LONG ISLAND

### INTRODUCTION

- Amphipods are sea dwelling microscopic invertebrates (Hughes & Ahyong, 2016).
- They are an awesome bio-indicator to biologists because they are relatively present in water environments (Hughes & Ahyong, 2016).
- They are small enough that one can get an accurate reading of how the environment is developing, and the impact of chemicals polluting our oceans and bays (Hughes & Ahyong, 2016).
- We chose to barcode amphipods because they are quite difficult to tell apart by just looking at the anatomy of them with the bare human eye (Herbert & Gregory, 2005).
- Amphipods are easily affected by imbalances in water chemistry so by viewing the amphipods present in an environment and viewing the water quality of that same environment, we can see the relation between the two (Podlesińska, & Dąbrowska, 2019).
- Given the close proximity between us and the ocean and bodies of water around us, we affect both the species in the water as they reflect how it could affect us (Podlesińska, & Dąbrowska, 2019).
- The biodiversity of amphipods can tell us information about the ecosystem (Podlesińska, & Dąbrowska, 2019).
- We can also use their biodiversity to tell us if humans are greatly affecting the bay /ocean ecosystem; and figure out ways in which to reduce human impact on the loss of amphipod biodiversity (Podlesińska, & Dąbrowska, 2019).
- The research we are doing on the biodiversity of amphipods will eventually allow us to determine if as humans, we are having a great impact on the bays, oceans, and beaches surrounding Long Island (Kostel, 2014).

# HYPOTHESIS

If the pH (6.5-7.5), water salinity (35 parts per thousand), and dissolved oxygen (7.5 mg/l) are all at stable levels, then the amphipod species will be more diverse and a greater variety of amphipods will be collected.

## METHODS

#### Sample Collection







- Using our hands we searched for the comma-shaped amphipods on washed up coral and driftwood.
- Whenever we came across an amphipod we put it in a purple test tube and labeled it. **DNA Extraction**



To extract DNA we crushed the amphipods inside the test tubes using a pestle.

#### Sample Documentation



To document the amphipods we used a camera microscope to take pictures.

#### **PCR/Electrophoresis**



Electrophoresis was used to help identify if DNA extraction and PCR for CO1 gene worked.

# THE EFFECT OF WATER QUALITY ON THE BIODIVERSITY OF AMPHIPODS

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		Water Quality			DNA Extraction / PCR	
Sample ID	Location	Salinity (ppt)	рН	Temperature (C)	Electrophoresis Results	Positive
XNE-001	Heckscher	26	7	13	negative	
XNE-002	Heckscher	26	7	13	negative	
XNE-003	Heckscher	26	7	13	negative	
XNE-004	Heckscher	26	7	13	negative	
XNE-005	Heckscher	26	7	13	negative	
<b>XNE-006</b>	Heckscher	26	7	13	negative	
<b>XNE-007</b>	Heckscher	26	7	13	negative	
<b>XNE-008</b>	Heckscher	26	7	13	negative	
<b>XNE-009</b>	Heckscher	26	7	13	negative	Negetive Res
XNE-010	Heckscher	26	7	13	negative	90.0%
<b>XNE-011</b>	WI Beach	26	7	10	positive	
XNE-012	WI Beach	26	7	10	positive	
XNE-013	WI Beach	26	7	10	negative	Figure 5: T
XNE-014	WI Beach	26	7	10	negative	got from D
XNE-015	WI Beach	26	7	10	negative	got nom D
<b>XNE-016</b>	WI Beach	26	7	10	negative	
<b>XNE-017</b>	WI Beach	26	7	10	negative	<ul> <li>We did not</li> <li>Results that there was we had not the second secon</li></ul>
<b>XNE-018</b>	WI Beach	26	7	10	negative	
XNE-019	WI Beach	26	7	10	negative	
<b>XNE-020</b>	WI Beach	26	7	10	negative	
XNE-021	WI Beach	26	7	10	negative	
<b>XNE-022</b>	WI Beach	26	7	10	negative	
<b>XNE-023</b>	WI Beach	26	7	10	negative	We think the second secon
<b>XNE-024</b>	WI Beach	26	7	10	negative	We could n
<b>XNE-025</b>	WI Beach	26	7	10	negative	to get to th

Figure 3: Metadata collected for all samples: common name of amphipod, collection elevation 0 feet, samples were collected on Oct. 25, 2019 from Heckscher State Park (Latitude 40 42'1" N; Longitude 73 10'22" W) and on Nov. 11, 2019 from West Islip Beach (Latitude 40 41'15" N; Longitude 73 18'31" W), all samples collected between 8:30am – 1:30pm. Collection site habitats were sand and rocks, exposed ground, algae, flat water, slight slope down to water.

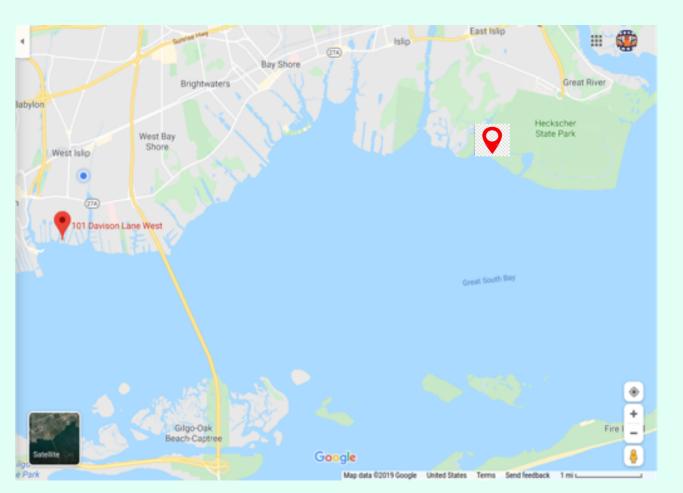
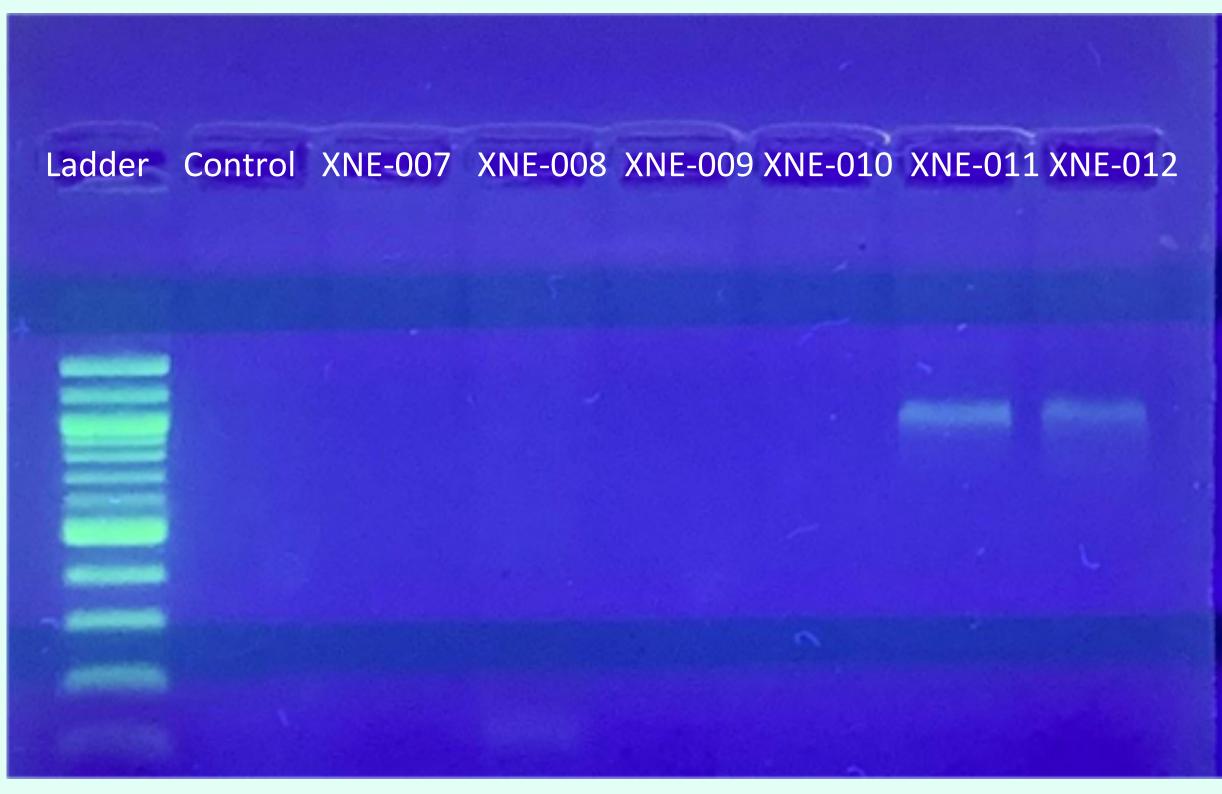


Figure 1: Amphipods were collected from Heckscher Park as part of the "A Day in the Life of a River" program and because location is less influenced by humans compared to the collection location of a beach in our town.



Figure 2: This is a common image of an amphipod and what they look like ("Amphipod").



results.

#### RESULTS

Figure 4: This is an example of our gel that shows our two positive

This chart compares the number of positive results we DNA Extraction and PCR compared to negative results.

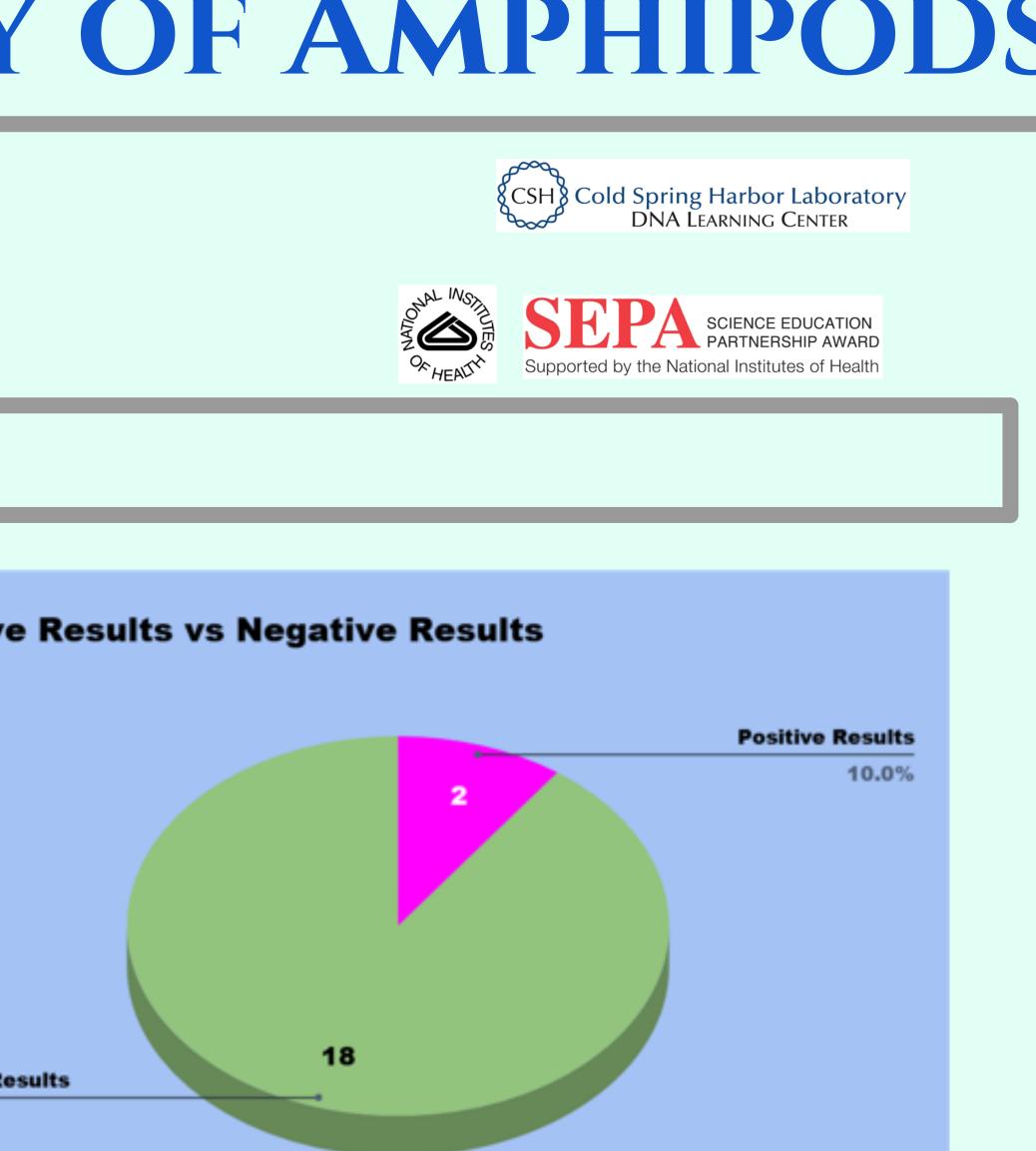
## CUSSION / CONCLUSIONS

- the DNA.

- to complete our research.

- samples.
- bioinformatics.

"Amphipod." Terminix, www.insect.com/pests/amphipod. Hebert, P. D., & Gregory, T. R. (2005). The promise of DNA barcoding for taxonomy. Systematic biology, 54(5), 852-859. Hughes, L. E., & Ahyong, S. T. (2016). Collecting and processing amphipods. Journal of Crustacean Biology, 36(4), 584-588. Kostel, K. (2014, May 18). Amphipods all the way down. Retrieved October 15, 2019, from https://web.whoi.edu/hades/amphipods-all-the-way-down/ Podlesińska, W., & Dąbrowska, H. (2019). Amphipods in estuarine and marine quality assessment—a review. Oceanologia, 61(2), 179-196.



ot get many positive results.

nat were positive had a very faint band, which means that very little DNA extracted from our samples.

this is because the amphipods that we had were very small. not tell if we crushed them completely to open up the cells

• This could help us for our research next year because we now know not to choose such tiny organisms to work with in the future or to find a better way to get DNA from such small organisms.

• We were not able to identify the organisms because we were not able

#### FUTURE RESEARCH

• In the future, to continue this research we would need to collect more

 We would have to keep extracting DNA and going through the process of PCR and electrophoresis until we get enough positive results. • Once we have the required amount of results, we would be able to identify them by their DNA barcode using Sanger sequencing and

### REFERENCES