Biodiversity of Marine Worms on Long Island

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Abstract

This DNA barcoding project studied the biodiversity of marine worms across Long Island and how varying water salinities affect the marine worm biodiversity. Studying marine worms and the effect of water salinity on their growth and respiration is very important because the results can provide reasoning behind why in certain bodies of water on Long Island, on either shore, there is a greater biodiversity present. The collection of such marine worms took place at the Waterfront Center in Oyster Bay, New York, which served as the samples from the North Shore, and for the South Shore worms, collection took place at Jones Beach, Long Island. Research had been done that indicates that marine worms that live in environments with higher water salinity contents tend to respire less and have stunted growth. Adapting to high salinity environments is quite difficult for most organisms, especially marine worms. Thus, previous data supports that waters with high salinities affect the amount of biodiversity of marine worms able to be living in that water. The results showed that the South Shore had a higher water salinity than that of the North Shore, but the North Shore did not have more species variation than that of the South Shore, showing a similarity in biodiversity.

Introduction

Long Island is home to a plethora of diverse organisms. It is divided into two shores-the North Shore and the South Shore. The Long Island Sound, a tidal estuary of the Atlantic Ocean, is the body of water that surrounds the North Shore, whereas the Atlantic Ocean surrounds the southern shore ("What Makes Long Island Sound So Special?"). The biodiversity of Long Island remains to be a commonly sought out research topic. Researchers commonly use a tool known as DNA barcoding to determine the species of certain organisms. With the use of DNA barcoding, one can then use the results to test interspecies relatedness among said organisms. Barcoding an organism's DNA can provide an efficient and accurate test to determine its species. This species identification technique utilizes an isolated gene region referred to as the CO1 (Cytochrome c oxidase I) when dealing with vertebrates and invertebrates ("What is DNA Barcoding"). By barcoding the aforementioned isolated gene region, the species of an organism can then be determined when the barcoding procedure is executed correctly.

The purpose of this DNA barcoding project is to identify biodiversity in marine worms, a specific aquatic invertebrate, across Long Island, using locations from both the North and South shores as collection sites. Salinity of the water from where the marine worms will be collected will be the factor that is studied on whether it can affect the amount of biodiversity of marine worms across Long Island. There are many environmental factors that affect biodiversity: they include pollution, nitrogen levels, food sources, salinity, etc. The salinity or salt content in the water can have a tremendous effect on the organisms that inhabit it. Salinity levels can affect a variety of biological processes in marine organisms (Beadle). Osmotic regulation must be adjusted by organisms living in water as the salinity of the water changes. Studies have found that with reduced salinities, metabolic rates in certain organisms were increased. In contrast, with increased salinity levels, oxygen consumption has been found to decrease (Beadle). Only certain organisms, like the sheepshead minnow, have the ability to adapt to varying water salinity levels ("Changes in Marine Salinity Levels"). The variations in water salinity between the North Shore and the South Shore on Long Island have an effect on the organisms and the amount of biodiversity present in the waters. In order to be able to observe how the varying salinities on the opposite shores of Long Island are affecting the amount of biodiversity that can be present, a specific marine invertebrate-marine worms- will be used to mirror the larger effects of salinity levels on biodiversity as a whole on the island. Marine worms are often used as indicator species of a myriad of environmental conditions. Water quality is one of the environmental conditions that marine worms can act as indicators for (K. Harlan). Water quality measurements include the measurement of salinity, pesticides, herbicides, and heavy metals present in the water. Being an indicator for water quality and pollution in water, marine worms will act as the model or tested species whose results lead to the creation of broader conclusions about the biodiversity of all marine organisms on Long Island. This research can also have implications for the human population on Long Island. Being that marine worms are the test subjects of this project and are useful indicators of water quality and pollution of waters, they can provide information about where clean, uncontaminated water is present, and also where the water has been sullied. This can help inform the human population on Long Island where clean, pure water is present, and which areas of water need to be purified.

The South shore, because of the body of water that encompasses it, should have higher salinity levels when compared to the levels of the North Shore water. Because of the salinity difference, the species variety of marine worms should be greater on the North Shore where the salinity levels are lower than those in the South Shore. Therefore, if the salinity levels of the South Shore waters are higher than those of the North Shore, then there should be a greater biodiversity of marine worms observed and recorded from the North Shore waters, as a greater variety of marine worms can live without certain biological processes being altered due to high water salinity levels.

The image to the left shows the gel electrophoresis results of the samples amplified via CPR. The samples sent for sequencing are 2, 4, 6, 8, 9, and 10.

Results

Collection Site	Water Salinity
Oyster Bay Waterfront Center (North Shore)	Hydrometer: 5-7 Refractometer: 22-12-20 YSI Multiparameter: 4.8-3-3.3-12.4
Jones Beach (South Shore)	Hydrometer: 8-9 Refractometer: 23-24-21 YSI Multiparameter: 6.8-9.8-15.3

Figure 1:
Figure 1 shows the different water salinities of the North Shore and South Shore collection sites, as calculated by a hydrometer, refractometer, and a YSI multiparameter instrument.

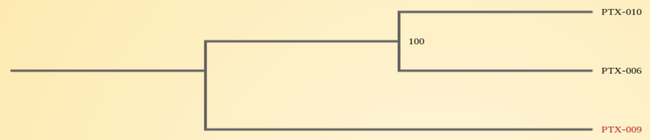

Figure 2: Figure 2 displays the phylogenetic tree compiled of the samples collected from the South Shore on Long Island.

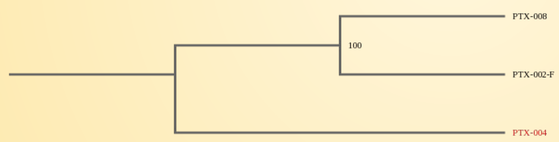

Figure 3: Figure 3 displays the phylogenetic tree compiled of the samples collected from the North Shore on Long Island.

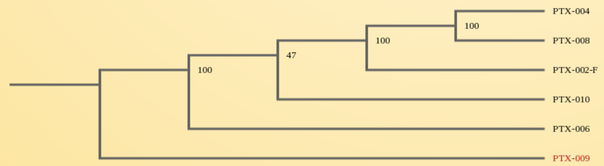

Figure 4: Figure 4 displays the phylogenetic tree compiled of all the samples collected that were sent to sequencing in this barcoding project.

Figure 5. Scientific and Common Names of Samples

Sample2-Alitta virens-sandworm
Sample 3-Capitellidae sp. CMC01-common name could not be determined with research
Sample 4- Alitta virens-sandworm
Sample 5- Capitellidae sp. CMC01-common name could not be determined with research
Sample 6-Capitellidae sp. CMC01-common name could not be determined with research

Methods and Materials

The samples of Marine worms were collected for the DNA barcoding from both the North Shore and South Shore on Long Island. There were 11 samples collected, but after amplification, 6 feasible ones remained to be sent for sequencing. Photographs of each were taken when in their natural habitat and in the lab. A sample of the surrounding water was also collected, so that the water salinity could be tested. Once the specimens were collected and documented, the DNA was isolated and amplified. To begin the amplification through the process of PCR, the samples were broken down and isolated through multiple steps of using aliquot distilled water, lysis solution, silica resin, and wash buffer. The purpose of isolating the DNA was in order to purify it so that it could be used for amplification.

Finally, to amplify a specific region of the mitochondrial genome by polymerase chain reaction, the PCR tubes were be placed in a thermal cycler. Then, the PCR products were analyzed by gel electrophoresis and thee samples that amplified the best were sent out to a company known as "Genewiz" for sequencing. The sequences were input into DNA Subway where the collected marine worms' DNA sequences were trimmed and analyzed which allowed for proper data interpretation.

In order to find salinity we used three methods. A hydrometer, a refractometer, and a YSI conductivity sensor.

Discussion

The results of this experiment did not correspond with the predicted hypothesis. Water from the South shore did have a higher salinity than that of the North Shore, but the phylogenetic trees created demonstrated a similarity in the biodiversity of marine worms in both the North and South shores of Long Island, rather than there being a higher rate of biodiversity in the North Shore. As with most experiments, there were several areas in which error and/or mistake could have influenced the results. First off, the more samples collected, the more accurate results are likely to be. There was a very minimal amount of marine worms collected in this experiment, making it difficult to really qualify a rate of biodiversity with only three marine worms from each area. Also, of the small number of worms that were collected, only about half were able to be sequenced and used for the phylogenetic trees. If more samples had been sequenced, more accurate and maybe different results would have been observed. In addition, there was a large room for error when collecting the marine worms, as it was difficult to keep variables in nature consistent for both collection sites. The temperature, windiness, and cloudiness were different between the collection sites in the North Shore and the South Shore. Different weather conditions could have influenced how many samples were collected and what kinds. Lastly, the validity of an experiment's results can always be improved when multiple trials are carried out. This experiment only had one trial, making the results less accurate. Although there could have been several errors within this experiment, it was still successful in serving as a stepping stone for further barcoding projects concerning biodiversity not just on Long Island, but anywhere. The collection and laboratory procedure used can serve as a basis for future studies of marine worms and how salinity may affect their biodiversity.

References

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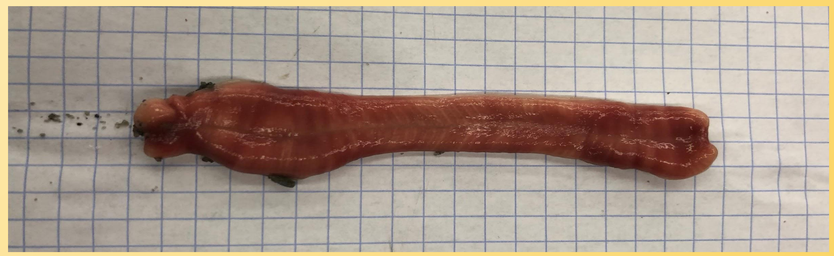

The above picture shows one of the many marine worms collected for the purpose of this barcoding project.

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