Collecting and Identifying DNA of Micro Aquatic Invertebrates in Massapequa Preserve to determine the Biodiversity the environment

Authors: Matthew Calfayan, Alexander Ramsawak, Frank Sulawa

Mentor: August Eberling

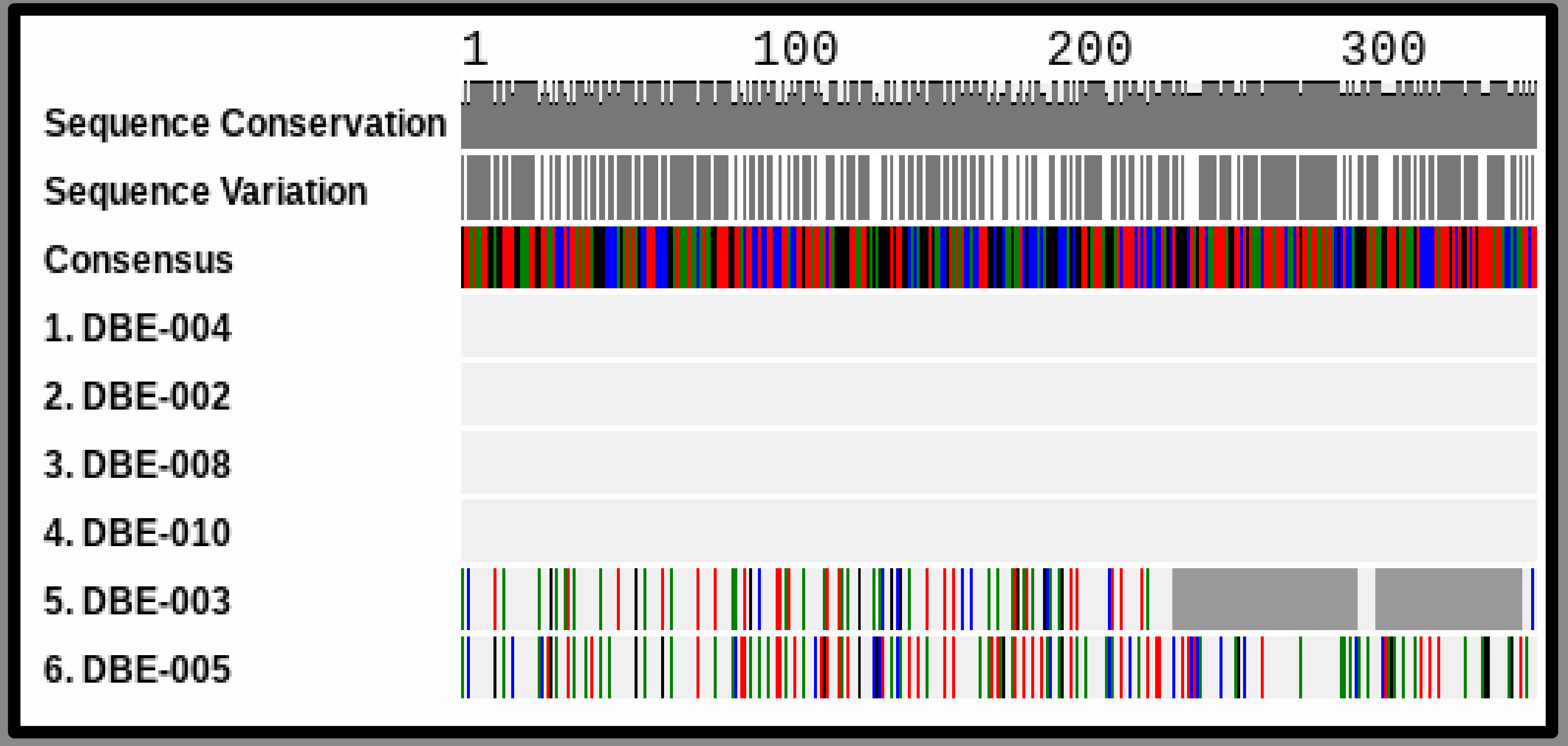
Abstract

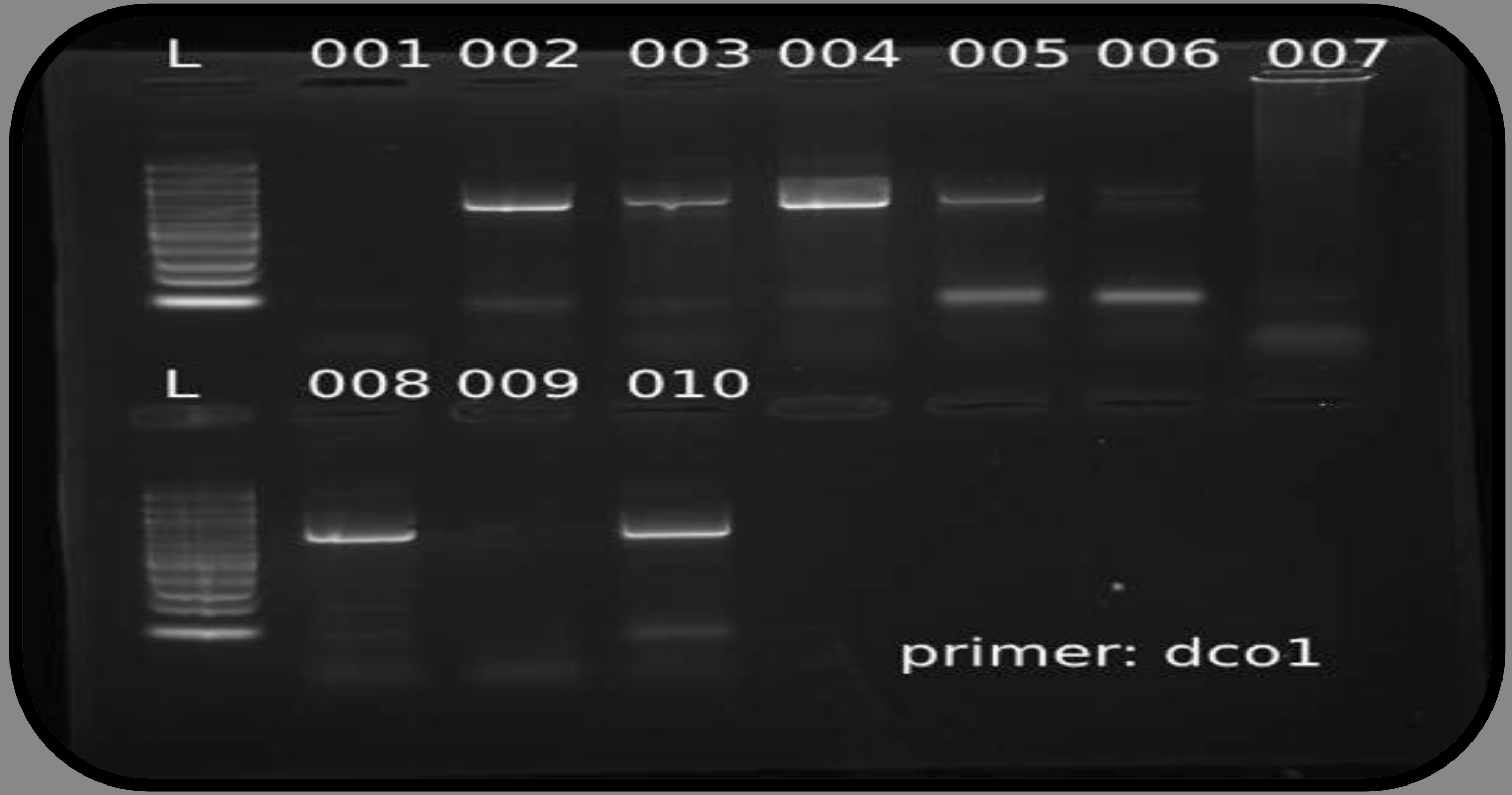
Biodiversity is the variety of life in the world or in a particular habitat or ecosystem, which is crucial due to its significant support to ecosystems by offering stability and resilience to ensure that other species can survive and thrive. The objective of this experiment was to determine whether there was a high or low level of biodiversity within the Massapequa Preserve. In order to obtain a better understanding of this objective, several specimens had to be collected and examined in order to determine whether they contained different DNA to one another. A total of 8 specimens were collected and examined and it was found that through the process of *Gel Electrophoresis* that there was a small amount of biodiversity within the Massapequa Preserve. To put this into simpler terms, with the support of scientific methods, these results show that there was very little biodiversity within the Massapequa Preserve.

Introduction

This experiment was conducted to determine whether there was a high or low level of biodiversity within the Massapequa preserve. The Massapequa preserve is a temperate deciduous forest with different levels of biodiversity, either high or low can be caused by climate change or urbanization. If the biodiversity in the Preserve is at a high level, that means the environment is healthy and stable, but if the level is low that means the environment has trouble thriving and remaining in balance between species. This experiment is measuring the percentage of relatability, the higher the relatability the less biodiversity there is and vice versa.

Massapequa Preserve





Results

The results show that samples 4, 8, 12, 2, and 10 were all Caecidotea racovitzai isolate. The third sample was identified as Ceratopogonidae sp. The fifth sample was identified as Aquarius remigis. Among samples 4, 8, 12, 2 and 10 they were 100% similar indicating a low level biodiversity, however samples 3 and 5 were both different species than the rest.

Discussion

Within our results we didn't get many different animals but all of the animals were from North American and non-invasive. Since there aren't many animals within the preserve there is a low biodiversity which is seen in our results. The preserve needs more biodiversity to make sure the ecosystem can continue to thrive for many generations later.

Sample 3: Ceratopogonidae *sp.*

Sample 5: *Aquarius remigis*

Samples 2, 4, 8, 10, 12: *Caecidotea racovitza*

Methods

1. Traveled to designated location in Massapequa preserve to collect Specimens that would be used for the experiment.
2. Specimens were examined and photographed
3. Specimens then were placed into test tubes filled with ethanol.
4. At Cold Spring Harbor, they were then grinded up and then PCR was performed to copy DNA.
5. Gel electrophoresis was then done to compare each specimen to one another to see if they contain CO1.
6. After obtaining results from Gel electrophoresis, they were then sent to Sanger Sequencing
7. Lastly, all specimens were put into DNA Subway to determine each species.

References

Leon-Alvarado OD, Miranda-Esquivel DR. Phylogenetic diversity and North Andean block conservation. PeerJ. 2023 Dec 6;11:e16565. doi: 10.7717/peerj.16565. PMID: 38077412; PMCID: PMC10710123

Marseille MR, Lindley SJ, Cook PA, Bonn A. Biodiversity and Health in the Urban Environment. Curr Environ Health Rep. 2021 Jun;8(2):146-156. doi: 10.1007/s40572-021-00313-9. Epub 2021 May 12. Erratum in: Curr Environ Health Rep. 2021 Sep;8(3):266. doi: 10.1007/s40572-021-00321-9. PMID: 33982150; PMCID: PMC8115992.

Acknowledgement