



## **Abstracts of the 11<sup>th</sup> Annual Mississippi Association of Entomologist, Nematologist, and Plant Pathologists Meeting, October 31<sup>st</sup> – November 1<sup>st</sup>, 2022**

### **Oral Presentations**

#### **The effects of types and queen cell size on development and birth characteristics of honeybee queens**

Abou-Shaara, Hossam and Esmail Amiri

Plastic queen cell cups have become an indispensable element of honeybee queen rearing activities. Currently, many different types of plastic cups are available on the market. We aimed to evaluate the effects of ten different types of commercially available plastic cups on the development of honeybee queens. We began by measuring the physical characteristics of cups followed by standard queen rearing approaches. According to their diameter, cups were divided into three groups (small, medium, and large). A single-source queen was used to provide young larvae to graft and three queenless colonies for nursing the grafted larvae. The experiment was repeated six times. For each cup type, we measured the acceptance rate, weight of larvae, and deposited Royal Jelly three days after grafting. We also recorded the emergence rate, the weight, and morphological characteristics of newly emerged queens. The results showed significant variations in the larval weight and deposited royal jelly among cup types, although no significant differences in morphological characteristics among emerged queens from different cup types. Although the amount of royal jelly was higher in medium and larger cups, acceptance, capping, and emergence rates were significantly lower in larger cups. Our findings are discussed regarding the suitability of available commercial cup types for queen rearing.

#### **Virome of bean leaf and banded cucumber beetles in Mississippi**

Aboughanem-Sabanadzovic, Nina, Fred Musser, and Sead Sabanadzovic

Bean leaf beetle (*Cerotoma trifurcata*) and banded cucumber beetle (*Diabrotica balteata*) are important agronomic pests in Mississippi and the southern US. This study, aimed to gain preliminary data on RNA viruses associated with these two insects, was carried out on 10 pools of samples (five for each beetle) collected in August/September 2021 in different locations/production fields in the state. Preliminary results generated by high-throughput sequencing revealed presence of numerous new and known viruses in studied samples, with higher number of viruses associated with bean leaf beetle compared to banded cucumber beetle.

#### **Preliminary data on tick-associated viruses in Mississippi**

Aboughanem-Sabanadzovic, Nina, Jerome Goddard, and Sead Sabanadzovic

Ticks are important vectors of several important pathogens, including viruses, that cause

diseases in humans. The number of tick-borne diseases reported in the US has significantly increased in recent years, leading the Centers for Disease Control and Prevention (CDC) to make this issue a high priority in public health policy. Therefore, due to a complete lack of information, a pilot study on viruses associated with four major tick species in Mississippi has been initiated in 2021 to generate baseline knowledge for the state and seed data for major funding. Here we present preliminary results based upon limited number of tick samples tested in the past year. They include several first reports on some for the state/region and discovery of a few new viruses. The project is ongoing.

### **Changes in microbial composition, diversity, and functionality in the *Amblyomma maculatum* microbiome following infection with *Rickettsia parkeri***

Adegoke, Abdulsalam and Shahid Karim

Ticks are the primary vectors for emerging and resurging pathogens of public health significance worldwide. Analyzing microbial composition and functionality is crucial for designing new strategies to control ticks and prevent tick-borne diseases. Here, we explored the microbial communities across developmental stages and tissues of the Gulf-Coast ticks (*Amblyomma maculatum*). Using a high-throughput sequencing approach, the influence of blood meal and *Rickettsia parkeri* infection in driving changes in microbiome was determined. This study shows that the core microbiome of *Am. maculatum* comprises ten core genera. The genus *Rickettsia*, *Francisella*, and *Candidatus\_Midichloria* displayed positive interactions within each developmental stage and tissues tested. Blood meal and *R. parkeri* led to an increase in the bacterial abundance in the tissues. Functional analysis revealed an increase in energy metabolism genes with blood meal. Correlation analysis identified an increase in *Candidatus\_Midichloria* and a decrease in *Francisella* in *R. parkeri* infected ticks. The abundance of *Rickettsia* and *Francisella* predominate in the core microbiome of *Am. maculatum*, whereas *Candidatus\_Midichloria* and *Cutibacterium* prevalence increase with *R. parkeri*-infection. Network analysis suggest that *R. parkeri* interacts positively with *Candidatus\_Midichloria* and negatively with *Francisella*. We conclude *R. parkeri* establishes infection by interacting with the core microbiome of the tick vector.

### **Longitudinal Monitoring of Honey Bee Colonies Along an Agricultural Intensification Gradient in Mississippi**

Catchot III, Angus, Urita Agana, Audrey Sheridan, Priyadarshini Chakrabarti Basu and Jeffrey Gore

Honey bee (*Apis mellifera* L.) colony declines have been reported extensively nationally and globally over the past decade. Pesticides and poor nutrition are two important factors causing such declines. The main purpose of this study is to evaluate the interactive effects of both pesticide exposure and poor nutrition on honey bee colony health across an agricultural intensification gradient in Mississippi. These field sites also vary in their availability of natural forage. Overall colony health, pesticide exposure and forage availability will be evaluated during an entire year from four field sites across the state. Visual inspections, pollen traps and landuse mapping will be used to determine the availability of forage in these areas. In addition, pesticide residue analysis will be conducted on pollen and nectar samples to assess the field realistic exposures to such pesticides. Various colony health parameters will be recorded in addition to collecting data on pests, parasites and pathogens from these colonies. The information gleaned from this study will help us determine if optimal nutrition can counteract the detrimental impacts of pesticides, if any, over long term in a field realistic scenario.

### **Updates from the MSU Pollinator Health and Apiculture Lab: One year old and buzzing!** Chakrabarti, Priyadarshini

The MSU Pollinator Health and Apiculture Lab ([www.priyadarshinichakrabarti.com](http://www.priyadarshinichakrabarti.com)) shares updates about the various interdisciplinary pollinator research, teaching and outreach activities of the lab. The graduate and undergraduate students in the lab are conducting research on primarily three themes: (i) Impacts of pesticides on bees; (ii) Bee nutrition; (iii) Impacts of multiple stressors on bees (such as climate change and pesticides, nutrition and pesticides etc.). The talk will highlight one-two key research projects in each of the thematic areas. In addition, the lab is extensively involved with teaching (Honey Bee Biology and Beekeeping course offered every Fall) and outreach activities housed at the newly established Chakrabarti-Basu Research Apiary at Clay Lyle Entomology Building, Mississippi State University.

### **Effect of fungicides on *in vitro* growth of *Athelia rolfsii* isolates causing southern blight of soybean in Mississippi**

Connor, Adam, Tom Allen, Alejandra Jimenez Madrid, and Tessie Wilkerson

Southern Blight (SB), caused by the fungus *Athelia rolfsii*, has increasingly impacted Mississippi soybean production with economic losses in recent years rising from \$123,803 in 2017 to \$9,508,412 in 2021. Currently, there are no fungicides recommended for use in SB management; therefore, deep tillage and crop rotation are the only suggested strategies. The objective was to evaluate mycelial growth inhibition by using five fungicides: pyraclostrobin, flutriafol, thiophanate-methyl, fluxapyroxad, and fluazinam, at concentrations of 10, 5, 1, 0.5, 0.1, 0.05, 0.01, and 0.001 µg/µl of active ingredient. Based on their distribution across the state of Mississippi, four SB isolates were selected for sensitivity evaluation. A 5mm disk of a pure culture was placed on fungicide amended PDA media with each treatment being repeated twice. Measurements were taken when the control, non-amended medium, reached the margin of the plate, and the mycelial growth inhibition was determined.  $EC_{50}$  values were determined for pyraclostrobin (0.0067±0.0018 µg/ml), fluazinam (0.009±0.0008 µg/ml), fluxapyroxad (0.026±0.0007 µg/ml), and flutriafol (5.01±4.48 µg/ml). Mycelial growth inhibition of thiophanate-methyl did not exceed 10%, therefore, no  $EC_{50}$  value was determined. With limited strategies to manage SB, continued research on fungicide efficacy is needed to manage the impact of SB on MS soybean production.

### **Deciphering the Interplay Between Selenoproteins and the Unfolded Protein Response in Pathogen Infection Using an *Ixodes scapularis* Cell Line**

Downs, LaToya and Shahid Karim

Tick-borne diseases are a public health issue and affect people daily. Despite a robust immune response, pathogens find a way to persist inside of the tick and be transmitted to a host. *Borrelia burgdorferi* (*Bb*) is transmitted to humans by the tick, *Ixodes scapularis* (*IS*). Little research on pathogen infection within the tick contributes to understanding its mechanism to survive within the tick. To uncover the molecular determinants of pathogen infection, we used an *IS* tick cell line (ISE6) to determine the involvement of the unfolded protein response (UPR) and antioxidant selenoproteins in successful pathogen infection inside the tick vector. We hypothesized that the tick UPR and selenoprotein defense mechanisms play a crucial role in pathogen maintenance. Our results show that pathogen infection causes a significant upregulation of selenoproteins and the UPR, and that the response is stress-specific. Additionally, the loss of UPR and selenoprotein components resulted in an increase in pathogen load. These results suggest an interplay between

selenoproteins and the UPR and that they both play an essential role in pathogen survival and replication.

### **Influence of Imidacloprid Seed Treatment Rate on ThryvOn Cotton**

Farmer, Brett, Jeff Gore, Angus Catchot, Whitney Crow, Don Cook, and Brian Pieralisi

In the Mid-South, thrips are an important early season pest on cotton. Mississippi planted over 500,000 acres of cotton in 2020, all of which were infested with tobacco thrips *Frankliniella fusca* (Hinds), which resulted in about \$6.5 million of economic losses. Therefore, cotton is typically treated with a preventative thrips control product at planting and generally about 25-30% requires an additional foliar treatment to reduce damage from thrips. A new *Bacillus thuringiensis* trait (ThryvOn®, Bayer CropScience, St. Louis, MO) has been developed that provides good control of thrips. Currently, there is some debate about the need for an insecticide seed treatment to improve thrips control. We conducted a study to determine if the addition of an imidacloprid seed treatment improves efficacy against tobacco thrips and to determine if reduced rates of seed treatments (100, 75, 50, 25, and 0% of the labeled rate) provide benefits for thrips control in ThryvOn cotton. Preliminary results suggest that a 50% seed treatment rate of imidacloprid provided similar control and yield protection as a 100% imidacloprid seed treatment rate. These preliminary data suggest that ThryvOn cotton could be utilized with a reduced rate of imidacloprid compared to other current commercial varieties.

### **Efficacy of Insect Growth Regulators on Lepidopteran Pest of Soybean**

Hopkins, Sawyer, Whitney Crow, Don Cook, Jeff Gore, and Angus Catchot

Co-application of an insect growth regulator insecticide and fungicide in soybean at the R3 to R4 growth stage commonly occurs in Mississippi. Diflubenzuron is the most commonly used insect growth regulator in these situations. These applications typically are made prior to insect infestations occurring. Diflubenzuron has been effective in managing velvetbean caterpillar when used in this manner. The impact of these insect growth regulator applications on pest and beneficial insects along with the economic benefits to soybean production have not been thoroughly investigated. The objective of this study is to determine the impact of selected insect growth regulators on insect pest infestations and soybean yield. Studies were conducted at the Delta Research and Extension Center in Stoneville, MS in 2022 to evaluate three common insect growth regulators (novaluron, methoxyfenozide, and diflubenzuron), chlorantraniliprole (an industry standard for caterpillar management in soybeans), and an untreated check against soybean looper. By utilizing a cost-effective insect growth regulator at a timing that producers are already making an application, could potentially reduce production costs for Mississippi producers.

### **Novel Viruses Identified in a Worldwide Survey of Bed Bugs**

Hunter Walt, Michael Sheele, Jose Pietri, and Jonas King

Bed bugs (Hemiptera: *Cimex spp.*) are a globally distributed hematophagous pest. Although bed bugs have routinely fed on humans for centuries, they have not been linked to disease transmission or outbreak. Bed bug populations were significantly reduced in developed countries after the widespread use of modern pesticides but have undergone a population resurgence in recent decades. Because of the bed bug resurgence, more studies on their capabilities as disease vectors should be conducted. Here, we subjected single wild-caught and lab-reared bed bugs to deep, high-throughput sequencing (*Cimex lectularius*: n=19, *Cimex hemipterus*: n=6) from nine distinct locations around the world. We used an RNA-seq based approach so that we could concurrently detect RNA viruses

and active microbes. We found full or substantial genome segments for two previously characterized RNA viruses associated with bed bugs (Shuangao bedbug viruses 1 and 2), and four putatively novel viruses: a toti-like virus, sobemo-like virus, a reovirus, and a tenui-like virus. Notably, none of the viruses detected are closely related to vertebrate pathogens. We also corroborate previous suggestions that a *Rickettsia* species may be a secondary endosymbiont of bed bugs and report the first molecular detection of *Cimex hemipterus* (Tropical Bed Bug) in Ohio.

### **An Evaluation of Square Retention Monitoring Methods in ThryvOn and non-ThryvOn Cotton Production Systems.**

Huoni, Michael, Whitney Crow, Jeff Gore, Don Cook, and Angus Catchot

Tarnished plant bug, *Lygus lineolaris* (Palisot de Beauvois), is the most economical insect pest of cotton, *Gossypium hirsutum* L., in the mid-south region of the United States. Yield losses from tarnished plant bug damage can occur as early as squaring and until the end of the bloom. Foliar applications of neonicotinoids, organophosphates, pyrethroids, sulfoximines or a tank-mixture of two are used for control. Alternating modes of action is always recommended when controlling tarnished plant bug; generally, pre-bloom control is reliant on cost effective options with lower levels of efficacy. ThryvOn, a genetically engineered trait utilizing novel Bt genes, has the potential to provide some season long suppression of tarnished plant reducing the number of foliar applications once commercialized. Studies were conducted at the Delta Research and Extension Center in Stoneville, MS in 2022 to reevaluate square retention methods to determine the best monitoring methods in both a sprayed and unsprayed environment with and without ThryvOn technology. The objective of this study was to compare different methods of square retention and determine the optimum method that improves scouting efficiency and tarnished plant bug management.

### **Characterization of antifungal activity of the endophytic *Burkholderia* sp. MS455 against *Aspergillus flavus***

Jia, Jiayuan, Kate Phillips, Emerald Ford, Sonya M. Baird, and Shien Lu

An endophytic bacterium MS455, isolated from soybean and identified as a strain of *Burkholderia*, exhibited broad-spectrum antifungal activity against plant pathogens, including the aflatoxin-producer *Aspergillus flavus*. The objectives of this research were to characterize the antifungal activity and evaluate efficacy on prevention of aflatoxin production on corn. Random and site-specific mutations revealed that the genes required for antifungal activity of MS455 share high homology to the *ocf* gene cluster of *Burkholderia contaminans* strain MS14, which is responsible for production of the antifungal compound occidiofungin. Transcriptional analysis demonstrated ORF1, a homolog to the LuxR-type regulatory gene *ambR1*, regulates occidiofungin biosynthesis in MS455. Corn kernel assays under lab conditions showed that growth of *A. flavus* and aflatoxin production were inhibited significantly by MS455. Fungal growth and aflatoxin production were significantly reduced when the fungus was inoculated with MS455 under greenhouse and field conditions. Genome wide search showed that the MS455 genome harbors multiple antimicrobial-related genes. Collectively, the results demonstrated that production of occidiofungin is essential for antifungal activity of the endophytic bacterium MS455. This research has provided insights to development of biological approaches to prevent aflatoxin contamination in plant production.

### **Developing a Pollen Nutrition Database for North America: Healthy Food for Healthy Bees**

Jennings, Lauren, Max Simon, Ramesh Sagili, and Priyadarshini Chakrabarti Basu

Poor nutrition is one of the major stressors of bee species and is a main contributor to loss in pollinator populations. Bees are currently faced with many nutritional challenges including loss of forage habitat and monoculture. The aim of this project is to promote better nutrition for bees by learning which floral resources are nutritionally optimal for all bees based on the nutritional composition of their pollens. This study will first use various methods of pollen collection in order to collect sufficient pollen from each target species of plants. Next, the collected pollen samples will be analyzed in the lab using basic biochemical assays, as well as mass spectrometry based methods, to determine the nutritional quality of the pollen. The pollen will be analyzed for its concentration of proteins, lipids, amino acids, sterols, metabolites, and phytochemicals. Finally, all of this data collected will be compiled into an online database showcasing the nutritional quality of each plant species' pollen. This database can be used by beekeepers, conservation groups, and growers to scientifically select forage plants for pollinators.

### **Mother Mite I: Evaluate Insecticides used to Manage Twospotted Spider Mites**

Krob, Jessica, Whitney Crow, Angus Catchot, Don Cook, and Jeff Gore

A novel foliar-applied pesticide containing the active ingredient isocycloseram has insecticidal and miticidal properties. This product is currently under review by the environmental protection agency (EPA) to be approved for managing pests in cotton, including tarnished plant bugs, stink bugs (Penatomidae), and twospotted spider mites (TSSM) (*Tetranychus urticae* (Koch)). Limited research has been done on this product, and there is currently no information on the residual activity of isocycloseram. Therefore, a hybrid field-lab bioassay study and a field study were completed in 2022 to evaluate the residual activity of isocycloseram and commonly used foliar miticides used to manage TSSM. The hybrid-lab bioassay study was performed by collecting cotton leaves from the field that were either untreated or treated with a miticide using a mud-master. Leaves were collected from the field at multiple intervals after the first application. Preliminary results will be presented, and as this product becomes available, the results from this research will be useful to cotton producers as they make decisions for managing TSSM in cotton.

### **Managing Rice Stink Bug in Mississippi: Where do we go from here?**

Lytle, Mary Jane, Jeff Gore, Whitney Crow, Don Cook, Angus Catchot, and Jason Bond

Mississippi rice producers have historically relied on pyrethroids to effectively manage rice stink bug (*Oebalus pugnax* F.) due to the cost effectiveness of insecticides within the chemistry. Damage caused by rice stink bug has the potential to lead to direct yield loss as well as decreases in grain quality in rice. In recent years, failed pyrethroid applications have been reported across a number of Mississippi rice acres, potentially indicating a reduction in efficacy due to increased tolerance of rice stink bug to the chemistry. In 2021 and 2022, laboratory bioassay experiments were conducted evaluating the efficacy of lambda-cyhalothrin on Mississippi rice stink bug populations at the Delta Research and Extension Center in Stoneville, MS. The study was comprised of liquid scintillation vials each treated with technical grade lambda-cyhalothrin at various doses and a nontreated control. Rice stink bug populations were collected throughout the Mississippi Delta region and one rice stink bug was placed per treated vial. Mortality assessments were collected 24 hours following infestation of the treated vials. Data analysis is ongoing, and results will be discussed regarding lambda-cyhalothrin control on rice stink bug and future management recommendations.

**Antibiotics induce changes in the microbiome and alter antioxidant gene expression in *Apis mellifera***

Oeth, Michael, Latoyia Downs, Surendra Sharma, and Shahid Karim

*Apis mellifera* or the European honeybee is subject to adversities year-round either due to different forms of disease-causing agents, climate change, pesticides/herbicides, and deforestation. One of the most prevalent problems in the honeybee world is the vector parasite varroa destructor which transmits deformed wing virus which is one of the larger causes of colony collapse disorder in honeybees during the winter. In this experiment, we fed sample sizes of European honeybees' tetracycline and tunicamycin to observe the effects of the antibiotics on the microbiome, deformed wing virus presence, and Reactive oxygen species quantification. We used qualitative real-time PCR to see changes in the core bacteria in the microbiome as well as SOD2 to measure gene expression in relation to increasing/decreasing oxidative stress. I hypothesized that Tetracycline and Tunicamycin feeding in *Apis mellifera* will cause a decrease in ROS production and an increase in ROS-related gene expression due to the perturbation of the core microbiome. Lastly the goal is to see if antibiotics like tunicamycin can serve as treatment for prevalent disease-causing pathogens, to develop a microbiome-free honeybee as a research tool, and to see correlative differences in oxidative stress, disease causing pathogens, and the microbiome of the European honeybee.

**Climatic limits to the present and future distribution of redbanded stink bug.**

Paul, Thomas, Angus Catchot, Tyler Towles, and Samuel Ward.

The non-native redbanded stink bug (RBSB), *Piezodorus guildinii* (Westwood), (Hemiptera: Pentatomidae), first emerged as an economically important pest of soybean in Louisiana in 2000. Drivers of interannual fluctuations in the distribution of RBSB populations are poorly understood, but such fluctuations may depend on the cold tolerance of overwintering RBSB, a chill susceptible species. Combining RBSB occurrence and historical climate data, we developed ecological niche models to identify areas suitable for RBSB persistence under current and future climatic regimes. The effects of warming winters on the range dynamics of RBSB and the insect's associated impacts on soybean will be discussed.

**Biogeography of the Gulf Coast tick, *Amblyomma maculatum* Koch, in a period of rapid environmental change**

Sabet, Afsoon, Jerome Goddard, and Samuel Ward

The Gulf Coast tick, *Amblyomma maculatum* Koch (Acari: Ixodidae), is a three-host tick species of growing medical and veterinary importance. It is a known disease vector of *Rickettsia parkeri*, a rickettsial disease in humans, and *Hepatozoon americanum*, the causative agent of American canine hepatozoonosis. This Nearctic and Neotropical pest has a historical range along the Gulf Coast in the United States, but established populations have been recently reported as far north as Connecticut. We developed an ecological niche model to identify current and future areas with suitable climates for Gulf Coast tick across North America. Models were developed by linking occurrence data from the National Tick Collection with WorldClim bioclimatic variables. We hope understanding the potential range of this pest may aid in implementing integrated pest management tactics in at-risk areas and enable researchers and public health entomologists to optimize disease surveillance.

### **Sublethal effects of thiamethoxam seed treatment on the development and reproduction of small hive beetle**

Sheridan, Audrey, Elijah Johnson, Armelle Vallat– Michel, Gaëtan Glauser, Jeffrey Harris, Peter Neumann, Lars Straubs.

Recent studies have shown that very low levels of thiamethoxam, clothianidin and imidacloprid residues in agricultural soil can have negative impacts on reproduction, longevity and abundance of soil-dwelling arthropod species. However, most of these studies have focused on the oral route of insecticide exposure to arthropods, and little information is currently available on contact toxicity to these organisms. The small hive beetle (*Aethina tumida* Murray, Coleoptera: Nitidulidae) is a globally distributed honey bee pest that completes development from larva to adult in the ground. As the beetle occurs in agricultural environments and does not ingest treated soil, it could potentially serve as a model for research on contact toxicity of neonicotinoids to beneficial arthropods (i.e. ground-nesting bees). In the present study, a commercial thiamethoxam insecticide (Cruiser 5FS) was used as a soil treatment, and several biological parameters were measured upon emergence of adult beetles from the treated soil. Thiamethoxam rates ranged from 25 to 200 ng g<sup>-1</sup>, and beetles were exposed for 16 days. Mating pairs were established from each treatment group and provisioned with food and water for two weeks, during which time egg counts were made daily. Results showed that all tested rates of thiamethoxam negatively affected emergence mass, onset of oviposition (days) and reproductive output (eggs laid over time) of small hive beetles when compared to untreated controls.

### **Invitro Fungicide Sensitivity Assessments of *Athelia rolfsii* from Mississippi Peanut Fields**

Tripathi, Subina, Alejandra Jimenez Madrid, Tom Allen, Alan Henn, Tessie Wilkerson, and Adam Connor

Southern blight (SB), caused by *Athelia rolfsii* (AR), is a soil-borne disease affecting peanut. This pathogen produces sclerotia that serve as inoculum the following season. SB can cause losses up to 80%. In the absence of resistant varieties, applying fungicides is the easiest and most common control method. The present study evaluated fungicide sensitivity of six fungicides. AR sclerotia were isolated on potato dextrose agar. After 7 days, white mycelia were observed. Tan to dark brown or black sclerotia were observed after 20 days. DNA was extracted from six isolates. The isolates were confirmed based on morphological characteristics and PCR-based method. *Invitro* sensitivity to prothioconazole (FRAC 3), azoxystrobin (11), fluxapyroxad (7), fluazinam (29), and pyraclostrobin (11) fungicides were evaluated. A 5mm actively growing fungal plug was placed on fungicide amended plates (10, 1, 0.1, 0.01, 0.001, 0 µg/ml) and colony diameter was measured after 4 days of incubation at 25°C. This experiment was arranged as RCBD with three replications. The experiment was repeated three times. All isolates were less sensitive to azoxystrobin (EC<sub>50</sub> from 3.35 to 8.41 µg/ml) and highly sensitive to other fungicides. Based on this study, fungicide sensitivity levels of AR populations should be regularly monitored in Mississippi.

### **Potential impacts of shade treatments on dormancy of overwintering redbud (*Cercis canadensis* L.) trees at southeastern nurseries**

Werle, Christopher, Anthony Witcher, and John Adamczyk

Dormancy accrual is an important process in mitigating the abiotic stressors of overwintering trees at ornamental nurseries, with frost-damaged tree crops at heightened risk of ensuing biotic insect and disease injury. As mean global temperatures rise, overwintering nursery crops will break dormancy sooner. Using potted eastern redbud (*Cercis canadensis* L.) trees placed under two types of shade cloth, in full sun, or in walk-in coolers, we measured



stem, air and root zone temperatures, accrual of chill hours and mean time to bud break at two sites. While there was no significant difference between the two shade treatments, shade cloths did moderate both high and low temperatures that trees were exposed to. Differences in stem temperatures and mean time to bud break were observed from shaded trees vs. those in full sun at each site. It may be useful to alter our shading design to continue protecting from overnight lows while preventing excess warming from daytime highs, thus promoting tree dormancy and limiting late-season frost injury, but further tests will be required.

### **Exploring aeolian and phoretic dispersal capacity of crapemyrtle bark scale**

Wright, Erika, Kevin Chase, and Samuel Ward

Crapemyrtle bark scale, *Acanthococcus lagerstroemiae* Kuwana (Hemiptera: Eriococcidae; CMBS), is a non-native sap-feeder that severely reduces the aesthetic value of commonly-planted crapemyrtles (*Lagerstroemia* spp.) by facilitating the growth of sooty mold and inhibiting flower production. Since its initial detection in 2004, this pest has become widely established throughout urban landscapes of the southeastern US. However, as females are flightless and only mobile as immatures, the modes of between-tree dispersal by CMBS remain unknown. Similar insects can disperse via wind and phoresy, and field studies have documented airborne CMBS. To investigate wind speeds that dislodge and potentially disperse CMBS from various substrates (e.g., host twigs and leaves), we used a custom-built wind tunnel. Additionally, we explored the phoretic dispersal capacity of CMBS by quantifying behavior of individual CMBS crawlers placed into Petri dishes and onto potted crapemyrtles with feathers and rodent fur. Our results highlight the potential for CMBS crawlers to be dislodged from various substrates at wind speeds as low as one m/s and the willingness and ability of immatures to crawl onto birds and mammals.

## **Poster Presentations**

### **Study of cotton leafroll dwarf virus in Mississippi (2019-2021)**

Aoughanem-Sabanadzovic, Nina, Tom Allen, Tessie Wilkerson, Jodi Scheffler, and Sead Sabanadzovic

Cotton leafroll dwarf virus (CLRDV, genus *Polerovirus*, family *Solemoviridae*), traditionally reported to negatively impact cotton industry in South America and Asia has recently been introduced in the United States. Since its original discovery in Mississippi during 2018/2019 season, a collaborative study involving MSU and USDA-ARS scientists, has been carried out with a focus on: 1) evaluating incidence of the virus, 2) improving diagnostic protocols, 3) studying virus population, 4) high throughput genome sequencing. Furthermore, non-cotton samples collected from cotton production fields, or nearby areas, have been tested to identify alternative hosts for the virus in the state. This presentation is an overview of CLRDV-centered research activities over the past three years along with specific results obtained during that period.

### **Deciphering the role of *Amblyomma maculatum* hemocytes during *Rickettsia parkeri* infection**

Adegoke, Abdulsalam and Shahid Karim

The increase in tick-borne diseases is a significant threat to public health without preventive measures. The tick immune system is divided into cellular and humoral immune responses. Immune cells, commonly called hemocytes, are a critical component of the immune system and produce immune factors that either facilitate or suppress pathogen development in a

tick. Despite their importance in pathogen development, understanding of their basic biology and molecular mechanisms is limited. In this study, a combination of pharmacological and molecular tools was utilized to investigate the functional role of tick hemocytes in rickettsiae infection. In *Amblyomma maculatum*, we morphologically identified five types of hemocytes. *In-vivo* bead phagocytosis led to identifying phagocytic and non-phagocytic populations of hemocytes. Clodronate liposome was used to deplete phagocytic hemocytes and elucidate their role in immune response against *Staphylococcus aureus*, *Escherichia coli*, and *Rickettsia parkeri* infection. Bulk RNA sequencing of hemocytes with and without *R. parkeri* infection revealed a total of 39,249 mRNA transcripts, with 11,301 identified as immune-related. We employed a reverse genetic approach (RNAi) to functionally characterize two differentially expressed marker genes in hemocyte phagocytosis. Together, these results represent a significant advancement in our understanding the biology of tick hemocytes and immune responses.

### **Relating Insecticide Efficacy to Honey Bee Toxicity**

Catchot III, Angus, Jeffrey Gore, Whitney Crow, Angus Catchot Jr., Donald Cook, Priyadarshini Chakrabarti Basu, and Jacob Smith

The use of foliar insecticides is critical for management of tarnished plant bug (*Lygus lineolaris*) in cotton. In the Mid-South region of the U.S., multiple insecticide applications are generally required each year to prevent severe economic losses. Although foliar insecticides are important for crop protection, they have been linked to honey bee (*Apis mellifera* L.) decline in many parts of the world. The physiological and colony responses of honey bees to multiple insecticides is highly variable, but so is the level of control of tarnished plant bug in cotton. Therefore, it is important to consider both efficacy against the target pest species as well as toxicity to honey bees when choosing insecticides for crop protection especially when honey bees are present in the vicinity of the crops being sprayed. The information presented in this poster will combine both of these important factors in revisiting a new rating system which adheres to both crop protection and bee protection.

### **Multi Stressor Impacts on Honey bee Physiology and Gut Microbiome**

Agana, Urita, Hunter Walt, Angus Catchot III, Audrey Sheridan, Lauren Jennings, and Priyadarshini Chakrabarti Basu

Honey bees (*Apis mellifera* L.) are the major insect pollinators of many different crops. A drastic decline in the honey bee populations has been reported over the past decade. While many factors have contributed to this decline, pesticides, poor nutrition, and *Varroa* mites are the most common concerns noted by scientists and beekeepers. Both pesticides and poor nutrition affect colony health, bee physiology and disrupt their ability to perform designated chores in the hive. The primary objective of this study is to examine the impacts of field realistic pesticide exposures and poor nutrition on honey bee gut microbiome diversity and individual bee physiology. For this study, 16 honey bee colonies were placed in each of the four different locations across Mississippi along an agricultural intensification gradient and with varying degrees of natural forage availability. Pollen and nectar samples have been collected from these field sites to analyze for pesticides residues. In addition, live honey bees have been sampled for physiological assays and gut microbiome analysis. The experiment is currently ongoing, and the information gleaned from the results will reveal valuable insight about the interactions between these two stressors and their impacts on honey bees under field conditions.

### **Morphological and functional classification of the *Amblyomma americanum* immune cells**

Hanson, Julia, Abdulsalam Adegoke and Shahid Karim

Ticks are a diverse group of obligate blood feeding arthropods and transmits a wide array of human and animal pathogens. The increase in tick-borne diseases is a significant threat to public health without preventive measures. The tick immune system is primarily divided into a cellular and humoral component. The cellular arm of the immune system is mediated through phagocytosis, encapsulation or nodulation of invading microbial pathogens, while the humoral response engages in the production of effector molecules such as antimicrobial peptides. Cellular immunity in ticks is mediated by the action of immune cells commonly referred to as hemocytes and are the equivalent of mammalian white blood cells. In this study, we utilized a combination of morphological, functional and pharmacological assays to characterize hemocyte population and immune functions in *Amblyomma americanum* ticks. Our study revealed five distinct hemocyte populations. We observed that the population of individual hemocyte types changes following blood meal. In-vivo beads phagocytosis assay allowed us to distinguish between phagocytic and non-phagocytic hemocytes. In addition, the use of clodronate liposome to deplete phagocytic hemocytes led to increased tick mortality following *Escherichia coli* and *Staphylococcus aureus* infection. This study advances our understanding of the tick hemocyte function and cellular immunity.

### **Morphological variation among the small hive beetles in honeybee colonies**

Hardy, Julie, Hossam Abou-Shaara, and Esmaeil Amiri

The Small Hive Beetle (SHB) is an invasive insect that is a pest to European honeybee colonies. SHBs are known for their high adaptability to new environments and display developmental plasticity in their adult size. Body size is the most fundamental feature of an organism that influences nearly all aspects of biology. In this study, we explored the morphological variation both between and within the sexes of SHBs in infested honeybee colonies. To do so, we randomly collected SHBs from 12 colonies, and then sorted the samples based on their sex. Subsequently, the weight, length, and width of each individual SHB were measured for either sex. Our results showed the presence of different sizes between and within the sexes of SHBs. We tentatively divided them into groups of small males vs small females, and large males vs large females and applied statistical analysis. The result showed significant differences within sexes for body weight, width and length, but not between sexes of each group. Large females were more abundant in bee colonies than small females and males. Our results present insight into size variations within SHBs population and pave the way for more research directions and questions.

### **Monitoring Bollworm Feeding in Three-Gene Cotton**

Lytle, Mary Jane, Jeff Gore, Whitney Crow, Don Cook, Angus Catchot, and Jason Bond

Previous research has shown that white flowers are important initial feeding sites for bollworm, *Helicoverpa zea* (Boddie), larvae on transgenic Bt cottons. However, no research has been done to determine the fate of bollworm larvae that leave white flowers and begin feeding on different plant structures of three-gene Bt cotton. In order to maintain effectiveness and use of three-gene cotton, it is necessary to understand the temporal and spatial feeding dynamics of bollworm larvae on different cotton plant structures expressing Bt toxins. In 2022 a laboratory bioassay was conducted to evaluate feeding locations and cotton fruiting structure impacts on bollworm growth and mortality at the Delta Research and Extension Center in Stoneville, MS. The study was comprised of two, three-gene cotton technologies, Bollgard 3 and Widestrike 3. Anthers (flowers) were collected from

each technology and one neonate bollworm was placed on each set of anthers. After 7 days (1 week) mortality was evaluated and surviving bollworms were weighed. Subsets of surviving bollworm larvae were placed on flower anthers, whole medium sized squares, whole thumb-sized bolls, and meridic diet. After 7 days, bollworms were again rated for mortality and surviving bollworms were weighed. Data analysis is ongoing, and results will be reported regarding Bt expression and bollworm survival.

### **The Ants of Coal Creek Farm, Cumberland, TN**

MacGown, Joe A., JoVonn G. Hill, and Zach Brown

The Coal Creek Farm is mountainous 5000+ acre tract of land owned by philanthropist George Lindemann in the Cumberland Plateau in Cumberland County, Tennessee. With support from Lindemann, Mississippi Entomological Museum (MEM) staff has collected ants at Coal Creek on various dates spanning from early August 2018 to the fall of 2022. Here we list the species collected from the property, note basic habitat/species associations, and discuss functional groupings of the ants found. We collected 49 species in 24 genera and six subfamilies at the property, all of which are native except for the Red Imported Fire Ant, *Solenopsis invicta* Buren. Of the 49 species collected, only five were restricted to open areas, whereas all others were found in woodlands or at woodland/open area edges. We collected species in the following functional groups: Cold Climate Specialists (6%), Dominant Dolichoderinae (6%), Subordinate Camponotini (14%), Cryptic Species (23%), Generalized Myrmicinae (23%), and Opportunists (29%). Functional groups are useful to note because they may aid ecologists in better understanding habitat usage.