



Moth Diversity over Long Island

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Abstract

Although moths are a common insect, there isn't much data on their species distribution. One experiment, *Surveying Moths using Light Traps: Effects of Weather and Time of Year*, showed that temperature is important to consider. It was predicted that there was no unknown invasive species. The hope was to get a brief overview of the species of moths from Long Island. During collection, different traps and lights were used to see if there were any links. There were two different traps used and each location tried the regular light bulb and the blue light. After collection, they were sent through PCR to begin sequencing and analyzing the results. Almost every sample had an almost perfect match. The blue light was much more effective in attracting moths. Although the PCR results were great, there were three samples with a high amount of mismatches. Most importantly, there were no signs of an invasive species on Long Island.

Introduction

What is the overall moth diversity of Long Island? Are there any invasive or unknown species?

- DNA Barcoding aids correct identification
- Invasive species can upset balance in an ecosystem if not monitored properly
- Light source, Surroundings, Type of traps, and Temperature are all important factors for catching moths

Materials & Methods

- 3 locations
- 2 different types of lightbulbs, and traps were used
- Zymo Research *Quick-DNA Tissue/Insect Miniprep Kit* Cat No. D6016 was used for processing using the Sanger sequencing method

Results

- 16 Moths with PCR product after gel were sent for testing
- Only two out of the three locations caught moths
- More success from blue light and powered trap
- 13 samples had low mismatches; PWK-003, PWK-006, PWK-007, PWK-008, PWK-012, PWK-301, PWK-302, PWK-306, PWK-004-F, PWK-005-R, PWK-303-F, PWK-304-F, PWK-305-F
- Sequences sent through DNA subway and Bold (If high number of mismatches)

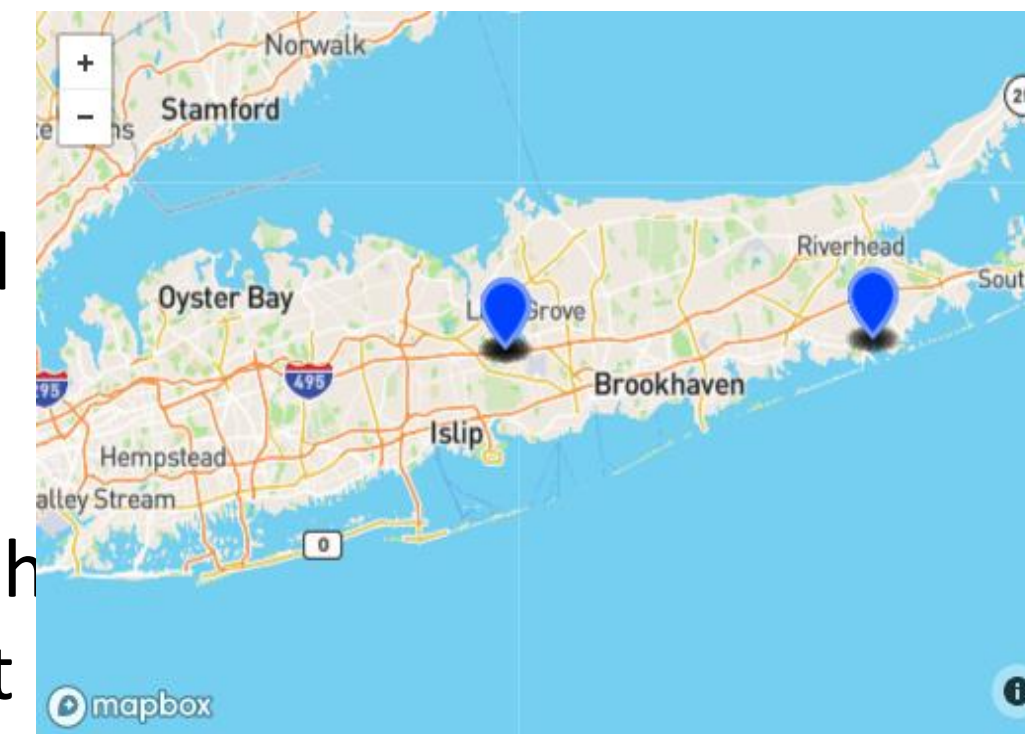


Figure 1: Map showing collection sites

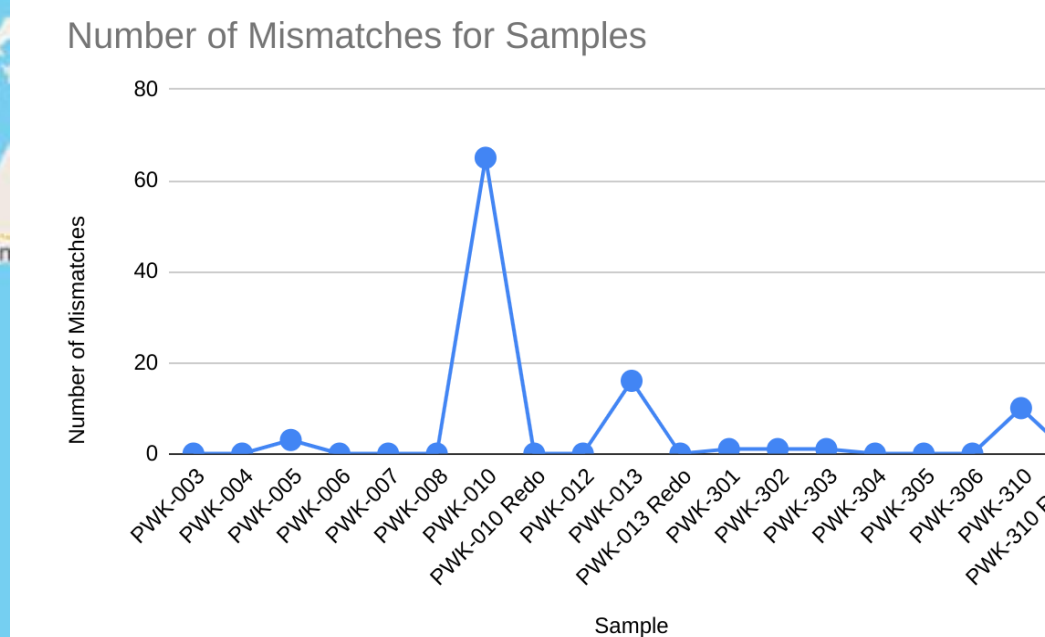


Figure 2: Graph showing number of mismatches in samples

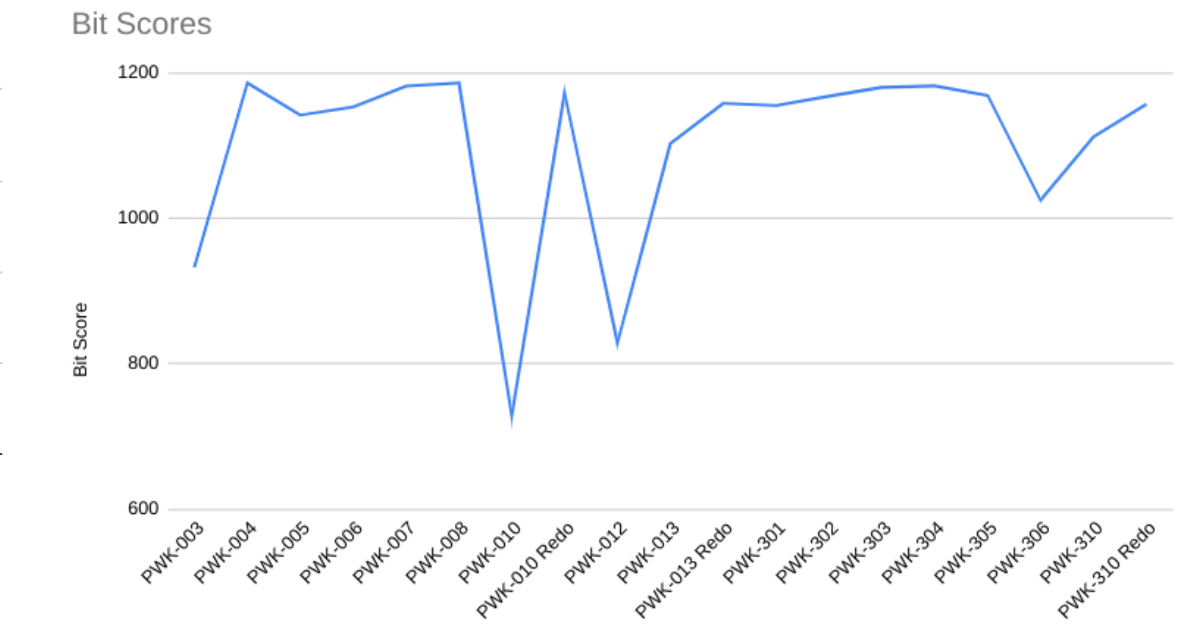
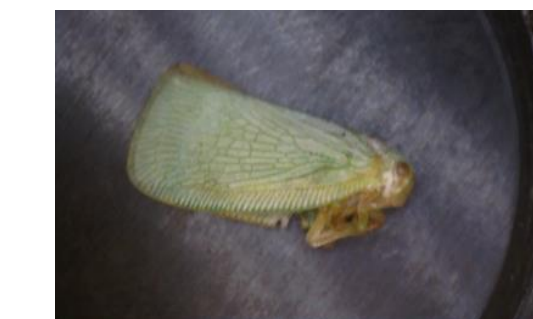


Figure 3: Graph showing bit scores per sample

Discussion

- PWK-303 was an error in the lab, where the actual sample was switched with a different sample, that wasn't supposed to be tested
- Some samples returned missing either the forward or reverse
- 3 samples had more than 10 mismatches, so they were resequenced
 - All 3 returned with better results
 - PWK-010 is *Helicoverpa zea*
 - PWK-013 is *Udea rubigalis*
 - PWK-310 is *Orthonama obstipata*
- All of the 16 samples had strong bit scores and alignment lengths
- 3 of the samples were identified as *Helicoverpa zea*
 - *Helicoverpa zea* and *Mythimna unipuncta* are an invasive species and pests
 - Shouldn't affect ecosystem on Long Island because of cold temperatures in the winter



PWK-303 Sample



PWK-303

References

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Acknowledgements

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