The Biodiversity of Marine Macroinvertebrates in a Creek Adjacent to a Power Plant

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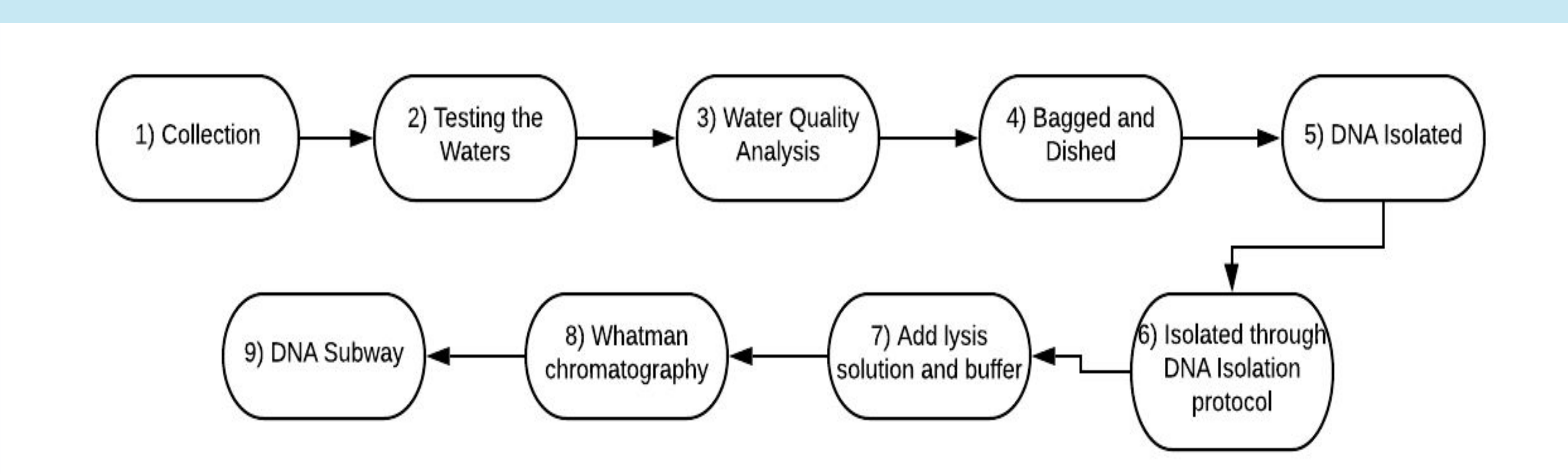
Abstract

The Shoreham nuclear power plant was finished in 1984 in hopes to light 500,000 homes, but ultimately it failed. This power plant never truly operated because of mass protests due to rising costs and environmental issues. The building of Shoreham power plant is believed to have caused immense devastation to the environment and affected factors such as biodiversity and water contamination. Through analysis of macroinvertebrates in this environment, results exemplifying the decrease of biodiversity is believed to be true. Due to the development of a power plant, it is believed that biodiversity increases s as distance increases from the powerplant.

Introduction

- The nuclear power plant built in Shoreham, Long Island was completed in 1984, this nuclear power plant that was initially sold as a solution for a power-hungry island sparked controversy.
- Many power plants across the nation exhibit influence on the surrounding wildlife.
- Whilst wildlife may be affected throughout the operation of the nuclear power plant, majority of the influence derives from building the plant.
- Building this powerplant released such an immense amount of radiation because of the uranium that was mined for fuel.
- Although the fuel was never used throughout operation, the presence of uranium caused an output of radiation.
- The process of mining and refining the uranium ore and producing the reactor fuel, requires a large supply of energy (Weisser, 2007).
- When building a power plant, mass amounts of carbon dioxide are emitted during construction. This is because nuclear power plants use uranium as fuel. The presence of uranium can cause a copious amount of radiation of the surrounding vicinity.
- It is hypothesized that the biodiversity of the macro invertebrates is significantly decreased the closer to the nuclear power plant.

Materials and Methods

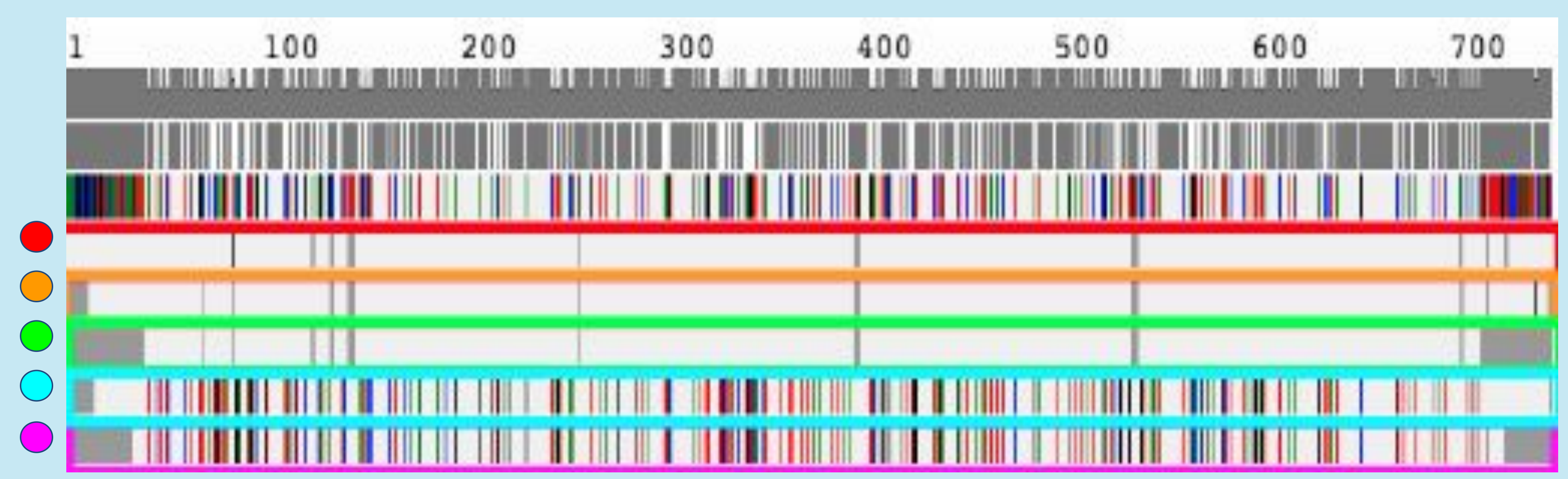


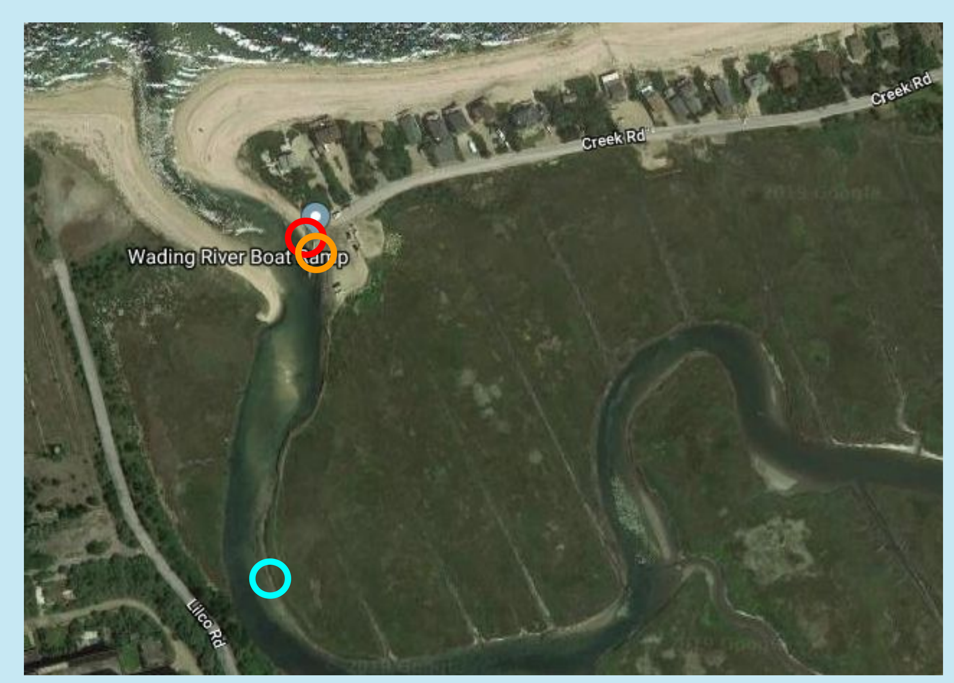
Results

Results are presumed to be that as distance increases from the power plant, the biodiversity of macroinvertebrates increases as well. Additionally, the cause of the vast curvatures within the rivers and land, are hypothesized to be a direct cause by the building of the nuclear power plant.

Samples 1, 2, 3, 4, 9, 17, 19, and 20 showed no signs of any gel electrophoresis bands. Samples 5, 6, 7, 8, 16, and 18 showed signs of bands within the gel; however, only samples 6, 7, 10, and 18 were accepted. After retrieving data to BLAST the sequences, we discovered that sample 18 did not sequence. The samples and their relation to other marine organisms are shown below

Tables & Figures





Sequence Similarity (%)

	C	XMX_006	XMX_007	SB	XMX_010	CC
C	-	99.18	99.72	99.70	74.38	72.91
XMX_006	99.18	-	99.17	99.70	73.00	71.75
XMX_007	99.72	99.17	-	99.85	73.48	72.16
SB	99.70	99.70	99.85	-	71.12	71.27
XMX_010	74.38	73.00	73.48	71.12	-	99.71
CC	72.91	71.75	72.16	71.27	99.71	-

C - Consensus

SB - Semibalanus Balanoides

CC - Chondrus Crispus

Discussion

The original purpose of this research was to analyze the biodiversity of the macroinvertebrates in a creek adjacent to a nuclear power plant. Through DNA barcoding we were able to successfully obtain the barcodes of three of the twenty samples collected. Although we are not able to draw a conclusion on the biodiversity based on just these sequences, it is evident based on the samples we were able to identify visually that the biodiversity of the macroinvertebrates decrease as the distance from the powerplant decreases.

However, through this process we were able to make the conclusion that it is imperative to look at more than just one gene sequence to successfully identify an organism. We were able to visually identify XMX_006 as a barnacle through our prior knowledge of macroinvertebrates and XMX_007 as a mud snail. However, when we analyzed the DNA sequences of these samples, a 99.17% sequence similarity was shown. Generally we would have utilized that sequence to identify which organism it is but since we are fully confident that these two samples are two different organisms it is clear that a single sequence cannot determine the organism. Therefore, simply looking at one gene (CO1 Gene) is not sufficient to distinguish organisms.

References

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