Barcode Long Island

Native and Invasive mosquito species on the Conscience Bay Shore, Long Island .

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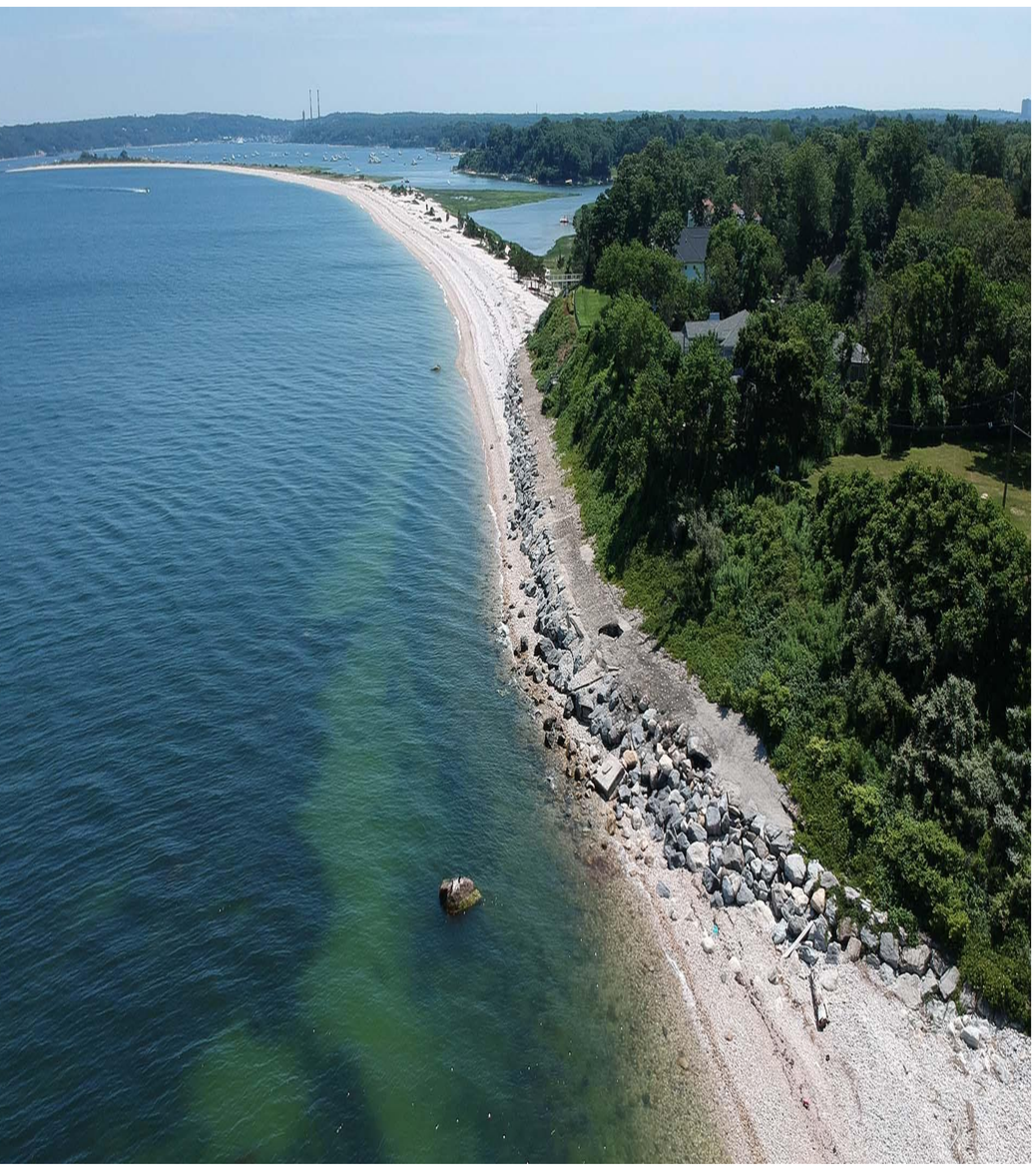
Abstract

Mosquitoes' adaptability, expansion of their range of habitat, and their ability to transmit viruses such as West Nile and Zika Virus have made themselves classified as some of the most invasive and dangerous species in the world. We collected mosquitoes in various locations with large mosquito populations using traps and used DNA Barcoding and agarose gel electrophoresis in order to isolate the genomes in the mosquitoes' DNA. We used the data in DNA Subway to compare our genome sequence with other genome sequences in the database. Upon analysis of the genomes, many matched to non-mosquito insects such as Exechia seriata, Mycetophila fungorum, and Chironomus flaviplumus, only catching one native mosquito, Culex salinarus. However, some of the other insects (namely M. fungorum) were caught well outside their natural habitats. Our preferred method of capture did not work as efficiently as we thought it would, but our capturing of non-native insects highlights the potential they may have on the diversity of the native ecosystem as they can outcompete the native species we captured.

Introduction

Our project focused on the native and invasive species of mosquitoes in the Conscience Bay area. Our research question was whether man-made still water containers were a more prevalent source of Mosquito breeding areas and populations of Mosquitoes. Through DNA extraction using silica residue and barcoding of DNA using DNA subway, we find out the answers to our questions above.
DNA Barcoding is advantageous to scientists working in the fields of Ecology, Evolution, and Zoology as it allows the scientific community to classify both known and novel organisms with one or few gene regions. Our project is of scientific interest as it allows the scientific community to receive more barcodes of previously barcoded mosquitoes and allows scientists to track the mosquito population in a specific ecosystem on Long Island. Learning whether the mosquitoes are native or invasive species has various implications on the health of the Long Island ecosystem. Culex Pipiens, the invasive mosquito species, are vectors of diseases such as West Nile virus, serve as a pest and are commonly found in still waters in the New York Area. If we could prove the frequency of Culex Pipiens across Long Island through sample collection from still water traps and DNA barcoding, We can advocate for the use in pesticides within manmade containers of still waters would be effective as Culex Pipiens prefer areas of still water for breeding. The use of pesticides in man-made still water areas will reduce both the cost of using pesticide in natural habitats such as marshlands, temporary ponds, and thick shade forest edges and would reduce the use of pesticides on floral /marshland environments such as the Conscience Bay shore.



Methods and Materials

Sampling/Collection devices and locations.

The Gravid Trap:

The Gravid Trap is a plastic wash bin with a still liquid named mosquito soup, it is one of the traps we used to collect our samples.

The BG sentinel:

The BG sentinel trap uses a battery powered fan to suck in and trap the mosquitoes. This is another trap we used to trap the mosquitoe
We collected from 3 sites:
50 Jefferson Landing Circle
Latitude: N 40.945390
Longitude: W -73.045660

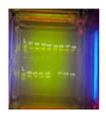
20 Skyview Lane
Latitude: 40.91411
Longitude: -73.13928

28 Conscience Circle, (Shoreline and house property.)
Latitude N 40.9579375°
Longitude W 73.1214358°
(Water edge)

Property:

Latitude N 40.95739°
Longitude W 73.13147°

Experimentation:
For experimentation we used DNA Isolation using Silica Resin Protocol (Courtesy of DNALC.)
Gel electrophoresis chambers with agarose gel were used to figure out whether the samples would be sent for sampling.
We also used PCR, Polymerase chain reaction to amplify the DNA during extraction.



Data processing:

For data processing we used the blue line of the DNA subway website in order to analyze our sequences.

Results

We found a wide variety of flies! Not mosquitoes though.

002: Crane-fly

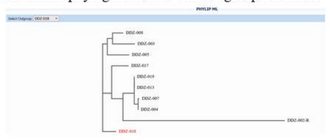
003: Long-legged fly

004: Fungus gnat

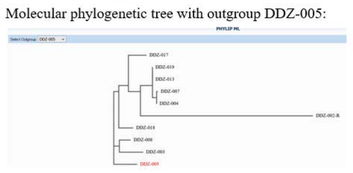
005: Nonbiting midges

007: Fungus gnat

Molecular phylogenetic tree with outgroup DDZ-018



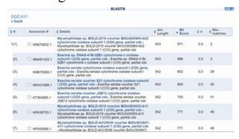
Molecular phylogenetic tree with outgroup DDZ-005:



008: crane-fly

013: Fly

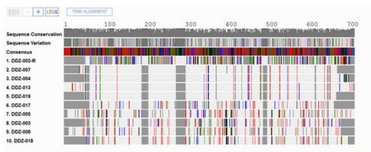
017: Fungus Gnats



018: Unbanded salt marsh mosquito

019: Fungus gnats

DNA Barcode:



References/ Acknowledgements

References:

Thank you to Mr. Altug for mentoring our project through the review phase of the proposal. Thank you to the staff at the DNALC who helped us learn DNA Isolation using silica resin.
Thank you parents who allowed us to capture mosquitoes on your property.
Thank you to all the group members who worked on the poster.

Discussion/Future Directions

Discussion: In conclusion, from our samples, we were not able to determine whether the hypothesis was true or false, due to the lack of mosquitoes collected. Out of the 20 samples, after blasting the DNA sequences, we found there was only 1 mosquito, and the majority of the samples were fungus gnats, or another type of gnat. The one mosquito that we collected was caught in our trap placed in Conscience Bay, and it was an unbanded salt marsh mosquito(Culex Salnarius). We believe that Conscience Bay, a mostly stagnant body of water, contains many mosquitoes, but the conditions we had for collection were not ideal. This could be because the weather in March and April, when the mosquitoes were collected, was too cold, and did not provide ideal conditions for the mosquitoes. Before we sent the samples in for sequencing, we did not have a microscope to accurately check the species of each specimen, so it was surprising to see how many specimens we believed to be mosquitoes were a type of gnat.

Future Direction: In the future, we believe that a more ideal time for sample collection would be in the summer, when the mosquitoes are more active, so we could get the correct species of specimen to observe. After we can get more mosquitoes, we could use DNA sequencing to find the species of the mosquitoes. Then, we would have to observe the environment from which the mosquitoes were collected, whether stagnant, or moving bodies of water, and observe which environment has a higher percentage of mosquitoes that possibly carry mosquito-borne diseases.