# DNA Barcoding To Test The Biodiversity of The Massapequa Preserve



### By. Sophia Fiorentino, Leah Johnson, Anabelle Kahn, Sophia Morgan, Jeff Petracca, August Eberling

#### **Abstract:**

There are over 1,000,000 species of insects. With there being so much wildlife, there is still so much that humans have not discovered. There are believed to be over 7-10 million insects in the wild. Biodiversity is crucial to the health of ecosystems. To determine biodiversity in the Massapequa Preserve, specimens were collected from the freshwater environment. Samples will be used to determine the biodiversity by the abundance or uniqueness of each sample through DNA barcoding. DNA barcoding is a way to identify species based on the sequence of their DNA in its genome. We found numerous species of different taxas. In conclusion, significant amounts of biodiversity are present in the Massapequa preserve considering that only two out of ten specimens matched.

#### Introduction:

In this experiment, the main idea exhibited is testing the biodiversity, or the amount of contrasting specimens of the Massapequa Preserve, and seeing if there are new organisms we haven't discovered and labeled yet. The river was entered in the preserve and sifted through sediment to find invertebrates. Our findings were brought to the Cold Spring Harbor Laboratory and preformed a PCR experiment in the C01 region to determine the species that were instituted. According to Frontiers In Ecology and Evolution, they state that Urbanization is one of the most intensive and rapid human-driven factors that threat biodiversity. Since this has been a problem, it is crucial to test for a variety of species in habitats, and if this is the cause, we can work towards an alternate solution.

## **Procedure**: DNA barcoding was ran on specimens Gloves, waders, kicknets, and sifters were used to obtain specimens

Coordinates of specimens were found

Specimens were labeled and photographed

Stored in test tubes containing 95% ethanol inside of a refrigerator















Sequence Conserva
Sequence Variation
Consensus
1. CSE-010
2. CSE-02
3. CSE-09
4. CSE-01
5. CSE-05
6. CSE-04
7. CSE-03
8. CSE-08

Gel electrophoresis showed that the PCR failed for CSE-006 as well as CSE-007. Other than those errors the results were conclusive. After using DNA subway on these species, the results were supported. Also, CSE-002 and CSE-009 results show them to be the same species based on their DNA sequence. Out of the experiment, two creatures were proven to be the same while the other five were different varieties of insects or tiny creatures.



#### **Conclusion:**

After processing our results in DNA subway all results were viable except CSE-004, CSE - 006 as well as CSE - 007 (species four is going to be re-ran). The first specimen was *Eukerria saltensis* which is an Earthworm with native origins to South America. Specimen number two is *Hyalella azteca*, a *Amphipod crustacean* from North America where they are able to thrive in fresh waters. The third species is known as *Tipula furca* but better known as crane flies. Tipulas have over 2,000 species all around the world. Species number four is being looked at in closer considerations. The fifth species with the name of Helobdella *modesta* are freshwater leeches that occur all around the world and do not suck on blood. As previously said, both species six and seven are not viable as seen in the gel electrophoresis. Species eight has a scientific name of Anyphaena pectorosa but better known as a ghost spider in the Anyphaenidae family. This spider is only seen in the United States as well as Canada. The ninth species is Hyalella azteca, an Amphipod crustacean which is the same as species number two. Species number ten was predicted to be Crematogaster cerasi, which is an ant within the Crematogastrini tribe.

#### **Gel Results**





### Work Cited



### **Acknowledgments:**

Thank you Jeff Petracca, Sharon Pepenella, and Cold Spring Harbor Labs for helping us conduct this experiment as well as Mr.Eberling for mentoring us through it.