

# Mapping genetic diversity and insecticide resistance of *Aedes aegypti* in Florida

by Jessica Quiñones, Helen Wagner, Andre Costa-da-Silva, Matthew DeGennaro

Abstract Id: 541 Submitted: March 8, 2019 Event: Conference for Undergraduate Research at FIU 2019  
Topic: Biology

*Aedes aegypti*, a vector for the pathogens that cause diseases like yellow fever, dengue, and Zika, has become highly adapted to living alongside humans. Despite the continued use of insecticides, mosquito species such as *Ae. aegypti* are still thriving in Florida. Considering that insecticide use across the regions in Florida varies, mosquitos that live in different regions may have been exposed to different levels of insecticides. Insight into possible different levels of resistance in *Ae. Aegypti* can be crucial for effective population control by utilizing targeted measures and improving preventative methods being used in Florida. In this project, genomic sequencing will be used to determine possible variations in populations. Traps will be placed around Florida for gravid females to lay eggs that will be collected. These traps have the secondary benefit of reducing populations by moving eggs away from the wild and into the laboratory. These eggs will then be hatched and sent out as adults for whole-genome sequencing, allowing for greater variation and range that is not seen in single nucleotide polymorphism genotyping (SNP). The genotype sequencing from each region's mosquitos will provide insight into the variation structure of the populations, including genetic variation associated with insecticide resistance.