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If samples are collected from the Massapequa preserve then, it will provide an Idea of the biodiversity in the preserve in late September of 2022. By taking muddy samples, dry samples, floating samples, and samples submerged in the narrow part of the creek. Once the samples are collected, they will be observed visually and analyzed biochemically, through DNA barcoding, a technique that amplifies a conserved sequence of DNA and then compares it to online genetic databases, to analyze to determine the genus of the organisms.

Intro

In this experiment, samples were taken at the Massapequa preserve in late September. This was done to get a general idea of the biodiversity in the freshwater streams in Massapequa preserve. During the experiment, macroinvertebrates were collected directly from the stream, and taken in for DNA isolation, PCR amplification, gel electrophoresis, and DNA sample sequencing. These various processes were all completed to be able to know the exact species of the samples collected, and how the samples compare to one another. By knowing the specific species in an area, an idea of the level of biodiversity in the area can be attained. Biodiversity is the amount of various organisms in an ecosystem and the variety of the species. When an ecosystem is more diverse, there is a greater amount of different species that can adapt to changes in the environment. This allows the ecosystem to be more stable even when there is a great change in the environment such as disease, climate change, or a fire. Therefore, by knowing the biodiversity of the streams in Massapequa preserve, then the stability of Massapequa preserve can be known, as well as its ability to recover after a disaster.

Methods for identifying sample:

DNA was obtained using silica gel bead extraction technique from Cold Spring Harbor.

Use PCR to isolate Co1 using Cold Spring Harbor's procedure. Use Gel electrophoresis to amplify samples.

Sequence of PCR product.

Use DNA Subway to analyze sequences.



Methods:

A: For Finding the Location:

• Using the gps coordinates find the location of sample collection using a map app or google maps

When searching for samples in shallow water, wear waist high waders, when searching in deep water, wear chest high waders.



1a. For Finding Samples in Dirt:

Using a shovel collect a small amount of dirt and rocks and place it in the sifter, and sift through the dirt and rocks to find samples. If a sample is found, carefully place it in a tube to preserve it, making sure to be wearing gloves throughout the entire process.



2a. For Finding Samples in Water:

Wear waders and wear standard blue disposable gloves
Walk through the water and look for any plants, or samples.
After a sample is found, carefully place it in a test tube to preserve



References

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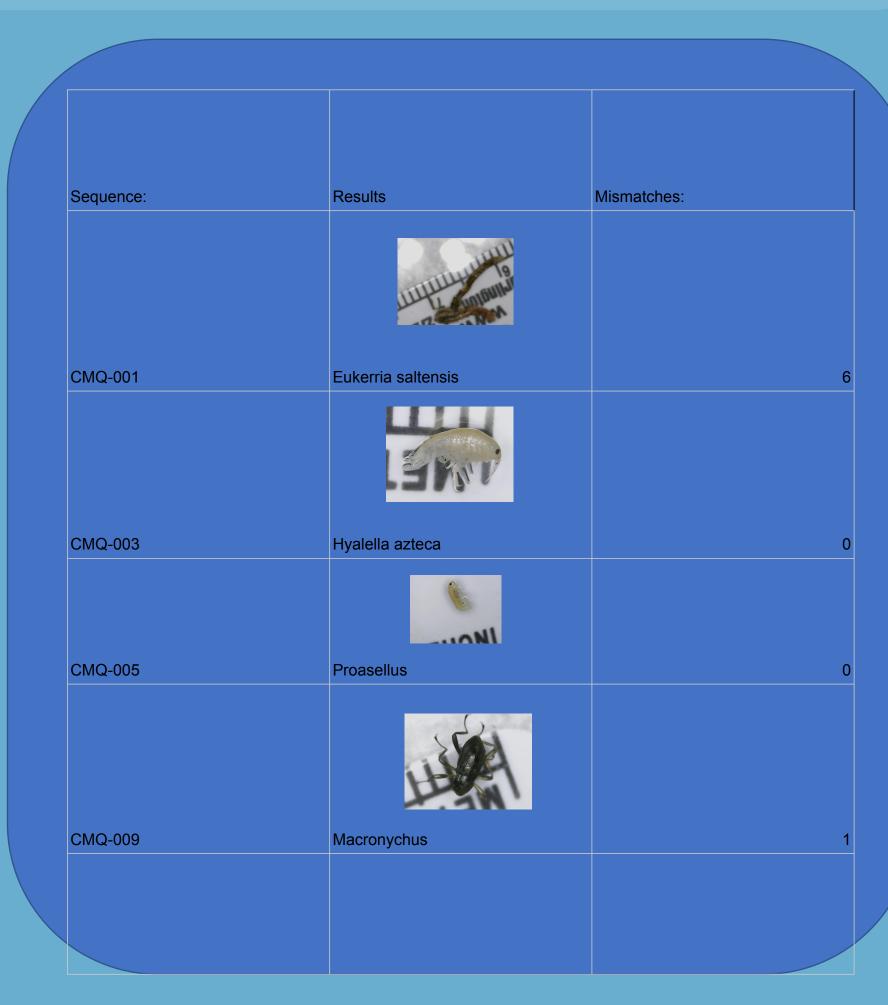
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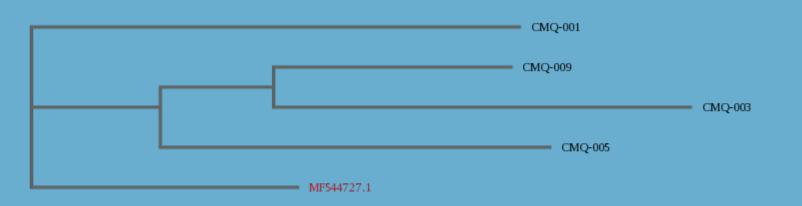
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Materials:

- 1. Sterile disposable nitrile gloves
- 2. Metal sifters(preferably more than two)
- 3. Short handheld shovels or a few spades
- 4. Fishing waters (waist and to chest) depending on depth of water
- 5. Sterile collection tubes
- 6. Sterile tweezers to help with collection(optional but helpful)
- 7. Phone or gps
- 8. A net without handles (will be use by dragging through deeper water)
- 9. Walking stick (optional but recommended for working in water)
- 10. Phone or notebook to record coordinates





Results

As shown in the table, sequence CMQ-003 and CMQ-005 were identical matches with the sequences of two other recorded sequences. Sequence CMQ-003 can be identified as Hyalella azteca, which is a species of amphipod crustacean that is found in North America.

On the other hand, CMQ-005 had a match with Proasellus which is an isopod crustacean. The Sequence CMQ-009 had only one mismatch and was identified as Macronychus or the more commonly known riffle beetle which is usually found in North America. Sequence CMQ-001 had 6 mismatches which was more than the other sequences, but it can be identified as Eukerria saltensis which is an aquatic earthworm originally from areas in South America.

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