

Invertebrates In the Long Island Sound vs Huntington Bay

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Abstract:

Invertebrates are organisms that don't possess a backbone. This experiment is meant to compare the diversity and density of invertebrates in the Long Island Sound versus Huntington Bay. While it was obvious that both environments would have an ample number of invertebrates for collection, it was predicted that the Sound would have a greater density and diversity of organisms than the Bay. While the fact that the Sound is a much bigger body of water than the Bay may be a reason for a differences in results, it was predicted that the environmental characteristics of the Sound would be better for a large population of invertebrates than the Bay. This is because the sample area of the Sound was at the mouth of a marsh, creating perfect conditions for mollusks such as snails to thrive. After the invertebrates were collected, amplified, and sequenced, only three of fourteen samples yielded DNA. Due to poor storage techniques and time limitations, only three of the samples showed DNA when run through an electrophoresis gel. While DNA couldn't be used to analyze results, simply observing the diversity and number of organisms collected can show the greater diversity of invertebrates in the Sound. Not only was it much easier to find organisms in the Sound sample area, there were many different types of invertebrates while the samples from the Bay consisted of only two different species.

Introduction:

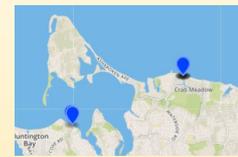
This experiment is made to determine the similarities and differences in microorganisms found in the Sound versus Huntington Bay using DNA barcoding. "DNA barcoding is a fast, accurate, and standardized method for species level identification, by using short DNA sequences"(Kumari 1). "Short DNA barcodes, about 700 nucleotides in length, can be quickly processed from thousands of specimens and unambiguously analyzed by computer programs"(DNA Barcoding Homepage). It is extremely helpful in identifying a variety of species in any environment, and is used in labs around the world. Although DNA barcoding can be used on nearly any species, this experiment is focused on barcoding marine invertebrates to compare the diversity and density of invertebrates in two different environments.

Invertebrates are essentially organisms that don't have a backbone. These organisms can come in many shapes and sizes, but the most common invertebrates in the sample areas are predicted to be mollusks. Mollusks usually "have a soft body and a hard or "calcareous" shell(marinebio 1), and can be found in every habitat found in the ocean. While there aren't many scientific experiments involving invertebrate diversity in the Long Island Sound or Huntington Bay, it is predicted that the samples area in the Sound will have a greater organism diversity and density due to differences in environment.

The environmental factors surrounding invertebrates can cause them to develop traits and dependencies that differ from those in another environment. Two different environments that may shape how invertebrates evolved or selected a habitat are the Long Island Sound and Huntington Bay. While connected, the two bodies have different environmental factors such as temperature, seabed (rocks, mud, sand at the bottom of the water), and size. With the area of the Long Island Sound at 1,320 square miles, the Sound is much larger than the bay(Long Island Sound Study 1). It is predicted that the Sound will have more species variety and organism density as the sample area is a marshland opening into the Sound. This marshland will provide a better habitat for specific organisms while the open water of the sample area in Huntington Bay will support other organisms.

Materials:

- 20 sample tubes
- Seining net
- Small Shovel
- 2 1 gallon buckets
- Rubber gloves



Methods:

Collection: Samples will be collected with a seining net held by two people at both locations. The net will be passed at the same location until 7 samples have been retrieved from each location. In the event that the net does not yield any samples, samples will be found in shallower water using gloves. Collection will take place simultaneously at both locations to ensure as many environmental constants as possible. A variety of invertebrates will be collected, and types of invertebrates will be compared after sequencing.

Sequencing: After collecting the samples, the DNA will be isolated by using the Silica DNA Isolation. This is started by grinding that sample in a lysis solution. Silica resin will be used to extract the DNA while leaving behind the larger sample pieces. Buffer will be added to the resin to purify DNA before amplification. The DNA will then be amplified using the COI primer set and put in the thermal cycler for multiple cycles at varying temperatures. The products are then put on ice until the next step. The amplified DNA is then analyzed using gel electrophoresis. Once it is verified that the DNA was amplified correctly, the DNA is sent off to GenWiz.

Results:

Ultimately, the experiment resulted in a failed gene sequencing. Although DNA could not be amplified from our samples we were able to analyze the diversity of each environment from a phenotypic standpoint. There was wider variation of collected species in the Long Island Sound than Huntington Bay. What phenotypically appeared to be 4 separate species were collected from the Long Island Sound, while only two phenotypically classified species were collected from Huntington Bay.

Discussion:

While the collected samples were unable to be genotypically confirmed, phenotypical analysis provides insight on what results may have shown had we been able to amplify DNA. There was a greater variety of species collected in the Long Island Sound, showing that it may be a more diverse habitat for marine invertebrates than Huntington Bay. The fact that it was much easier finding samples in the Sound also leads to the conclusion that the collection area of the Sound has a greater density of invertebrates than that of the Bay.

Acknowledgements:

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