PLANTS, INSECTS AND MICROBES SYMPOSIUM

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ABSTRACT BOOK

Academic Classroom and
Laboratory Complex (ACLC)

Room Information
ACLC 012: Oral Presentations
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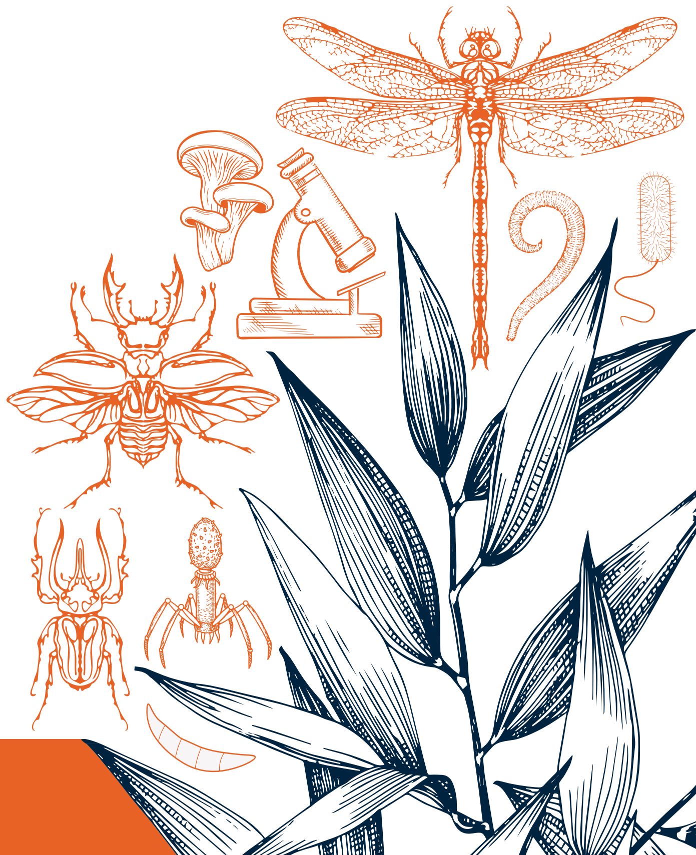

AUBURN
Entomology and Plant Pathology

ORAL PRESENTATIONS

O-1 A Novel System for Virus-induced Gene Silencing in Cotton with CLRDV

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Virus-induced genome silencing (VIGS) is a valuable research tool that leverages the natural antiviral defense mechanisms of plants to silence or downregulate specific targeted genes. However, studying gene functionality in cotton poses challenges due to its large diploid or allotetraploid genomes and low transformation efficiency. Interestingly, an infectious clone of the cotton leafroll dwarf virus (CLRDV) from Alabama has previously exhibited over 50% infection rates in *Gossypium hirsutum* L. without inducing any viral symptoms. This study aims to convert the CLRDV clone into a silencing vector and assess the levels of downregulation. Given that CLRDV is a low-titer, phloem-limited virus, it becomes crucial to compare the levels and locations of silencing with an established VIGS system previously used in cotton, tobacco rattle virus (TRV). In designing the CLRDV-VIGS vector, a multicloning site was integrated into the 5' untranslated region of the virus, allowing the insertion of target gene sequences. The chloroplast-associated genes CLA1 and PDS, known to induce tissue photobleaching when silenced, are utilized to verify the functionality of the CLRDV silencing vector in two host plants: cotton and *Nicotiana benthamiana*. Currently, the two virus vectors and the two target genes are being tested across all possible combinations in both host plants. This research aims to leverage a novel virus clone to introduce a new method for conducting studies in cotton, potentially offering advantages for certain applications due to its phloem limitation.

O-2 Predicting the phenology of herbivorous insects

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Models of herbivorous insect phenology can be used to make agriculture more sustainable and to better manage the effects of climate change on natural communities. The phenology of herbivorous insects depends on heat-time, but exactly how it varies across populations, and the causes of this variation are unclear. Here, with multilevel Bayesian models, we perform a comparative analysis of 601 published herbivorous insect phenology models. We find that variation in herbivorous insect phenology can be explained by variation in insect taxonomy, adult body size, feeding site, host plant taxonomy, geographic location, and the approaches that researchers used for model parameterization. Contrary to previous analysis, we also find that the minimum temperature required for development varies across life stages in a way that suggests a more complex role for temperature during the egg stage. Our analysis shows how we can make better and more generalizable predictions of herbivorous insect phenology by incoporating more information about how insect populations and their environments vary. We continue trying to further enhance our ability to predict herbivorous insect phenology by exploring how local scale weather (e.g. precipitation) during development might impact herbviorous insect phenology.

O-3 Pathogens on the prowl: Do abiotic stress-driven changes help pathogens exploit and overcome disease resistance more rapidly?

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Disease resistance remains a key strategy for sustainable plant health management. However, its durability may be compromised when plants experience simultaneous abiotic stress, posing risks to crop production. In the southeastern U.S., tropospheric ozone (O_3) levels frequently surpass the plant-tolerable threshold (40 parts per billion) during summer and are expected to rise. Previous studies showed that elevated O_3 alters plant physiology and defense mechanisms, leading to variable disease pressure across different pathosystems. This study examined how pathogen adapts to disease-resistant plants under simultaneous elevated O_3 stress. A field experiment was conducted using open-top chambers to control O_3 levels while challenging resistant and susceptible pepper cultivars with a mixed inoculum of two *Xanthomonas perforans* strains, mimicking natural mixed infections. Disease progression and pathogen dynamics were tracked, focusing on inoculated strain abundance and mutations over a growing season. Elevated O_3 led to increased but more variable disease severity on resistant cultivars but had no significant effect on susceptible cultivars. A single strain persisted on susceptible cultivars, while both strains remained in resistant cultivars under ambient conditions, indicating differential fitness across hosts. However, elevated O_3 altered strain dynamics during the colonization of resistant cultivars. Notably, the pathogen population from resistant cultivars exhibited high genetic polymorphism, with O_3 stress increased transient and deleterious mutations. These finding highlights the unpredictable nature of pathogen adaptation to hosts under abiotic stress, emphasizing the need for multi-generational studies. Understanding parallel *de novo* mutations retained over time may offer insights into pathogen adaptation mechanisms, informing future disease management strategies.

O-4 What Good Are Soldiers During Peacetime? Foraging Efficiency of Fire Ant Soldiers

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Division-of-labor is a hallmark of eusociality. In addition to the division between the reproductive and non-reproductive castes, numerous species have evolved further divisions within the non-reproductive caste, such as distinct soldier and minor worker castes. However, the function of the soldier caste is not always clear, especially in species that display continuous polymorphism rather than clearly distinct worker and soldier morphs. Here we test whether larger workers contribute to colony success by (1) foraging faster, and/or (2) carrying weight more efficiently. We ran 190 fire ant workers (*Solenopsis invicta*) that varied 24-fold in mass on an untethered automatic tracking system for a total of 12 minutes each. Larger workers travelled at a higher velocity than small workers, but their velocity was proportionally slower relative to their body size. Regarding transport of weight, larger workers travelled with a higher momentum, both absolutely and in proportion to their body size. We then tested whether the increased momentum of larger workers provided an advantage when carrying weight by measuring velocity and momentum of 142 workers carrying brood. Larger workers carrying brood ran at the same velocity as smaller workers but had a four-fold increase in momentum. Ant soldiers may thus be more efficient at transporting large food items and brood, which could explain how they contribute to colony success outside of defensive roles in the colony.

O-5 Common floral forage found in the southeastern United States and their biometric effects on the western honey bee

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Known by beekeepers to produce copious amounts of nectar utilized by the western honey bee (*Apis mellifera*), tallow (*Triadica sebifera*) (TAL) is an invasive flowering tree species commonly found in the southeastern United States. The role it plays in honey bee nutrition is poorly documented. To better understand that role, we assessed hypopharyngeal gland acini width (HPG), vitellogenin (VG) relative expression, and longevity (30 days) by conducting dietary cage trials. For these trials, we utilized newly eclosed workers and fed them pollen treatments for 10 days. The pollen treatments included common floral resources that are found in the US southeast including: crape myrtle (*Lagerstroemia indica*) (CM), Fabaceae (*Melilotus*/*Trifolium*) (FAB), and Magnolia spp. (MAG). We tested each pollen type singly (CM, FAB, MAG, TAL), and two combination polyfloral blends PFT (w/w CM/FAB/MAG/TAL) and PF (CM/FAB/MAG), and a no pollen negative control (NP). For HPG, all pollen treatments were significantly larger than NP; for Vg expression, FAB (β = 41.55 ± 18.18 95% C.L.) and MAG (β = 381.55 ± 18.18 95% C.L.) had higher expression than the other treatments; and for survival, FAB lived 1.56 more days than all other treatments (1.00, 2.42; lower and upper C.L.). These results suggest that the pollen sources investigated vary in their honey bee biometric responses, and that each potentially plays a role in honey bee health. Future studies should investigate colony level responses to the pollen treatments.

O-6 Evaluating best fall management practices of pollinator plantings in southeastern agriculture systems.

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USDA programs provide funding for landowners to establish wildflower plantings for pollinators. However, best management practices to maintain diverse and abundant forage for visiting insects are unclear due to a lack of empirical evaluation, particularly in the southeastern United States. In this study, we compared the effects of mowing, light disking, and a combination treatment against a no-management control on the diversity and density of wildflower blooms and foraging bees. Three experimental plots were sown with a mix of 20 native wildflower species at the E.V. Smith Research Center in Shorter, AL in April 2022. Consistent with USDA requirements, species were chosen to ensure at least three were in bloom throughout the growing season. Each plot was divided into sixteen subplots (n = 48) which were randomly assigned one of the three treatments or control. Treatments were applied first in December 2022 through February 2023 and again in November 2023. Blooms were counted three times per year through the 2023 and 2024 growing seasons. We plan to analyze the density and diversity of wildflower blooms among the treatment and control groups.These results will help to establish recommendations on how to best manage wildflower plantings to provide forage for pollinators.

O-7 Transcriptomic Discovery of RNAi Targets for Sex-Specific and Lethal Gene Silencing in the Poultry Pest *Alphitobius diaperinus*

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Alphitobius diaperinus, the lesser mealworm, is a widespread pest in poultry production, contributing to disease transmission and structural degradation. As chemical control options become increasingly limited by resistance and regulatory concerns, RNA interference (RNAi)—a species-specific gene-silencing mechanism—offers a promising alternative. This study presents the first sex-differentiated transcriptomic analysis to identify RNAi targets in *A. diaperinus*. Total RNA was extracted from male and female beetles, sequenced using Illumina paired-end technology, and assembled *de novo* into a reference transcriptome. Differential gene expression analysis identified both sex-biased and constitutively expressed genes across samples. Transcript abundance data from male and female groups were used to prioritize candidate targets with annotated functions related to sex determination, development, and essential cellular processes. These genes provide a basis for control strategies such as sex-sorting approaches (e.g., male-only release programs) and RNAi-based insecticidal applications for population suppression. Selected candidates were validated using quantitative real-time PCR (RT-qPCR) on independent biological replicates. These results lay the groundwork for developing RNAi-based tools to manage *A. diaperinus* through biologically targeted and environmentally responsible strategies.

O-8 In-furrow insecticide persistence and effects on peanuts and cotton in Southeast Alabama.

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Across Southern Alabama cotton and peanuts are the most common crop roatation, both crops have early season insect pests which transmit plant pathogens. *Cotton leafroll dwarf virus* (CLRDV; genus *Polerovirus*, family *Luteoviridae*) is transmitted by the cotton aphid (*Aphis gossypii*). In 2017, based on symptoms alone, incidence ranged from 3-30%, and yield losses were estimated at an average of 560 kg/ha across this area, which was valued at $19 million dollars. In peanuts, *Tomato spotted wilt virus* (TSWV; genus *Tospovirus*, family *Bunyaviridae*) is transmitted by nine species of thrips. The predominant thrips species in Alabama are *Frankliniela fusca*, and *Frankliniela occidentalis*. There are several systemic in-furrow insecticides available to growers to combat insect pests including phorate, aldicarb, and imidacloprid. Although not widely used in cotton production, phorate is known to control thrips and reduce *Tomato spotted wilt virus* in peanuts by inducing a plant disease defense response. Thus, the objectives of this research are to i) quantify the amount of time these insecticides persist in plant tissue, ii) determine their impact on insect populations, and iii) determine their impact on CLRDV incidence and incited yield loss. To conduct this research, we collected cotton and peanut tissue samples at 15, 30, 42, 56, and 70 days after planting, to analyze the insecticide levels present in the plant over time by AOAC 2007.01. As well as aphid counts in cotton, thrips injury ratings in peants, and CLRDV PCR in cotton and TSWV ratings in peanuts.

O-9 Method Development for Use of Synthetic Tomato Xylem to Study Biofilm Formation of the Plant Pathogen *Ralstonia pseudosolanacearum*

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Ralstonia pseudosolanacearum is a soil-borne bacteria that causes bacterial wilt disease across numerous economically important crops. *R. pseudosolanacearum* invades the root system, colonizes plant xylem vessels, and forms thick biofilm reducing or even stopping the flow of water to the rest of the plant. Studying *R. pseudosolanacearum* and other biofilm forming plant pathogens' behavior in xylem vessels is difficult as the vessels are hidden within the plant. End-point destructive sampling also does not allow for the examination of biofilm dynamics. Depending upon live plants leads to a number of potential confounding factors including the need to maintain live plants for an extended period of time before being able to run an experiment.

Currently within this project, we have demonstrated that a xylem-inspired microfluidic system with a cellulose-like coating has the potential to give rise to techniques useful in studying the behavior of *R. pseudosolanacearum* attachment and biofilm formation. We found that *R. pseudosolanacearum* attachment to surfaces and biofilm formation are highly dependent on xylem flow rate, and that biofilm formation under flow is a complex phenomenon with many contributing factors such as settling time, flow rates, the presence of bacterial adhesins, extracellular polysaccharides, etc. The future goals of my research will be to further optimize the system to a point where *R. pseudosolanacearum* behaves and expresses genes as closely as possible to actual tomato xylem infection.

O-10 Exploring the role of rhizosphere microbiome in hemp plant growth and defense against two-spotted spider mites

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Hemp (*Cannabis sativa* L.) is a versatile crop with significant industrial and medicinal value. As cultivation expands, understanding the ecological dynamics of hemp, particularly the role of rhizosphere microbes in plant defense is essential. Beneficial soil microbiomes contribute to plant health by promoting growth and enhancing resistance to insect herbivores. Despite their importance, the specific impacts of rhizosphere microbes on hemp pest resistance remain largely unexplored. This study investigates the composition of the hemp rhizosphere microbiome and its potential role in enhancing plant defense against the two-spotted spider mite (*Tetranychus urticae*), a major pest in hemp production. We hypothesized that the composition of the hemp rhizosphere microbiome influences hemp growth and defense against spider mites. Two hemp cultivars, Cherry Citrus and BaOx, were assessed to identify potential microorganisms contributing to resistance against *T. urticae*. Plant and root dimensions were recorded for twelve plants per cultivar at the flowering stage. Spider mite damage was evaluated using a 0-to-5 scale, and rhizosphere soil and root samples were collected for microbial DNA extraction. Bacterial 16S ribosomal RNA (rRNA) genes were amplified to profile microbial communities. The results of this study will contribute to the development of sustainable pest management approaches by identifying microbial taxa associated with natural pest suppression.

O-11 Optimizing Gel Bait Toxicity for all developmental stages of American Cockroach (*Periplaneta americana*) (Blattodea: Blattidae): The Role of Competitive Food Availability

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The American cockroach (*Periplaneta americana* (L.); Blattodea:Blattidea) is a peridomestic pest with public health significance. This study evaluated the toxicity of eleven insecticidal gel baits containing active ingredients such as abamectin B1, boric acid, clothianidin, dinotefuran, emamectin benzoate, fipronil, imidacloprid, and indoxacarb, against several developmental stages of *P. americana* (adults of both sexes and nymphs of varying sizes) with and without competitive food. A completely randomized block design was used to estimate mortality and median survival times (MSTs) over a 14-day period. Gel baits, preferred for their efficacy and reduced environmental contamination, demonstrated variable effectiveness. Hotshot (Dinotefuran 0.05%) and Alpine (Dinotefuran 0.5%) did not cause significant mortality ($P > 0.05$) compared to the control both with and without competitive food. Combat (Fipronil 0.01%) and MaxForce FC Magnum (Fipronil 0.05%) exhibited the highest efficacy, achieving the lowest MST of 48 h across all tested stages. All other gel baits were also moderately effective against all the developmental stages. Boric acid (33.3%), except for small and large nymphs, was efficient in controlling other stages of *P. americana*. Experiment without competitive food indicated gel baits were significantly effective, suggesting that the availability of alternative food sources may influence bait uptake and efficacy. These findings highlight the potential of fipronil-based gel baits as a reliable tool for managing all the stages of *P. americana* populations, emphasizing the importance of active ingredient selection for optimal pest control.

O-12 Xylem sap-mediated growth and biofilm formation of *Xylella fastidiosa* and its potential role in host adaptation and virulence

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Xylella fastidiosa (Xf), a xylem-limited plant pathogen, causes devastating diseases such as Pierce's disease (PD) in grapevines, blueberry leaf scorch, and almond leaf scorch disease (ALSD), among others. Some *Xf* strains isolated from one host can infect and cause disease in multiple hosts. Since xylem sap is the sole growth medium for *Xf* in plants, we hypothesize that strain-specific growth and biofilm formation in xylem sap influence colonization and virulence across hosts. This study compared *Xf* strains' in vitro growth phenotypes and biofilm production from almonds, grapes, and blueberries. Strains were grown in artificial media (PD3) amended with 25%, 50%, or 75% xylem sap from susceptible *Vitis vinifera* 'Chardonnay' grapevines. Additionally, some strains were grown in PD3 supplemented with 25% xylem sap from resistant and susceptible *Vaccinium* spp. blueberries to evaluate strain adaptation to different host environments. Biofilm formation varied among strains, increasing at higher grape sap concentrations in some strains while decreasing in others. Also, biofilm production was greater in susceptible blueberry sap than in resistant sap. Results from microfluidic chambers, used here as 'artificial xylem vessels,' also aligned with the *in vitro* results. Preliminary findings suggest that biofilm formation in xylem sap may be associated with virulence *in planta*, based on limited virulence testing. Currently, more extensive virulence assays are being performed in the greenhouse across multiple strains and host plants to validate these findings. This study aims to assess the potential virulence of diverse *Xf* strains based on their growth and biofilm formation in xylem sap.

O-13 Mechanisms and Management: Impact of Alternating Insecticide Selection in *Aedes aegypti*

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This study investigated the dynamics of insecticide resistance development in *Aedes aegypti* to two commonly used insecticides, permethrin and malathion, and evaluated the effectiveness of an alternating application strategy in mitigating resistance. A field-derived population was subjected to three treatment strategies: continuous selection with permethrin or malathion for five generations, and alternating selection with both insecticides over seven generations. Continuous permethrin exposure led to a sharp increase in resistance, reaching a 2,700-fold resistance ratio. Alternating permethrin and malathion delayed the onset of high-level resistance but did not prevent its rapid resurgence once permethrin was reintroduced. Synergist assays and gene expression profiling revealed that P450-mediated detoxification—particularly the overexpression of *CYP325V1* and *CYP6BB2* was a major mechanism of permethrin resistance. Sequencing of the voltage-gated sodium channel (VGSC) gene further identified the F1534C mutation, confirming target-site insensitivity as an additional resistance mechanism. Together, these pathways contributed synergistically to high resistance levels. In contrast, malathion selection did not substantially increase resistance, which remained low and was primarily associated with modest overexpression of *CYP6BB2* and *CYP6M11*, without detectable mutations in the *ace-1* gene. Collectively, these findings highlight the multifactorial nature of insecticide resistance in *Ae. aegypti*, involving both metabolic detoxification and target-site mutations. They underscore the value and limitations of insecticide rotation strategies, which can delay resistance progression but cannot fully prevent it under continued selection pressure. This study provides critical insights for optimizing resistance management and preserving the efficacy of insecticides in vector control programs.

O-14 From Seed to Shining Seedling: The Soil Steaming Effects on Spermosphere Assembly and Plant Health

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The spermosphere is the area around an imbibing seed where exudates drive microbial interactions. The developmental stage from seed to seedling is one of the most vulnerable to disease, but few studies have researched the role of microbiome assembly. Soil steaming disinfestation can reduce the number of pathogens present to prevent disease. Therefore, understanding how assembly differs in steamed and non-steamed soil and the impact of steaming on plant health are vital for managing seedling diseases. To accomplish this, ITS and 16S amplicons were sequenced from soybean (*Glycine max*) epiphytes, steamed spermosphere, non-steamed spermosphere, steamed rhizosphere, and non-steamed rhizosphere using Illumina MiSeq. We hypothesize that more seed-associated microbes will be transferred from seed to spermosphere in steamed versus non-steamed soil, which may translate into positive plant health outcomes. Plant biomass and seed pod yield were recorded to indicate plant health. Preliminary results show that the prokaryote composition of the steamed soil communities differed from that of non-steamed soil communities and soybean epiphytes. Moreover, the non-steamed soil was more stable in compositional variation across each sample. Plant biomass did not differ between treatments, but steaming significantly increased yield. Steaming alters community structure for both spermosphere and bulk soil samples. Stochastic variation among steamed soil was higher for beta diversity metrics than non-steamed soil. We also found that some taxa were differentially abundant from planting to the spermosphere, and some could be seed-originating since they were also found on the seed surface.

O-15 The Hidden Arsenal: How *Xanthomonas perforans* Wields T6SS for Survival and Defense

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In the microscopic arena of the phyllosphere of infected tomato plants, a bacterial pathogen, *Xanthomonas perforans* (*Xp*), has evolved virulence strategies to evade plant immune response. However, little is known about how it can overcome competition with the resident microflora. Type VI secretion system is known to mediate interbacterial interactions and has been hypothesized to play an important role in manipulating host microbiome. *Xp* harbors two clusters of this T6SS, yet their specific functions are poorly understood. We hypothesized that *Xp* employs T6SS clusters to interact with specific members of the tomato phyllosphere and to survive abiotic stressors. Through a mix of fluorescence-based assays, microscopy and real time PCR, we found that *Xp* activates both of its T6SS clusters at a low level, indicative of basal constitutive expression. However, co-existence of specific members of the phyllosphere with *Xp* that engage in competitive interactions leads to stronger activation of T6SS clusters, suggesting that a defensive role of T6SS in *Xp*. T6SS cluster activation was also observed in response to osmotic stress and low levels of pH. Our findings reveal the *Xp* uses its T6SS more than just a microbial killer to eliminate other bacterial competitors but as a tool for survival, giving *Xp* the upper hand in both biological battles and abiotic conditions endurance. Understanding this bacterial warfare could help us develop better strategies to manage tomato diseases.

O-16 Stable pair coordination enables change in the order of mating behavior sequence in a termite

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Animal mating behavior often consists of a sequence of stereotyped actions leading to mate acquisition. Previous studies have focused on how addition or subtraction of behavioral repertoire can diversify mating behavioral sequences. However, changes in the order of behaviors in a sequence may also contribute to diversity of mating behaviors. In termites, winged adults fly from the original nests to find a mate and a site for colony foundation. In most species, alates must shed their wings before obtaining a partner as wings hinder tandem running, a courtship behavior by which partners move together in search for potential nesting sites. However, here we describe a unique tandem running behavior of an Australian termite, *Microcerotermes nervosus*; they can perform tandem runs with wings and are more likely to shed their wings in the presence of a partner. A comparison of tandem stability in *M. nervosus* before and after wing-shed revealed that removal of wings in this species contributed to higher tandem stability. Additionally, we compared the tandem stability of *M. nervosus* to seven sympatric species and found that *M. nervosus* displayed greater tandem speed and stability than most tested species. Our results suggest that extremely stable tandem runs may be required for termites to display tandem running behavior with wings. This discovery provides an example of how mating behavior can be diversified by restructuring the order of behavioral events in a mating sequence.

O-17 How honeybees process dead mice in the nest

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Particularly during winter, conditions such as warmth and food availability inside a honeybee nest cavity appeal to potential animal intruders, including mice. Beekeepers have documented instances of finding skeletal mouse corpses that bees have coated in propolis in their hives. Propolis, a mix of plant resins and beeswax, is anti-microbial in nature. This mouse-mummifying phenomenon resembles other biological processes at the cellular level, like melanization and foreign body response. However, the progression from newly dead mouse to "mummy" has never been tracked and reported. Using modified observation hives, we tracked multiple colonies in processing provided dead mice and described and quantified their behaviors. Colonies processed mouse corpses without the detectable assistance of other animals, through behaviors like chewing and tugging at fur and flesh and even sucking of decay fluids. However, no replicates resulted in mice coated in propolis. Our study is the first to describe how honey bee colonies process decaying vertebrate corpses in their nests. Honey bee nests are constantly exposed to stressors, and the threat of vertebrate intruders is no exception. As climate change continues to exacerbate trends in extreme weather, this threat and its subsequent immune challenges may become more common during the most challenging season for honey bee colonies.

O-18 Monitoring cotton soilborne seedling diseases through metabarcoding and shotgun metagenomics

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A two-year, multi-state effort was undertaken to identify soilborne pathogens causing cotton seedling diseases by sequencing fungal and oomycete communities from bulk soil, rhizosphere, and root tissue. Field sites were part of the National Cotton Council - National Cottonseed Treatment Program, which included 15 sites from 10 states in 2023 and 16 sites from 11 states in 2024. These data were modeled with soil traits and environmental conditions post-planting to explain variation in plant emergence. Metabarcoding revealed that *Fusarium oxysporum*, *F. solani*, and *F. incarnatum-equiseti* sp. complexes were of high relative abundance, and there was a negative relationship between rhizosphere fungal species richness and plant emergence. For oomycetes, a distinct split was noted in the mean relative abundance of *Globisporangium irregulare* and *G. ultimum* along 90°W (around the Mississippi River). Soil oomycete species richness decreased as plant emergence increased, and oomycete community composition in rhizosphere and root tissue was influenced by plant emergence. Including functional gene content with shotgun metagenomic sequencing will further elucidate pathogen diversity patterns and uncover biological processes linked to plant emergence, soil and/or environmental factors. Usage of these data may also be incorporated into prediction models for plant emergence. Understanding patterns in pathogen diversity in agriculture is essential to discern why disease pressure may vary across regions and to improve location-specific disease management recommendations.

O-19 Field Edges as Refuges: Conserving Ground-Nesting Wasps in Tilled Landscapes

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Society benefits from the ecological processes sustained by healthy communities of beneficial insects. Among these are diverse assemblages of aculeate wasps (Order Hymenoptera). Although often misunderstood, these wasps provide essential ecosystem services—as natural enemies of agricultural pests and as pollinators of flowering plants. Their contributions could reduce reliance on chemical inputs and help support more resilient and productive agroecosystems.

Most aculeate wasps nest below ground, making them particularly vulnerable to disturbances in the soil layer. Conventional tillage is a management practice of particular concern due to the intensity of soil disruption it causes. In this work, we focused on quantifying differences in wasp assemblages between two contrasting treatments: Conventional Tillage and Field Edges. Using soil emergence traps, we intensively sampled wasp emergence from spring through early fall in 2021 and 2022, conducting 54 sampling rounds and deploying 2,592 emergence traps.

Our results revealed stark contrasts: field edges supported dramatically higher wasp abundance and higher observed richness than conventionally tilled plots. Overall, the wasp assemblage in the conventionally tilled plots exhibited signs of community degradation. This included lower observed species richness and the loss of dominant species that were otherwise abundant in field edges. These findings underscore the critical role that minimally disturbed semi-natural areas play in maintaining wasp diversity and associated ecosystem functions, highlighting the benefits of incorporating such areas into agricultural landscapes .

O-20 Environmental DNA as a detection approach for *Tropilaelaps* mites, invasive honey bee mites of global concern

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Mites in the genus *Tropilaelaps* parasitize the western honey bee (*Apis mellifera*), causing severe damage. These mites have spread far beyond their native range (especially *Tropilaelaps mercedesae*), and could impact wild and managed *Apis mellifera* populations worldwide. Environmental DNA (eDNA) techniques are used for early detection of other invasive species and could be applied to detect *Tropilaelaps* in samples from honey bee colonies, and complement the current detection approaches that are overly time consuming. To determine which sample types are appropriate for eDNA testing, and how colony infestation levels influence DNA detection we collected multiple sample types from 106 *A. mellifera* colonies in Thailand and South Korea, where *Tropilaelaps mercedesae* mites are present. These samples were tested for *Tropilaelaps* DNA using a qPCR assay. We determined the *Tropilaelaps* infestation rate of the colonies by uncapping worker cells. For each sample type, we determined a detection threshold – the infestation of *Tropilaelaps* required to provide 50% probability of detection in the qPCR assay. We found that samples collected using a moistened swab through the hive entrance performed consistently well across both countries. This method detected *Tropilaelaps* in all tested hives in Thailand regardless of infestation levels and had a detection threshold of 2.6% *Tropilaelaps* brood infestation (infested cells per 100 cells) in Korea. We conclude that eDNA methods are viable for *Tropilaelaps* detection, and discuss their suitability for monitoring programs, based on considerations of sensitivity, processing cost and time needed for sample collection.

POSTER PRESENTATIONS

P-1 Vaccination of Plants for General Disease Resistance: a novel perspective on the 30 years of discovery

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Abstract:
Pathogen attack is a major threat that restricts plant growth and yield. Many studies have identified a large pool of resistance (R) for crop improvement. Unfortunately, genetic engineering of plants modifying these R genes to overcome disease constraints appears to be at a standstill. Their ectopic expressions tend to confer protection against just one or a few pathogens, while suppressing critical aspects of plant growth. To search for novel and feasible approaches to engineer disease resistances, several studies including ours have highlighted "plant growth-promoting rhizobacteria (PGPR)-induced systemic resistance (ISR)" as a unique mechanism capable of priming long-lasting, broad-spectrum disease resistance without the growth penalty that usually accompanies the resistance. Leaders in plant pathology have identified 'the understanding of ISR' as a major future challenge, especially "what is the mobile signal(s)?", and this is answered in this study. We show that PGPR trigger the accumulation of jasmonate (but not salicylate) hormones in the inoculated roots and send 12-oxo-phytodienoic acid (OPDA, a primary jasmonate precursor) as a phloem-mobile signal to the uninoculated leaves where it bind/activate a receptor (CYP20-3)-dependent OPDA signaling. We are performing grafting studies using different combinations of wild type and/or cyp20-3 KO mutant rootstocks (RS) and scions. This will confirm that CYP20-3 is required to respond to the ISR signal in the systemic scions but is not required in the inoculated tissues to produce the ISR signal, and—to the end—help generating transgenic plants with enhanced biotic stress resistance while maintaining or improving growth and yield.

P-2 Comparison of the virome of the Tobacco thrips (*Frankliniella fusca* Hinds) from peanut (*Arachis hypogea*) and clover (*Trifolium repens*) field in Auburn, Alabama collected in 2022 and 2023

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Tobacco thrips (*Frankliniella fusca* Hinds) are major agricultural pests and vectors of plant viruses, particularly in peanut and clover fields. This study employed RNA sequencing (RNA-seq) to characterize the virome of *F. fusca* collected from Wiregrass, Alabama, in 2022 and 2023. A total of 80-85 thrips were collected from peanut and clover fields each year, revealing 25 different viruses. RNA-seq analysis identified 10 viruses in *F. fusca* from clover in 2023 and 3 in 2022, whereas 4 viruses were detected in peanut fields in both years. Most viruses belonged to the order *Bunyavirales*, comprising 33% of those detected in peanut fields in 2022, 67% in 2023, 67% in clover fields in 2022, and 41% in 2023. Shared virus occurrences were limited, with one common virus between peanut field samples from 2022 and 2023, one between clover samples from both years, one between clover and peanut in 2022, and four in 2023. *Orthotospotomatomaculae* was the only virus consistently present across both crops in both years. Overall, *F. fusca* collected from clover in 2023 exhibited greater viral diversity than those from peanut fields, suggesting that thrips feeding on clover host a more diverse virome compared to those on peanut crops. These findings provide insights into virus diversity in *F. fusca* and highlight the potential role of clover as a reservoir for plant viruses.

P-3 Evaluating fall *Varroa destructor* treatments and their impact on amitraz resistant mite populations.

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Varroa destructor mites are a leading cause of honey bee colony losses worldwide. Compounding this problem, some populations of *Varroa* mites have developed resistance to amitraz, one of the most widely used acaricides to treat for *Varroa*. This experiment was designed to determine the effectiveness of different *Varroa* mite treatments while also characterizing the impact different treatments had on amitraz resistant *Varroa* mite populations. Treatment groups included an untreated control, amitraz, formic acid, hops beta acids, and oxalic acid vapor. Treatments were implemented in early October and colonies were assessed 63 and 133 days later. We found that the amitraz, formic acid, and hops beta acids treatment groups kept *Varroa* infestation levels throughout the study, but they did not decrease infestation levels. Contrarily, the untreated control and oxalic acid vapor treatment groups saw a significant increase in *Varroa* infestation at the midpoint sampling event. For colony survival, we saw elevated queen loss in the formic acid treatment group, but we saw only minor differences in colony strength metrics. Genetic analysis showed that amitraz resistance allele frequency increased after the application of amitraz, but this change disappeared over time after overwintering. Additionally, alternative treatments did not change amitraz resistant allele frequency in *Varroa* populations which suggests amitraz resistance may not have a fitness cost, and there does not appear to be cross-resistance of amitraz to other treatments.

P-4 Natural Mutation in the Movement Protein (NSm) of Soybean Vein Necrosis Virus Enables Expression and Delay Cell Death in Plants

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Soybean (*Glycine max* L). is the fourth planted crop in Alabama, valued at $195.8 million in 2023. Soybean vein necrosis virus (*Orthotospovirus glycininecrovenae*, SVNV) is an ambisense single-stranded RNA virus transmitted by the vector *Neohydatothrips variabilis* in a persistent, propagative manner. Symptoms of SVNV include necrotic patches that vary from brown to dark between the veins. SVNV has three genomic segments that carry six open reading frames (ORFs), including NSs (putative non-structural silencing suppressor), N (nucleocapsid), NSm (putative non-structural movement), G_N and G_C (glycoproteins), and L (RNA-dependent RNA polymerase). NSm of SVNV was selected in this study to understand infection and the cause behind the necrotic symptoms of this virus. The original sequence of NSm isolated 15 years ago from Tennessee (accession: GCF_004789395.1), and a representative sequence from Alabama isolated in 2023 (accession: PP855220.1) were used. The two sequences were cloned into a pENTR-d-TOPO vector and then into a pSITE-2CA vector expressing Green Fluorescent Protein (GFP). *Nicotiana benthamiana* plants, also a host for SVNV, were infiltrated with NSm tagged with GFP, and a confocal microscope was used to capture images at two through four days post infiltration (dpi). These images revealed that NSm of TN does not express and causes cell death at four dpi, which was confirmed with a SYTOX blue stain. However, NSm of AL showed protein expression and did not cause cell death at four dpi. These findings indicate the evolution of SVNV-NSm protein and will further our understanding of SVNV infection and potential new management strategies.

P-5 Investigation of isolation, characterization and storage methodologies on *Ramularia* species

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In the United States, areolate mildew is a significant disease in cotton due to its impact on yield. This disease is caused by two distinct species of *Ramularia*: *R. gossypii* and *R. pseudoglycines*. Traditionally, *R. gossypii* has been the predominant species linked to areolate mildew in the southeastern cotton belt. However, in 2022, *R. pseudoglycines* was identified in cotton fields in Mississippi. This study aims to assess the prevalence of these two *Ramularia* species in Alabama. Cotton leaves showing areolate mildew disease symptoms were collected in 2023 (n=10) and 2024 (n=20) from the cotton growing areas across the state. Samples were subjected to fungal isolation on optimal growth media followed by DNA extraction. The rDNA region was amplified using ITS1-F/ITS4-R; ACT-F/ACT-R and TEF1-α-F/TEF1-α-R primers to determine the species of *Ramularia*. The results indicated that modified V8 juice agar and modified Kirchoff's media favored *Ramularia* growth. Sanger sequencing results revealed that all the ten of the 2023 isolates were *R. gossypii.* For 2024 isolates, the sequencing results revealed the presence of both *R. gossypii* and *R. pseudoglycines* in the same isolate. Further studies are in the process of obtaining a pure culture to clarify the results. The results describing population diversity will help us understand the distribution of the pathogen and will be a basis for studying disease dynamics to improve management implications for growers.

P-6 Rooting for Sustainability: Utilization of Plant Growth-Promoting Rhizobacteria as a Biological Control in Turfgrass Management

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In turfgrass management, the soil borne fungal pathogen *Rhizoctonia solani,* causes destructive patch diseases. Symptoms of *R. solani* infection are predominate around spring green-up or fall dormancy, leading to damage if left untreated. Chemical fungicide and fertilizer inputs play a crucial role in maintaining healthy, disease-free turf. With negative impacts of conventional pesticides under scrutiny, biological alternatives have become a useful tool for disease suppression. Plant growth-promoting rhizobacteria (PGPR) are naturally occurring, soil dwelling microbes that enhance growth through a number of mechanisms. PGPR strains from collections at Auburn University have proven effective as biofertilizer and biocontrols in several plant systems. This study explores the potential of PGPR as a sustainable disease management and plant enhancement tool in turfgrass management. Through a series of in vitro and greenhouse trials, 110 PGPR strains were characterized for mechanisms of growth promotion, antagonism against *R. solani,* and direct plant health enhancement in zoysiagrass. The results of these studies enabled the creation of three PGPR consortia targeting *R. solani*, while enhancing nutrient uptake within the rhizosphere of turf. In a 2-year field evaluation, these PGPR treatments were compared to Heritage (azoxystrobin) and Densicor (prothioconazole) in an augmented factorial randomized block. Data from soil health assessments, disease ratings, suggests PGPR-induced disease suppression and nutrient enhancement could be a useful tool in sustainable management systems in turfgrass.

P-7 Exploring sand excavation potential in dark southern drywood termite *Kalotermes approximatus* (Blattodea:Termitidae)

Rebecca A. Valentine, Nobuaki Mizumoto

Termites exhibit diverse nesting behaviors, with a major transition between one-piece nesters, whose entire colony life is completed within a single piece of wood, and foragers, who use physically separated food sources often by connecting them with underground tunnels. Among termite diversity, Kalotermitidae is a lineage of primarily one-piece nesters, and many species are adapted to using a limited amount of wood resources. However, it remains questioned if such strict one-piece nesting is the ancestral state of the Kalotermitidae evolution. In this study, we investigate the potential to excavate tunnels in sand in *Kalotermes approximatus.* This species is a typical one-piece nester in the southeastern United States and is an early diverged (basal) species of Kalotermitidae diversity. We found that *K. approximatus* engaged in tunneling behavior to find other food sources. In a planar arena filled with sand, termites constructed complete tunnels between food sources (separated 7 cm) within 48 hours, with larger groups constructing tunnels more quickly. Their behavioral repertoire of tunneling is similar to that of *Paraneotermes simplicicornis*, a unique kalotermitidae species classified as a forager, where termites kick substrates back to the next termite in line rather than grabbing substrate with their mandibles and carrying it out of the tunnel. These observations imply that the common ancestor of Kalotermitidae had the potential to build tunnels.

P-8 Exploring the Role of *Salmonella enterica* Effectors in Plant Cell Localization and Infection

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Foodborne illness linked to fresh produce has been on the rise in recent years. *Salmonella enterica* has been repeatedly found in contaminated produce and is a leading cause in human foodborne illness. *Salmonella* utilizes its Type III Secretion System (T3SS) in mammalian hosts to invade host cells and promote intracellular survival. Similarly, plant pathogens like *Pseudomonas syringae* and *Xanthomonas campestris* employ a T3SS to inject effector proteins into plant cells to modulate host immunity and facilitate infection. Given the similarity in infection strategies, *Salmonella* may also use its T3SS to interact with and infect plant hosts. We hypothesize that *Salmonella enterica* may use its T3SS to translocate effector proteins into plant cells, similar to the mechanism used by plant pathogens. To test this, we are using transgenic *Arabidopsis thaliana* plants expressing specific *Salmonella* effectors tagged with GFP to assess the localization of these effectors in plant cells. Interestingly, we found that a number of Salmonella Type III effector proteins targeted multiple organelles and cell types in plant, including plasma membrane and the endoplasmic reticulum in leaf pavement cells and stomata. These observations will guide future studies aimed at investigating the possible roles of these effectors in plant colonization and immune modulation.

P-9 A pathogenicity accessory chromosome in *Fusarium oxysporum* f. sp. *vasinfectum*

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Members of the *Fusarium oxysporum* species complex are known to harbor accessory chromosomes that play critical roles in virulence. These chromosomes have the ability to be horizontally transferable between fungal isolates, posing a potential threat due to the spread of pathogenic traits. In this study, we investigated a highly virulent *Fusarium oxysporum* f. sp. *vasinfectum (Fov)* strain, 89-1A, and identified a unique accessory chromosome containing a gene cluster that encodes a lactamase which has been confirmed to be a virulence factor for cotton. A GFP tag was introduced into this chromosome, and two single-spore isolates carrying the GFP-tagged chromosome were obtained. A hydroponic test tube virulence assay confirmed the GFP insertion did not affect the virulence of strain 89-1A. Using one of the GFP-tagged isolates, we performed flow cytometry screening and successfully isolated 44 conidia lacking GFP fluorescence, indicating they may have spontaneously lost the target chromosome. Subsequent virulence assays revealed isolates with a marked reduction in virulence. Sequence analysis of the accessory chromosome identified eight genes potentially involved in host specificity. Among them, qPCR analysis showed that *FUN_000082 and FUN_001597* were significantly upregulated—by approximately 200-fold and 60-fold, respectively—at 15 hours post-infection of cotton. Ongoing research will employ molecular biology techniques and virulence assays to further elucidate the functions of these two genes. By identifying key genes and clarifying their roles during infection, this study provides novel insights into the function of pathogenicity-related accessory chromosomes, and may offer potential strategies for developing effective and sustainable measures to manage cotton diseases.

P-10 Salt-Tolerant PGPR: A Dual Approach to Suppressing *Meloidogyne incognita* and Promoting Cotton Production

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Southern root-knot nematode (*Meloidogyne incognita*, sRKN) remains a persistent threat to cotton production, prompting the search for sustainable, biologically based management tools. This study investigates using salt-tolerant plant growth-promoting rhizobacteria (ST-PGPR) to enhance cotton health and suppress sRKN through key mechanisms such as nitrogen fixation, siderophore production, and direct nematicidal activity.

A total of 222 ST-PGPR strains were initially screened in vitro. Nitrogen fixation was evaluated using nitrogen-free JNFb media, where pH-induced color changes and pellicle formation signaled active nitrogenase activity. By Day 3, strains like *Curtobacterium oceanosedimentum* (ST-42), *Bacillus velezensis* (ST-68), *Pseudomonas neuropathica* (ST-177), and *Pseudomonas koreensis* (ST-217) demonstrated strong nitrogenase activity, with 38% of isolates exhibiting notable fixation potential. Siderophore production was assessed on Chrome Azurol S (CAS) agar, with iron-chelating activity indicated by orange/yellow halo formation. Strains *Pseudomonas glycinae/kribbensis* (ST-170/211), *P. anguilliseptica* (ST-161), and *Luteibacter yeojuensis* (ST-7) were particularly effective, with ST-170 producing the largest halo (1.42 cm). To determine nematicidal potential, all 222 strains were subjected to an in vitro J2 mortality assay against sRKN second-stage juveniles (J2), with 1×10^7 CFU/ml bacterial suspensions. Several strains induced high mortality, including *Psychrobacter nivimaris* (ST-97, 97%), *Isoptericola halotolerans* (ST-105, 97%), *Bacillus vietnamensis* (ST-167, 95%), and *Bacillus safensis* (ST-172, 94%). Based on the in vitro results, 38 promising strains were selected for greenhouse trials, which are ongoing to validate their efficacy for nematode suppression and cotton growth.

This study highlights the potential of ST-PGPR as a multifunctional bioinoculant capable of improving nutrient availability and offering biocontrol against sRKN, laying the groundwork for sustainable solutions in cotton production.

P-11 Pollinator and Pollinator Plant Communities within restored Montane Longleaf Pine Ecosystems

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Historically the fire-dependent and biodiverse longleaf pine (*Pinus palustris)* ecosystem was the dominant ecosystem of the Southeastern US. This ecosystem's range was massively reduced due to land conversion and fire exclusion efforts, causing loss of many native species. Efforts to restore and protect longleaf pine stands are now ongoing with the goal of expanding habitat and refuge for threatened species. Differences in restoration practices and prior land use may influence the extent to which restored habitat patches can support pollinators and their plants. This study compared pollinator plant biodiversity between two neighboring restored montane longleaf pine stands that differed in prior composition. Surveys were repeated each month from February to November of 2024. Pollinator plant richness, abundance, and diversity were greater in prior timber plantation plots than in prior mesophied forest plots. Prior plantation plots contained 27 species that were missing from prior forest plots, but the community composition did not differ significantly between site histories. Seasonality was a stronger influence on community composition than prior land management. Soil samples from prior plantation plots were lower in LBC, Mn, P, Zn, and had a higher pH. The only soil measurements that correlated with changes in community composition were LBC and P. The results of this study can inform future restoration management efforts by identifying conditions and strategies that best assist longleaf pine understory community recovery, increase local pollinator biodiversity, and provide refuge for endangered species suffering from habitat loss.

P-12 A Computational Search: Discovering Type VI Secretion System Effectors in *Xanthomonas perforans*

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With whole genome sequencing becoming a prevalent research technique, the wealth of data available for study is growing exponentially. This resource is not only used for population genomics but can be leveraged to answer questions in molecular biology. One such question is finding the effector repertoire of the type 6 secretion system (T6SS) in the plant pathogen, *Xanthomonas perforans* (Xp). Unlike the type 3 secretion system, there is no universal secretion signal for T6SS effectors. This presents a challenge in identifying new effectors computationally. To address this problem, this study aims to develop a computational pipeline for the discovery of new effectors. First, genomes are downloaded from the NCBI database and undergo a BLAST search for the core genes *tssA* and *tssB* which flank the T6SS gene clusters. This identifies the location of the T6SS gene clusters and after filtering out known core and regulatory genes, the remaining genes are viewed as putative effectors. To find potential orphan effectors spread throughout the genome, the SecReT6 database of experimentally validated effectors is searched against all Xp genomes using BLAST and HMMER. Once a list of putative T6SS effectors is formed, the effectors are characterized using Google's AlphaFold and Foldseek for structural and functional analysis, and PaperBLAST and EggNOG-mapper for annotation and domain indentification. The information gleaned from these analyses will be used to reveal the function of T6SS in addition to the potential physical limitations of the system such as effector structure, charge, unfolding force, or size. This study not only exposes the effector diversity of Xp but also serves to show the potential for genomic data to be useful in addressing questions in molecular biology.

P-13 Plant Growth-Promoting Rhizobacteria-Mediated Crop Protection Against Plant Virus

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The Green Revolution, while significantly boosting global crop yields, also incurred substantial environmental costs due to intensive chemical inputs. There is a growing recognition of the transition from chemical-dependent practices to organic practices. This study explores the role of plant growth-promoting rhizobacteria (PGPR) in enhancing crop growth, particularly their ability to modulate virus infections. In this study, we evaluated the effectiveness of PGPR in mitigating virus infections using two significant virus species for vegetable crops and four PGPR species previously shown to positively affect crop health against viruses. Our methodology included quantifying virus titers before and after PGPR treatment and monitoring expression of defense-related genes. Our study showed that both Cucumber mosaic virus and Potato virus Y could successfully infect tobacco and *Arabidopsis* plants systemically. Furthermore, treatment of the plant with four different PGPR species differentially regulated the expression of defense-related genes and limited the infection by both viruses. This study underscores the potential of PGPR as a sustainable alternative to chemical interventions, reducing environmental pollution, preserving beneficial soil organisms, and promoting overall ecosystem health. Embracing organic practices supported by PGPR presents a promising pathway toward achieving agricultural sustainability in the face of mounting environmental challenges.

P-14 Unveiling Viral Diversity in *Aphis gossypii*: Discovery and Characterization of Novel Iflaviruses

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Understanding the viral communities associated with economically important insect pests is crucial for developing comprehensive pest management strategies. This study investigated the viral community in the cotton aphid, *Aphis gossypii*, using samples collected from cotton fields across five Alabama counties: Autauga, Henry, Macon, Escambia, and Lee. RNA sequencing of pooled aphid samples enabled the identification of viruses through de novo assembly and taxonomic classification. These analyses revealed viruses from at least seven families, including both plant-infecting and insect-infecting viruses, each exhibiting distinct geographic prevalence patterns across the sampled counties. PCR-based validation confirmed 12 out of 13 selected viruses, spanning diverse taxonomic groups. Notably, three novel iflavirus species -- positive-strand RNA viruses belonging to the family Iflaviridae -- were identified within the virome assembly and further validated through whole genome resequencing using PCR, T/A cloning, and 5′/3′-RACE techniques. Phylogenetic analysis grouped these viruses within the same clade as other aphid-infecting iflaviruses while distinguishing them into two separate subclades. Additionally, the detection of negative-strand RNA in two of the three iflaviruses indicated their replication within the aphid host. Despite the confirmed presence of these novel iflaviruses, the overall infection rates in aphid populations were below 1% in the collected samples. These findings highlight the complexity of the viral communities associated with *A. gossypii* and underscore the importance of future research into the ecological and agricultural impacts of these viruses on aphid biology and cotton crop health.

P-15 Factors affecting the success of biofertilizers in bermudagrass pastures

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Regenerative agriculture focuses on reduced chemical inputs and improving soil health, while maintaining high productivity. Forage production, with frequent defoliation and regrowth, is heavily reliant on chemical fertilizers. Plant growth promoting rhizobacteria (PGPR) have promise to reduce chemical inputs and maintain comparable growth with reduced fertilizer inputs, but there are concerns about consistent performance in biological products. We investigated how common soil, stand, and environmental factors contribute to the responses of *Paenibacillus riograndensis* DH44, a gram positive PGPR strain with documented success in forage grass. In greenhouse experiments, we determined 10^5 CFU/mL was the lowest concentration of DH44 to achieve growth promotion in bermudagrass and this was further tested in the field. Data from routine soil and phospholipid fatty acid (PLFA) tests were collected on samples from the 7 production sites used in this trial. Principle component analysis was used to visualize 1) key factors that contribute variation based on clustering due to treatment performance and 2) the relationship between soil factors and growth responses (forage height and mass).

P-16 Exploring Phyllosphere Yeast-Bacterial Interactions and the Evolutionary Placement of a Novel *Cystobasidiomycetes* Yeast

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Microbial interactions play a crucial role in shaping community structure and function, yet plant-associated yeasts' contribution to these dynamics remains relatively understudied compared to bacteria. This study investigates yeast-bacterial interactions using an *in-vitro* plate assay, finding a spectrum of effects on bacterial growth, ranging from neutral to positive or negative. Contact-dependent and contact-independent interactions indicated that yeasts influence bacterial communities through direct contact, agar-diffusible compounds, and/or volatile compounds. In addition, a comparative genomics approach was employed to identify potential adaptive features at the genomic level among *Cystobasidiomycetes*. Phylogenetic analysis using multiple loci and whole-genome sequencing data was conducted to determine the placement of a novel *Cystobasidiomycetes* yeast, EMM_F5, isolated from *Magnolia grandiflora* leaf surface. Phylogenetics based on ITS, LSU, SSU, *TEF1-α, RPB2*, and *CYTB* loci suggests that this novel yeast belongs to the family *Microsporomycetaceae*, and comparison with available genomes suggests it is closely related to *Millanazyma bloemofonteinensis, Millanazyma cladoniphila* and *Microsporomyces hainanensis* in the basal lineages of *Cystobasidiomycetes*. However, further comparative analyses are necessary to refine its taxonomic placement by identifying features shared with closely related species. This study highlights the need for functional genomics and metabolomic profiling of these yeasts to understand the evolutionary drivers of fungal adaptation. Additionally, it provides insights into yeast-bacterial interactions and their potential role in shaping microbial communities in the phyllosphere. Future studies are needed to elucidate the underlying molecular mechanisms driving these interactions and their ecological significance, particularly within phyllosphere microbiomes.

P-17 Impact of Seed Treatment on Soybean Yield in Alabama

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The impact of seed treatments in Alabama was observed at six locations across the state. This study monitored the effect of insecticide, fungicide, and a combination of insecticide/fungicide seed treatments targeting primary pests to increase yield in Alabama soybeans. Pest populations, yield, and return on investment were observed to determine the benefit of each seed treatment on soybean productivity.

P-18 Genome Characterization and Virulence Potential of Two *Fusarium solani* Species Complex Isolates Infecting Soybean

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Fusarium solani species complex (FSSC) includes multiple pathogenic species known for infecting a wide range of hosts. In this study, we characterized two virulent isolates—*Fusarium solani* Cherokee5 and *Fusarium falciforme* Progeny4—identified through preliminary virulence assays on soybean. Genomic DNA was extracted using the Qiagen protocol and sequenced using Oxford Nanopore Technology. Assemblies generated using Canu were polished with Racon and Medaka, resulting in 22 contigs (~58 Mb) and 24 contigs (~62 Mb) for *F. solani* and *F. falciforme*, respectively. Gene prediction via AUGUSTUS identified 17,606 genes in *F. solani* and 17,900 genes in *F. falciforme*. To investigate their natural product biosynthetic potential, we analyzed secondary metabolite gene clusters using antiSMASH, which predicted 46 clusters in *F. solani* and 47 clusters in *F. falciforme*. Comparative genomics using *Fusarium vanettenii* 77-13-4 as a reference allowed delineation of core and accessory genome regions. Future work includes transcriptome analysis of these isolates in the presence of soybean seed exudates to identify candidate genes involved in manipulating the spermosphere and candidate genes that could be involved in early root colonization. Select candidate genes will then be targeted for functional validation using CRISPR-Cas9-mediated gene editing to assess their role in influencing the spermosphere and pathogenicity. This study provides genomic insights into two virulent members of FSSC and lays the foundation for understanding their infection mechanisms.

P-19 Understanding a New Fast-growing Potentially Novel Strain From the Diversity of Epichloe Endophytes in Tall Fescue From Alabama.

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Epichloë endophytes are symbiotic fungi that benefit cool-season grasses such as Tall Fescue (*Schedonorus arundinaceus)* by enhancing stress tolerance and herbivore resistance. However, they also produce alkaloids that can lead to livestock toxicoses, notably fescue toxicosis. Traditionally, *Epichloë* species are known to grow slowly in culture, but we recently isolated a strain from Tall Fescue in Alabama that exhibits notably rapid growth. Morphological and molecular analyses, including internal transcribed spacer (ITS) and partial *tef1* gene sequencing, indicate that this isolate aligns with the *Epichloë* genus yet displays distinct characteristics, suggesting it may represent a novel variant. Its accelerated in vitro growth points to possible unique adaptations affecting the grass–endophyte dynamic, with implications for both local ecological interactions and agricultural applications. Ongoing research is investigating the alkaloid profile, symbiotic effectiveness, and potential impact on forage quality and livestock health. A better understanding of this fast-growing *Epichloë* strain could inform breeding strategies aimed at balancing the agronomic benefits of endophyte infection with mitigation of livestock toxicoses. Ultimately, this work underscores the evolutionary plasticity of *Epichloë* endophytes and their capacity to shape Tall Fescue performance under diverse environmental conditions.

P-20 Utilizing Drought-Tolerant Plant Growth Promoting Rhizobacteria for Sustainable Management of *Meloidogyne incognita* in Cotton

Bhandari, Gayatri, Chhetri, Prativa; Lawaju, Bisho Ram; Lawrence, Kathy

Cotton (*Gossypium hirsutum*) is increasingly threatened by drought and root-knot nematode (*Meloidogyne incognita*, sRKN) infestations, leading to compromised plant health and yield loss. This study evaluates the potential of drought-tolerant plant growth promoting rhizobacteria (DT-PGPR) for enhancing plant resilience and suppressing nematode populations. A diverse collection of 235 bacterial strains, isolated from plants roots in La Luz, New Mexico was screened for nitrogen fixation, siderophore production, and nematicidal activity, Approximately 25% of the isolates demonstrated active nitrogenase function with *Promicromonospora alba* (DT-15), *Bacillus velenzensis* (DT-59), *Bacillus cabrialesii/ inaquosorum* (DT-62), *Paenibacillus endophyticus* (DT-72), emerging as top nitrogen fixing candidates based on visual calorimetric evaluations using liquid JNFb media. Siderophore production, assessed in Chrome Azurol S agar media showed the highest halo zone in *Pseudomonas monteilii* (DT-14) at 9.8mm, followed by Bacillus velezensis (DT-105, 8.7mm), *Arthobacter nitrophenolicus* (DT-129, 7.3mm), and *Bacillus siamensis* (DT-8, 7.2 mm) as highly competitive strains for iron acquisition. In vitro nematode bioassays targeting second-stage juveniles, evaluated using NaOH viability test, revealed significant mortality ranging from 0% to 36%. *Chryseobacterium elymi* (DT-3) induced highest juvenile mortality (36%), followed by *Sphingomonas kyeonggiensis* (DT-204, 32%), *Bacillus velezensis* (DT-59, 32%), and *Variovorax ureilyticus* (DT-64, 30%)- all significantly higher than the control ($P \leq 0.0001$). Based on these findings, 37 DT-PGPR strains have been selected for greenhouse trials to evaluate plant growth promotion and biological nematode suppression. This research will lay the foundation for selecting top-performing strains for field trials in sRKN infested fields, assessing their potential for sustainable nematode management through biological control.

P-21 The Calcium-Virulence Connection: Conservation Across *Xylella fastidiosa* Strains

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Xylella fastidiosa (*Xf*), a xylem-limited bacteria, is transmitted by insect vectors and infects 713 host plants, causing devastating diseases in grapes (Pierce’s disease) and blueberries (bacterial leaf scorch), among others. *Xf* has developed the ability to manipulate the mineral composition of the xylem, a nutrient-poor environment subject to continuous flow. We showed that calcium (Ca) is a key regulator of virulence by enhancing virulence traits (biofilm formation, twitching motility) in the bacterium, and *Xf* infection induces higher Ca levels in xylem sap of multiple host plants However, the effect of Ca on virulence among strains from different subspecies has not been studied.

Here, we investigate the impact of Ca supplementation on virulence and disease development across *Xf* strains from five different subspecies isolated in the US and Europe. Preliminary results show that adding Ca to growth media increases biofilm formation across genetically diverse strains. Interestingly, strains isolated from an island in Spain showed stronger responses, suggesting a potential role of geographic origin in Ca responsiveness. Comparative genomic analysis will assess the makeup of Ca-binding proteins across all *Xf* genomes. Twitching motility plate assays show that Ca enhances motility, which will be further tested in microfluidic chambers mimicking flow conditions. Ongoing experiments in the greenhouse are testing the hypothesis that Ca amendments to potted plants increase symptom development by *Xf* strains. By combining wet lab, molecular microbiology techniques, and bioinformatics, this study will help understand the regulation of virulence by Ca among *Xf* strains.

P-22 Development of qPCR Assay for Detection and Quantification of *Paenibacillus reograndensis* DH44.

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Paenibacillus reograndensis is an endophytic plant growth-promoting bacterium (PGPB) that is a potential bio-stimulant alternative to synthetic N fertilizer, and using this bacterium may help reduce associated costs. However, tools to identify and quantify them must be developed to validate their effects and compare them with N fertilizers in field scenarios. Here, we attempted to develop a strain-specific quantitative PCR (qPCR) assay to identify and quantify DH44, a strain previously shown to be beneficial to turfgrasses. A comparative genomic analysis of DH44 against 1122 *Paenibacillus* genomes using K-mers Exclusion by Cross-referencing (KEC) yielded 59 unique regions, from which ten primer pairs were designed, ranging from 105 to 176 bp in length. Endpoint PCR confirmed specificity to DH44 for nine out of ten primer pairs. Subsequently, the qPCR assays performed with these primer pairs were optimized to refine primer concentrations and thermal cycling conditions. Primer pairs KEC 12 and KEC 13 emerged as the most robust primers with 99.4% and 90.08% primer efficiency, respectively. The limit of detection (LOD) was obtained at 0.1 pg DNA, equivalent to approximately 124 DNA copies, ensuring high assay sensitivity. Our future directives include comprehensive *in planta* validation of the qPCR assay to ensure feasibility.

P-23 Engineering a hypervirulent strain of *Beauveria bassiana* through expression of a repressed secondary metabolite

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Beauveria bassiana, an entomopathogenic fungus known to infect a wide range of insects, is a widely used biocontrol agent in managing insect pests. In this study, we engineered a hypervirulent strain *of B. bassiana* through the disruption of *BbSMR1,* a negative regulator of a transcription factor for the oosporein biosynthetic cluster using a CRISPR/Cas9 gene editing system by inserting a resistance cassette for geneticin as a selective molecular marker into the Cas9 cleavage site. The *B. bassiana BbSMR1* mutant displayed over production of oosporein, a secondary metabolite characterized by the red pigmented phenotype. Virulence assays with the mutants on *Galleria mellonella* demonstrated a remarkable increase in insecticidal activity with reduced lethal times. Conidia from wild type and geneticin present mutants were mixed and grown on media without selective marker which allowed the parasexual recombination and growth of marker-less transformants. Those transformants were screened and grown on liquid media and the marker-less mutants were confirmed with the production of a red phenotype. This study emphasizes the utility of genetic engineering in developing enhanced biocontrol agents and will enable generation of marker-less strains for use in sustainable agriculture for environment-friendly pest control.

P-24 Impact of Peanut Variety and Insecticide on Thrips Management in Nematode Infested Fields

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A trial was done at the Wiregrass Research and Extension Center in Headland, AL in 2023 and 2024 to evaluate the management of tobacco thrips (*Frankliniella fusca*) and the transmission of tomato spotted wilt virus (TSWV). Two varieties, GA 06-G and GA 12Y, were planted at a seeding rate of 6 seed per foot on 36-inch rows. Treatments consisted of a non-treated control and at-plant applications of aldicarb (AgLogic, 7 lb/A), phorate (Thimet, 5 lb/A), and oxamyl (Vydate, 17 oz/A). Evaluations were done by making whole-plot visual estimations of thrips injury and seedling vigor at 15, 22, and 29 days after planting (DAP). Additional data collection included seedling % TSWV incidence and percent green canopy closure at 50 and 56 DAP. Finally, plots were harvested to determine treatment effects on yield.

P-25 Ants in the City: How Urban Landscapes Shape Diversity in the Southeast

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Urbanization is reshaping ecosystems globally, but its effects on biodiversity vary across cities and regions. In high-latitude cities, studies often report neutral or even positive impacts of low-level urbanization on biodiversity, suggesting that urban areas can act as biodiversity reservoirs. Toward the equator, however, urbanization tends to have more negative effects, though the reasons remain unclear—partly due to limited research in low-latitude cities compared to temperate counterparts. To address this gap, we conducted the first survey of insect diversity in Atlanta, Georgia, focusing on ants, to assess urbanization's impacts in the southeastern U.S.—a biodiversity hotspot relative to northern cities. We examined both direct effects of urbanization (e.g., impervious surface cover, vegetation complexity) and indirect effects via invasive species, which are especially prevalent in southeastern urban areasWe sampled ant communities at 47 sites across three habitat types along a gradient of urban stress: fragmented greenspace (most urban), manicured parks (moderately urban), and forested parks (least urban). Contrary to patterns observed in northern cities, where biodiversity typically declines with increasing urbanization, we found a non-linear pattern: species richness peaked in moderately urban manicured parks and was lower in both highly urban and minimally urban sites. The unexpectedly low diversity in forested parks was associated with the presence of *Brachyponera chinensis*, the invasive Asian needle ant. These results align with broader latitudinal patterns, suggesting that invasive species may be a primary driver of biodiversity loss in low-latitude cities—raising concerns for conservation in global biodiversity hotspots.

P-26 Integrated pest management of chilli thrips in Alabama nurseries

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Chilli thrips (*Scirtothrips dorsalis Hood*) are economically important pests of ornamental, fruit, and vegetable production. In ornamental crop systems, this species causes significant damage resulting in drastic reduction in plant marketability. While chilli thrips are found worldwide, establishment in Florida and Alabama have only recently been documented (1991 and 2017 respectively). Furthermore, resistance to insecticides has been observed within their native range and recently in Florida. Due to this rapid range expansion and reported resistance, investigating seasonal phenology and alternative management strategies has become a necessity. This study aims to investigate biological control strategies, potential volatile attractants, insecticide resistance, and seasonal flight patterns/abundance of chilli thrips within Alabama. In a two-year study conducted in Mobile, Alabama, sticky cards were collected from plant nurseries to determine abundance and seasonal distribution. We observed that chilli thrips were most abundant in 3-month periods during the spring and fall, with peaks being observed in April and October. Spring 2024 results may even indicate grower surveys and treatment within their nurseries, though we are surveying growers for confirmation. A biocontrol assay was performed determine the efficacy of two predatory species (minute pirate bugs and *Amblyseius swirskii* mites; individually and together) in controlling chilli thrips populations in a nursery setting. This assay includes host plants of *Distylium, Cleyera*, rose, and azalea with heavy chilli thrips populations and damage in Auburn and Mobile. These results may indicate sustained control over a five-week period. This assay is being repeated in Fall 2024 to confirm these results.

P-27 Foliar bacterial pathogens: The unexpected allies of root invaders

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Plants encounter multiple pathogens throughout their lifetime, and sometimes they face simultaneous infections. However, our understanding of plant disease outcomes mainly focuses on binary interactions between a single pathogen and the plant. This approach neglects the complex interdependencies among the plant and multiple pathogens and how the outcome of simultaneous infections may not simply be the sum of individual infections. Consequently, managing simultaneous pathogen infections may not be straightforward. In this study, we investigated whether simultaneous presence of foliar pathogen and root parasite may alter overall disease outcome and resistance-based management of root parasites. In Southeastern U.S. fields, both root-knot nematodes and *Xanthomonas* are endemic pathogens, and growers rely on *Mi*-resistant tomato lines to control nematode infestations. In the study, we investigated single and simultaneous infection in tomato plants by parasitic root-knot nematode *Meloidogyne* species and foliar bacterial spot pathogen *Xanthomonas perforans*. We assessed resistance efficacy of nematode-resistant varieties that are near-isogenic line for the *Mi* resistance gene. In planta greenhouse experiments showed an increase in *M. incognita* nematode population with the *X. perforans* co-infection in nematode-resistant tomato cultivar Monita, with no significant influence on nematode-susceptible cultivars. Meanwhile, *Mi*-mediated resistance to nematode did not confer resistance to *X. perforans* irrespective of nematode infection. Overall, the study suggests that foliar bacterial infection may compromise *Mi*-mediated resistance to parasitic nematodes, and it is essential to understand the mechanism of simultaneous infections by multiple pathogens when ensuring the long-term durability of host resistance.

P-28 Taxonomic and functional convergence of the soybean spermosphere microbiome across different soils

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The interactions between seeds and soil microbes are important to the establishment of seedlings with outcomes often resulting in seed or seedling death. However, few studies have investigated the microbiome assembly process from seed sowing to seedling development. Therefore, we present the microbiome of developing seeds, focusing on the spermosphere, the small and short-lived zone surrounding an imbibing seed before radicle emergence. Previous research has shown crop-specific microbiome assembly in the spermosphere within 18 hours of sowing soybean or cotton. In this study, we aim to identify the microbes and fucntions commonly selected for in the spermosphere despite different microbial pools. Therefore, we sampled the soybean spermosphere from different soils around the U.S. at 0, 8, 12, and 16 hours post planting. Bulk soils without seeds planted were also sampled. Emergence data was recorded to indicate plant health outcomes. Fungal and bacterial amplicon libraries were sequenced and analyzed to reveal the microbes commonly enriched in the soybean spermosphere. Future work will involve the exploration of the functional convergence of the spermosphere microbiome using metagenomics. Overall, this research will enhance management strategies for seedling diseases, identify key microbes for robust seedling growth and protection, and underscore the significance of early plant microbiome assembly in influencing plant health.

P-29 influence of planting date on the insect complex in alabama cotton

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Tarnished plant bug and multiple species of stink bug are both significant pest of cotton in the Southeast. In Alabama this Insect Complex on average account for over $20 million in economic losses. Replicated small plot research trials were conducted in Alabama to document the effects of planting date, variety selection, and management practice on this bug complex in Alabama cotton. Plots were planted on May 2nd and May 24th with both a ThryvOn and non-ThryvOn variety. Half of the plots were managed for insects in the bug complex at threshold and the other half of the plots were no spray plots. Early planted cotton had significantly higher pest pressure from the bug complex, however it also yielded substantially higher, as there was a late season drought this past season in Alabama. ThryvOn plots were significantly lower in plant bug pressure when compared to non-ThryvOn plot, however there was no differences in regard to stink bug pressure. Lastly, plots that were managed at threshold for insects were significantly lower in pressure on average throughout the growing season

P-30 Variance in Microbial Diversity Among Drought-Tolerant and Drought-Susceptible Peanut Cultivars

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Drought has been identified as a dominant threat to the peanut industry (National Peanut Board, 2025). As the severity and duration of droughts are expected to increase alongside rapidly changing environmental conditions, new strategies are being developed to increase crop resilience to drought and other abiotic stressors. The host-associated microbiome acts as an extended layer of immunity and provides tolerance towards biotic and abiotic stressors. This work aims to seek understanding of the contribution of the microbiome in drought tolerance. To investigate this, microbial DNA samples from three rhizocompartments (rhizosphere, endosphere, and bulk soil) were extracted and characterized from nine peanut cultivars of varying levels of drought tolerance (water-saver, water-spender, and sensitive) from Auburn University's peanut breeding program. Results show statistically significant differences in community assembly and diversity among the drought-tolerant categories, in additon to shifts in selection pressure among the three rhizocompartments of each genotype. This work poses a foundation for further research into the contribution of host genotypes in structuring microbial communities and can potentially help growers identify novel mechanisms of microbe-associated immunity against drought stress.

P-31 Evaluation of Reklemel™ as a specific chemical nematicide for *Meloidogyne incognita* and its effects on the associated *Fusarium oxysporum* f. sp. *vasinfectum* disease complex in Alabama

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Reklemel is a nematicide that has been brought to the market as a less harmful alternative to traditional products. One of the specific organisms targeted by Reklemel is the southern root knot nematode, *Meloidogyne incognita*. This organism causes severe crop damage and loss each year and can form a disease complex with the causative agent of cotton fusarium wilt, *Fusarium oxysporum* f. sp. *vasinfectum* (FOV). Nematicides have historically been very harmful to soil ecology and are not specific in their impacted populations. The objectives of this study are to 1) evaluate the effective ranges of Reklemel in FOV isolates in an in vitro assay, 2) assess the impact of Reklemel use in field/greenhouse trials on plant growth and yield and 3) determine the effects of Reklemel on commensal bacterial, fungal and nematode soil populations. Media will be prepared containing serial dilutions of Reklemel to be used for the in vitro assay and field trials will be done at the Plant Breeding Unit of Auburn University's E. V. Smith Research Center near Tallassee, AL. Statistical analysis will be performed with SAS Proc Glimmix to determine rates of FOV infection compared to *M. incognita* egg density. This study aims to determine whether Reklemel is both effective in preventing damage from the *M. incognita*/FOV disease complex and specific with its target of plant parasitic nematodes.

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