

# Biodiversity of moths found around light poles in varying locations on Long Island



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## Abstract:

Light poles act as good sites for collecting moths because of the fact that moths, in general, are attracted to man made lights such as porch lights, light poles, or fires. The hypothesis suggested that there would be a large biodiversity of moths on Long Island. The aims of this project were to determine the biodiversity of moth species found within various locations on Long Island, to determine genetic similarities within the genomes of the different moth species, and to find a possible common ancestor based on the similarities and differences and create a phylogenetic tree to show the evolutionary relationship. Paper cups, index cards and plastic bags were used to collect the moths that were to be tested.

## Introduction:

Biodiversity, or the variety of life on Earth, is extremely important to ecosystems all around the world due to the fact that it allows for a balance of species within the ecosystem. Determining the biodiversity of moth species found in different locations on Long Island will be an extremely important goal for this experiment. Having a variety of moths would prove important to the ecosystem because it could allow different niches for moths to occupy that may provide benefits to the ecosystems that they are present in.

There are many things that moths may do that could help or hurt human well-being. Specifically, moths have a large impact on plants and food crops. Certain types of moths help these crops by pollinating them. Therefore, without moths, food crops would be unable to produce a good harvest (3). On the other hand, there are some species of moths that are detrimental to food crops. One species of moth, the gypsy moth, is especially detrimental to plant species on Long Island (2).

Light poles act as good sites for collecting moths because of the fact that moths, in general, are attracted to man made lights such as porch lights, light poles, or fires. Many people believe that this is caused by the fact that artificial light may cause problems with moths' internal navigation systems (5). Therefore, by observing light poles as the source of collection for this experiment, there will be the ability to collect a large variety of moths with very different characteristics, such as size, color, etc.. In addition, by observing light poles from different ecosystems, and comparing the diversities of the moths living there, an understanding of the biodiversity of moths within different local ecosystems can be obtained. In New York State, there are approximately 83 recorded species of moths (1). However, after a literature review, no studies recording the amount of moth species found specifically on Long Island could be observed.

The method be used to determine the species variation within the ecosystems of Long Island is DNA Barcoding. DNA Barcoding involves looking at a specific portion of a gene within the genome of an organism (in this case, the CO1 gene for animals) and comparing that gene to the same portion of the gene within other similar organisms. This method, created by Paul Hubert, provides a quick and simple way of identifying plant and animal species, as opposed to the more complicated and less effective use of morphological features that was previously the primary method (4). Using this method of DNA Barcoding it is expected that a larger variety of moth species will be identified as compared to the use of taxonomic keys, due to the similarities in the morphology of moth species.

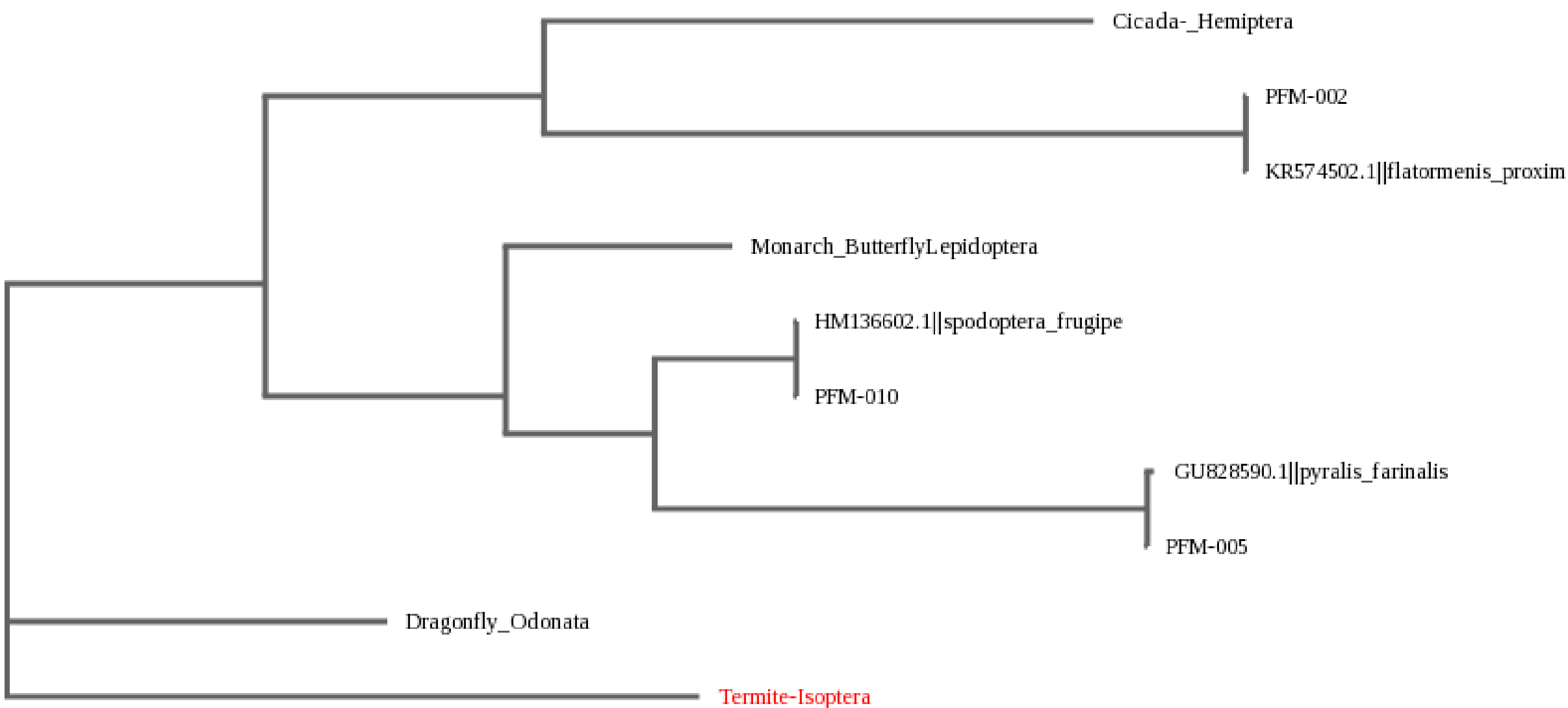


Figure 1: Phylogenetic tree of moth species compared to other similar insect species and showing termites as an outgroup.

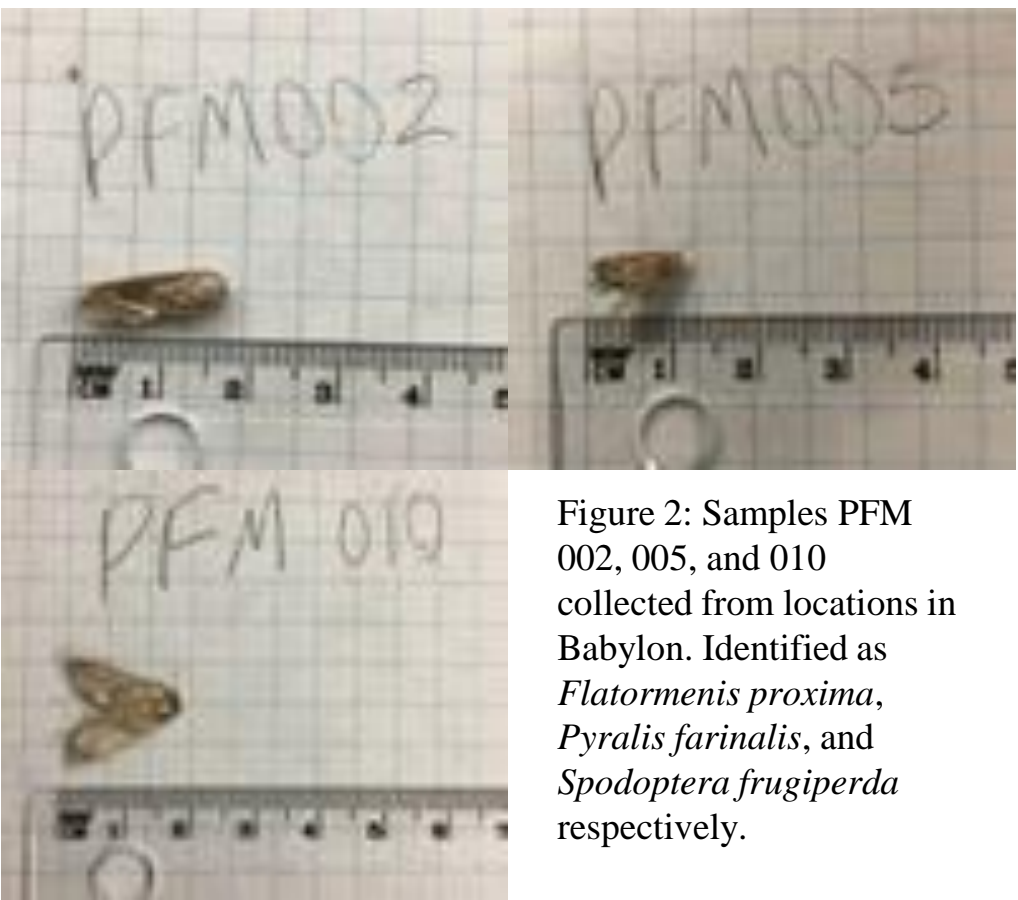


Figure 2: Samples PFM 002, 005, and 010 collected from locations in Babylon. Identified as *Flatormenis proxima*, *Pyrallis farinalis*, and *Spodoptera frugiperda* respectively.



Figure 3: Map from DNA Subway showing where all samples came from.

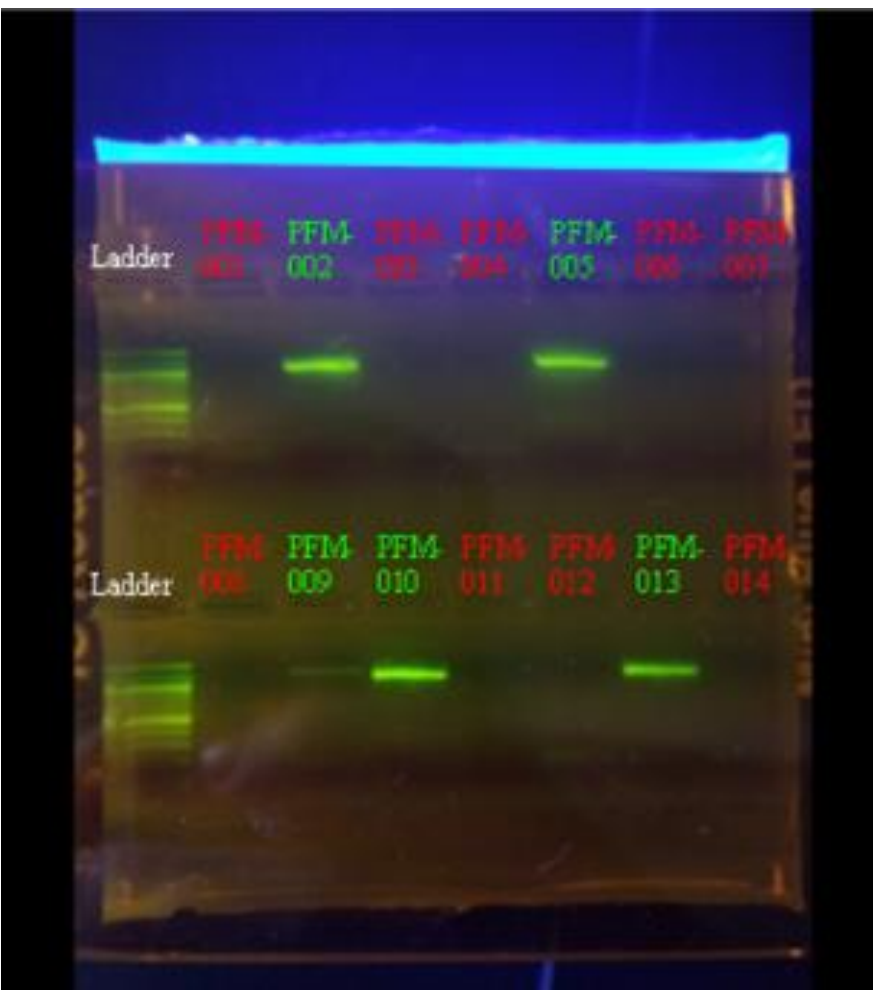


Figure 4: Gel picture for sequenced samples. White = Ladder Green = Sequenced Red = Not Sequenced

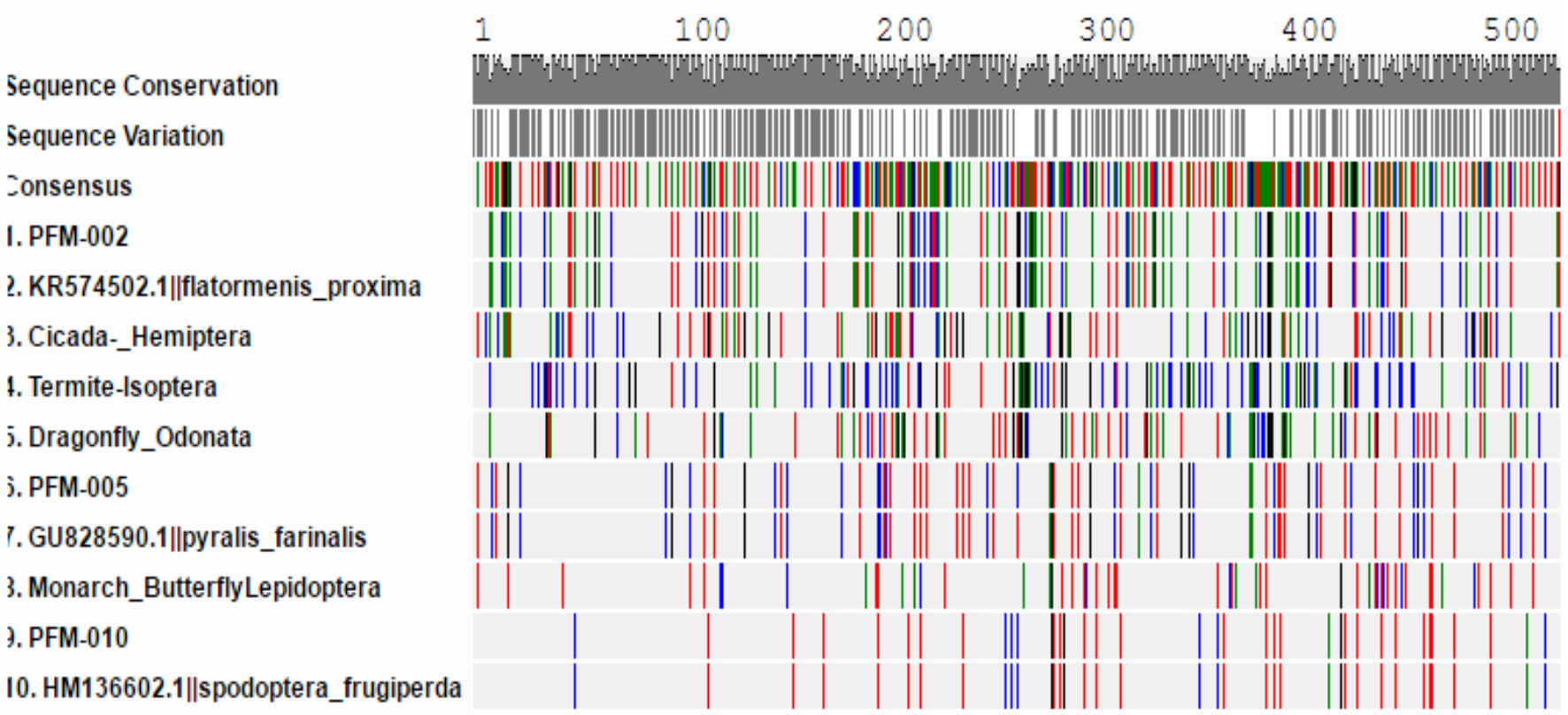


Figure 5: MUSCLE from DNA Subway showing each banding pattern in relation to the compared organisms.

## Method:

The samples of moths from light poles found on Long Island were obtained from locations in Babylon, Patchogue and East Islip. The collected samples were observed and their specific locations, latitude and longitude, masses, physical appearances, length and the initial field identification will be logged.

The captured moths were placed in a plastic freezer bag in order to completely secure the moth, with no chance of escape. These moths, once completely secured in their respective freezer bags, were frozen for storage until they are ready to be DNA Barcoded.

Each sample was documented along with the locations in which they were obtained. This includes picture documentation, of both the locations where the specimen was obtained as well as pictures of the samples, and accurate labeling of all the samples after putting them into separate tubes.

The collected samples were brought to the DNALC laboratory in Cold Spring Harbor so the samples can be prepared for analysis. Once all of the samples were analyzed, the different samples will be compared with each other in order to determine the biodiversity between species from the different locations on Long Island in which they were collected from. The samples were also compared in order to determine a possible common ancestor between them. A phylogenetic tree was created in order to represent the evolutionary relationship between the various moth species present in different ecosystems on Long Island.

## Discussion:

Based on the data collected, it is not certain that Long Island has a very large biodiversity of moths. However, the conclusion that there are multiple species of moth on long island can be drawn. This is known because out of the three samples that were able to be sequenced, all three were different species of moths. However, in order to obtain a better idea of the biodiversity of Long Island, more samples of moths would have to be sequenced successfully.

## References:

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