



The Biodiversity Of Macroorganisms In Argyle Lake

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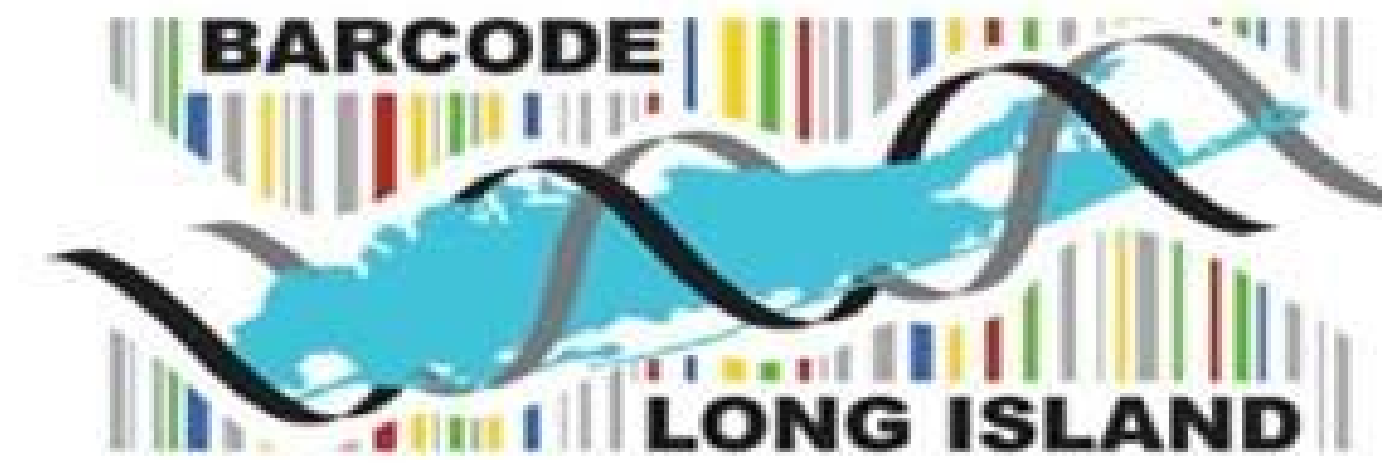
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Cold Spring Harbor Laboratory
DNA LEARNING CENTER



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Abstract

Argyle Lake is a habitat for many freshwater benthic macroorganisms. Through the process of obtaining and examining macroorganisms from Argyle Lake, biodiversity will be determined throughout specific parts of the lake. The sample collections from various parts of Argyle Lake will be compared to other known species. The different types of macroorganisms will be obtained by collecting samples from various parts of the bottom of the lake. The DNA will be collected from the organisms found and will be compared to other known organisms and each other using DNA barcoding. Three out of the eleven samples taken from Argyle Lake were able to be sequenced.

Introduction

Freshwater benthic macroorganisms have many important roles in the ecosystem and the food chain. These organisms are found in freshwater sediments, are diverse and abundant, but are often patchily distributed and relatively difficult to sample, especially when they live in deep subsurface sediments (2). They help in their ecosystem by burrowing down deep into layered sediment and accelerate nutrient cycling, as well as helping increase the rates of recycling of macronutrients (2). They are also prey for many organisms, supporting life within the ecosystem.

Argyle Lake is located in Babylon, New York. It is formed by a dam across the Carll's River flowing out to the Great South Bay (3). The lake is a freshwater lake surrounded by trees and a park on one side; however there are also residential houses, a school, and a road on the other sides of the lake, which could have a definite impact on the water quality of the ecosystem.

Benthic macroorganisms help indicate the water quality of an ecosystem, frequently used as bioindicators for environmental stress in aquatic ecosystems at different levels. The total number of species and the differences between their roles are currently unknown, so to help determine the biodiversity of the lake would give a greater understanding of the local ecosystem.

Results

Results showed that only three out of the eleven samples ended up with DNA sequences. These sequences were NRJ 006, NRJ 008, and NRJ 011 and all of these samples are diverse.



Figure 1: Location of benthic macroorganisms sampled

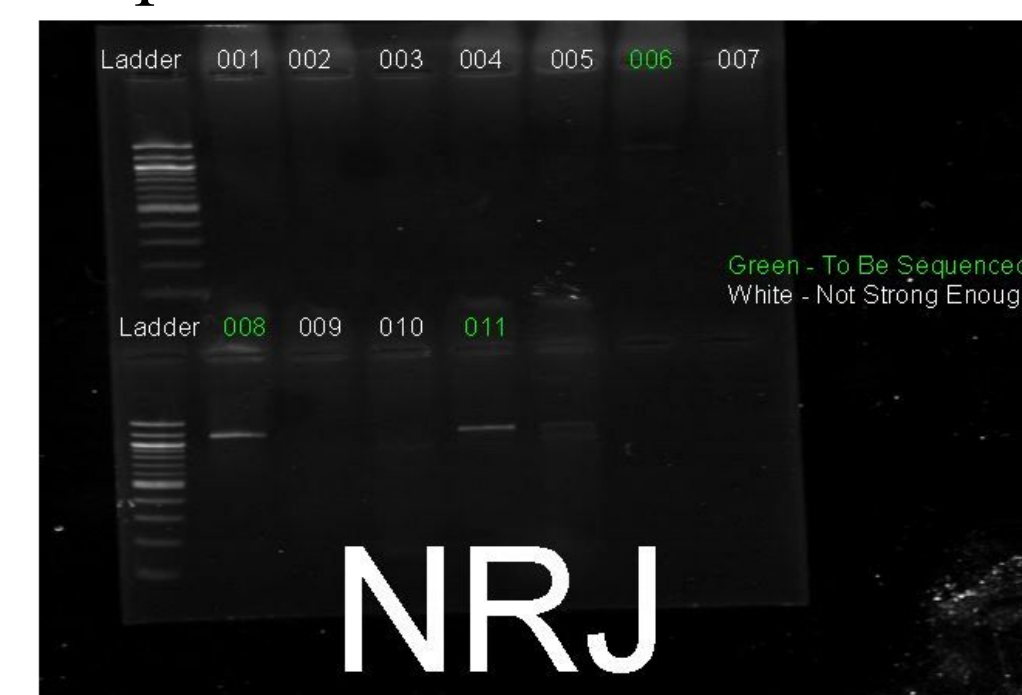


Figure 2: Gel results of PCR. Sample 006, 008, and 011 are circled in green as they were sequenced.

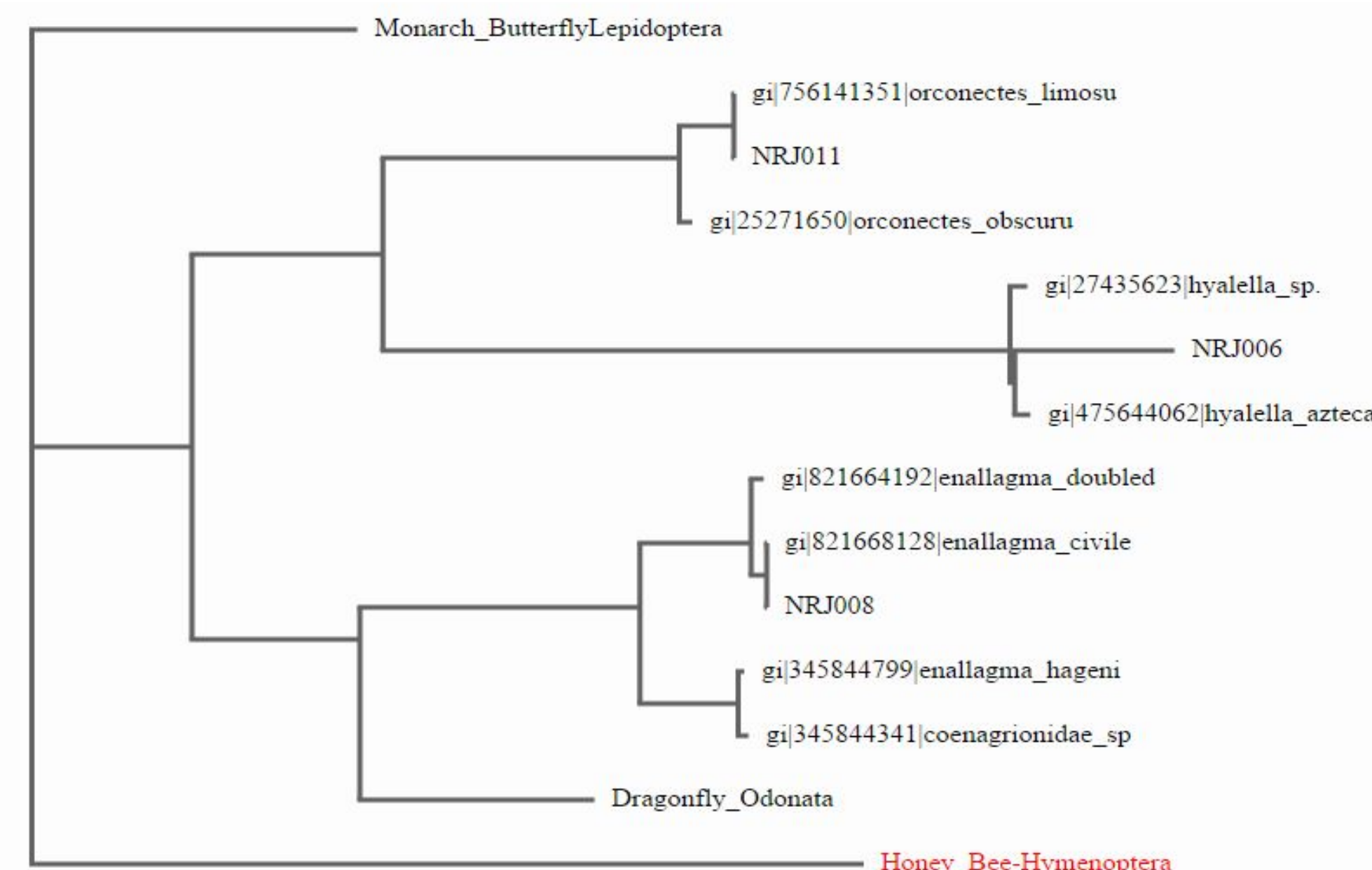
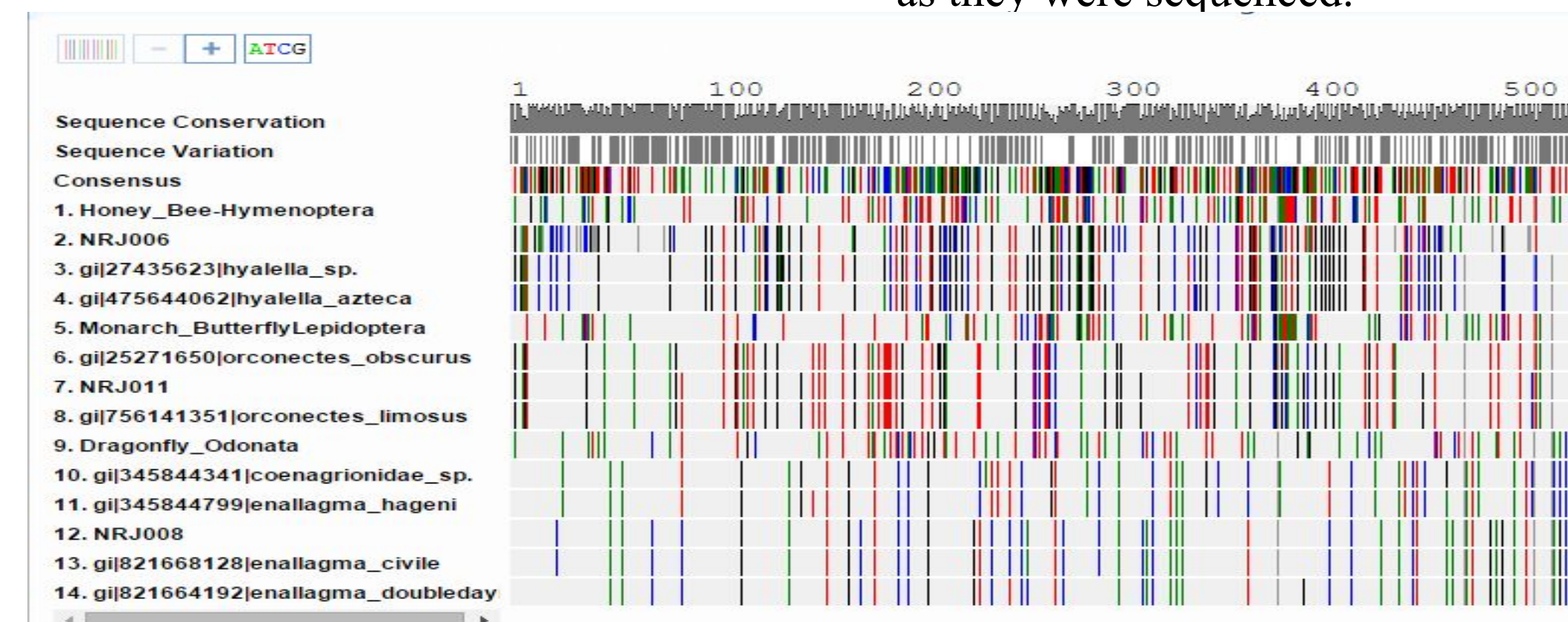


Figure 4: The ML phylogenetic tree of the three samples, blast results. And the outgroup showing relationships in COI gene/

Methods

The sample collection of twenty macroinvertebrates were obtained from different parts of Argyle Lake using leaf pile nets. The specific location in the lake, the color, the taxonomically determined genus and species, and the life stage of each organism found was logged in a data table.

To process the benthic macroinvertebrate DNA, standard DNA extraction techniques were used from Barcode Long Island protocols and laboratory equipment. Following DNA extraction, samples were sequenced according to Cold Spring Harbor Laboratory protocols. The DNA from the macroinvertebrates was compared to each other.

Discussion

The results showed that not all of the samples were able to be sequenced. However, the samples that were able to be sequenced all showed very different DNA barcodes. These samples help to show the biodiversity throughout Argyle Lake. If all of the samples had been able to be sequenced it would further show the genetic diversity of the organisms in Argyle lake. In the future one could collect samples from different areas throughout a town and compare the DNA sequences of the organisms from the different areas to determine biodiversity throughout that town or village. This future study would expand the original study to determine biodiversity over a larger area.

References

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