2022 - 2023 Florida Coordinating Council on Mosquito Control

FDACS Grant Research Abstracts

- Below are the final report abstracts from the researchers for the 2022 -2023 fiscal year. If you are interested in reading the complete report, please contact Caitlin Gill (Caitlin.Gill@fdacs.gov) with the title and Principal investigator.
- If you have specific questions regarding the research, please reach out to the researcher directly.

"Nontarget effects of adulticide and barrier treatment applications on Lepidoptera: Resilience of larvae to feeding from treated host plants"

FDACS Contract #29021

Principal Investigator: Dr. Lawrence Reeves [1] lereeves@ufl.edu

Co-PI: Dr. Nathan Burkett-Cadena [1] nburkettcadena@ufl.edu

Abstract:

FL DACS Contract # 29021 (UF Project # 0279023) constitutes a project designed to improve understanding of the real-world impacts of mosquito adulticide applications on a group of non- target invertebrates: lepidopteran larvae. Lepidoptera are ecologically important as pollinators, and economically important in Florida where a small industry of commercial breeders produce and sell butterflies and butterfly-based attractions exhibit live butterflies. Research on the nontarget impacts of mosquito adulticide applications on Lepidoptera has largely focused on laboratory tests of the acute susceptibility of adult butterflies, and, to a lesser extent, caterpillars, to mosquito adulticides. Such laboratory-based assays do not account for more nuanced factors related to environment or variation among species in biology and life history that may affect the extent to which these insects are impacted in the field. Given this, our understanding of the actual impacts of mosquito adulticide applications on Lepidoptera in nature remains incomplete. This project addresses this issue through a series of semi-field experiments that assess the susceptibility and resilience of lepidopteran larvae to feeding from adulticide-treated host plants. This project was completed with support from the Lee County Mosquito Control District (LCMCD), which facilitated the aerial and truck-based treatments of plants with naled and permethrin, respectively.

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"Investigation of metabolic resistance in Florida Culex quinquefasciatus mosquitoes" FDACS Contract #29037

Principal Investigator: Dr. Eva Buckner[1] eva.buckner@ufl.edu

Abstract:

Culex quinquefasciatus is one of the primary vectors of West Nile and St. Louis encephalitis viruses in Florida. Over-reliance on pyrethroid and organophosphate insecticides by mosquito control programs has led to mosquito populations becoming resistant to them. Given that Cx. quinquefasciatus is such an important disease vector in our state, it is important to study its resistance status and mechanisms responsible. Very limited research has been conducted on resistance in Florida Cx. quinquefasciatus mosquitoes. Even fewer studies have investigated resistance mechanisms in Florida Cx. quinquefasciatus mosquitoes. To fill this gap in knowledge, the objective of this study was to conduct the first known attempt of a statewide survey of metabolic resistance in Florida Cx. quinquefasciatus mosquitoes. Toward this goal, we successfully compared α-EST, β-EST, GST, and P450 activity levels in Cx. quinquefasciatus mosquitoes from 29 counties (43% of state) in Florida to the α-EST, β-EST, GST, and P450 activity levels in susceptible Cx. quinquefasciatus mosquitoes. We found that esterase (specifically β-EST) and GST were the most consistently elevated metabolic enzymes in Florida Cx. quinquefasciatus mosquitoes, indicating that they are most likely responsible for influencing phenotypic insecticide resistance levels seen. Because PBO has been shown to inhibit P450s and esterases, our results

suggest that formulated mosquito control products containing PBO could be helpful in overcoming metabolic resistance in Florida Cx. quinquefasciatus mosquitoes.

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"Non-target effects: impact of residual environmental Bti on mosquito biology and behavior"

FDACS Contract # 29038

Principal Investigator: Dr. Eric P. Caragata [1] e.caragata@ufl.edu

Abstract:

The need to develop novel mosquito control products has led to the development of highly effective microbial-derived biopesticides, such as the range of products derived from the *Bacillus thuringiensis* subvariant *israelensis* (Bti) which rapidly kills mosquitoes after exposure. Bti-based products are widely utilized by mosquito abatement programs, and also at the household level, to treat standing water and reduce mosquito bites. Over the counter Bti products typically prescribe a regular treatment frequency. In the absence of re-treatment, residual Bti persists in the environment, which might lead mosquitoes to be exposed to sub- lethal or non-optimal doses. This could potentially lead those mosquitoes to become resistant to Bti, but also could affect other aspects of their biology, and even impact their ability to transmit pathogens like dengue virus. In this project, we ask the question: 'What are the non- target effects caused by exposure of *Ae. aegypti* mosquitoes to this residual environmental Bti in water?

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"A population genomics approach to predicting insecticide resistance mechanisms in Aedes aegypti"

FDACS Contract #29039

Principal Investigator: Dr. Derrick Mathias [1] d.mathias@ufl.edu

Co-PI: Dr. Eva Buckner[1] eva.buckner@ufl.edu and Dr. Yoosook Lee [1] Yoosook.lee@ufl.edu

Abstract:

FDACS Contract #29039 (UF Project # P0273929) is a collaborative project among faculty at UF- FMEL (the PI along with Co-PIs Buckner and Lee) with assistance from Manatee County Mosquito Control District. This project takes a population genomics approach to predicting mechanisms of insecticide resistance in Aedes aegypti, an important vector of arboviruses in Florida. Due to the limited number of chemicals available for public health use, mosquito resistance to pyrethroid insecticides has become a widespread problem. Mutations in Ae. aegypti that cause target-site insensitivity (i.e., kdr resistance) are well known, but additional mechanisms (e.g., metabolic detoxification, cuticular resistance) work in combination with kdr to enhance resistance. In a preliminary study comparing genome sequences between populations differing in resistance status, we identified 115 highly differentiated single nucleotide polymorphisms (SNPs) in 20 genes involved in detoxification or in cuticular thickness or composition. In the resistant population, many of these genes had dramatic reductions in the number of polymorphic sites near the SNP(s) detected, a sign of recent strong selection. We hypothesized that these loci represented markers of metabolic and cuticular resistance, which usually result from the overexpression of genes in a handful of multigene families: cytochrome P450 monooxygenases, carboxyl/cholinesterases, glutathione-S-transferases, cuticle proteins, and ATP-binding cassette transporters. Our objective is to determine if we can use comparative genomics to predict pyrethroid-resistance mechanisms operating in Ae. aegypti in nature. We have re-sampled mosquitoes from the resistant population used in our preliminary study and will characterize resistance to a panel of active ingredients, measure genome-wide levels of gene expression following exposure to permethrin, and test for statistical associations between SNP genotype and transcript number for genes of interest. If successful, our data will lay the groundwork for identifying the range of mutations responsible for pyrethroid resistance in Ae. aegypti in Florida. Once these polymorphisms are known, we can experimentally determine their effect sizes and develop molecular assays for monitoring those that pose the greatest threat to controlling this important vector species.

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“Investigating the prevalence of novel kdr mutations among Aedes aegypti populations in Florida”

FDACS Contract #29314

Principal Investigator: Dr. Yoosook Lee [1] Yoosook.lee@ufl.edu

Co-PI: Dr. Eva Buckner[1] eva.buckner@ufl.edu

Abstract:

FL DACS Contract #29314 (UF Project # P0277092) is a collaborative project among faculty at UF-FMEL (the PI along with Co-PI Buckner) with assistance from Palm Beach County, Broward County, Monroe County, and Collier County Mosquito Control Districts. This project investigates the prevalence of novel kdr mutations in Aedes aegypti mosquito populations in Florida and examines their contribution to insecticide resistance knockdown rates. To improve our knowledge on the mechanism responsible for mosquito insecticide resistance, we sequenced 106 Ae. aegypti individuals collected throughout the state of Florida and examined mutations in the voltage-gated sodium channel (VGSC; AAEL023266), a known insecticide resistance gene, also known as knockdown resistance (kdr) gene. Through whole genome sequencing, we previously identified 2 novel nonsynonymous single nucleotide polymorphisms (SNPs), F174I and E478K, and 5 known SNPs, V410L, S723T, V1016I, D1763Y, and Q1853R (Figure 1). Except for V1016I, the other known SNPs were reported in Floridian Ae. aegypti for the first time. The two novel SNPs and the known SNP D1763Y were displayed at a low alternate allele frequency (approximately 1%), and were considered rare, all the others were displayed at a high frequency, and were considered common (Kosinski et al. 2022). Our objective was to customize a multiplex SNP assay to determine allele frequencies of these insecticide resistance mutations in a larger number of samples from four counties and examine their phenotypic contribution to pyrethroid resistance in Ae. aegypti. These counties included Broward (Miramar), Collier (Naples), Palm Beach (West Palm Beach) and Monroe (Upper, Middle and Lower Keys).

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