

UST ANNUAL RESEARCH SYMPOSIUM 2022: April 28-29, 2022

Abstract Submissions: Deadline April 3, 2022

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Abstract Title (limited to 20 words): Metagenomics Analysis of Viral Families Carried by *Aedes* Mosquitos in Houston

Student Author: Martin Silguero, Franklin Pham, Ana Hernandez, Sarah Strobel, Angelina Le, Ava Ngo, Michelle Najarro, Paola Gonzalez, William Maldonado, David Brittain

Faculty Advisor: Rosmarie Rosell, Ph.D., Maia Larios-Sanz, Ph.D.

Department: Department of Biology, Division of Natural Sciences, Mathematics and Engineering

Student Email: silguem@stthom.edu

Email Advisor: rosell@stthom.edu, lariosm@stthom.edu

Abstract Text (limited to 250 words)

Mosquitos are well-known vectors of many important viral diseases, but little is known about the complete collection of viral strains that they might carry. Historically, culturing techniques were used to study microbial diversity, but genomic analyses have demonstrated that culturing methods are biased and inadequate to understand true diversity. In our research, we used a metagenomic approach to characterize the viral populations carried by different species of mosquitos found in Houston. In this work, we sequenced the entire genetic material of pooled male or female mosquito samples and analyzed it with computational tools. We collected mosquitos from locations in Houston and separated them by species and sex using morphological characteristics. We then confirm our separations by using DNA barcoding. Total DNA and RNA were extracted from each sample, and RNA samples were converted to cDNA to facilitate sequencing. Combined DNA/cDNA pools were sequenced using 454 sequencing technology. We then used a modified BLAST workflow developed in-house by alumni David Brittain to analyze the returned sequences. Our first analysis involved samples of male and female *Aedes aegypti* mosquitos. A total of 51 different species of viruses were identified in the female sample, and 40

different species in the male sample. We are in the process of building libraries from new samples of mosquitos. We also plan on further analyzing the unknown sequences obtained, many of which may be viral in origin. These studies will help us better understand the viral collections carried by different mosquitos in Greater Houston.