# Project Mosquito

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## Abstract

DNA barcoding was used in addition to traditional taxonomy to scientifically identify each mosquito collected across areas of Long Island. DNA barcoding was important as many mosquitoes are phenotypically similar. We paired sequencing and checked if certain species of mosquitoes would feed to specific hosts. We wanted this information to allow for better environmental management due to the growing mosquito problem and their ability to transmit diseases.

## Introduction

Mosquitoes are becoming a big problem in warm and humid places, islands, tropical locations, etc. because mosquitoes are disease vectors. Emergent zoonotic infections may be transmitted to humans through vector mosquitoes.

Analysis of mosquito blood meals will help to relate mosquito species diversity to their host preference. Linking species with host preferences may inform environmental management to responsibly manage mosquito populations. More informed management practices will be beneficial to overall environmental, and by extension, human health.

## Materials & Methods

Samples were collected at night with the BG-2 Sentinel Mosquito Trap and light traps. Samples were provided by the Suffolk County Department of Health Services.

DNA was extracted by cutting of and grinding one leg and a part of the stomach. Gel electrophoresis was used to check for successful amplification.

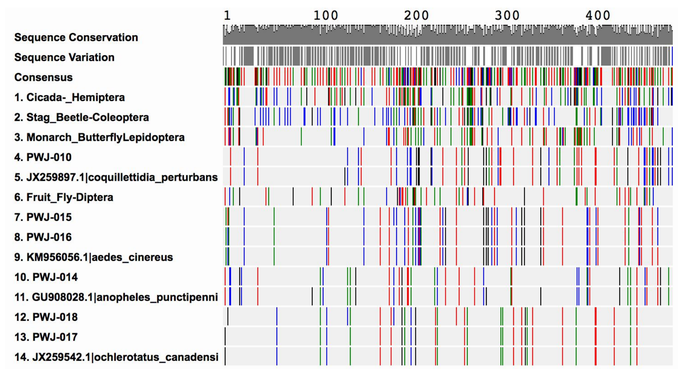



Figure shows allignment of samples with species sequences

**PWJ-010**

**PWJ-014**

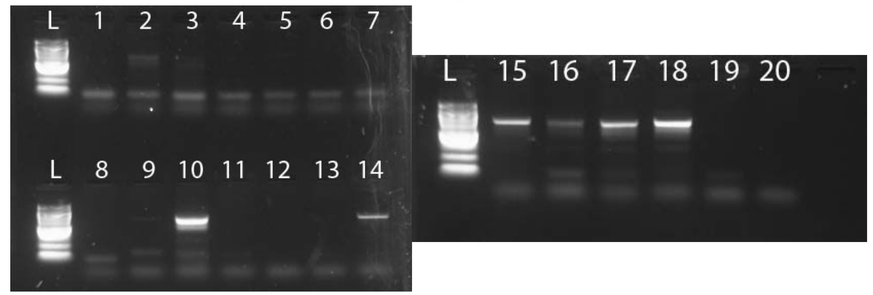
**PWJ-016**

**PWJ-016**

Samples that tested positive for different hosts. An "**X**" represents it being present.

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **A-pig** | | | | | X | | | | | | | X | | | | | | | | |
| **B-human** | X | X | | X | X | | X | X | X | X | X | X | | X | X | X | X | X | X | X |
| **C-goat** | | | | | | | | | | | | | | | | | | | | |
| **D-dog** | | | | | | X | | | | | | | | | | | | | | |
| **E-cow** | | | | | | | | | | | | X | | | X | X | X? | X | X | X |

Many mosquitoes showed human amplification. This may be a mistake from cross contamination as humans are managing the samples.




## Results

We analyzed 20 samples from mosquitoes provides by the Suffolk department of health that had feed on different hosts. BLAST provided the scientific identification of the mosquitoes. Many BLAST identifications differed from the taxonomic identification provided. This may be incorrect taxonomic identification due to phenotype similarities.

## Discussion

For PWJ-010, there was a mistake in GenBank when analyzing and identifying the mosquito. When looking at the picture, we confirmed it is actually Coquillettidia perturbans instead of Anopheles.

Our results also showed human amplification in almost all the samples that were analyzed. We are not sure if the human amplification on all the samples is accurate. This amplification can be a mistake from cross contamination where humans are managing the samples as well as humans actually being fed on or being the real host.

## Acknowledgements

We would like take this poster space to thank the Cold Spring Harbor Labs including Dr.Fernandez in asisting us in our research.