# The Use of DNA Barcoding Techniques to Determine Biodiversity of Algae in the Great South Bay, Long Island, NY



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### Abstract

Within Long Island waters, macroalgae are an integral part of the many dynamic ecosystems present. Macroalgae can contribute to algal blooms, which are detrimental to human health and marine ecosystems. The purpose of this study was to identify species of algae present in the Great South Bay (GSB), determine nativity, and investigate links to algal blooms. Researchers gathered twenty samples of algae from the GSB. Metadata, such as water and air temperature, salinity, humidity, and nitrate levels were also collected at each site. Researchers extracted the DNA from each sample, performed PCR on the rbcl gene, and ran it through electrophoresis using techniques learned from DNAbarcoding101.org (Cold Spring Harbor DNA Learning Center, 2014). Ten out of twenty samples were sent to Genewiz for sequencing and the data was analyzed using DNA Subway. Four species were identified and they were all native to Long Island. These results refuted the hypothesis that the GSB has a large degree of algal biodiversity.

#### Introduction

- Macroalgae are an important part of the Long Island ecosystem, and can be a source of food for some animals, but some can also produce harmful toxins or contribute to algal blooms in different bodies of water. Algal blooms and toxins produced by the algae can harm marine ecosystems as well as human health.
- Our research can be classified as unique considering that no other scientists have barcoded and determined the specific species of macroalgae in the Great South Bay, while also determining if they are native or non-native species.
- The barcoding and identification of macroalgae in the Great South Bay has significant scientific importance because it can allow scientists to link certain species with harmful algal blooms as well as determine if they are non-native species. This research could potentially lead to the implication of certain procedures that could, in turn, hinder certain algae species from flourishing in the Great South Bay.
- The purpose of this study was to identify different species of algae and determine if they are linked to algal blooms as well as if they are native or non-native species. This study will also seek to determine that if the algae species are invasive, what impact they might have on the Great South Bay ecosystem.

### Materials and Methods



Figure 1: Map indicating the areas used for sample collection in Gardiner Park. Photo taken from Google Maps.





Figure 2: Members of Kelp Company collecting samples of algae in the Great South Bay using a strainer and scissors. Photo taken by researchers.



Figure 3: Scientific After pictures were

## **Results:**

- According to the data obtained through DNA Subway, researchers collected four different species out of the ten samples sent to be analyzed.
- The species identified included: Ulva flexuosa, Zostera marina, Valonia sp. and Ulva compressa (Table).
- The barcodes that were made were of a high quality and were deemed reliable.
- All the species identified in the study were common in Northeastern Atlantic waters.

Table: Metadata collected and the results of each sample analyzed using DNA Subway.

ample ID	Habitat Description	pH of Water	Salinity of Water (ppm)	Nitrates (ppm)	Water Temp (Celsius)	Bit Score	E Value	r ma
PCN- 001	Shallow river bank	6.2 to 7.0	25.6	0.0 to 2.5	16.6	917	0	7
PCN- 003	Shallow river bank	6.2 to 7.0	25.6	0.0 to 2.5	16.6	928	0	5
PCN- 004	Shallow river bank	6.2 to 7.0	25.6	0.0 to 2.5	16.6	1002	0	3
PCN- 005	Shallow river bank	6.2 to 7.0	25.6	0.0 to 2.5	16.6	1029	0	2
PCN- 006	Muddy shoreline	8.4	25.6	0.0 to 2.5	16.6	825	0	18
PCN- 009	Rocky, sandy shoreline	8.5	27	0.0 to 1.0	18.8	1081	0	0
PCN- 010	Rocky, sandy shoreline	8.5	27	0.0 to 1.0	18.8	1050	0	7
PCN- 012	Cove	8.4	26.3	0.0 to 2.0	18.4	1061	0	3
PCN- 013	Cove	8.4	26.3	0.0 to 2.0	18.4	1052	0	3
PCN-	Shallow Inlet	8.1	28.3	n/a	19.9	1054	0	3

picture was for PCN-017. taken, DNA extraction procedure detailed by CSHL was followed. *Photo* taken by researchers.





Figure 4: Isolated rbcl gene for ten out of the twenty algae samples collected. Both PCR and Electrophoresis processes were conducted to obtain these results. The acceptable samples were sent to CSHL to be sequenced and were analyzed in DNA Subway. Photo courtesy of Cold Spring Harbor Laboratory's DNA Learning Center.

#### Discussion

- species.

- to the coast.
- areas with a greater concentration of algae.
- characteristics of the species found.

#### References

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Lvellia aspera-Polytrichale



• The results refute the original hypothesis of the study, due to the fact that the samples collected are all common to North America. They also refute the hypothesis by showing that out of many samples, there were only four different

• Although these species were non-invasive, these species were all very closely related (Fig 5).

• The phylogenetic tree shows that many samples obtained either share a common ancestor or are the same species. • This lack of biodiversity could be hazardous to human health. A lack of biodiversity means that large parts of ecosystems can easily be damaged by disease, toxins, or abiotic factors. If this were to happen, the economy of the island would be harmed and toxins that could build up in organic matter could pose a significant risk to those who go

• However, nitrate levels found around the collected samples were extremely low. This could be a cause of the small amount of algae found near the actual collection sites. The nitrate levels (toxins) would most likely be a problem in

• For future study, researchers may investigate algae species in other locations, the low nitrate levels, and

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