellaris*, and ultimately will promote the development of resistance to CLB in soybean.

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Identification of QoI-resistant *Septoria glycines* isolates.

D. L. Neves[1], A. Wang[2], J. D. Weems[1], D. S. Mueller[3], H. M. Kelly[4], C. A. Bradley[1]

[1]University of Kentucky, Princeton, KY; [2] University of Illinois, Urbana, IL; [3]Iowa State University, Ames, IA; [4]University of Tennessee, Jackson, TN

Brown spot, caused by *Septoria glycines*, is a common foliar disease of soybean (*Glycine max*). Excessive sprays of quinone outside inhibitor (QoI) fungicides in soybean have contributed to the development of resistant populations of *Septoria glycines*. We investigated the molecular mechanisms of resistance to QoIs in these populations for the target gene cytochrome b (cytb). Isolates of *S. glycines* were collected from several soybean fields sampled in different seasons in Illinois, Iowa, Kentucky and Tennessee. A single discriminatory dose (0.1 μg/ml) of azoxystrobin, which was completely inhibitory for the QoI-sensitive strains but allowed growth of resistant strains, was used to measure the sensitivity of 410 isolates. Using Next Generation Sequencing and bioinformatics, the cytb gene was identified in the *S. glycines* genome and a set of primers were developed into PCR assays to amplify the cytb and another set of primers, to discriminate QoI-resistant and -sensitive isolates. QoI-resistant isolates made up 38% of the *S. glycines* tested by discriminatory dose. The change from glycine to alanine at position 143 (G143A) was detected for *S. glycines* isolates. For every isolate tested, two PCR reactions allowed discrimination between QoI-resistant (210 bp) and –sensitive (409 bp) isolates.

Genome-wide polymorphic microsatellite markers in *Phytophthora sojae*

Guohong Cai, Tomara J. Fleury, and Ning Zhang

Phytophthora sojae causes stem and root rot in soybean. It is one of the most serious soybean pathogens in the United States, especially in the Midwest region. Understanding genetic and pathogenicity diversity of the pathogen is important for disease control. Microsatellite markers are an ideal tool to examine population genetic structure and dynamics. Currently there are a small number of microsatellite markers available. In this study, we took advantage of the availability of genome sequences from multiple isolates and designed a bioinformatic pipeline to simplify of the development of microsatellite markers. We identified 157 high-quality, informative microsatellite markers in this oomycete pathogen. Experimental validation of 20 loci supported bioinformatics predictions. Our approach can be readily applied to other organisms.

Identifying Soybean Varietal Resistance to Cercospora Leaf Blight and Describing a Leaf Disk Assay for Rapid Resistance Screening

Brian Ward, Paul Price III, Thanos Gentimis

Cercospora leaf blight (CLB) is a serious disease of soybean in the southeastern United States. The disease occurs in the later drier summer months and can defoliate fields in severe cases, leading to annual losses estimated at $45-50 million in the southern 16 states. To further compound issues, the disease is caused by three similar *Cercospora* species (*C. kikuchii*, *C. flagellaris*, and *C. sigesbeckiae*), with unknown distribution and differences between the species. There are currently no resistant soybean cultivars, fungicide resistance has been documented in pathogen populations, and climatic conditions are shifting to be more conducive for disease.

Widespread testing of commercial varieties and breeding lines across 7 states in the mid-south has yielded a starting point for breeders to incorporate resistance and helped to categorize the sporadic varietal resistance over location. At least 5 breeding lines show consistent resistance to CLB. And while no common commercial varieties show strong resistance, there are relative resistances between them. There were numerous susceptible varieties identified, which should be avoided if conditions are favorable for CLB development.

To aid in the breeding selection process, a resistance screening assay has been developed that is fast and reproducible. The assay uses the purified toxin cercosporin produced by the pathogens in lieu of actual pathogen inoculation. The toxin is applied to greenhouse-grown soybean leaf tissue (R5 growth stage) and chlorophyll A is extracted and measured via spectrophotometer to assess the relative resistance of a variety to the toxin. While the assay does not account for biotic-based resistances it can be used to remove very toxin-susceptible lines early in the screening process, and fast-track resistant lines for further testing. The assay can also account for much of the variation observed across locations based upon soil nutrient availability and will further aid breeders in rapid screening for specific locations. These nutritional differences can also have large effects in increasing resistance on a varietal basis, with certain varieties responding to fertilization better than others.

These studies give breeders an excellent starting position to acquire resistance, give growers more data to make informed decisions, and give researchers an easy screening method for testing toxicity issues and varietal resistances on soybean.

Early detection of soybean sudden death syndrome using high-resolution satellite imagery

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Abstract

Sudden death syndrome (SDS) is one of the major yield-limiting soybean diseases in the Midwest. Effective management for SDS requires accurate detection in soybean fields. Since traditional scouting methods are time-consuming, labor-intensive and often destructive, alternative methods to monitor SDS in large soybean fields are needed. This study explores the potential of high-resolution (3 m) PlanetScope satellite imagery for early and accurate detection of SDS using a random forest classification algorithm. We used four spectral bands including red, blue, green, and near-infrared (NIR) and calculated normalized difference vegetation index (NDVI) to detect healthy and SDS-infected quadrats (3 m wide × 1.5 m in length) in a soybean field experiment located in Boone, Iowa. Data collected during the 2016, 2017 and 2018 soybean growing seasons were analyzed in this study. The results indicate that spectral bands of high-resolution PlanetScope imagery along with calculated NDVI can accurately predict SDS in soybean plots even before foliar symptoms develop. Healthy and diseased soybean quadrats were detected with more than 85% accuracy and with kappa statistics, a measure of inter-rater agreement, of more than 68% in all growing seasons. These promising results suggest that high-resolution satellite imagery has tremendous potential for detection of SDS in soybean fields. Our findings highlight that this technology can facilitate large-scale monitoring of SDS and possibly other economically important soybean diseases to guide recommendations for site-specific management in current and future seasons.

Nematodes population distribution and densities as affected by soil type and crop rotation in Tennessee row crops

Rufus Akinrinlola and Heather Kelly

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Plant parasitic nematodes cause up to $80 billion worth of crop damage every year on a worldwide basis, and United States alone has reported up to $8 billion annual yield loss. Monitoring nematode population distributions and densities, and understanding the factors influencing their populations can provide insights on possible management strategies to reduce crop damage. Hence, this study was conducted with two objectives in mind: (1) To determine the population distributions and densities of major plant parasitic nematodes in row crop fields in Tennessee, (2) To determine which, if any, crop, nutrient level, and/or soil type may influence nematodes populations. In 2018, 169 soil samples were collected across 18 counties in Tennessee and 5 counties in Kentucky. From each sample, 100 cc was processed for the presence of plant parasitic nematodes.

Spiral, soybean cyst (SCN), lesion, stunt, dagger, root-knot, and reniform nematodes were the most predominant nematodes found in the samples, with their population occurring in 84, 47, 25, 20, 8, 4, and 4% of the samples, respectively. Their population densities, reported as juveniles in 100 cc of soil, ranged from 7 to 547 for spiral, 7 to 100 (115 to 4,569 eggs) for SCN, 7 to 62 for lesion, 7 to 69 for stunt, 7 to 23 for dagger, 23 to 446 for root-knot, and 38 to 324 for reniform nematodes. Additional samples and data are being processed and analyzed, including HG type testing of SCN populations. Total results and analyses from 2018 will be presented. At this time, growers with significant nematode populations should consider developing appropriate preventive strategies to limit nematode populations increase and spread that can cause potential crop damage and yield loss.

Kew words: Nematodes, field crops, soybean cyst nematodes, root knot nematodes, reniform nematodes

The effects of *Soybean vein necrosis virus* (*Bunyaviridae: Tospovirus*) on soybean (*Glycine max*) yield

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Soybean (*Glycine max*) is a crop of global importance and the United States is the world's largest soybean producer. Several viruses can infect soybean and result in significant yield loss to growers. *Soybean vein necrosis virus* (SVNV), a tospovirus, was first reported in Tennessee in 2008 and has since been found in 12 additional states: Alabama, Mississippi, Arkansas, Oklahoma, Kansas, Missouri, Kentucky, Ohio, Iowa, Wisconsin, Illinois, and Michigan. Like all tospoviruses, SVNV is transmitted by thrips in a persistent and propagative manner. This virus was observed in West Tennessee in the 2018 growing season. This study aimed to: (1) identify and collect symptomatic and asymptomatic plants; (2) confirm virus presence by enzyme-linked immunosorbent assay (ELISA); and (3) evaluate and compare yield parameters of sampled plants. Symptomatic and asymptomatic plants were identified and tagged in five experimental field trials across two locations in West Tennessee, Milan (Gibson county) and Jackson (Madison county). From each sampled plot, paired asymptomatic and symptomatic leaf samples were taken at growth stage R6 and whole plants were harvested at growth stage R8. Five yield parameters were recorded: plant height, number of pods per plant, number of seeds per pod, plant yield, and 100-seed weight per plant. Presence of SVNV was detected by an ELISA test in all the symptomatic samples across both locations and all asymptomatic samples were negative, except one sample from Jackson. None of the yield parameters of the symptomatic plants were significantly different from those of the asymptomatic plants. A nested real-time PCR assay is forthcoming to quantify the amount of SVNV present across all samples.

Keywords: *Glycine max*, *Tospovirus*, ELISA, yield parameters

Has *Cercospora kikuchii* vanished in the U.S.? Comparative genomics provides new clues

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Cercospora leaf blight (CLB) has become one of the most prevalent foliar diseases of soybean in the southern U.S., and has become increasingly more common in Midwestern states. Although the causal agent of CLB was originally described as *Cercospora kikuchii*, recent studies have identified two other pathogens associated with CLB: *Cercospora* cf. *flagellaris*, and *Cercospora* cf. *sigesbeckiae*. Intriguingly, recent surveys of pathogens associated with CLB across the U.S. failed to detect *C. kikuchii*. This has led to the question of whether *C. kikuchii* fell victim to 'strain replacement' by *C.* cf. *flagellaris* and *C.* cf. *sigesbeckiae*, or if there are other genetic or epidemiological mechanisms underlying this apparent shift. To address these questions, we sequenced the genome of a historical isolate of *C. kikuchii* (isolated in the late 1990s from soybean in Indiana), and two isolates of *C.* cf. *sigesbeckiae* (isolated from soybean in Louisiana in 2012, and Arkansas in 2017). High quality genome assemblies were obtained for all three strains. Surprisingly, the majority of the genomes (>70%) of all three strains were virtually identical, which indicated an extremely close taxonomic relationship. Intriguingly, the portion of the genomes that differed the most between *C. kikuchii* and *C.* cf. *sigesbeckiae* were clustered into distinct regions that were spread broadly across the assembly scaffolds (and thus presumably the chromosomes). The regions that distinguished *C. kikuchii* and *C.* cf. *sigesbeckiae* were highly conserved in the two *C.* cf. *sigesbeckiae* strains despite the amount of time and physical distance distinguishing their original collections. Together, these factors suggest that the genomic polymorphisms distinguishing *C. kikuchii* and *C.* cf. *sigesbeckiae* are introgressions resulting from interspecific hybridization. The high level of genomic identity among the three strains suggests that the hybridization event was relatively recent. Furthermore, the extremely high level of genomic identity between the two *C.* cf. *sigesbeckiae* strains implies that sexual reproduction is either uncommon or does not occur in this species. In sum, these findings indicate that *C.* cf. *sigesbeckiae* is a hybrid derived from *C. kikuchii* and another as-yet unknown *Cercospora* species, and it has a propensity for clonal propagation. These results suggest that species barriers among *Cercospora* spp. are semi-permeable to the exchange of genetic information, which will be an important consideration for breeding strategies to control *Cercospora* diseases of soybean.

Evaluation of field soils collected from the Mid-southern United States for differences in soybean cyst nematode egg density and reproduction

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The soybean cyst nematode (SCN; *Heterodera glycines*) is a plant parasitic nematode of soybean that is widespread throughout the soybean growing regions of the United States and Canada that is responsible for more than $1 billion in monetary losses annually. In parts of the Mid-Southern U.S., there is evidence to suggest that SCN has virtually disappeared from soybean-growing areas where the nematode was historically present, indicating the possible development of SCN suppressive soils. To better understand why these reductions in SCN may have occurred, a study was constructed to: i) evaluate if SCN is still present in soil collected from five geographically diverse locations in the Mid-South, and ii) determine if SCN reproduction on a susceptible soybean cultivar differs among field sites. For this study, a 5-gallon sample of field soil was collected from each of five soybean producing sites in four states (Missouri, Arkansas, Mississippi, and Louisiana) representing geographically and agronomically diverse areas of the region. Each soil sample was thoroughly mixed and processed for cysts using an elutriator. Cysts were ground to release eggs which were counted to obtain initial SCN egg densities. SCN eggs were detected in all soils except for the northern Arkansas site (ranging from 0 to 10,500 eggs/250 cc of soil), indicating that SCN has not disappeared from soils where soybean is still produced in any of the four states. After initial egg counts, a greenhouse assay was conducted using the naturally infested and SCN-inoculated field soil to measure SCN reproduction on the SCN-susceptible cultivar Williams 82 when grown for 30 days. The assay was repeated twice with each treatment replicated five times. Females were washed from the roots and processed for final cyst counts and plant weights were recorded. Initial results suggested decreased reproduction of SCN in the soil from Louisiana despite inoculation with 500 SCN eggs per plant. To further explore this difference, a second greenhouse assay was conducted with a subset of soil from the Louisiana location, the Missouri location, and laboratory soil serving as the negative control which were autoclaved and used for comparison to non-autoclaved soil from each respective location. In addition, half of the autoclaved and non-autoclaved treatments were inoculated with 500 SCN eggs per plant to ensure root colonization. Each treatment was replicated four times. The SCN-susceptible cultivar Williams 82 was grown for 30 days and females were washed from the roots and counted. In all greenhouse assays, SCN females were present in all treatments including those with an egg count of zero. Of note was the presence of SCN eggs, but diminished reproduction by the nematode in the soil from Louisiana. Even though SCN reproduction was reduced in the soil from Louisiana, the mechanism or cause for suppression is unknown.

Soybean variety response to *Xylaria* sp., causal agent of taproot decline

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Taproot decline is a newly discovered disease of soybean. The causal agent, *Xylaria* sp., is a novel species most closely related to *Xylaria striata* within the *Xylaria arbuscula* aggregate. Foliar symptoms include interveinal chlorosis and necrosis, and upon further investigation, there are often dead plants adjacent to symptomatic plants within the row. Many other soybean diseases have similar foliar symptoms; therefore, further investigation is required for proper identification. Soybean debris from previous years is suspected to be the primary source of inoculum. Plants may be infected at any point during the growing season, often resulting in premature death. Precision planting, reduced tillage, and soybean monoculture contribute to increases in disease incidence and severity. There have been no studies related to sources of resistance to taproot decline.

The pathogen is easily isolated from the pith or lateral roots of infected plants after surface sterilization and subsequent placement on potato dextrose agar. For this study, the pathogen was cultured on twice-sterilized Japanese millet, and soybean varieties (n=147, seed obtained from 2016 LSU AgCenter Official Variety Trials) were inoculated (1cc infested millet/6-inch pot) in the greenhouse. There was no effect of non-infested millet on plant growth; therefore, non-inoculated plants served as controls. Final emergence was counted after 21 days. Whole plants were harvested, washed of growth medium, cut at the crown, oven-dried until final moisture, and roots and shoots were weighed. Emergence, root weight, and shoot weight were compared for each variety using a paired t-test (α=0.05).

Significant reductions in emergence, root weight, and shoot weight were observed in some varieties. Since initial germination of seed was unknown, emergence data are not presented. Shoot weight was correlated with root weight, and TRD is a root disease; therefore, root weight reduction data were used to delineate varieties. There were significant reductions ranging from 48 to 85% in 56 varieties; therefore, varieties with root weight reductions of $\geq$48% were considered susceptible. Varieties (n=25) with root weight reductions ranging from 36 to 48% were considered moderately susceptible. Those (n=16) with root weight reduction ranging from 24 to 36% were considered moderately resistant, and varieties (n=7) with <24% reduction were determined to be resistant. In field confirmation experiments, varieties showing significant height and yield reduction when inoculated were susceptible in greenhouse studies. Varieties deemed resistant in the greenhouse showed no significant effects on height and yield from the inoculum in the field. Results from these studies indicate that commercial sources of resistance to taproot decline are available to soybean producers. More field research is needed to corroborate these results.

Identification of alternative hosts for *Xylaria* sp., the pathogen of taproot decline of soybean

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Taproot decline (TRD) of soybean is caused by an undescribed species of *Xylaria*. The disease is characterized by the breakdown of the taproot leading to foliar symptoms such as interveinal chlorosis, necrosis, and occasional plant death. Stroma, a cushion-like mass of vegetative hyphae, serves as the diagnostic feature on the taproot of affected soybean plants. Deadman's fingers, or stromata, can be observed on soybean residue from the previous growing season and are believed to serve as overwintering structures. Five *Xylaria* sp. isolates from geographically distinct locations in Mississippi were used to inoculate corn (*Zea mays* L.), cotton (*Gossypium hirsutum* L.), rice (*Oryza sativa* L.), sorghum (*Sorghum bicolor* L.), wheat (*Triticum aestivum* L.), and soybean (*Glycine max* L.). These hosts were chosen to represent row crops traditionally grown in areas adjacent to or in rotation with soybean. Soybean was included as the standard host. In 10-cm plastic pots, *Xylaria* sp.-infested-corn cob grit (1.25 g) was spread in a 3.5 × 5 cm furrow in direct contact with surface disinfested seed. Experimental units were arranged in a randomized complete block design with five replicates (pot) of each *Xylaria* sp. isolate and within each pot three host plants served as sub-samples. The greenhouse was maintained at ≥ 24°C to achieve an average soil temperature of 27°C. The experiment was conducted three times. At 10 weeks, each plant was subjected to destructive sampling where shoots were separated from the roots and stored at 4°C until analysis. Plant height and fresh weight of shoots was recorded before being placed in a drying oven at 60°C for 5 days and subsequently weighed again. The root systems were rinsed in 2.5% sodium hexametachloride solution, rinsed in distilled water three times, and towel-dried. Root systems of the host plants were weighed and evaluated for disease incidence and severity. A binary observation was made for incidence where: 0 = absence of stroma and 1 = stroma produced on roots as a result of colonization by *Xylaria* sp. on the root system. To assess the severity of stroma colonization on the root system, a visual evaluation was made based on a 0 to 4 scale where: 0 = absence of stroma; 1 = 1 to 25% stroma colonization of root system; 2 = 26 to 50% stroma colonization; 3 = 51 to75% stroma colonization; 4 = 76 to100% stroma colonization. Plant height, plant fresh and dry weights, root weight, root disease severity, and incidence data were subjected to analysis of variance using PROC GLM in SAS. The midpoints of the root disease percentage range were used to analyze the root disease severity. The percentages were also arcsine transformed then back transformed for the presentation of the data. When significant (α=0.05), means were separated using Fisher's protected least significant difference. Data were pooled across experiments as there was no isolate by experiment interaction. *Xylaria* sp. produced stroma on corn, cotton, rice, sorghum, wheat, and soybean. There were no differences among *Xylaria* sp. isolates with respect to their effect on the six host species. Root disease severity was low across hosts with a range of 5.4 to 13.6%. Soybean had significantly greater disease severity when compared to non-soybean hosts. However, incidence ranged from moderate to high (42.9 to 85.9%), with wheat plants having the lowest incidence and sorghum and soybean having the greatest.

Functional genomics in *Phomopsis longicolla* as a tool to dissect Phomopsis seed decay at the molecular level

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Phomopsis longicolla (Hobbs) causes Phomopsis seed decay, one of the most prevalent and potentially damaging diseases of soybean seed worldwide. Currently, little is known about the molecular basis of pathogenesis in *P. longicolla*, in part because crucial tools for molecular genetics, such as targeted gene deletion, have not been demonstrated in this organism. In other filamentous fungi, the heterotrimeric CCAAT-binding complex is involved in diverse aspects of growth and development, including secondary metabolism, morphogenesis, and pathogenesis. In this study, a putative component of the CCAAT-binding complex (*HAP3*) was identified in *P. longicolla* and characterized through functional genomics. The *HAP3* gene was successfully deleted via homologous recombination, and the mutant was genetically complemented via reintroduction of the wild-type gene. *HAP3* deletion strains had significantly reduced pathogenicity on soybean seeds and stems. Expression profiling during colonization of soybean seeds identified 2353 genes differentially regulated following deletion of *HAP3*, including genes predicted to encode plant biomass degrading enzymes, effector proteins, and structural and enzymatic components of secondary metabolism. This study establishes the involvement of the CCAAT-binding complex in *P. longicolla* pathogenesis and demonstrates the feasibility of targeted gene deletion in this organism. Phenotypic similarities between *HAP3* deletion mutants of *P. longicolla* and other plant pathogenic fungi potentially indicate a broad involvement of the CCAAT-binding complex in plant pathogenesis.

Taxonomic diversity of *Diaporthe* species associated with soybean in Arkansas

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Diaporthe species can be pathogens, endophytes, or saprobes, and are associated with a wide range of plant hosts. Some *Diaporthe* species were identified as pathogens associated with soybean. However, the diversity of *Diaporthe* species associated with asymptomatic tissues of soybean has rarely been studied. To study the diversity of *Diaporthe* in Arkansas, 184 isolates were obtained from asymptomatic stem tissues of soybean plants in four locations: Marianna, Rohwer, Stuttgart, and Keiser in Arkansas, USA in 2015. Phylogenetic Bayesian Inference and joining neighbor trees were constructed from a combined multilocus dataset (ITS, TEF1-α, TUB2, and CAL) to evaluate species diversity. Additionally, the pathogenicity of 114 isolates was evaluated with a cut-stem inoculation technique. Isolates of *Diaporthe* clustered in four distinct clades with high support, corresponding to four known species. The following distribution was observed: 133 isolates clustered with *D. longicolla,* 41 isolates clustered with *D. unshiuensis,* 8 isolates clustered with *D. ueckerae,* and 2 isolates clustered with *D. pescicola*. Although the distribution and diversity of these clades varied throughout Arkansas, *P. longicolla* was dominant in all locations. Isolates that clustered with *D. unshiuensis* were obtained from only three locations, and isolates that clustered with *D. ueckerae* were isolated from only two locations. Furthermore, all 114 isolates evaluated for pathogenesis caused lesions on soybean stems. Thus, this study significantly expands the current knowledge regarding the distribution of *Diaporthe* species associated with soybean in Arkansas.

Wilting response of soybean leaves to culture filtrates of *Corynespora cassiicola* isolates from cotton and soybean

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Corynespora cassiicola, the causal agent of target spot disease, is a fungal pathogen with increasing importance in cotton and soybean producing countries. Severe disease symptoms and significant yield losses can occur when the pathogen is not properly controlled. The use of resistant or tolerant cultivars have been recommended as a long-term strategy to control the disease but this option is not always available. The lack of studies on screening methodologies to select germplasm resistant or tolerant to target spot make screening difficult in early phases of soybean breeding. The choice of representative isolates and the methodology used to screen germplasm are the main problems faced for plant pathologists and plant breeders. Specific genes known as cassiicolin-encoding genes (*Cas2*, *Cas6*, and *Cas2+6*) were found in *C. cassiicola* isolates from cotton and soybean in Alabama, reflecting an overall genetic diversity of the isolates. Under all circumstances, it is highlighted the need for a reliable screening methodology of soybean germplasm. For this reason, we assessed the wilting response of soybean leaves to culture filtrates of several *C. cassiicola* isolates from cotton and soybean in Alabama as a potential screening methodology of soybean germplasm. For the culture filtrates production, mycelial growth of *C. cassiicola* in PDB was vacuum filter-sterilized through a set of Millipore membranes. Trials included cultures filtrates from *C. cassiicola* isolates sampled from soybean, later isolates from cotton were tested. For each trial, trifoliate soybean leaves (tolerant and susceptible) collected at the greenhouse were immediately immersed in the solution: culture filtrates + water (50% v/v) for 24 hours. Water was used as the negative control. The degree of wilting was grouped into three categories (1 – mild, 2 – moderate, or 3 – severe). Data collected was analyzed using SAS 9.4 PROC GLIMMIX, and LS-means separated using Fisher's Protected LSD ($P \leq 0.05$). For the first trial, the use of different soybean germplasm, and culture filtrate were significant ($P \leq 0.05$). Susceptible soybean germplasm exhibited higher wilting ($P \leq 0.05$) compared to the tolerant. Two out of six isolates, PBU06 (*Cas2*) and LIM13 (Cas0) induced higher wilting of soybean leaves ($P \leq 0.05$). Only culture filtrates were significant ($P \leq 0.05$) for the second trial not the soybean germplasm (tolerant or susceptible). PBU06 (*Cas2*) isolate induced higher wilting of soybean leaves, followed by FHP01 (Cas0) ($P \leq 0.05$). The other six isolates exhibited lower induction of soybean leaf wilting, similarly to the negative control (water) ($P \leq 0.05$). In summary, some *C. cassiicola* isolates from soybean were not toxic enough to be used in this screening methodology, and most of the isolates from cotton exhibited no effect on soybean leaf wilting indicating some host-specificity. Those preliminary results might indicate a leaf-wilting bioassay as a methodology to assess the indirect response of soybean germplasm to *C. cassiicola*.

Analysis of systemic resistance caused by *Bacillus* sp. in *Meloidogyne incognita* infested *Glycine max*

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Meloidogyne incognita is an endoparasitic nematode that causes yield losses in soybeans. *Glycine max*. Management of the nematode includes chemical nematicides, cultural control and biological control. Due to the low manufacturing cost and environmental benefits, biological control agents are becoming more popular as a control method for this nematode. Biological control agents can work by direct or indirect antagonism. Indirect antagonism includes the upregulation of plant defense pathways. This specifically refers to induced systemic resistance pathway, which utilizes jasmonic acid, and the systemic acquired resistance pathway, which utilizes salicylic acid. Determining which pathway a biological control agent, with an indirect method of antagonism, stimulates is essential to the integration of the biological control agent into a successful pest management program. This research will examine five *Bacillus* species and their ability to stimulate a systemic response to *M. incognita* within soybean. Experiments will include a greenhouse test, an in vitro assay, and a split root assay. Results of the greenhouse test will determine the efficacy of the *Bacillus* sp., while results of the in vitro assay and split root assay will determine whether the mechanism of action is direct or indirect for each species. The findings of this research will help implement these biological control agents in an integrated pest management program for nematodes, specifically *M. incognita*.

Determining the role of new soybean germplasm in reducing losses associated with poor quality grain in Mississippi soybean

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Major economic losses in the southern U.S. soybean production system may be attributed to poor grain quality which can result from delayed harvest. In extreme situations grain elevators have reported an average of 7% damage. In some years, Phomopsis seed decay, caused by *Phomopis longicolla* (PL), can have an economic impact by affecting harvested soybean grain quality resulting in losses for soybean farmers at the grain elevator. In addition, PL can occur in soybean seed production fields and subsequently result in seed exhibiting slow seed germination or no germination. The objective of this research was to determine differences in grain damage between soybean entries under environmental conditions conducive to reducing the quality of harvested grain. Field trials were established under rainout shelters (n=2) consisting of greenhouse cold frames covered with two-ply semi-clear plastic in 2018. Each shelter contained twenty-one entries planted as single row plots, on 30-inch centers measuring 12 foot in length, replicated three times. All plots in Shelter 2 were inoculated at the R5.5 growth stage using a PL spore suspension consisting of beta conidia while plots in Shelter 1 remained non-inoculated. The soybean plots in Shelter 2 received a 4 fl oz/acre application of trifloxystrobin + prothioconazole (as Stratego YLD) at beginning maturity (R7) while the plots in Shelter 1 remained non-treated. Shelters were simultaneously overhead irrigated for approximately 200 hours. Plots were hand-harvested at full maturity (R8) to determine plot weight and associated grain damage. Observations of grain damage were based on observations of a composite of symptoms associated with Phomopsis seed decay that included: presence of white mycelium considered to be PL, as well as individual kernels with a shriveled, elongated or cracked appearance. Hundred kernel weights were determined from post-harvest grain samples and seed viability was measured using a simple germination test consisting of three subsamples from each harvested plot sample incubated at 22°C for 7 days. Data were subjected to analysis of variance using PROC GLM in SAS. Significant differences were observed in the non-fungicide shelter between entries with a 78% difference in weight between Progeny 4211 (selected check) and 11030-541-210 and an 81% difference in damage between 11030-541-210 and DB06X06-093, two advanced entries from the USDA breeding program. No significant differences in harvested weight, hundred kernel weight or grain damage were observed in the fungicide-treated shelter. Additional research is needed to determine the potential of germplasm in reducing seed quality losses.

Fungicide Sensitivity Screening for *Corynespora cassiicola* and Field Evaluations

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Target spot (TS), caused by the fungus *Corynespora cassiicola*, is a foliar disease of cotton and soybean. Over recent years, TS has become a disease of concern, although Frogeye Leaf Spot (FLS), caused by the fungus *Cercospora sojina,* has greater potential for impacting yield. In 2010, *C. sojina* isolates were reported to have resistance to quinone outside inhibitor (QoI, FRAC Group 11) fungicide group. Since then, evaluating *C. sojina* for QoI resistance has been of interest in Tennessee and other soybean production states. With the emergence of TS, interest now includes monitoring for fungicide sensitivity in both pathogens. The objective of this study is to conduct fungicide screening to monitor sensitivities and resistances in *C. cassiicola* and *C. sojina* in Tennessee soybean and cotton production.

Fungal isolates were collected from research field trials as well as from grower soybean and cotton fields. The sensitivity of 18 *C. cassiicola* isolates to 8 technical grade fungicides across multiple fungicide groups (FRAC Groups 1, 3, 7, and 11) was evaluated based on mycelial growth inhibition assays. The effective concentration of each fungicide to inhibit 50% of the fungal growth (EC_{50}) was calculated. All active ingredients had EC_{50} > 100 µg/mL with the exception of difenoconazole which EC_{50} varied among isolates from 3 to 40 µg/mL.

In addition to laboratory assays, field trials were conducted at 3 locations. Five fungicide tank mixes were evaluated for control of TS and FLS among 3 soybean varieties of differing susceptibility. Ratings on a 0-100% scale were used to evaluate control of FLS and TS. There were no significant interactions between variety and fungicide product on yield. While all treatments reduced FLS compared to the non-treated check, only Miravis Top significant increased yield. Similarly, only Miravis Top and Quadris Top significantly reduced TS compared to the non-treated check.

Based on the EC_{50} values and lack of control with products not containing difenoconazole one can conclude there is lack of efficacy and/or resistance already in the isolates tested… the poster presenting this data will allow the audience to vote and give their opinion on which might be the case and how one would justify their opinion or further investigate.

Impact of seed treatment and seed quality on soybean emergence and yield

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Soybeans are negatively affected by seedling diseases which can significantly reduce stands and yields. These diseases are strongly dependent on environmental conditions, particularly soil physical and chemical properties, soil temperature and moisture and pathogen diversity. Another factor that can interact with these soil factors is seed quality. Most commercial soybean seed is of high quality (high seed vigor, low seed infection), but lower quality seed may be marketed if demand is high and seed supplies are low. The primary control for seedling diseases is the use of a seed treatment. There are several commercially available seed treatments, most with multiple fungicides and some with insecticides. The effectiveness of these seed treatments may depend on the environment and on the pathogens present. The objective of this study was to evaluate the efficacy of commercially available soybean seed treatments on high and low quality seeds across a range of environments.

The test was conducted with the soybean cultivar UA5715 GT. In order to obtain low quality seed, high quality seed of this cultivar were exposed to 100% relative humidity at 40oC for one week. This resulted in a high quality seed lot that had 80% standard germination (SG) and 77% germination in accelerated aging (AA). The low quality seed lot had 65% SG and 60%. These seed were treated at labeled rates with nine commercially available seed treatments: ApronMaxx RFC, Cruiser 5 FC, CruiserMaxx Vibrance Beans, Avicta Complete Beans, Maxim 4 FS, Vibrance, EverGol Energy, Trilex, and Alligiance FL. The control treatment was treated with water. The tests were planted in a randomized complete block design with 5 replications at four Arkansas, locations (Rohwer, Marianna, Keiser and Kibler) with two sowing times (early May and June) except for the Marianna location that had only a June planting. Plant stand were determined at 14 and 28 days and yields were taken at the end of the season.

At four of the locations, between one and four seed treatments resulted in greater stands than the control with high quality seed. These treatments included Alligiance, CrusierMaxx Vibrance Beans, EverGol Energy, Trilex and Vibrance. With low quality seed, significantly greater stands than the control occurred at two locations with two or three treatments: ApornMaxx, Avicta Complete Beans and CrusierMaxx Vibrance Beans. However, EverGol Energy at two locations, Trilex at three locations, and Vibrance at all locations resulted in significantly lower stands than the control with low quality seed, but not high quality seed. At most locations and planting dates, yields were not significantly affected by seed quality or seed treatment except the late planting at Keiser. The yields low quality seed treated with Allegiance, ApronMaxx, Avicta Complete Beans, Cruiser 5 FC or CrusierMaxx Vibrance Beans had yields similar to the best yields of the high quality seed.

Southern United States Soybean Disease Loss Estimates for 2018

Allen, T.W.[1], Bissonnette, K.[2], Bradley, C.A.[3], Damicone, J.P.[4], Dufault, N.S.[5], Faske, T.R.[6], Isakeit, T.[8], Kemerait, R.C.[9], Koehler, A.[10], Mehl, H.L.[11], Mueller, J.D.[12], Padgett, G.B.[7], Price, P.P.[13], Sikora, E.J.[14], Thiessen, L.[15], and Young, H.[16]

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Since 1974, soybean disease loss estimates for the southern United States have been published in the annual proceedings of the Southern Soybean Disease Workers (SSDW). Summaries of the results from between 1977 and 2010 have been published in numerous refereed scientific journals (10; 12-21; 23-24). Disease loss estimates from 2010 to 2018 have been published annually in the SSDW proceedings (1; 3-9; 11) and most recently in a publication that included the estimates from 2010 to 2014 in Plant Health Progress that includes the loss estimates from the entire soybean production region including the southern and northern states (2). In addition, a website through the University of Illinois Extension Service is available and summarizes the estimated yield losses from both the northern and southern U.S. from 1996 through 2014. The website can be accessed at:

http://extension.cropsci.illinois.edu/fieldcrops/diseases/yield_reductions.php

Various methods were used to obtain the disease losses, and most individuals relied on multiple methodologies to arrive at estimates. The methods employed included: field surveys, plant disease diagnostic clinic samples, variety trials, and questionnaires to Cooperative Extension staff, research plots, grower demonstrations, private crop consultant reports, foliar fungicide trials, sentinel plot data, variety trial ratings, and "pure guess". The production figures for each state were collected from the USDA/NASS website in early February 2019 due to the government shutdown these were a little later than normal. Production losses were based on estimates of yield in the absence of disease. One additional topic that was added to the 2018 data summary was the comparison of environment from within each state. Numerous states indicated that seed decay issues (Phomopsis seed decay) were more problematic during 2018. In an attempt to keep data collection and reporting simple a centroid from each state was determined based on designated geographic centroid for each state and were obtained from Wikipedia (https://en.wikipedia.org/wiki/List_of_geographic_centers_of_the_United_States). In situations where environmental data were not available in close proximity to the centroid a different location was selected. State, county and designated centroid location are presented in Table 1. Environmental data representing the most current 30-year normal (1981-2010) were downloaded for each corresponding location from the National Centers for Environmental Information data tools which includes climate normal (https://www.ncdc.noaa.gov/cdo-web/datatools/normals).

Table 1. Location of state centroids used to download environmental data for the 2018 season from each state in the southern soybean production system.

State	County/Parish	Location
Alabama	Chilton	Clanton
Arkansas	Pulaski	Little Rock
Delaware[a]	Sussex	Georgetown
Florida[a]	Leon	Tallahassee
Georgia	Twiggs	Macon
Kentucky	Bayle	Danville
Louisiana[a]	Rapides	Alexandria
Maryland[a]	Baltimore	Baltimore
Mississippi[a]	Madison	Canton
Missouri	Miller	Jefferson City
North Carolina	Chatham	Sanford
Oklahoma	Oklahoma	Oklahoma City
South Carolina	Richland	Columbia
Tennessee	Rutherford	Murfreesboro
Texas	McCulloch	Brady
Virginia[a]	Buckingham	Lynchburg

[a] Location moved based on lack of 30-year normal data, lack of temperature data for 2018, or a lack of a complete set of precipitation data for 2018 from the corresponding defined state centroid.

The 2018 total acres harvested, average yield (bushels/Acre), and total production (yield in bushels) from each state are presented in Table 2. Soybean acreage in the sixteen southern states in 2018 increased compared to that reported in 2017 by 2.6% (1). Ten states (AL, AR, FL, GA, LA, MO, NC, OK, SC, and TX) reported an overall reduction in the harvested number of acres between 2017 and 2018. The 2018 average per acre soybean yield was 42.3 bushels per acre, a 6.2% decrease in average yield compared to the 2017 average yield (45.1 bu/A). As opposed to 2017, when 13 southern states recorded a record yield, only one state reported a record yield (MS; +1.5 bu/A over the previous record). In 2018, more than 951 million bushels were harvested from approximately 20.5 million acres from the 16 southern states accounting for a 7.3% decrease in the total harvest compared to 2017.

Production losses associated with disease severity estimates were based on the formula used to derive production losses: potential production without disease loss = actual production ÷ (1-percent loss) (decimal fraction). Rounding errors may occur in the tables provided below due to the presence of "trace" estimates of disease which were estimated by the state pathologist rather than assigning the value that had been used in the past to be approximately 1×10^{-9}. Total losses

in the form of percent disease loss by state and total losses in millions of bushels were determined by averaging the loss by state with the inclusion of the trace estimates.

Percentage loss estimates from each state are specific as to causal organism or the common name of the disease (Table 3). The total estimated average percent disease loss for 2018 was 9.8%, a 2% increase losses compared to 2017. In terms of the top five diseases encountered during 2018, some minor shifting occurred between what was observed in 2017 and this season. Phomopsis seed decay, soybean cyst nematode (SCN), root-knot nematode, Cercospora leaf blight, and purple seed stain were the top five diseases, respectively. Three of the top five diseases were similar between 2017 and 2018, but the seed rot observed in most states throughout the southern region accounted for a major increase in the estimated losses associated with Phomopsis seed decay. Breaking the diseases down into plant categories impacted by the diseases within that specific category nematode diseases (28.4%), root diseases (12.9%), foliar diseases (24.9%), seedling diseases (3.8%), and seed diseases (29.0%) highlights the importance of specific groups of diseases and which disease areas are causing the greatest estimated losses. Diseases included in the category "other diseases" could not be separated into separate categories. As a whole, 13 states reported an increase in percent disease losses compared to 2017 (AL, AR, DE, FL, KY, LA, MD, MS, NC, OK, SC, TN, TX). In addition, and one important note regarding the diseases observed and reported during 2018, a greater number of states continue to report losses associated with target spot. In 2016 only seven states reported observing target spot while this number increased to nine states in 2017 and increased to 10 states in 2018. An increasing number of states reporting this specific disease indicates that target spot is becoming a much more widespread concern.

In terms of the disease losses in millions of bushels, the 2018 disease losses accounted for 109.28 million bushels in lost potential production, a 15% increase compared to the estimated losses incurred during 2017 (Table 4).

Environmental conditions during 2018 were conducive for widespread development of seed rot issues throughout the southern soybean production system (Table 5). In addition, temperature for 2018 was also compared to the 30-year normal (1981-2010). In general, looking across the entire year, based on temperature averages for the whole year, nine states were observed to have temperature increases when compared to the 30-year normal. Looking at temperature data by month, seven months had average temperature increases with three of those months being May, June and July across the region. Taken as a whole, all but one state, Missouri, had increases in annual rainfall. The increases in percent rainfall by state ranged from a low of 3.4% (Georgia) to a high of 31.7% (Arkansas) more rainfall for the year.

Acknowledgments

Funding was provided from the United Soybean Board to collate the losses across the region as part of a larger effort to collect losses from the entire soybean producing area in the U.S. The members of the SSDW Disease Loss Estimate Committee see value in continuing to collect the estimates on an annual basis and will continue to seek funding sources to support the effort in the future.

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Table 2. Soybean production in 16 southern states in 2018.

State	Acres (1,000s)[a]	Bu/Acre[b]	Yield in Bu (1,000s)[c]
Alabama	340 (-)	41 (-5)	13,940 (-)
Arkansas	3,240 (-)	51 (0)	165,240 (-)
Delaware	168 (+)	42 (-9)	7,056 (-)
Florida	12 (-)	38 (4)	456 (-)
Georgia	135 (-)	40 (-2)	5,400 (-)
Kentucky	1,990 (+)	52 (-1)	103,480 (+)
Louisiana	1,200 (-)	52 (-2)	62,400 (-)
Maryland	515 (+)	47.5 (-3.5)	24,463 (-)
Mississippi	2,190 (+)	54.5* (1.5)	119,355 (+)
Missouri	5,800 (-)	45 (-4)	261,000 (-)
North Carolina	1,570 (-)	34 (-6)	53,380 (-)
Oklahoma	600 (-)	30 (1)	18,000 (-)
South Carolina	375 (-)	29.5 (-8.5)	11,063 (-)
Tennessee	1,670 (+)	46 (-4)	76,820 (-)
Texas	135 (-)	32 (-5)	4,320 (-)
Virginia	590	43 (-1)	25,370 (-)
TOTAL	**20,530**		**951,743**
		Avg. 42.3 (-2.8)	

[a] Difference from 2017 indicated in parentheses as either a decrease (-) or increase (+).
[b] Difference from 2017 indicated in parentheses as either a decrease (-) or increase (+) in addition to the value difference between 2017. Asterisk (*) denotes a state that set a yield record.
[c] Difference from 2017 indicated in parentheses as either a decrease (-) or increase (+).

Table 3. Estimated percentage loss of soybean yield due to diseases from 16 southern states during 2018.

	% yield suppression by state																
Disease	**AL[a]**	**AR**	**DE**	**FL**	**GA**	**KY**	**LA**	**MD**	**MS**	**MO**	**NC**	**OK**	**SC**	**TN**	**TX**	**VA**	**AVG**
Anthracnose	0.10	0.30	0.00	0.40	0.50	0.00	0.50	0.00	0.00	0.00	0.05	0.10	0.05	0.50	0.00	0.50	**0.19**
Bacterial diseases	0.00	0.10	0.00	0.10	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.01	0.05	0.00	0.00	0.00	**0.02**
Brown stem rot	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.01**
Cercospora leaf blight	1.00	1.00	0.50	0.50	0.50	0.05	3.00	0.10	1.50	0.50	0.80	0.20	1.00	0.03	0.00	1.00	**0.73**
Charcoal rot	0.25	0.40	0.50	0.25	1.00	0.15	1.00	0.20	0.80	0.10	0.00	0.80	0.05	1.40	0.00	0.00	**0.43**
Downy mildew	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.01	**0.01**
Frogeye leaf spot	0.40	0.70	0.00	0.40	0.10	1.00	1.00	0.01	0.10	0.40	0.40	0.10	0.50	1.50	0.10	0.50	**0.45**
Fusarium wilt and root rot	0.00	0.20	0.01	0.01	0.00	0.00	0.10	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	**0.03**
Other diseases[b]	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.05	0.00	**0.01**
Phomopsis seed decay	2.00	3.00	4.00	1.00	0.50	1.50	7.00	4.00	4.00	0.07	0.80	2.50	3.00	2.50	0.00	1.00	**2.30**
Phytophthora root and stem rot	0.00	0.10	0.00	0.01	0.00	0.30	0.10	0.00	0.00	0.50	0.70	0.05	0.00	0.02	0.00	0.01	**0.11**
Pod and stem blight	0.20	0.80	1.00	0.20	1.00	0.30	1.50	0.50	0.00	0.50	0.70	0.50	0.50	0.00	0.00	1.00	**0.54**
Purple seed stain	0.20	0.30	1.50	0.20	0.25	0.90	0.70	1.00	0.50	0.10	0.70	0.70	0.30	0.05	1.00	0.50	**0.56**
Reniform nematode	0.25	0.20	0.00	0.50	0.10	0.00	0.75	0.00	0.50	0.00	0.00	0.00	1.00	0.00	0.00	0.00	**0.21**
Root-knot nematode	0.50	4.50	0.50	0.50	3.00	0.00	1.50	0.01	1.10	0.01	1.00	0.50	3.00	0.00	0.00	1.00	**1.07**
Soybean cyst nematode	0.25	0.80	2.00	0.00	0.00	2.50	0.00	0.50	0.04	5.00	2.00	1.50	2.00	2.50	0.00	2.00	**1.32**
Other nematodes[c]	0.00	0.01	0.50	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.25	0.00	2.00	0.00	0.00	0.50	**0.21**
Rhizoctonia aerial blight	0.20	0.20	0.00	0.00	0.00	0.00	1.00	0.00	0.50	0.00	0.01	0.00	0.00	0.00	0.00	0.00	**0.12**
Sclerotinia stem rot (white mold - *Sclerotinia sclerotiorum*)	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
Seedling diseases	0.20	0.20	1.00	0.20	0.00	0.80	0.10	1.00	0.60	0.50	0.30	0.40	0.10	0.50	0.00	0.10	**0.38**
Septoria brown spot	0.40	0.20	0.00	0.20	0.00	0.40	0.40	0.00	0.80	0.00	0.10	1.00	0.30	0.50	0.00	0.10	**0.28**
Southern blight	0.25	0.20	0.00	0.50	0.25	0.00	0.10	0.00	0.50	0.00	0.00	0.05	0.15	0.00	0.00	0.10	**0.13**
Soybean rust	0.10	0.00	0.00	0.20	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.03**
Stem Canker	0.10	0.10	1.00	0.10	0.00	1.00	0.00	1.00	0.01	0.01	0.20	0.05	0.10	0.50	0.00	0.50	**0.29**
Sudden death syndrome	0.05	0.00	0.01	0.00	0.00	0.30	0.10	0.50	0.01	0.50	0.00	0.10	0.01	0.00	0.00	0.50	**0.13**
Taproot decline	0.25	0.30	0.00	0.00	0.00	0.00	1.50	0.00	0.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.14**
Target spot	0.10	0.10	0.01	0.00	0.00	0.08	0.25	0.00	0.08	0.00	0.01	0.00	0.50	0.30	0.00	0.01	**0.09**
Virus Diseases[d]	0.25	0.00	0.01	0.75	0.00	0.08	0.00	0.00	0.00	0.00	0.20	0.01	0.05	0.00	0.00	0.00	**0.08**
Total disease %	**7.05**	**13.71**	**12.64**	**6.12**	**7.30**	**9.36**	**20.90**	**8.93**	**11.24**	**8.19**	**8.24**	**8.57**	**14.67**	**10.30**	**1.15**	**9.43**	**9.86**

[a]Rounding errors may exist since some numbers presented carry decimal places beyond the hundredths place.
[b]Other diseases listed included: Phymatotrichopsis root rot (TX), red crown rot (LA, MS, NC, SC, VA).
[c]Other nematodes listed included: Columbia lance nematode (NC, SC), lesion nematode (AR, DE, VA), sting nematode (VA), stubby root nematode (VA).
[d]Virus diseases listed included: *Bean pod mottle virus* (KY, MS, NC, SC), *Soybean mosaic virus* (DE, MS, NC, SC, VA), *Soybean vein necrosis virus* (DE, KY, MD, MS, NC, OK, VA), *Tobacco ringspot virus* (KY, NC, SC).

Table 4. Estimated suppression of soybean yield (Millions of Bushels) as a result of disease during 2018.

	yield suppression by state (millions of bushels)																
Disease	**AL[a]**	**AR**	**DE**	**FL**	**GA**	**KY**	**LA**	**MD**	**MS**	**MO**	**NC**	**OK**	**SC**	**TN**	**TX**	**VA**	**TOTAL**
Anthracnose	0.01	0.57	0.00	0.00	0.03	0.00	0.39	0.00	0.00	0.00	0.03	0.01	0.00	0.43	0.00	0.14	**1.62**
Bacterial diseases	0.00	0.19	0.00	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.00	**0.31**
Brown stem rot	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.00	**0.07**
Cercospora leaf blight	0.15	1.91	0.04	0.00	0.03	0.06	2.37	0.03	2.02	1.42	0.03	0.01	0.00	0.02	0.00	0.28	**8.36**
Charcoal rot	0.04	0.77	0.04	0.00	0.06	0.17	0.79	0.05	1.08	0.28	0.03	0.01	0.00	1.20	0.00	0.00	**4.51**
Downy mildew	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.00	**0.04**
Frogeye leaf spot	0.06	1.34	0.00	0.00	0.01	1.14	0.79	0.00	0.13	1.14	0.03	0.01	0.00	1.28	0.00	0.14	**6.08**
Fusarium wilt and root rot	0.00	0.38	0.00	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.03	**0.53**
Other diseases[b]	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.00	**0.12**
Phomopsis seed decay	0.30	5.74	0.32	0.00	0.03	1.71	5.52	1.07	5.38	0.20	0.03	0.01	0.00	2.14	0.00	0.28	**22.75**
Phytophthora root and stem rot	0.00	0.19	0.00	0.00	0.00	0.34	0.08	0.00	0.00	1.42	0.03	0.01	0.00	0.02	0.00	0.00	**2.09**
Pod and stem blight	0.03	1.53	0.08	0.00	0.06	0.34	1.18	0.13	0.00	1.42	0.03	0.01	0.00	0.00	0.00	0.28	**5.110**
Purple seed stain	0.03	0.57	0.12	0.00	0.01	1.03	0.55	0.27	0.67	0.28	0.03	0.01	0.00	0.04	0.04	0.14	**3.81**
Reniform nematode	0.04	0.38	0.00	0.00	0.01	0.00	0.59	0.00	0.67	0.00	0.03	0.01	0.00	0.00	0.00	0.00	**1.73**
Root-knot nematode	0.07	8.62	0.04	0.00	0.17	0.00	1.18	0.00	1.48	0.03	0.03	0.01	0.00	0.00	0.00	0.28	**11.92**
Soybean cyst nematode	0.04	1.53	0.16	0.00	0.00	2.85	0.00	0.13	0.05	14.21	0.03	0.01	0.00	2.14	0.00	0.56	**21.73**
Other nematodes[c]	0.00	0.02	0.04	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.14	**0.32**
Rhizoctonia aerial blight	0.03	0.38	0.00	0.00	0.00	0.00	0.79	0.00	0.67	0.00	0.03	0.01	0.00	0.00	0.00	0.00	**1.91**
Sclerotinia stem rot (white mold - *Sclerotinia sclerotiorum*)	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.00	**0.04**
Seedling diseases	0.03	0.38	0.08	0.00	0.00	0.91	0.08	0.27	0.81	1.42	0.03	0.01	0.00	0.43	0.00	0.03	**4.48**
Septoria brown spot	0.06	0.38	0.00	0.00	0.00	0.46	0.32	0.00	1.08	0.00	0.03	0.01	0.00	0.43	0.00	0.03	**2.79**
Southern blight	0.04	0.38	0.00	0.00	0.01	0.00	0.08	0.00	0.67	0.00	0.03	0.01	0.00	0.00	0.00	0.03	**1.25**
Soybean rust	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.00	**0.06**
Stem Canker	0.01	0.19	0.08	0.00	0.00	1.14	0.00	0.27	0.01	0.03	0.03	0.01	0.00	0.43	0.00	0.14	**2.34**
Sudden death syndrome	0.01	0.00	0.00	0.00	0.00	0.34	0.08	0.13	0.01	1.42	0.03	0.01	0.00	0.00	0.00	0.14	**2.18**
Taproot decline	0.04	0.57	0.00	0.00	0.00	0.00	1.18	0.00	0.27	0.00	0.03	0.00	0.00	0.00	0.00	0.00	**2.09**
Target spot	0.01	0.19	0.00	0.00	0.00	0.09	0.20	0.00	0.10	0.00	0.03	0.00	0.00	0.26	0.00	0.00	**0.88**
Virus Diseases[d]	0.04	0.00	0.00	0.00	0.00	0.09	0.00	0.00	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.00	**0.17**
Total disease %	**1.06**	**26.25**	**1.02**	**0.03**	**0.43**	**10.69**	**16.49**	**2.40**	**15.11**	**23.28**	**0.76**	**0.24**	**0.02**	**8.82**	**0.05**	**2.64**	**109.28**

[a]Rounding errors may exist since some numbers presented carry decimal places beyond the hundredths place.
[b]Other diseases listed included: Phymatotrichopsis root rot (TX), red crown rot (LA, MS, NC, SC, VA).
[c]Other nematodes listed included: Columbia lance nematode (NC, SC), lesion nematode (AR, DE, VA), sting nematode (VA), stubby root nematode (VA).
[d]Virus diseases listed included: *Bean pod mottle virus* (KY, MS, NC, SC), *Soybean mosaic virus* (DE, MS, NC, SC, VA), *Soybean vein necrosis virus* (DE, KY, MD, MS, NC, OK, VA), *Tobacco ringspot virus* (KY, NC, SC).

Table 5. Deviation of the 2018 temperature from the 30-year normal and the total precipitation for 2018 and the 30-year normal from each of the 16 southern soybean producing states based on data downloaded from the centroid for each respective state.

	Deviation from the 30-year temperature norm (°F)												Total precip (in)		
State	**January**	**February**	**March**	**April**	**May**	**June**	**July**	**August**	**September**	**October**	**November**	**December**	**2018**	**30-year**	**Deviation**
Alabama	-1.3	9.6	1.1	-1.6	4.2	2.9	1.0	-0.4	5.1	-3.3	-4.4	-0.2	72.8	57.9	**14.9**
Arkansas	-2.7	0.8	3.9	-4.6	6.3	2.0	0.2	-3.1	-1.7	-1.5	-6.0	0.5	71.4	48.8	**22.7**
Delware	0.6	9.1	-3.7	-0.4	5.9	-0.4	0.1	4.0	3.9	3.3	-1.2	5.0	55.2	43.8	**11.5**
Florida	-5.3	-1.6	-1.7	-0.2	1.6	1.9	0.1	-1.0	3.7	4.3	-3.7	-0.2	74.0	58.1	**16.0**
Georgia	-1.4	8.1	-0.9	-1.8	0.9	1.5	-1.2	0.3	7.9	3.6	-5.0	1.1	49.1	45.7	**3.4**
Kentucky	-1.3	9.0	-3.8	-4.1	8.4	3.5	1.7	-1.3	2.6	0.6	-5.7	2.5	60.2	46.4	**13.8**
Louisiana	-5.2	6.0	2.5	-2.7	5.9	2.0	2.8	1.8	1.4	1.1	-4.8	0.4	67.0	55.9	**11.1**
Maryland	0.7	6.3	-4.4	-1.8	5.6	-0.5	0.5	2.6	2.1	1.5	-5.1	2.8	71.8	41.9	**29.9**
Missouri	-1.4	1.1	-4.0	-6.7	8.7	4.3	0.0	1.1	4.5	-0.8	-8.8	3.5	37.1	44.0	**-6.8**
Mississippi	-5.0	0.9	0.8	-4.3	3.4	0.4	-0.6	-1.9	-1.1	0.8	-10.5	-0.5	60.1	54.6	**5.5**
North Carolina	-3.0	8.9	-6.5	-1.9	4.0	1.5	-0.8	-0.2	2.6	0.3	-5.4	.	68.9	46.2	**22.7**
Oklahoma	0.1	-3.3	2.3	-4.6	4.8	2.2	-1.0	-4.3	-3.6	-4.6	-4.4	-1.0	45.9	36.5	**9.3**
South Carolina	-1.4	8.7	-1.4	-0.9	2.3	3.7	0.1	1.9	5.2	2.8	-5.8	-0.5	51.2	46.3	**4.9**
Tennessee	-5.0	6.9	-3.2	-7.7	5.3	1.8	0.2	-2.1	1.9	-0.4	-8.1	-0.2	62.8	53.4	**9.4**
Texas	-2.5	-1.1	3.3	-1.0	3.1	4.2	3.2	-1.6	-7.2	-7.4	-6.2	-2.6	33.3	27.6	**5.7**
Virginia	-1.2	5.6	-5.9	-2.0	6.5	1.7	0.6	0.8	2.5	1.1	-5.8	1.0	65.7	41.6	**24.1**
Avg.	**-2.2**	**4.7**	**-1.4**	**-2.9**	**4.8**	**2.0**	**0.4**	**-0.2**	**1.9**	**0.1**	**-5.7**	**0.8**	--	--	**12.4**

[a]Deviations of temperature were calculated based on subtracting the average temperature for each month from the 30-year normal. Negative numbers are deviations below the normal and positive numbers are deviations above the normal temperature for the 30-year period from 1981-2010.