



The Effect of Cadmium on the Biodiversity of Benthic Organisms



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Abstract

Cadmium is known to be toxic and detrimental to the health of organisms. One of the effects of cadmium is the potential link to cancer. The purpose of this experiment was to investigate how cadmium in the sediment of ecosystems affects the biodiversity of organisms in that area. It was hypothesized that there will be less diversity of organisms in areas that may have been exposed to cadmium pollution. Samples were collected from Gardiner Park (control) and the West Islip Beach (site adjacent to a past area that tested positive for low levels of cadmium). Additional metadata was collected during field research. DNA was found during extraction, then the CO1 gene was amplified by PCR. Positive samples after electrophoresis were sent for sequencing. After analyzing the DNA in DNA subway, 3 organisms had a large number of mismatches meaning they may be considered to be potentially new barcodes. There are more non barcoded organisms in Gardner Park which could lead to the conclusion that this cadmium free area can allow for more new organisms to inhabit leading to greater biodiversity.

Introduction

❖ Cadmium is known to be toxic and detrimental to the health of organisms. Cadmium is a priority pollutant, because of the ease with which it is bio-accumulated, due to its toxicity (Warren, Tessier, & Hare, 1998). Due to recent flooding, the EPA found increased cadmium in soil near our school from the Dzus Fastener Company.

❖ We believe the biodiversity of benthic invertebrates may be greatly affected, if cadmium and other pollutants are absorbed by the tissue of organisms. We compared biodiversity just south of a known polluted area to an area that was not polluted to observe the effect of the pollutants. We were not in danger of exposure since the area we tested was not part of the EPA danger area. If cadmium does affect biodiversity, we expect to find great diversity in the species of organisms found in the non-polluted areas, and very little diversity among species found in the cadmium contaminated areas (Kandeler, Kampichler, & Horak, 1996).

❖ Cadmium has been linked to causing disease in humans. It also can cause a decrease in bone mass, and can cause early development of osteoporosis (Godt, Scheidig, Siestrup, Esche, Brandenburg Reich, & Groneberg, 2006). In benthic organisms, scientists have found that elevated exposure to cadmium causes bivalves' mitochondria to decrease in resistance to hypoxia and reoxygenation (Ivanina, 2012). Cadmium affects benthic organisms because the cadmium seeps into the ground and is absorbed by the tissues of organisms. This can affect the ability of the organism to intake oxygen from the water.

❖ We collected organisms from a public park, on the south shore of Long Island, Gardiner's Park. Benthic organisms were collected from the Great South Bay, and this served as the non-polluted area. Our organisms from a possibly polluted source were extracted from where Lake Capri drains into the Great South Bay, as seen in Figure 1. After analyzing organisms' results from DNA Subway, we will determine the biodiversity in each of the two areas to see the effect of pollution on the organisms. Therefore, we observed the effect of cadmium on biodiversity of benthic invertebrates in the Great South Bay.

❖ We hypothesized that if different organisms are exposed to cadmium in each area, then biodiversity will be severely impacted. As stated, if organisms are more tolerant to cadmium than others, they will have much greater populations in the affected areas. This is bad, because a lack of biodiversity means that the ecosystem is very unstable.

Methods and Materials

❖ Sample Collection: We arrived at Gardiners Park, located posts in the Great South Bay, then measured a 6 inch quadrat around the post. After sifting through the mud, while using a seine, and a sediment corer, we collected samples of mud from different posts and labeled the test tubes we put the mud in. We collected any organisms that were less than 10 millimeters and stored them in plastic tubes.

❖ Sample Documentation: We took pictures of the organisms we collected, showing great detail. Next we placed the organisms into test tubes, and froze the samples until we were ready to extract DNA. We labeled the tubes based on the order in which the organisms were collected, and which site we obtained the organism from. This helped us to identify which organism was what, when extracting DNA.

❖ DNA Collection: To start DNA extraction, we crushed apart our specimen, then incubated it, and centrifuged. The next day, we used washed buffer, to clean it out, and then once again centrifuged. On the third day of DNA extraction, we set up the agarose gel. As that was cooling, we did PCR for our extracted DNA to copy the CO1 gene. On the final day of DNA collection, we did electrophoresis, and then viewed the gel results on a UV Trans-illuminator.

❖ Data Interpretation: DNA sequences will be analyzed in DNA Subway, for future research. We will then see how the biodiversity differs between the affected and unaffected areas. Metadata was collected in a data table to make sure that both collecting days are similar in outside variables, and that biodiversity is not due to other factors besides contamination.

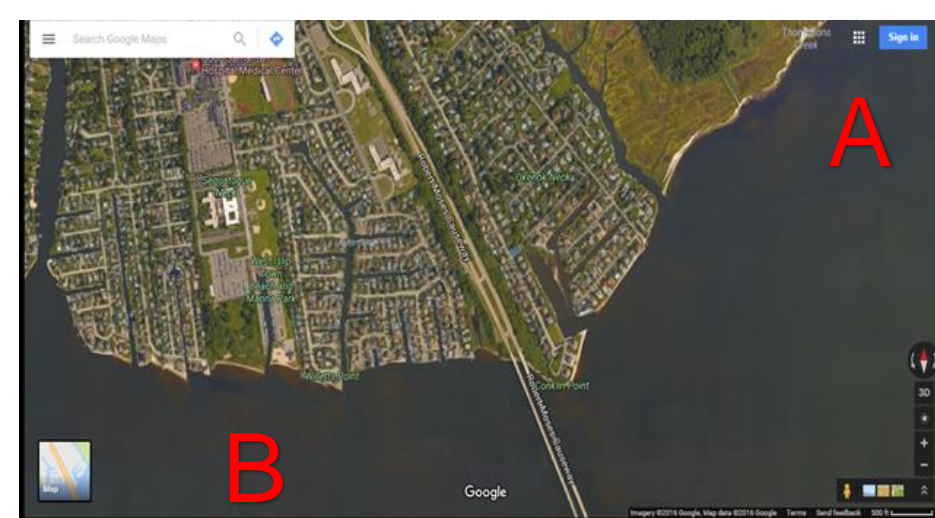


Figure 1: Collection site A located at Gardiners Park. Collection site B is located at West Islip Beach

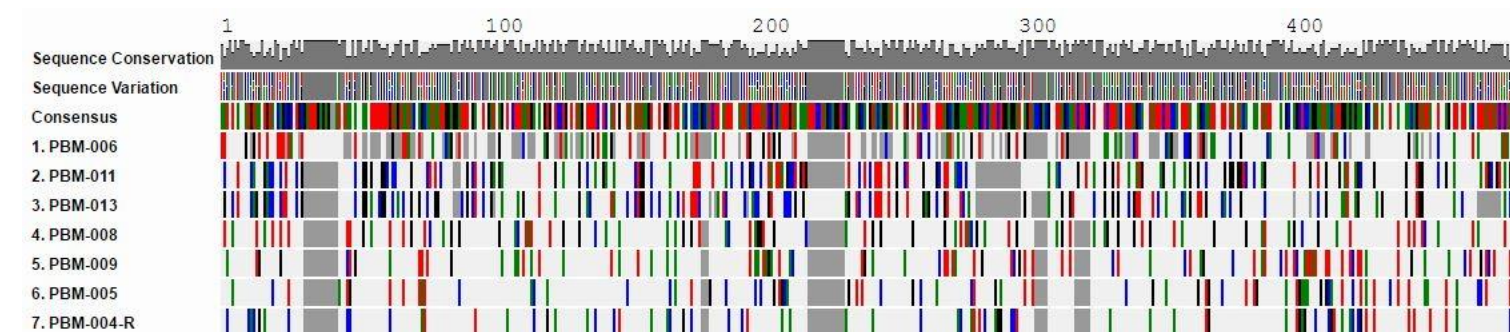


Figure 2: DNA sequences of all samples

Results

There were four samples sequenced in the control site and there were three samples sequenced from the cadmium site. The results also told us that there were two suspected novel organisms from the control site and one from the cadmium site. This is shown by the high amount of mismatches in the suspected samples.

Table 1: Samples collected from Gardiner Park (control site).

Sample ID	Common Name	Latitude	Longitude	Posts Description	Bitscore	E Value	Mismatch	Scientific Name
PBM-004	Worm	40.69N	-73.29W	Wood	711	0.0	116	Unknown
PBM-005	Slug	40.69N	-73.29W	Wood	1124	0.0	1	Crepidula convexa
PBM-006	Tube Worm	40.69N	-73.29W	Wood	244	7e-61	21	Parvamoeba rugata
PBM-008	Worm	40.69N	-73.29W	Wood	1040	0.0	53	unknown

Table 2: Samples collected from West Islip Beach (suspected Cadmium site).

Sample ID	Common Name	Latitude	Longitude	Post Description	Bitscore	E Value	Mismatches	Scientific Name
PBM-009	Moss	40.69N	-73.29W	Wood	1180	0.0	0	Nematoda sp.
PBM-011	Snail	40.68	-73.28	Wood	733	0.0	116	Unknown
PBM-013	Snail	40.68	-73.28	Wood	248	3e-62	96	Oleiphilus sp.

Discussion

- ❖ We received results because the DNA in our organisms was sent to Cold Spring Harbor Laboratories, where they used an evaporator to concentrate the DNA and get results.
- ❖ We expected to find a lack of biodiversity at our second organism collection site, however we have to wait for our sequence results from CSHL to see if biodiversity appears similar at both sites.
- ❖ Aside from DNA, biodiversity seemed to be limited at the second organism collection, based on the appearance of the organisms. Many of these organisms looked similar to each other, and had hard outer shells, like snails. Whereas at the original test site, there were no organisms we collected which looked similar to a snail. Therefore, our hypothesis may be supported, pending DNA sequencing results.
- ❖ Many days we wanted to collect organisms, it was too cold, or raining so it made it difficult to collect good quality samples. We were forced to take some samples that were not as good as the samples we originally obtained at Gardiner's Park.

Future research

- ❖ We can go to collect samples during a different time of year, when it's warmer outside, so it would make it easier to collect more samples.
- ❖ For future research, we could collect from more than just two sites, so we can get more results, that can help explain our results more thoroughly, as well as add more data to our experiment.
- ❖ Lastly, we can follow the DNA extraction procedure much more carefully, to increase our chances of receiving results without using the evaporation method at CSHL.

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Acknowledgements

We want to thank the scientist at CSHL for all of the help they gave us during our project. We also want to acknowledge Mrs. Kroll, our science research teacher, and all of the other science teachers that helped us collect samples.

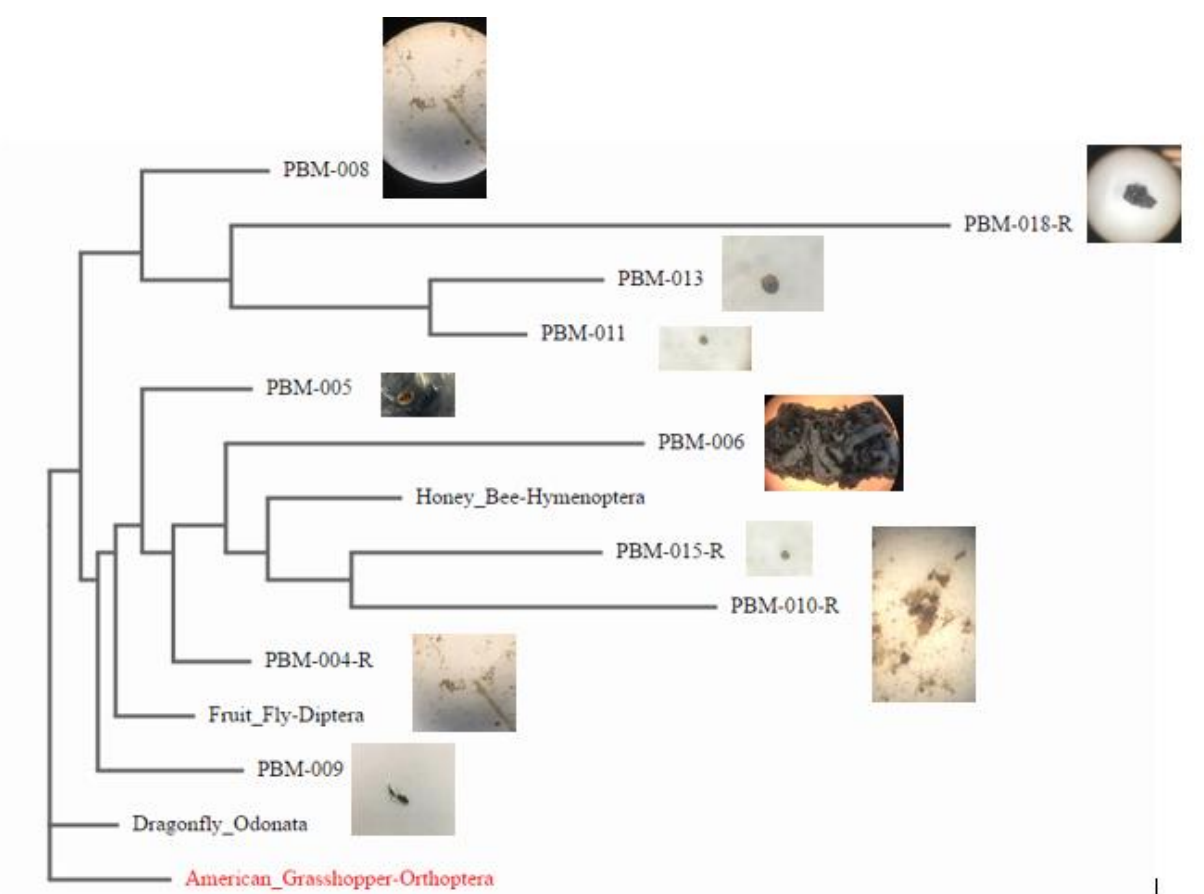


Figure 3: Phylogenetic tree of our organisms compared to reference organisms