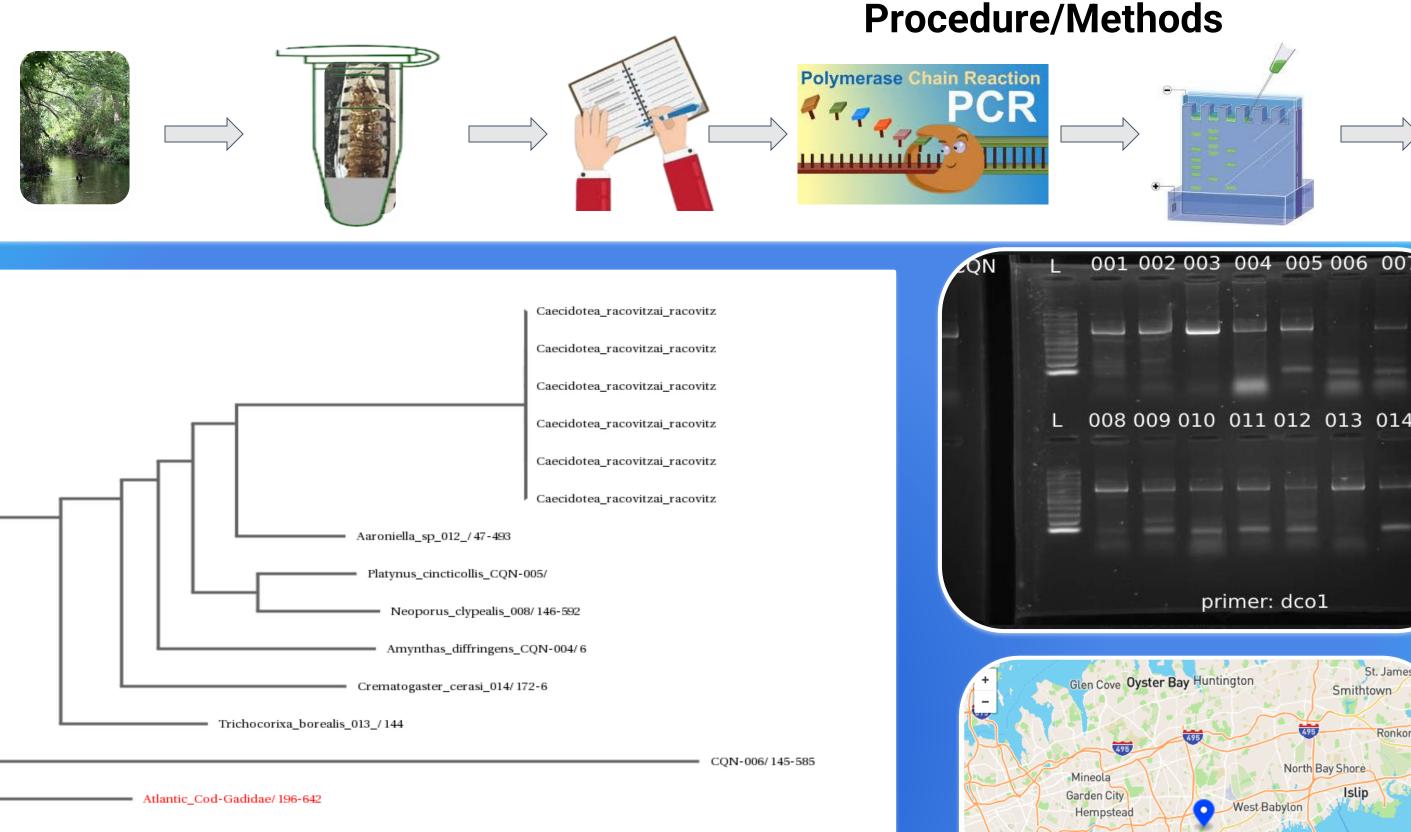
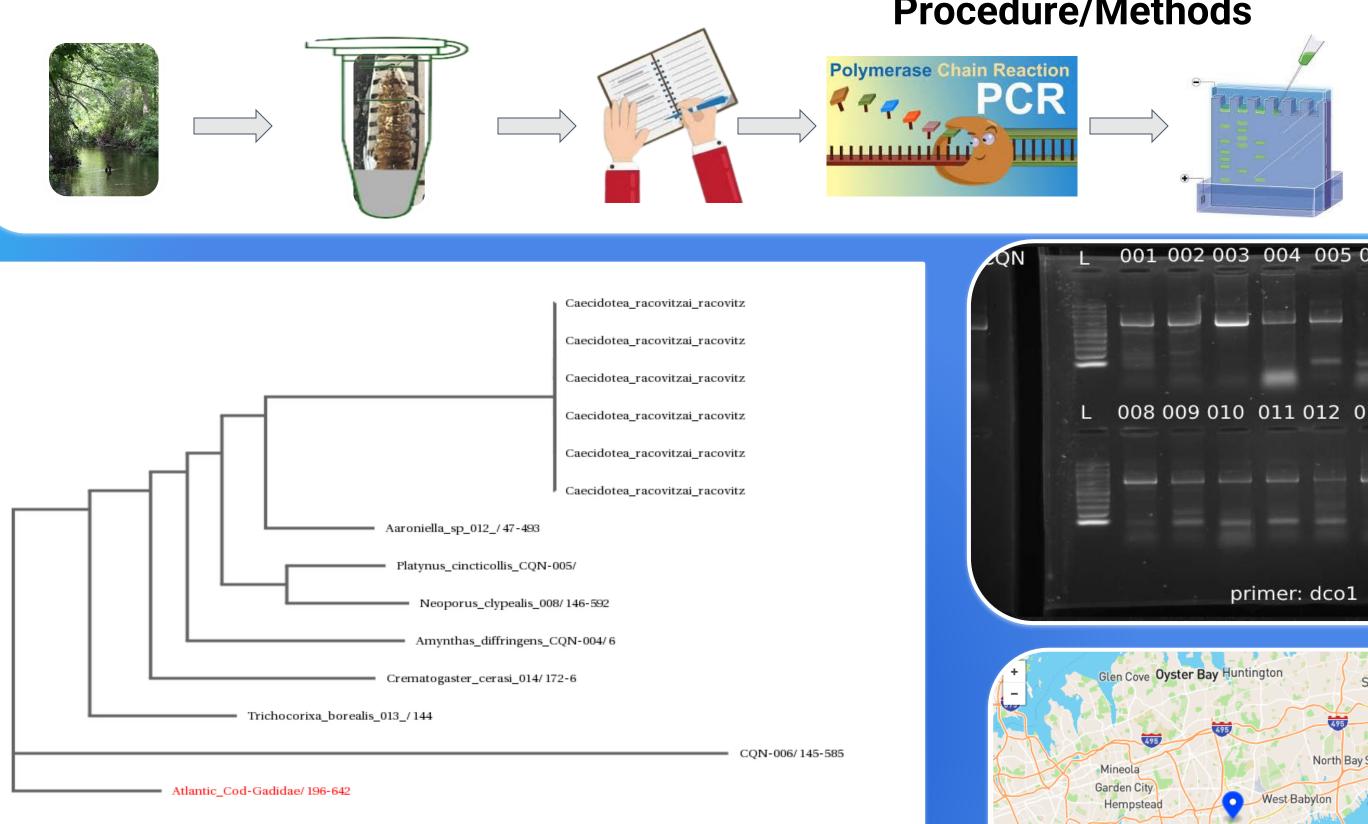
DNA Barcoding of Aquatic Macroinvertebrates to Determine the **Biodiversity of the Massapequa Preserve**

By Joseph Buckley¹, Benjamin Soehl¹, Nathaniel Stutz¹, August Eberling¹, Jeff Petracca² ¹Massapequa High School-Ames Campus, ²Cold Spring Harbor Laboratory DNA Learning Center

Abstract

The lack of Biodiversity in preserves/parks, such as the Massapequa Preserve, is an increasingly devastating problem affecting multiple countries world wide. This experiment sought to use DNA Barcoding to find and document evidence of biodiversity in the Massapequa Preserve and discern the level of restoration work, if any, that the Preserve needs to become a fully diversified environment/habitat. In the Massapequa Preserve, sixteen samples, a mix of terrestrial and aquatic macroinvertebrates, were collected. These samples were captured using various tools, including scoopulas, kicknets, and sifters. Afterwards, the samples were frozen; later their DNA from the C01 gene was extracted to determine the genus and species of each organism. Some of the genus and species names found include Caecidotea racovitzai racovitzi, Crematogaster cerasai, Neoporus clypealis, Platynus cincticollis, and Trichocorixa borealis. Based on our findings, we can see that the Massapequa Preserve does indeed have a high level of biodiversity, and has been able to fill in necessary niches possibly caused by urbanization 50-60 years ago.





Introduction

Biodiversity is very essential to the survival of humans and ecosystems. Biodiversity can contribute to positive human and ecosystem health and wellbeing in a variety of ways (Marselle, 2021). One such way is through medicine. Some plants have been found to hold the cure to certain seemingly untreatable diseases. More biodiversity in an ecosystem can allow for the production and discovery of more cures for deadly diseases.

To determine the biodiversity of an area, scientists use DNA barcoding. DNA barcoding is a molecular process by which a segment of DNA, usually 500-700 base pairs long, often taken from the C01 gene, is used to determine the species of the organism being tested. This is the method that we used in determining the genus and species of the samples we collected.



According to DNA Subway, this species was said to be an unidentifiable bacteria. This was thought to be the result of some bacteria contaminating the sample's DNA

Results

Data collected shows that six of the specimens collected were identified as Caecidotea racovitzai racovitzai, which is a species of isopods. Another identified species, labeled as CQN-004, was identified as Amynthas diffringens, a worm originally from Japan. This invasive species of worm has caused severe environmental damage on the countries it has invaded, including the U.S.A. Unfortunately, one of the labeled specimens, CQN-006, showed signs of being contaminated by unidentifiable bacterial DNA. However, judging from its appearance and structure, we can assume that sample CQN-006 is a Caecidotea racovitzai racovitzai.





CQN-006





CQN-004

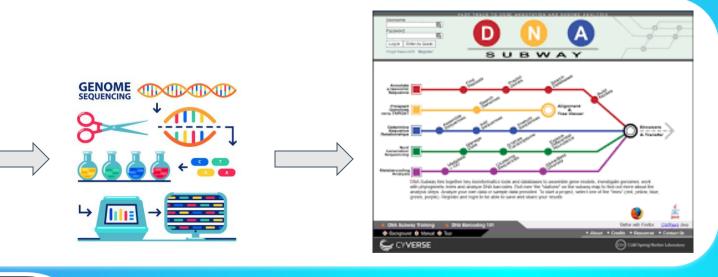
A.K.A. Amynthas diffringens. Originally from Japan, but has now invaded several countries, including the U.S. It has also caused severe environmental damage on the countries it has invaded.

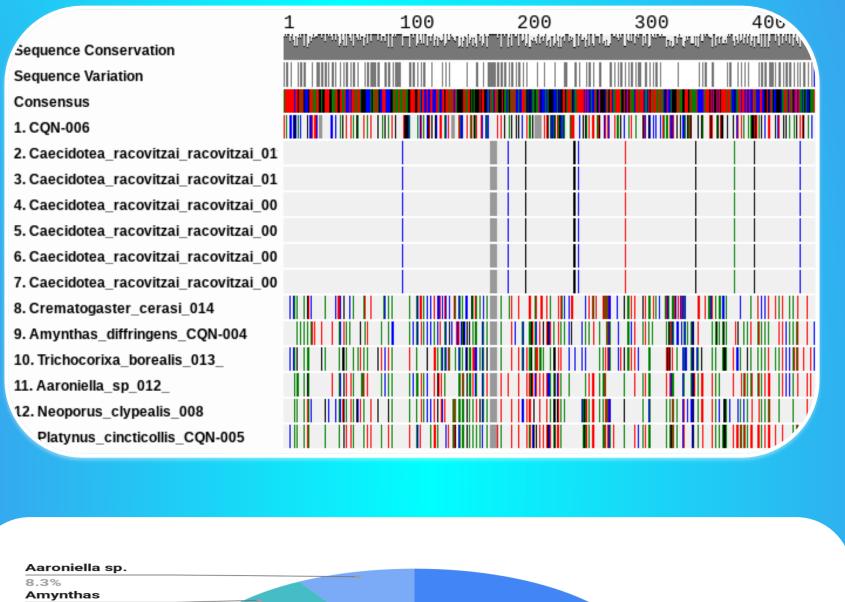
References and Acknowledgments

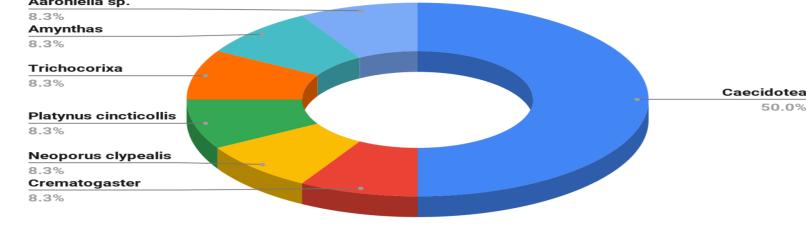
Please use the QR code provided to access the references and acknowledgements page.













In conclusion, the data collected shows that the Massapequa Preserve has a moderate level of biodiversity. This is evident because many of the samples collected were of various unique species. The samples collected in the preserve also show the presence of invasive species, such as Amynthas diffringens. This also shows that the Massapequa preserve is a stable ecosystem. In contrast to these exciting findings, there were some issues present in our sample data. For example the specimen CQN-003, which is shown as the brightest bands on the electrophoresis test, had insufficient data, possibly as a result of multiple specimens' DNA being present. CQN-006 was also unidentifiable due to bacterial contamination. These findings are significant due to the fact that it proves that biodiversity and invasive species are present in the deciduous forests of Long Island. This biodiversity is one of the may factors that keeps the ecosystem of the Massapequa Preserve stable and thriving.