

# Biodiversity of Moths on Long Island

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## Abstract:

Moths are a part of the insect order Lepidoptera which they share with butterflies. Moths are an excellent organism to barcode due to the large amount of unclassified moth species, as well as the difficulty trying to identify different species. The goals of this project are to determine the specific species of moths found around the town of Babylon, and to compare the species of the moths found at different locations around Long Island. To do this moths will be collected from various locations then sequenced according to BLI Protocol. The result will then be compared to achieve the projects goals. After the conclusion of the sequencing process, 8 of the samples were successfully sequenced. Out of the 8 samples, there were 6 different species. This shows that the moth population in Babylon is diverse. It would be beneficial to continue this experiment with a larger sample size to learn more about the biodiversity.

## Introduction:

Moths are a part of the insect order Lepidoptera which they share with butterflies. They are flying insects that begin their lives as caterpillars, consume large amounts of plant matter, and then use this abundance of plant matter to metamorphose into moths. Moths are very similar to butterflies, but can usually be differentiated by their antennae. Moths are mostly nocturnal, while there are a few species that are diurnal, such as the bordered straw (*Heliothis peltigera*). There are many different species of moths that can be found on Long Island. Many species of moths have not been classified yet, which makes them an excellent organism to barcode.

Moths are an excellent organism to barcode due to the large amount of unclassified moth species, as well as the confusion that often arises when trying to taxonomically identify different species. Moths are very important members of the ecosystem for three main reasons. Number one, as caterpillars they consume leaves of harmful weeds that could be detrimental to crop growth. Secondly, they are a food source for many creatures such as birds and bats. Lastly, they are thought to help with pollination. For all of these reasons, moths are an excellent species to barcode and collect genetic information on.

## Methods and Materials:

Moths were collected from various locations around the town of Babylon and compared to other samples from around Long Island found in the databases. Collection took place mostly around light sources, as moths tend to gather around them. Traps with honey and fermenting fruit were set around light fixtures to further attract the moths. A fresh set of sterile gloves was used to collect each sample, and the samples were then stored in separate ziplock bags in order to prevent cross contamination. The location of each sample was recorded then be stored in a freezer until they could be barcoded.

The first step in the barcoding process was to take a small sample of tissue from each organism. Next DNA was extracted by adding the tissue to a lysis solution and using a pestle to grind up the sample. The sample was incubated and centrifuged multiple times and eventually the Co1 gene was extracted from the supernatant. The Co1 gene was then be amplified through the process of PCR. The amplified gene was then sent to GeneWiz for sequencing. Using GenBank databases, the results were compared to those of other known species. Once the specific genus species of the samples was determined they were compared to genetic information from other species to analyze the biodiversity of moths on Long Island. This was done by comparing the species we found to the other similar species found in nearby areas on the GenBank.

## Results:

After the conclusion of the amplification process, 8 of the samples were successfully sequenced. The PDE-001 sample was an *Idia americalis*. PDE-002 was an *Agriphila ruricolella*. PDE-003 was a *Costaconvexa centrostrigaria*. PDE-004 and PDE-006 were both *Agrochola bicolorago*. PDE-005 and PDE-007 were both *Udea rubigalis*. PDE-008 was an *Alsophila pomataria*. The successfully sequenced samples were compiled into 2 different phylogenetic trees; one maximum likelihood tree and one neighbor joining tree.

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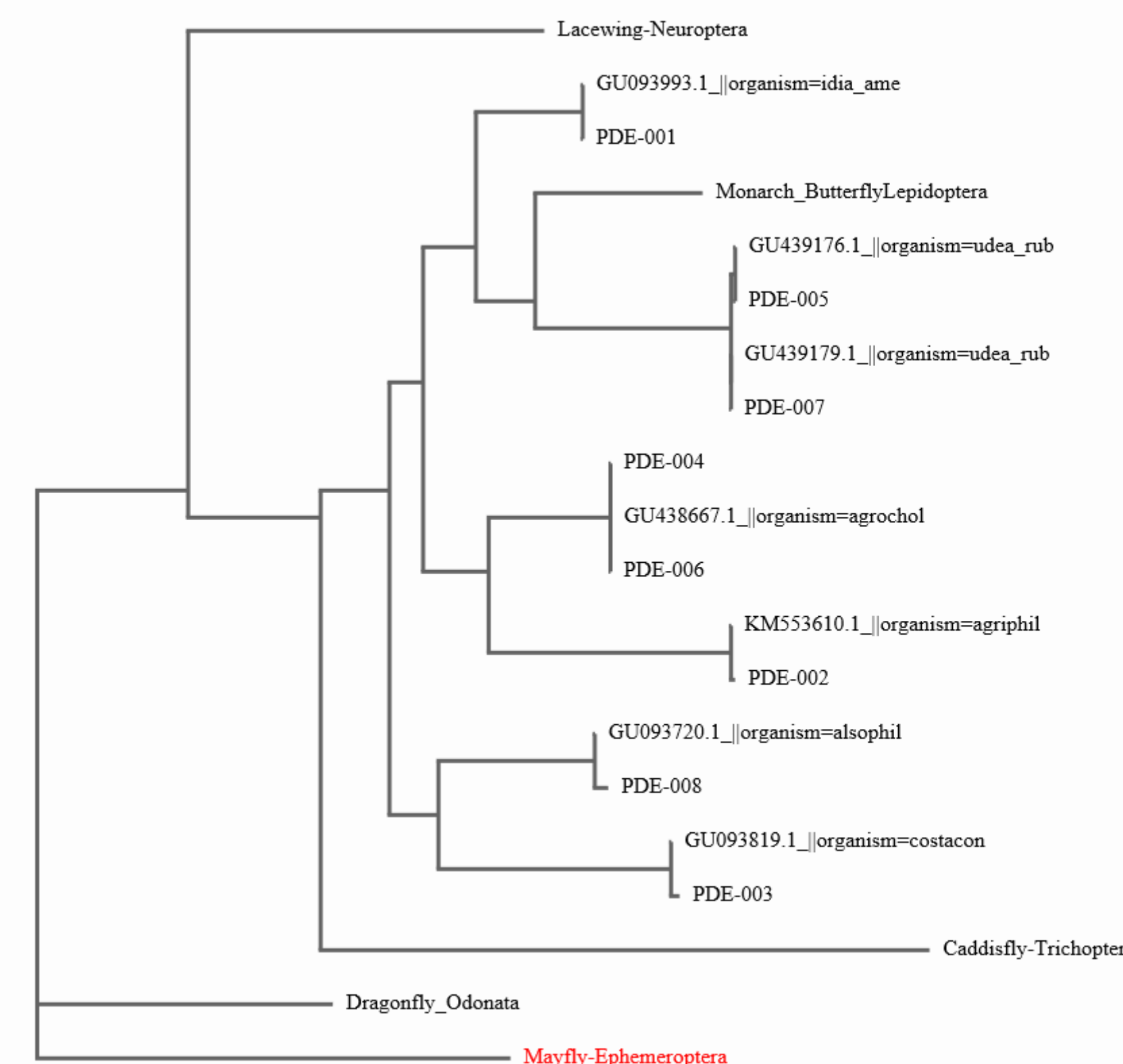


Figure 1: Phylogenetic tree of samples compared to other common winged insects for genetic comparison.



Figure 2: (LEFT) Image of samples PFA-006, identified as *Agrochola bicolorago*, (RIGHT) Sample PFA-001, identified as *Idia americalis*.

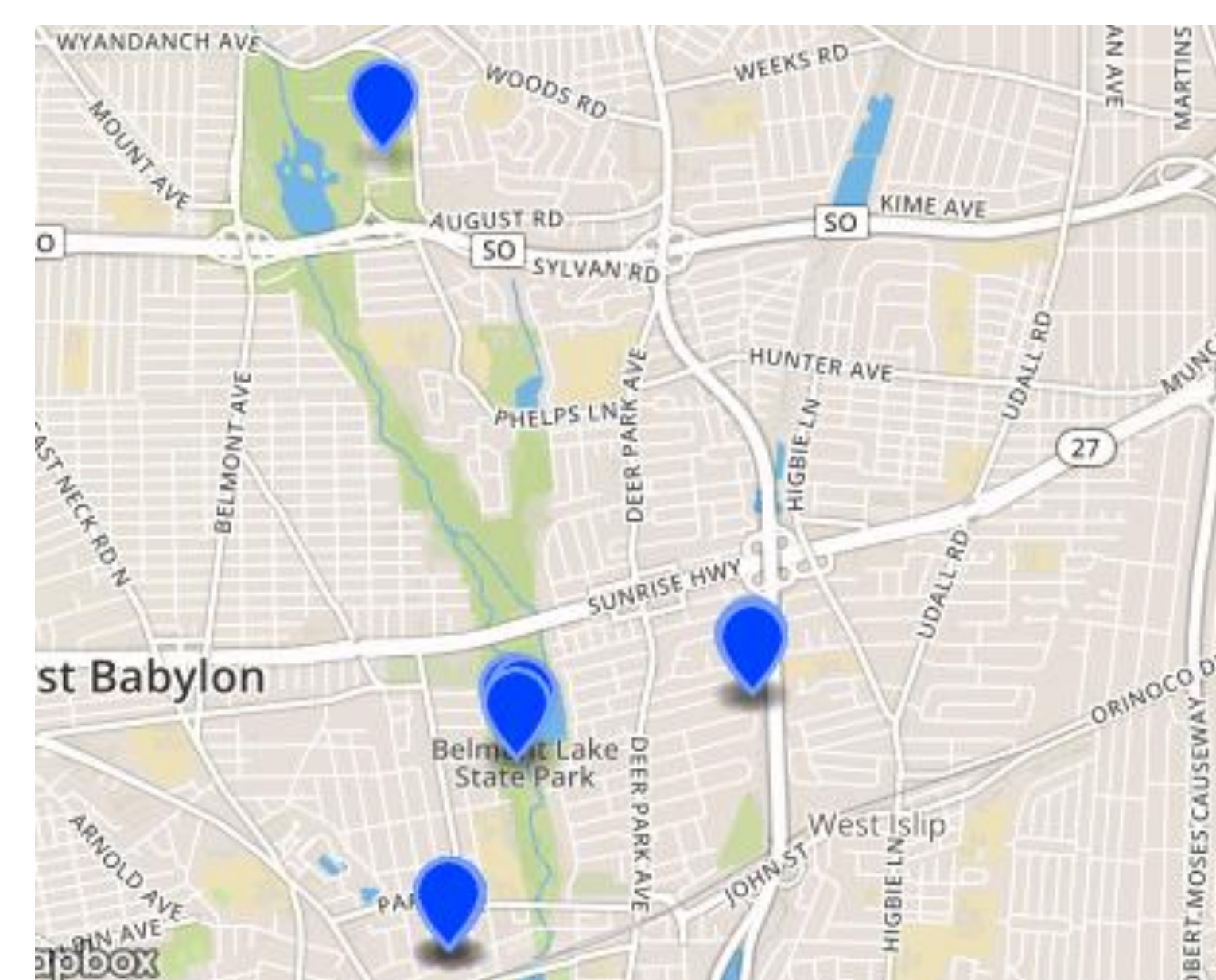


Figure 3: Map indicating various collection sites within Babylon.

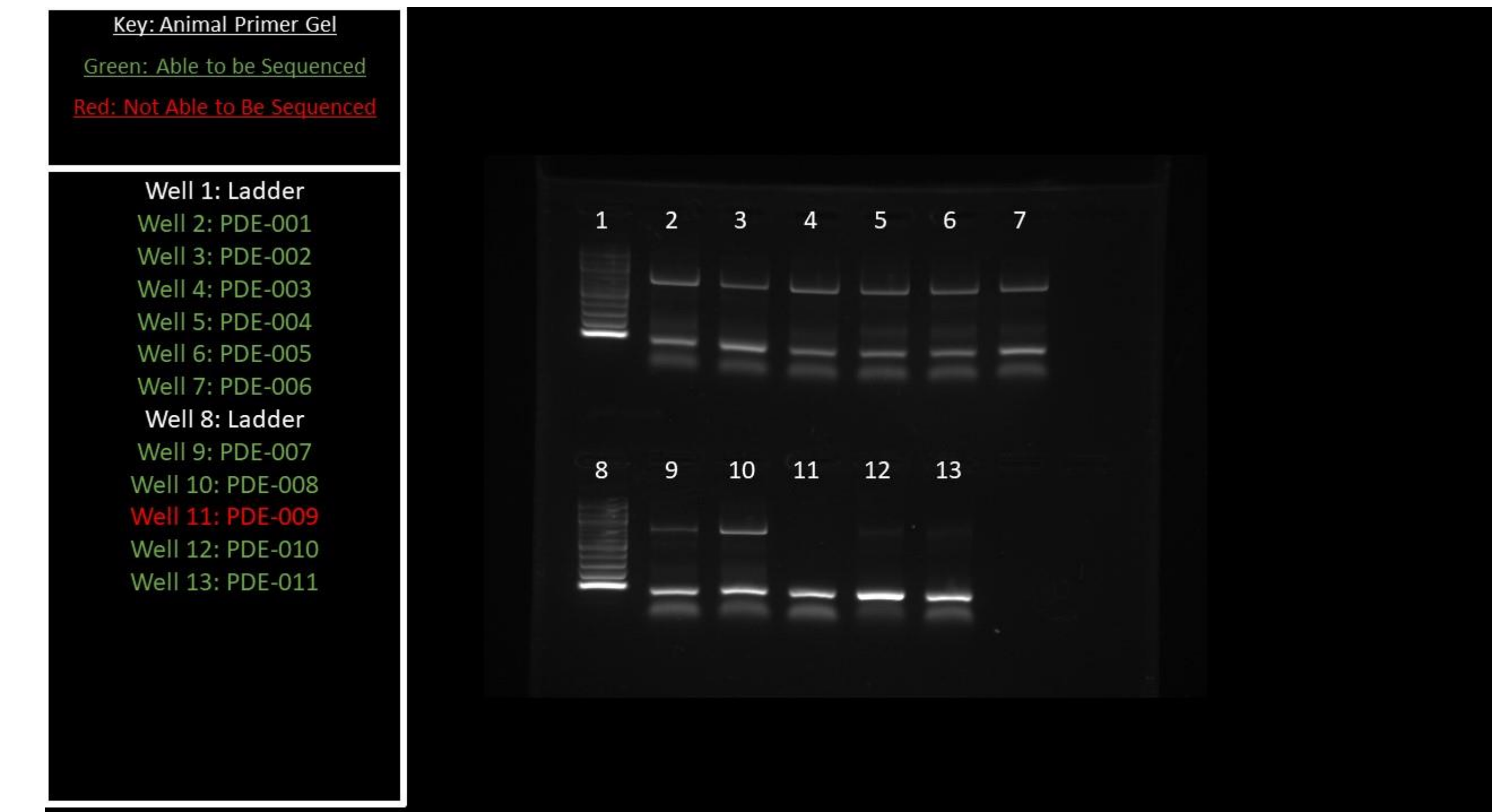


Figure 4: Gel electrophoresis of samples indicating which PCR was successful enough for samples to be sequences (red = unable to be sequenced, green = able to be sequenced via GeneWiz)

## Discussion:

The moths were collected from various areas around Babylon. In our results, there were no novel sequences as all the genes in question matched up to a species in the database. Samples PDE-004 and PDE-006 were both *Agrochola bicolorago* and were found in the same locations. PDE-005 and PDE-007 were both *Udea rubigalis* but they were found at two locations. Both locations were near fresh water meaning this type of environment may be favored by this species. Out of the 8 samples sequenced, there were 6 different species in total. This shows that the Moth population in Babylon is diverse. It is difficult to tell realistically though with such a small sample size. It would be beneficial to continue this experiment with a larger sample size to learn more about the biodiversity. It would also help to learn more about what environment different species favor as it is difficult to tell this with so few samples.

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