2019 Southern Division Meeting Abstracts (Part II)

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[2019 Southern Division Meeting Abstracts \(Part I\)](#)

Vertical distribution of nematodes as influenced by crop rotation and irrigation

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Sod-based rotation uses two years of bahiagrass followed by one year each of peanut and cotton compared with a conventional crop rotation. Reniform nematode (*Rotylenchulus reniformis*, RN) is a pathogen of cotton, but peanut and bahiagrass are not known to be hosts. Our study investigated plant-parasitic and free-living nematodes (FLN) at different soil depths in sod-based and conventional rotations with or without irrigation at a long-term field site in Quincy, FL. The objective was to understand the vertical distribution of these nematodes to assist with management practices. Soil samples were collected to a depth of 120 cm before planting (Spring 2017), after harvest (Fall 2017), and in the winter (Winter 2018) using a hydraulic probe. Nematode populations were analyzed in 30 cm-sections. No irrigation effects were observed in any of the sampling dates ($P > 0.05$). There were significant crop $\times$ depth interactions ($P < 0.05$) for FLN populations in Spring 2017, for both FLN and RN populations in Fall 2017, and for FLN populations in Winter 2018. Sod-based rotation reduced RN at all depths compared with second-year conventional cotton. Fungivore populations were greater following two years of bahiagrass at the 0–30 cm depth while at deeper depths there were no differences between the rotations. There were no differences in omnivore populations at the 0–30 cm depth, but at 30–120 cm depths populations were greater following two years of conventional cotton.

Distribution of *Puccinia triticina* races (pathotypes) in Northern Egypt

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Survey for wheat leaf rust disease was conducted in two growing seasons in five governorates in Northern Egypt during two growing seasons. Samples of wheat leaf rust were collected from commercial wheat fields and Egyptian Wheat Rust Trap Nursery. In the 1st season, 105 isolates of leaf rust were obtained in a frequency ranged between 11.43 and 29.52%. The highest number of isolates (31) was found in Kafr El-Sheikh (29.52%), while the least number (12) was obtained from Alexandria (11.43%). In the 2nd season, 88 leaf rust isolates were obtained with frequency ranged from 11.36 to 47.73%. Kafr-Elsheikh showed the highest frequency (47.73%), while Beheira and Dakahliya showed the least (11.36% each). In season-1, the most virulent race was TTTT (100%) followed by races, TTTS and STTT (93.75%, each) and races PTTS and TTJT (87.5%, each). Race TTTT was virulent to all 20 differential *Lr* genes (1, 2a, 2c, 3, 9, 16, 24, 26, 3ka, 11, 17, 30, 10, 18, 21, 2b, 14b, 15, 36 and 42). However, race BBBB was avirulence against all 20 differential *Lr* genes. The other races exhibited virulence ranged between 6.25 and 75.00%. In season-2, the most virulent race was TTTT (100%) followed by races STTT and TKTT (93.75%, each) and races STTS, TJTT, TSKT, TSPT and TTTJ (87.50%, each). Race TTTT was virulent to all genes. Race BBBB was avirulent to all 20 differential lines. The virulence of the other races ranged from 18.75 to 81.25%.

Dynamic growth of *Phyllosticta citricarpa* in response to temperature and relative humidity

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Phyllosticta citricarpa, the causal agent of citrus black spot, is an emerging fungal citrus pathogen in Florida which causes yield loss and reduced fruit marketability. Dead twigs in the tree canopy are proposed to be an asexual inoculum source. *P. citricarpa* growth on dead twigs in response to temperature and relative humidity (RH) is of interest. Artificially inoculated twigs were placed in enclosed microcosms containing saturated salt solutions for controlled RH levels (100, 94, 82, 72 and 43%) and incubated at various temperature levels (8, 12, 16, 20, 24, 28, 32 and 36°C) to determine the effect on fungal growth. Pycnidia, conidia, and fungal DNA quantification was performed on samples at 3, 5, and 7 weeks post-inoculation. Our findings suggest that *P. citricarpa* requires RH above 86% for fruiting body formation and above 91% for conidia production ($P < 0.0001$). Pycnidia formed between 12–32°C while sporulation occurred between 16–28°C but pycnidia at 32°C were observed to be sterile ($P < 0.0001$). For fungal biomass, temperature and RH and the interaction were found to be statistically significant ($P < 0.0001$). An increase in RH caused a corresponding increase in fungal biomass. Similarly, a temperature increase caused fungal biomass to increase until 32°C when it began to decline. Since no sporulation occurred at 32°C, it is likely that 28°C is the optimal condition for growth. These findings show that twigs can be an inoculum source in warm and humid environments.

Response of root-knot nematode (*Meloidogyne incognita*) and saponin content of quinoa (*Chenopodium quinoa*)

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Demand for quinoa (*Chenopodium quinoa*) is increasing due to its high nutritional content and lack of gluten. In order to reduce costs associated with removal of saponins, sweet varieties (low saponin) are being developed; however, little is known about impact of saponin on resistance to plant pathogens. The objective of this research was to determine if saponin levels in quinoa predict plant response to root-knot nematode (RKN - *Meloidogyne incognita*). Eggs (2100 per plant) served as inoculum. Three cultivars (9 plants per variety) were inoculated: 'Jesse' (sweet); 'Redhead' (high saponin); and QQ74 (moderate saponin). After 28 d, roots were washed and weighed, and galls were counted. Numbers of galls/g root were approximately 3.5× greater in 'Jesse' and QQ74 than in 'Redhead' ($P < 0.05$). Root mass was greater for 'Redhead' than the other two varieties, which did not differ. In a separate experiment, mobility of second stage juveniles (J2s) in aqueous extracts from uninoculated plants was tested. Oven-dried roots were autoclaved (15 mg/ml water), stored at room temperature (24 h), filtered, then re-autoclaved. Freshly hatched J2s were more sensitive to extracts from 'Jesse' than to extracts from 'Redhead' or QQ74 ($P < 0.05$). Since extracts did not foam when shaken, it is unlikely that bioactivity is due to saponins; therefore, other anti-nematodal compounds in roots may contribute to RKN tolerance. Further research is needed to fully understand tolerance in quinoa.

Gene cluster in onion bulb rotting bacteria contributes to virulence by conferring tolerance to reactive sulfur species

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Pantoea ananatis is endemic in onion (*Allium cepa* L) farmscapes of Georgia causing center rot with both foliar and bulb symptoms. To counteract bacterial infection, onions have developed robust chemical defenses, such as Allicin and other reactive sulfur species. We hypothesized that previously identified plasmid borne genetic loci in *P. ananatis* PNA 97-1R, termed the Onion Virulence Region (OVR A-D), contribute to virulence in onion and render tolerance to reactive sulfur species (RSS) in host. Deletion mutants of each region were generated and tested for fitness and virulence on red onion scales, in crude onion extracts (COE); as well as their tolerance to crude garlic extracts (CGE), and pure-chemical grade 'Allicin'. The deletion mutant PNA 97-1R^{ΔOVR A} had significantly reduced fitness, lesion area on red onions scales, reduced growth in COE, reduced tolerance to CGE, and reduced tolerance to Allicin compared to wild-type (PNA 97-1^{WT}) and other deletion mutant strains (PNA 97-1R^{ΔOVR B-D}). Further mutational analysis of OVR A indicates that tolerance to RSS produced by onion is conferred by a 10kb cluster containing 12 genes associated with sulfur redox reactions, such as thioredoxin reductase. Homologous genes in a similar arrangement have also been identified on plasmids of other onion bulb-rot pathogens in the Pacific Northwest US. The identification of plasmid borne RSS-tolerance helps inform our understanding of virulence and host-pathogen interactions in *P. ananatis*.

Evaluation of alternative fungicide spray programs for the management of bacterial spot on fresh-market tomatoes

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Bacterial spot, *Xanthomonas* spp., is one of the most damaging diseases of tomato worldwide. Due to limited disease management options, growers rely heavily on copper-based bactericides, which are often ineffective due to the presence of copper-tolerant *Xanthomonas* strains. This study was undertaken to evaluate the efficacy of Leap™ ES (*Bacillus thuringiensis* subsp. *kurstaki* strain ABTS-351), LifeGard™ WG (*B. mycoides* isolate J), Actigard® 50WG (acibenzolar-S-methyl), Harbour® (streptomycin), and three experimental nanomaterials (NC) loaded with copper (Cu) and/or chitosan (CHI) as potential alternatives to the grower standard, copper-mancozeb, under greenhouse and/or field conditions. In greenhouse studies, tomato plants treated with either Actigard® 50WG

at 0.4 g/L alone, or in combination with Harbour® at 1.2 g/L or Kocide® 3000 at 2.1 g/L (copper hydroxide), and Leap™ ES at 2.6 ml/L in combination with Harbour® at 1.2 g/L significantly reduced bacterial spot disease severity when compared to the grower standard and water controls ($P < 0.05$). In field trials, LifeGard™ WG at 4.5 oz/100 gal, and NC+CHI at 100 ppm/A significantly reduced bacterial spot disease severity when compared to the nontreated control without a significant impact on yield ($P < 0.05$). This study highlights the potential of several different products for the management of bacterial spot of tomato.

New species of *Bipolaris* infecting industrial hemp in Kentucky

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The 2014 Farm Bill permitted reintroduction of industrial hemp to the United States. A hemp leaf spot disease emerged in Kentucky that same year, with symptoms presenting as numerous 1–2 mm leaf lesions which frequently coalesced to form larger spots that, in severe cases, encompassed much of the leaf. Growers experienced symptoms ranging from minor disease to total crop loss, and a similar disease and pathogen was also reported in surrounding states. The causal pathogen was isolated from symptomatic fields in at least 11 Kentucky counties. Both multi-gene and whole genome analysis, as well as morphological traits, indicated that the pathogen was a previously undescribed *Bipolaris*. In contrast to known *Bipolaris* species, macroconidia sporulated from multiple intercalary cells as well as from the ends. Preliminary surveys of alternative hosts have thus far revealed only dicot hosts, further distinguishing this species from most other *Bipolaris* species, which are associated with monocots. Isolates of the hemp leaf spot pathogen varied in growth rates, colony appearance, sporulation, conidium size, and a putative microsclerotia. Understanding this disease and its causal pathogen is critical for developing and implementing effective management. As hemp acreage continues to increase, the potential impact of this disease may cause significant yield loss and influence that threatens the future of this new crop.

Salibro™ (Reklemel™ Active): A novel active ingredient for the control of plant parasitic nematodes in North America

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Plant-parasitic nematodes remain a significant threat and source of yield reduction in crop production around the world. Over the last two decades nematicidal products used for protection against these soil dwelling pests have come under significant regulatory pressure due to a range of toxicological and environmental issues. In response, the crop protection industry has initiated an intensive effort directed at the discovery and development of new biological and chemical nematode control products, as well as traits in plants. Salibro™ (Reklemel™ active) is a new highly effective and selective active ingredient for the control of plant-parasitic nematodes. Specificity for nematodes coupled with absence of activity against the target sites of commercial nematicides suggests that Salibro™ active has a novel mode of action. It is the first member from the novel chemical class of sulfonamide nematicides. Salibro™ has been extensively tested in laboratory, greenhouse, micro-plot and field trials in North America. In those trials Salibro™ was proven extremely effective against a range of important plant-parasitic nematode species. Salibro™ has a fit in nematode management programs in a range of crops in North America, including fruiting and cucurbit vegetables, root vegetables (carrot, sweet potato, potato), tree nuts, grapes, citrus, stone fruit, and tobacco. An introduction to the chemical and biological properties of this new nematicide will be presented.

Characterization of ‘*Candidatus Liberibacter solanacearum*’ haplotype virulence and competitiveness in field-grown potatoes

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Potato zebra chip (ZC) is putatively caused by ‘*Candidatus Liberibacter solanacearum*’ (Lso) which, is transmitted by the tomato potato psyllid (TPP, *Bactericera cockerelli*). In the US, there are two haplotypes of the pathogen (A & B), which predominately infect potatoes, and TPP can transmit both individually or as a mix (A+B). To determine virulence and competitiveness of the haplotypes, experiments were conducted in the spring of 2018 in which plants were infested with TPP carrying specific haplotypes or haplotype combinations. The treatments were arranged in a randomized complete-block design. Each of four replicate plots had four plants covered with a mesh cloth cage. Each plant under individual cages was infested at flowering with six psyllids carrying either A, B, or A&B, or 3 TPP carrying only A and 3 TPP carrying only B. Plants in un-infested cages served as negative controls. Seven weeks after infestation, tubers from each individual plant were harvested, sliced, and rated for ZC severity on 0 to 3 scale where 0 = healthy and 3 = severe symptoms. In addition, tissue samples were collected from tubers for Lso detection and quantification by RT-qPCR, followed by SYBR green analysis for haplotype identification. Data was analyzed with SAS software using PROC GLIMMIX. Haplotype B was significantly more virulent than all other haplotype treatments ($F=5.21$; $P=0.003$), but in plants infected by both haplotypes neither predominated. To our knowledge, this was the first study to investigate competition between haplotypes in mixed infections.

Impact of ‘*Candidatus Liberibacter solanacearum*’ haplotypes on seed potato sprouting

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Zebra Chip of potato, putatively caused by the bacterial pathogen '*Candidatus Liberibacter solanacearum*' (Lso), has been reported to affect sprouting of potato seed tubers. There are predominantly two haplotypes of the pathogen (A&B) that infect potatoes in the US, however the relative impact of the individual haplotypes on seed germination is currently unknown. To address this knowledge gap, a study was conducted in which potato tubers known to be infected with individual haplotypes (A, B, or A+B mix) were planted in pots arranged in a completely randomized design. Twenty tubers from each haplotype seed lot were planted and numbers of emerged plants was recorded daily. Forty days after planting height, width, leaf area index (LAI), and plant biomass were measured. Data were analyzed with SAS software using PROC GLIMMIX. Sprouts from all uninfected (control) tubers emerged followed by sprouts from tubers infected with haplotype A (85%), B (60%) and lastly A+B (45%). While there was no significant difference between tubers infected with A and the healthy control, sprout emergence from tubers infected with the other haplotypes was significantly less than that of the healthy control ($\alpha = 0.05$). Plant biomass from healthy tubers was significantly higher than those from infected tubers regardless of haplotype ($\alpha = 0.05$). Sprouts from tubers infected with A also had significantly higher biomass than those infected by either B or A+B haplotypes. Height, LAI, and stem width of sprouts emerged from tubers with different haplotype treatments followed a similar pattern as biomass.

In-vitro evaluation for measuring stem rot disease progress in peanut

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Peanut stem rot, caused by the fungi *Sclerotium rolfsii*, is one of the most severe soil borne pathogens for southeastern U.S. peanut production. There are not known strong resistances in cultivated germplasm. Wild relatives of peanut, on the other hand, present strong resistances to several fungal and viral diseases, and nematodes, and have the potential to offer novel alleles for resistance to stem rot. However, information on the resistance to these diseases is still lacking. The in-vitro evaluation for peanut stem rot is highly demanded for measuring the resistance of wild species due to their large architectural difference in comparison with the cultivated species. Results of evaluation will help researchers decide which wild species have new and strong resources of resistance and use it for introgression in breeding programs. Three evaluation methods were tested on cultivated peanuts and wild species. Firstly, the disease progress of peanut leaves inoculated by *S. rolfsii* on potato dextrose agar (PDA) was examined. Peanut stem with same inoculation method was used in the second method. The methodology of the third one was that peanut stem inoculated by *S. rolfsii* cultured in potato dextrose broth. Results from the first and second methods showed that *S. rolfsii* on PDA caused high disease pressure even on cultivars with higher resistance and no significant differences were shown. Preliminary results of third method showed significant difference among susceptible and moderately resistant cultivated peanuts, which was consistent with the field data. A diverse set of wild genotypes will be included in the future experiments.

In-vitro evaluation for measuring southern stem rot disease progress in peanut

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The in-vitro evaluation for peanut southern stem rot is highly demanded for introgressing new and strong resources of resistance from wild species. Three evaluation methods were tested on cultivated peanuts and wild species. Firstly, the disease progress of peanut leaves inoculated by *Sclerotium rolfsii* on potato dextrose agar (PDA) was examined. Secondly, peanut stem with *S. rolfsii* on PDA inoculation was employed as materials. Thirdly, peanut stem with *S. rolfsii* cultured in potato dextrose broth was used. Results from the first and second methods showed that *S. rolfsii* on PDA caused high disease pressure even on more resistance cultivars. Results turned into no difference. Preliminary results of third method showed significantly difference among susceptible and resistance cultivated peanuts, which is consistent with the field data. More genotypes will be included and replicated in the future experiments.

Monitoring plant health and quantifying fungal root pathogens within ultradwarf bermudagrass putting greens

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Root decline is associated with ultradwarf bermudagrass (UDB) greens during the summer months in the southeastern United States. Abiotic factors coupled with a complex of fungal root pathogens contribute to this syndrome. The goal of this study is to monitor plant health and to quantify the distribution of root decline pathogens within selected UDB greens. A fishnet grid system using ArcGIS was established for sampling ($n = 161$) putting greens at Mississippi State University Golf Institute (MSUGI). Aerification cores were collected within 2.4 m² of each centroid. Composite root samples were analyzed for root health using WinRhizo Pro and fungal quantification was based on multiplex qPCR assays. Normalized Difference Vegetation Index (NDVI) using a drone equipped with MicaSense and visual turfgrass quality ratings were conducted once monthly while UDB was actively growing. To date, *Gaeumannomyces* and *Magnaportheopsis* spp., and *Candidacolonium cynodontis* were detected across 86, 45, and 83% of centroids within green 2 at MSUGI, respectively, and across 65, 99, and 44% of centroids within green 12 at MSUGI, respectively. NDVI ratings were variable month to month within both selected greens with consistent areas of low reflectance occurring only in green 12, while root health averaged < 10% for all centroids under investigation. Results of this research may serve to represent the relationship between plant health and root pathogen presence.

Nematicide effects on non-target nematode ecological indices in bermudagrass

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In the southeastern US, nematicides are commonly used to reduce densities of plant-parasitic nematodes on golf course turfgrass, but little research has been devoted to investigating nematicide effects on non-target nematodes. In our field study, we evaluated the effects of four turfgrass nematicide formulations of abamectin (Divanem SC), fluopyram (Indemnify), furfural (MultiGuard Protect EC), and fluensulfone (Nimitz Pro G) on free-living nematodes in bermudagrass. Nematicides were applied four times at maximum labeled rates every four weeks as a summer treatment program from 7 June to 30 August, 2016 and 24 April to 18 July, 2017 in Citra, FL. Samples were collected before treatment and two days, two weeks, eight weeks, and thirty-four weeks after the final treatment each year for ecological analysis. Data from each nematicide treatment were compared to the untreated control at each sampling date using analysis of covariance with initial population counts serving as the covariate. Nematicides decreased Maturity Index, Maturity Index 2-5, Sigma Maturity Index, Enrichment Index, Basal Index, Structure Index, and Channel Index values at multiple sampling dates ($P < 0.1$). Faunal profile analysis indicated a decrease in structure over time. These results suggest nematicides can significantly impact nematode ecological indices, which could have a negative impact on soil health.

CRISPR/Cas9-mediated endogenous gene tagging in *Fusarium oxysporum*

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Fusarium oxysporum is an economically important pathogen that widely exists in the environment and is capable of causing serious problems in crop production. One important step for the characterization of a fungal protein with an unknown function is to determine its subcellular localization within a cell. To facilitate the study of important functional regulators or key virulence factors, we developed a CRISPR/Cas9-mediated endogenous gene tagging (EGT) system based on two different strategies, homology-independent targeted integration (HITI) and homology-dependent recombination integration (HDRI). The HITI strategy was able to facilitate integration of a large DNA fragment, ~8 kb in length, into the genome of *F. oxysporum* at the sgRNA cleavage site, and was used to insert a 3×sGFP tag to the 3' end of the *FoCHS5* gene and a mCherry tag to the 5' end of the *FoSSO2* gene. The HDRI strategy was used to tag the paralogous gene, *FoSSO1*, with a C-terminal mCherry marker. FoChs5-3×sGFP localized to conidia, some septa, and fungal tips. A majority of the FoSso1-mCherry was distributed in the conidia, septum, and hyphae distal from the fungal tips. While FoSso1-mCherry showed a very weak fluorescent signal at the fungal tips, mCherry-FoSso2 accumulated in the plasma membrane of conidia, germlings, fungal tips, hyphae, and phialides, suggesting *FoSSO1* and *FoSSO2* are regulated differently during fungal development. These results indicate this EGT system is efficient and can be another molecular tool to resolve the function(s) of proteins and infection strategies of *F. oxysporum*.

Comparative gene expression analyses of *Phytophthora parasitica* infecting periwinkle and citrus roots

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Phytophthora parasitica is wide host range oomycete plant pathogen that seriously damages the growth of many plants. In continental United States, it is a major pathogen of tobacco, tomato, and ornamentals produced in greenhouses including periwinkle *Catharanthus roseus*. *P. parasitica* causes leaf blight and root rot in periwinkle and it is also invasive to citrus causing root rot, fruit rot and stem infection. Here, we infected periwinkle and citrus roots with *P. parasitica* and collected tissues at different time points during infection for RNA sequencing and to study the host-*P. parasitica* interactions. We used the publicly available genome sequences of *P. parasitica* as reference genome for the gene expression bioinformatic analyses of effector disease related genes. We are currently in the process of identifying *P. parasitica* effectors genes that are induced during infection in both periwinkle and citrus. Candidate *P. parasitica* effectors will be assessed for virulence activity using Agrobacterium mediated transient expression followed by spore inoculation. Our long-term goal is to use these effectors for functional analysis in order to detect potential host susceptibility *S* factors in common between periwinkle and citrus hosts.

Training field agents and educators with practical skills and diagnostic techniques

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With shrinking budgets and reduced extension staffing, Cooperative Extension programs are shrinking across universities. Likewise, disciplines such as plant pathology include complex levels of diagnostic methods and techniques that may be out-of-reach for agents' and educators' skillsets. This scenario makes it more important than ever to train agents with applicable and relevant diagnostic skills that can be employed in the field and/or at the office. Based on communications, surveys, and verbal feedback, we developed a train-the-trainer certificate program in 2018 to teach some of these diagnostic skills. This program consisted of eight how-to webinars and a series of hands-on workshops for agents. Techniques included use of hand-held USB microscopes, slide preparation using office tape and cell phone flashlights, cell phone magnification aids, digital photo devices, and soil-root analysis. A range of diagnostic practices possible through these techniques included detection of bacterial streaming and identification of common fungal structures. This

training helped agents increase understanding and build confidence, thereby allowing them to better serve stakeholders. Short term results included more efficient and more effective service to growers, more accurate field diagnostics, and improved sample submission to the plant disease diagnostic laboratory. Long term, this adoption of diagnostic skills and use of simple tools will result in more accurate and more rapid solutions to stakeholder disease problems and cost savings for both Extension programs and for stakeholders.

Field evaluation of soybean germplasm to reduce losses associated poor soybean grain quality in Mississippi soybean

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Reduced soybean grain quality can occur as a result of delayed harvest. In some years, grain elevators report an average of 7% damage. In some years, *Phomopsis* seed decay, caused by *Phomopsis longicola* (PL), causes economic losses in the southern U.S. soybean production system. The objective of this research was to determine differences in grain damage between soybean entries under environmental conditions conducive to reducing seed quality. In 2018, field trials were established under rainout shelters (n=2) consisting of greenhouse cold frames. Each shelter contained single row plots of each entry, replicated three times. All plots were inoculated with a PL spore suspension at the R5.5 growth stage. Shelter 1 remained fungicide non-treated. Shelter 2 received a 293 ml/ha fungicide application (Stratego YLD) at R7. Shelters were simultaneously overhead irrigated for approximately 200 h. Plots were hand harvested at R8 to determine plot weight and grain damage. Significant differences were observed in the non-fungicide shelter between entries with a 78% difference in weight between Progeny 4211 and 11030-541-210 and an 81% difference in damage between 11030-541-210 and DB06X06-093. No significance differences were observed in the fungicide-treated shelter; however, numerical differences between entries were observed. Although differences occurred between entries, additional research is needed to determine the potential of germplasm in reducing seed quality losses.

Cropland connectivity: A risk factor for invasion and saturation by emerging pathogens and pests in the Caribbean

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Cropland connectivity is a risk factor for invasion and saturation by pathogens and pests. We apply a new cropland connectivity risk index (CCRI) to key crops produced in the Caribbean region. Networks of potential movement of pathogens and pests specific to each crop species were estimated based on the distance between pairs of cropland locations, and the cropping area. Identification of priority surveillance and management locations in the network included uncertainty quantification, to find locations that are important across the range of potential pathogen or pest dispersal kernels. We evaluated the CCRI in the Caribbean region for avocado, banana and plantain, beans, cassava, mango, potato, rice, sweetpotato, and yam. Haiti is an important location in the region across most of these crops, with high CCRI and as a potential bridge location for connecting neighboring countries. For banana and plantain, high CCRI in the Inter-Andean valleys of Colombian, all of Central and Western Ecuador, as well as in Haiti, are consistent throughout the parameter ranges evaluated in the uncertainty quantification. We are also integrating the CCRI, as one geographic risk layer, with geographic risk layers based on networks formed by extreme weather events and based on trading networks. Risk maps including the CCRI can inform national strategies for disease and pest management, such as the development of pest risk assessments (PRAs) in advance of potential invasions.

Transcriptome analysis of *Phytophthora parasitica* during infection in *Nicotiana benthamiana*

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Phytophthora spp. are oomycete plant-pathogens that can cause devastating effects on agricultural crops. *Phytophthora parasitica* is one of the most common *Phytophthora* species occurring in subtropical areas, causing citrus foot and root rot. It is commonly found in soil and on roots, but usually not infecting far above the ground. Here, we employed the model plant *Nicotiana benthamiana* to study the host-*P. parasitica* interactions at a molecular level. We developed a bioassay for *in vitro* study of the infection of *Nicotiana benthamiana* roots with *P. parasitica*. We also compared root infections with leaf infections using a detached leaf assay. Infected leaf and root tissues were collected at different time points during infection for RNA sequencing. Genome sequences of *P. parasitica* isolates from citrus IAC0195 and P1569 publicly available were used as reference genomes for the gene expression bioinformatic analyses of the infected tissues samples generated in this study. We found several *P. parasitica* RXLR type effectors differentially regulated at early time points of pathogen infection. Moreover, we detected differential expression of *P. parasitica* effectors between roots and leaves of *N. benthamiana* infected samples.

Possible causes for late-reproductive stage development of *Cercospora* leaf blight of soybean

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In Louisiana, *Cercospora* leaf blight (CLB) of soybean is primarily caused by *Cercospora* cf. *flagellaris*. *C. cf. flagellaris* produces cercosporin, a host non-specific toxin implicated in its virulence. Although CLB symptoms mostly appear during the R5 growth stage of soybean or later, low fungal populations can be detected earlier (V3-R2) in asymptomatic plants. Based on these findings, we investigated whether R2 and R5 soybean leaf extracts differentially affected the growth and cercosporin production of *C. cf. flagellaris*. Leaf extracts were made by grinding the leaves in water, collecting the supernatant after centrifugation and sterilizing it by filtration. Growth of *C. cf. flagellaris* and cercosporin production were found to be lower in the R2 leaf extract compared to R5 extract. We then investigated whether sucrose and auxin might be the factors that contributed to the observed differences. Fungal growth and cercosporin production in the sucrose-amended R2 (R2-suc) leaf extracts were more similar to those in R5 than R2 leaf extracts. Additionally, cercosporin-related genes were downregulated in *C. cf. flagellaris* grown in R5 and R2-suc, compared to those in the R2 leaf extract. Fungal growth and cercosporin production were also markedly reduced in auxin-amended media. Elucidation of the factors contributing to the suppression of CLB until the late reproductive growth stages of soybean will hopefully provide novel insights into CLB management strategies.