



The Oyster Cage is Your Oyster

Comparing Sessile Invertebrate Species Diversity in the Upper New York Bay and New York- New Jersey Bight

Author: Cayla Kushner¹
Dakota Rodgers²

Mentors: Manisha Jalan³ and Allison Mayle, PhD*

¹Fiorello H. LaGuardia High School of Music & Art and Performing Arts; ²Harbor School; ³Memorial Sloan-Kettering Cancer Center; *Urban Barcode Research Program, DNA Learning Center NYC

Abstract

We planned on collecting a random sampling of 10 sessile marine invertebrate samples from two oyster cages along the East River. We planned on measuring some key factors of water quality such as pH and nitrate concentrations to determine if water quality was an indicator of genetic diversity or of a specific species's presence. Our overall goal was to compare "Species Richness of Macroinvertebrates in New York Harbor: Buttermilk Channel in 2017", a similar project drawing from macroinvertebrates in the Buttermilk Channel, New York Harbor, with our study to determine similarities and differences in the DNA makeup of marine invertebrates found in oyster cages within the East River (Upper New York Bay) and Buttermilk Channel (Lower New York Bay). We focused on the gene Cytochrome oxidase subunit 1 (CO1), as the gene was studied in the previous 2017 project, and is studied in invertebrates. Due to limitations, however, we were unable to collect physical samples. Instead, we analyzed CO1 sequences from previous sampling in the DNA Barcoding Learning Center sequence database. Some marine invertebrate samples were successfully identified, and compared with the 2017 study. Further research will need to be made to determine the factors that influence genetic diversity of marine invertebrates in the New York Bay and beyond.

Introduction

During the early 19th century, the population of New York increased from approximately 60,000 to nearly 4 million inhabitants. Intense human settlement and lack of complementary waste processing infrastructure, as well as increased shipping port activity within New York Harbor (Upper New York Harbor and surrounding ports of New York and New Jersey) supplied excessive organic materials to algae and bacteria, which starved marine life of oxygen and made the area uninhabitable.

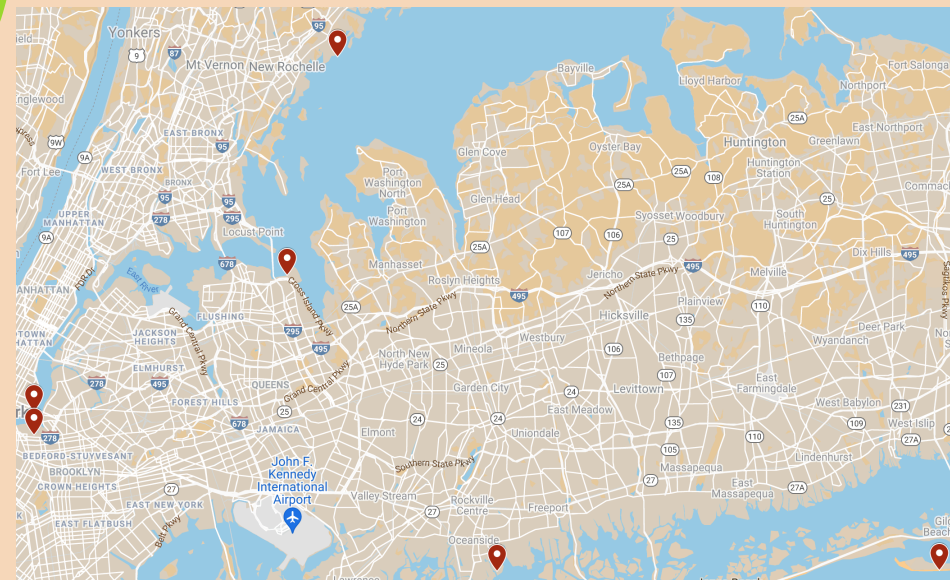
Oysters, shelled invertebrates that are often found in brackish environments, are present in New York Harbor and its feeding rivers when saltwater from the Atlantic Ocean intersects freshwater sources inland. Oysters feed off of algae suspended in the water and phytoplankton, removing algal biomass from their environment, and consume organic particles which would otherwise potentially trigger eutrophication and create algal blooms— which starve surrounding marine life from oxygen. Oysters shells also provide habitats for barnacles, measles, and anemones.

What are the similarities and differences in the DNA makeup of macro marine invertebrates between the East River and Hudson River oyster cages? How has the water quality of different areas in the New York Harbor affected marine communities? We attempted to answer these questions throughout this experiment.

Methods

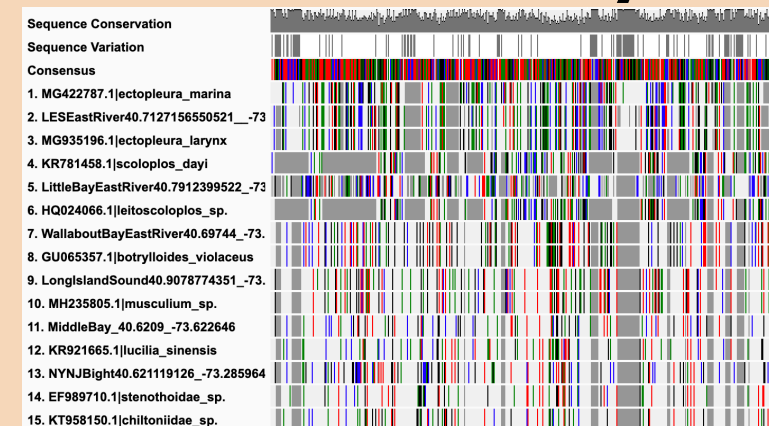
We planned on collecting at least 20 sessile invertebrate samples on the lower or upper East River. We could not complete the work due to COVID-19. Instead, we used DNA Subway/BLAST to identify 6 sample species from the DNA Learning Center's sequence database to analyze species phylogenetic relationships. Each sample was labeled with its location name and coordinates. Then, similar sequences from DNASubway.org were incorporated to create a PHYLIP NJ phylogenetic tree (See Figure 3).

Figure 1: Locations of Sequences Sampled



Map of the GPS coordinates of sequences used from the DNA Barcoding Learning Center Sequence Database.

Figure 2: Results from DNA Analyses

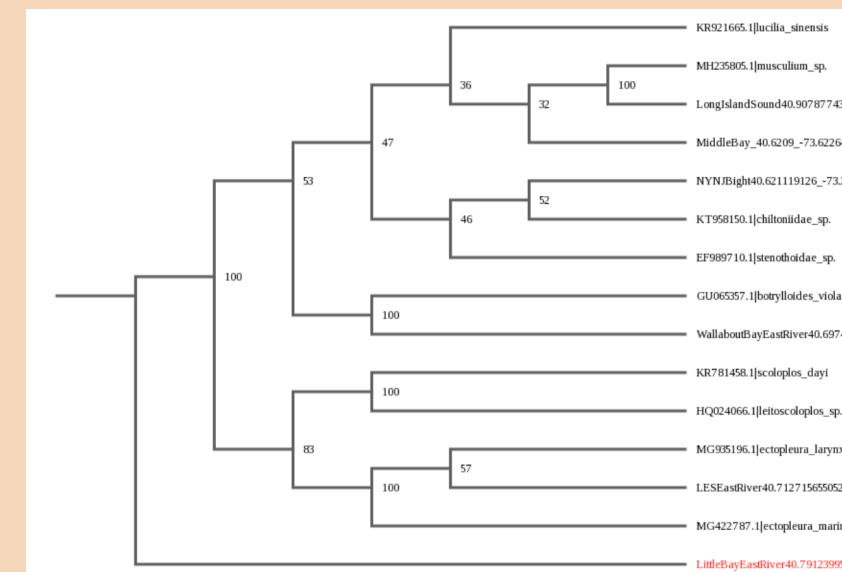


Results of DNA trimming and alignment of marine invertebrate samples used from DNA Barcoding Learning Center database and the DNA from similar species in the DNASubway.org website database.

Results

- Due to COVID-19, we were unable to collect physical samples. Instead, we analyzed CO1 sequences from the previous sampling in the DNA Barcoding Learning Center sequence database and compared them with sequences on the DNASubway.org website.
- Out of the samples that we did analyze, we found that the phylogenetic relationships were most definitive between marine invertebrates found throughout the East River, and that phylogenetic relationships were least definitive between marine invertebrates found in the New York-New Jersey Bight, the Long Island Sound, and the Middle Bay (which merges into the New York-New Jersey Bight, see Figure 1).
- The sample collected in Wallabout Bay, the East River was determined with a confidence value of 100 to be more closely genetically related to the botrylloides genus than other taxa. The sample collected on the Long Island Sound was also determined with a confidence value of 100 to be more closely related to the musculium genus than other taxa (See Figure 3).
- Despite this, the small sample size in the experiment obscures the confidence in these genetic relationships. Further sampling of invertebrates and

Figure 3: PHYLIP NJ Phylogenetic Tree



Sample sequences collected from the DNA Learning Center student sequence Database are labeled with the location names and GPS coordinates from which they were reported to be collected from.

Discussion

Due to COVID-19, our team was unable to feasibly collect macroinvertebrate samples from the East River. Further research will need to be made to determine the factors that influence the genetic diversity of marine invertebrates in New York Bay. Social distancing requirements made it difficult to carry out our original project report as planned, and communicative unresponsiveness led to us being unable to access the "Species Richness of Macroinvertebrates in New York Harbor: Buttermilk Channel in 2017" that was initially to be used to compare results. Although phylogenetic relationships were more definitively made between marine invertebrates collected in the East River, they should not be used as evolutionary evidence due to the small sample size collected, and possible disparities in collection procedures in those locations.

References

Bloomfield, C., & Obermayor, J. (2017). *Species Richness of Macroinvertebrates in New York Harbor: Buttermilk Channel* [Scholarly project]. In *New York Harbor SEALS*. Retrieved December 13, 2020, from <http://harborseals.org>

Shomu's Biology. (n.d.). Retrieved November 13, 2020, from <https://www.shomusbiology.com/>

Zhang, Zhi Qiang. "Animal Biodiversity: An Introduction to Higher-Level Classification and Taxonomic Richness." *Zootaxa*, 2011, mapress.com/zootaxa/2011/f/zt03148p012.pdf.

"Marine Life." *NYS Dept. of Environmental Conservation*, New York State, www.dec.ny.gov/animals/117322.html.

O'Neil, Judith M, et al. "New York Harbor: Resilience in the Face of Four Centuries of Development." *Regional Studies in Marine Science*, Elsevier, 17 Feb. 2016, [stelar.edc.org/sites/stelar.edc.org/files/R_3EJXVUJHW5uskYb_Elsevier.pdf](http://www.stelar.edc.org/sites/stelar.edc.org/files/R_3EJXVUJHW5uskYb_Elsevier.pdf).

Acknowledgements

I would like to thank Dr. Mayle and Dr. Jalan for their patience and guidance throughout this project, and for providing Dakota and I with the software and resources necessary to (if only attempt to) answer our questions. Additionally, this project would not be possible without the opportunity that the Urban Barcode Research Program, supported by the Pinkerton Foundation and Science Sandbox, provided us.

