The Effect of Different Post Locations on Finding Various Marine Invertebrates

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Abstract

This project's goal was to find marine invertebrates at different posts. Researchers hypothesized that if samples were collected near a cement post, there would be a greater abundance of marine invertebrates because a study by Zajac et al., (2000) stated the greater amount of species were found in mud and mixed rubble. A cement post is closer to mixed rubble. 20 samples of marine invertebrates were collected at three different posts (wood, cement, metal) and barcoded to try to identify the samples. 10 samples were approved for sequencing and many samples were not pure enough which resulted in poor sequencing, aside from 2 samples. The 2 samples refuted the hypothesis because they were found near wood posts. These results could show a problem of the lack of diversity near specific areas because if organisms cannot feed near posts other than wood, the whole food web could be at risk.

Introduction

- By finding the biodiversity of animals using DNA barcoding, scientists can expand their knowledge of the ecosystem.
- If macroinvertebrates die out due to dredging and human pollution, the entire food web of Long Island's ecosystem could be jeopardized.
- It was hypothesized that if samples were collected near a cement post, there would be a greater abundance of marine invertebrates because a study by Zajac et al., (2000) stated the greater amount of species were found in mud and mixed rubble. A cement post is closer to mixed rubble.
- The purpose of this investigation was to expand the knowledge of marine invertebrates and how different post habitats can affect the marine diversity on Long Island.

Materials & Methods

Sample Collection: On October 13, 2016 researchers collected marine organisms at Gardeners Park in Bay Shore, New York. According to figure 1, this shows where we collected samples at three sample locations.

Figure 1: Where we collected our samples.

Documentation: While two partners were collecting, the other student was collecting data. According to figure 2, this is the data that corresponds to the data collected. Temperature of the water and the air in degrees Celsius was recorded using a thermometer. Also, pH of the water was measured with a PASCO pH probe measured from 0-14 (1-6 acidic, 8-14 basic). Salinity and other factors typically stayed constant when samples were collected. Air temperature was recorded at every post and every time an organism was collected.

DNA Barcoding: The CSHL barcode protocols were followed and the CO1 gene was used throughout the PCR protocol. DNA subway was used to identify the organisms. Also, DNA subway was used to see if the DNA submitted was sufficient enough to barcode.
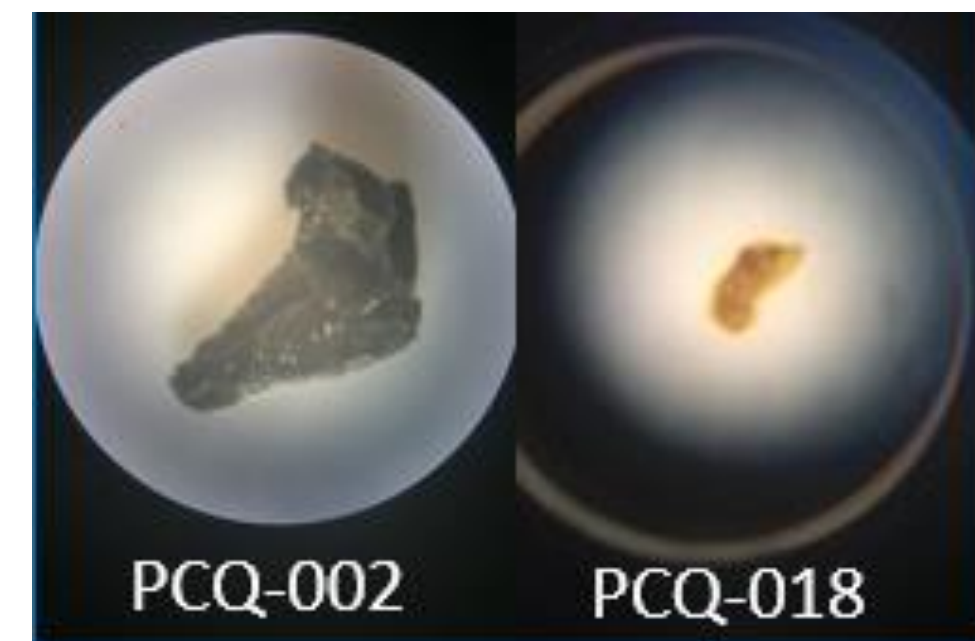

Figure 2: These are pictures of our samples after we collected them. We took pictures of the samples under a microscope.
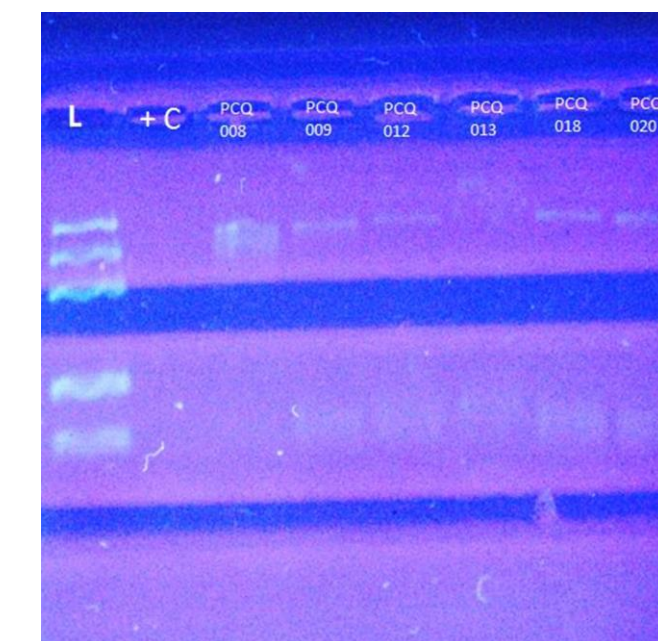

Figure 3: Sample PCQ-018 was sequenced and approved from CSHL from these gel results.

Table: Metadata and DNA Subway data collected for each sample that was sequenced

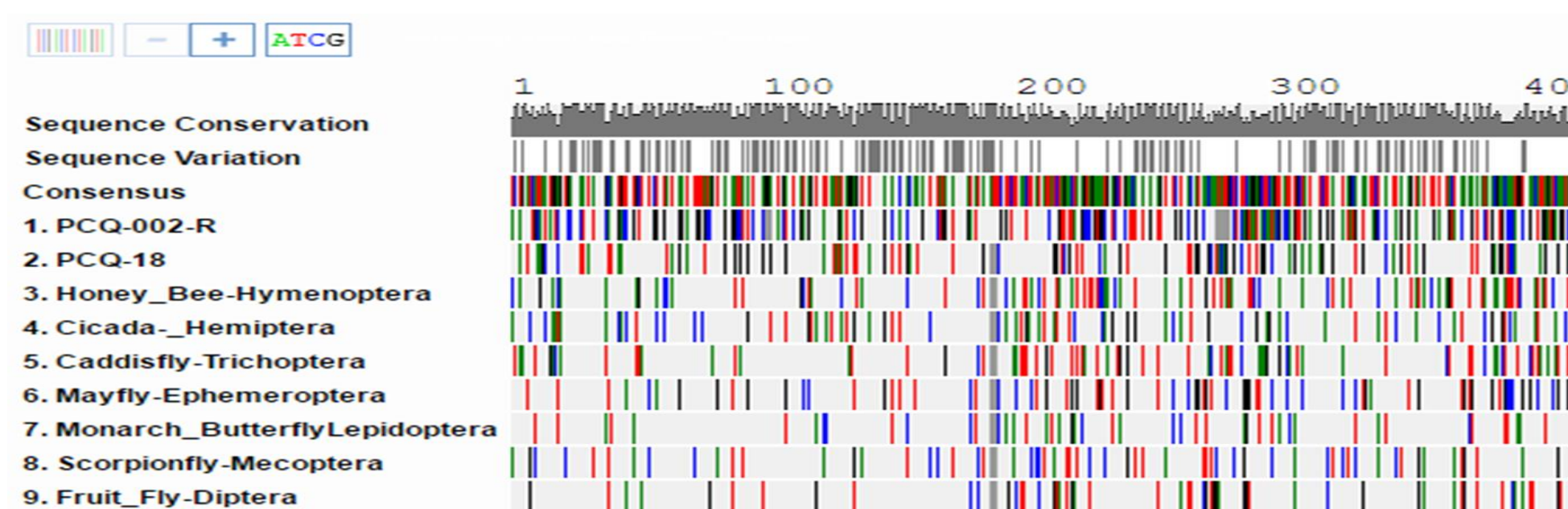| Sample ID	Location	Common Name	pH	Habitat	Water Temp. ºC	Post Type	Water Salinity ppt	Bit Score	e value	Mis-matches	Scientific name
PCQ-002	40º 41'35" North	Worm	7.2	Bay Water	6.6	Wood	29	562	1e-156	85	Polychaeta environmental
PCQ-018	40º 41'35" North	Shrimp-Like	7.2	Bay Water	6.6	Wood	29	746	0	5	Cliona celata

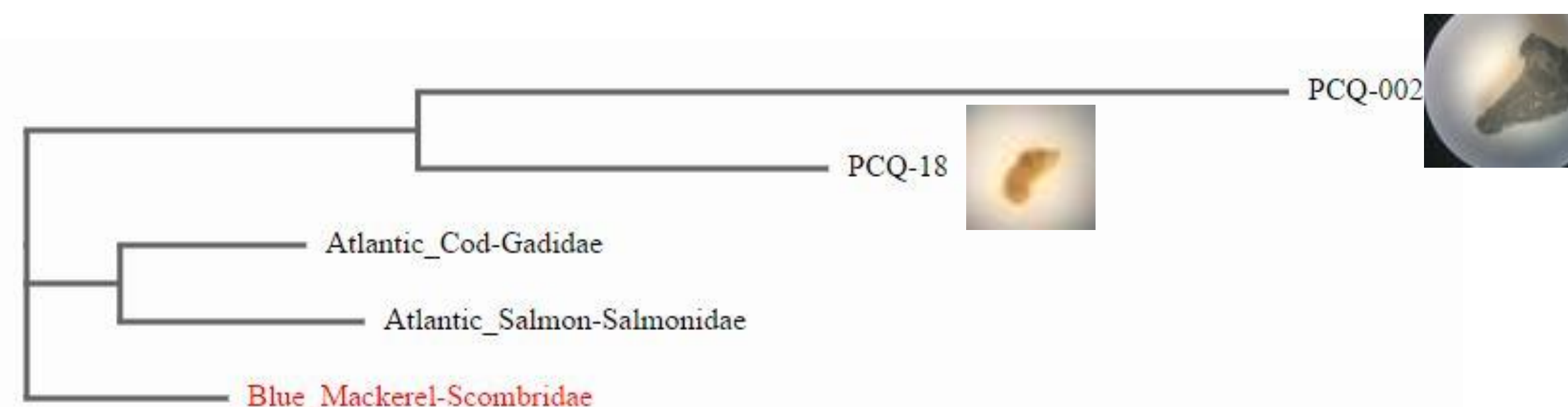Figure 4: This alignment is where we compared our results to other samples.

Figure 5: The Phylogenetic Tree shows that our samples are more closely related to each other than to the reference samples.

Results

- Only two samples were sequenced because the quality of the other eight sources were not good.
- Sample PCQ-002 had an e- value of 1e - 156, a bit score of 562 and 85 mismatches. Sample PCQ-018 had an e-value of 0, a bit score of 746 and 5 mismatches.
- The e-value of 0 showed that the results were not by chance and rather because of the data entered. Any e-value of 1 or greater means that results were possibly determined by chance and not because of data entered.
- The bit score was the score of the alignment, so the higher the bit score the better the alignment.
- The number of mismatches showed that one sample was not really different from other samples.

Discussion

- Unfortunately, there is not enough data to refute or support the hypothesis but the 2 samples collected were found near wood posts which is different than the suspected cement posts.
- One reason why only 2 samples were approved was because the samples were not crushed enough. To ensure sufficient DNA for sequencing in the future, the samples would have to be crushed more in order for the DNA to be pure and the extraction to be more effective.
- The results approved and unapproved should be experimented multiple times to ensure that future errors will not occur and that the results are true and valid. The more samples that are sequenced, the more valid our results become.

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