A Comparison of Macroalgae in the Little Hell's Gate Salt Marsh vs. the East River

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Introduction

- Hypothesis: the salt marsh will contain more species than the East River
- 6000 species of macroalgae but 3
 main categories: red algae, brown
 algae, green algae (Pereira, 2021)
- Algae need brackish water to survive
 includes salt marsh (Sandrin, 2009)
- Algae requires a substrum makes Little Hell Gate Salt Marsh a favorable place (Editor's of Randall's Island Website, Edited 2023)
 - East River is moving body of water so less favorable
- Increased pollution in East River which could have negative effect on biodiversity
- Aim to determine the difference
 between species in East River vs
 Salt Marsh on Randall's Island



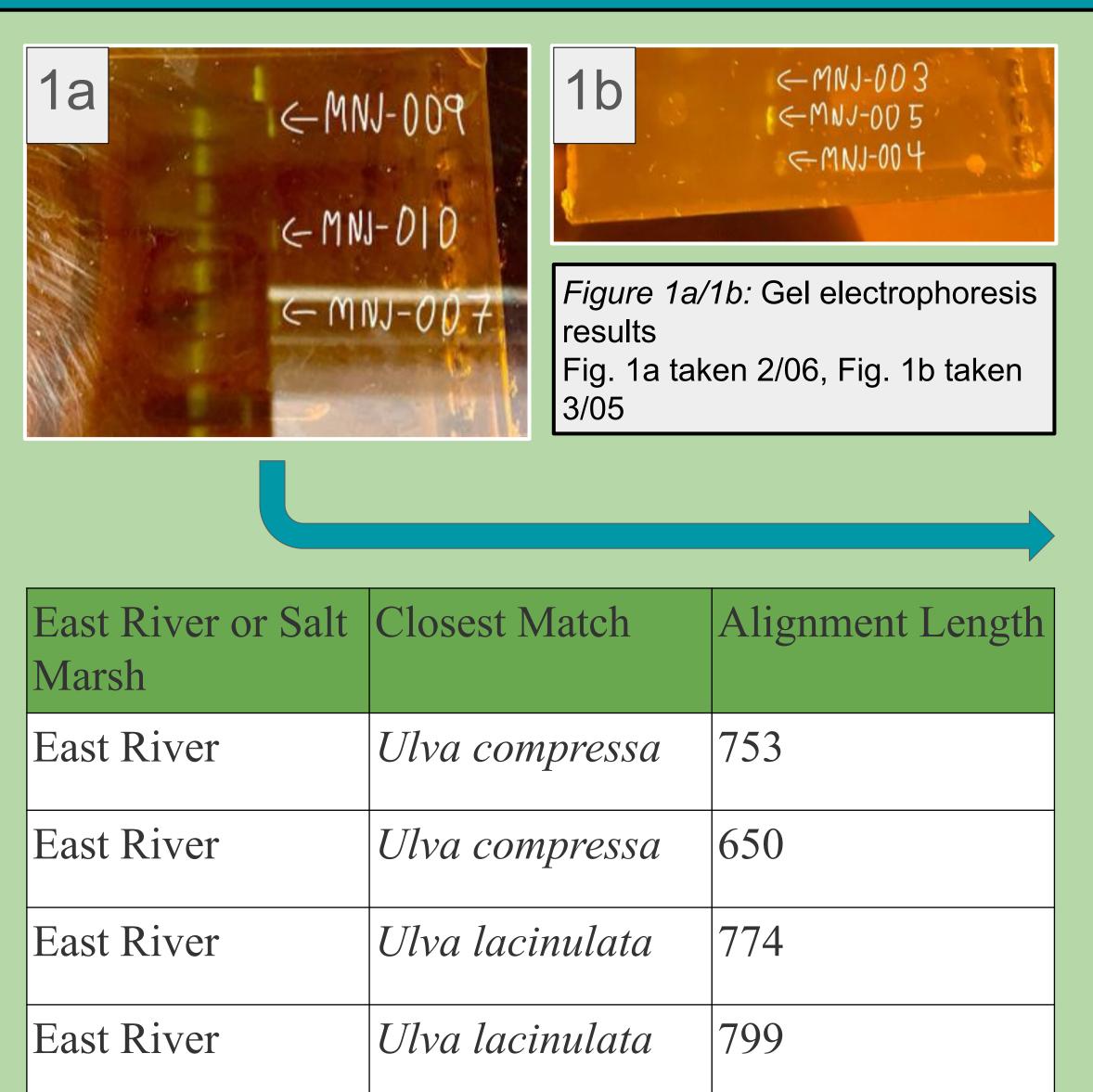




Fucus Ulva lactuca Phylum vesiculosus rhodophyta

Materials and Methods

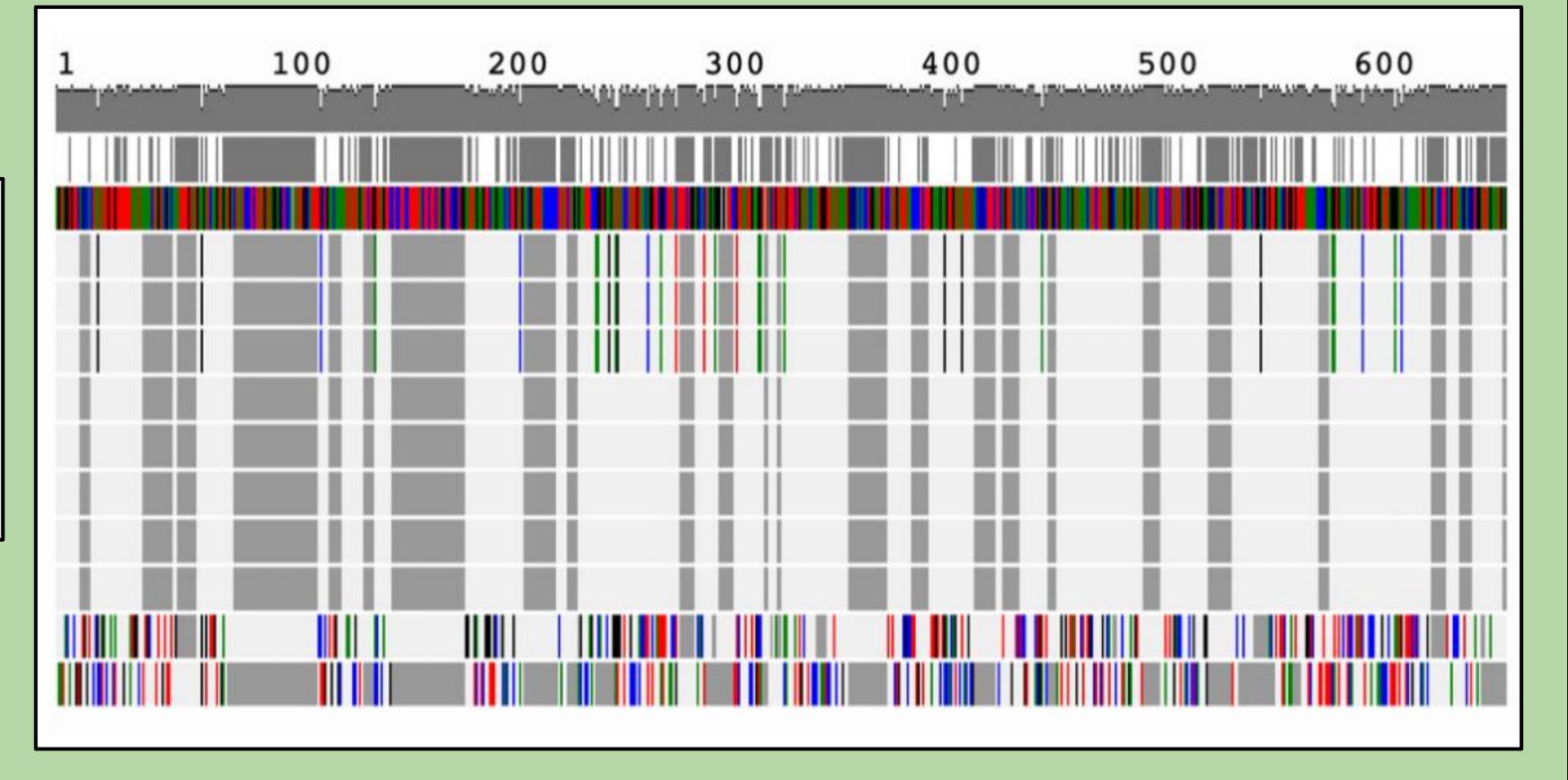
- Twenty-five algae samples collected along two 20-meter transects, one at East River, one along the Salt Marsh.
- Flags were placed at 4 m intervals, and samples were collected at ¼ square meter quadrats placed at each flag interval.
- DNA isolated by centrifuging, lysis solution, silica resin, and an ice-cold wash buffer
- Isolated DNA then amplified via PCR with
 UBP-issued TUFA primer specific to algae
- PCR results analyzed by gel electrophoresis, positive samples to Azenta for sequencing
- Returned sequences entered in BLAST on Cyverse DNA Subway database to identify the species of algae
- Identified species entered into MUSCLE program to align DNA sequences
- Then entered in NJ PHYLIP to create a maximum likelihood phylogenetic tree



East River or Salt Marsh	Closest Match	Alignment Length
Salt Marsh	Unsuccessful	N/A
Salt Marsh	Unsuccessful	N/A
Salt Marsh	Unsuccessful	N/A
Salt Marsh	Ulva compressa	751
Salt Marsh	Ulva compressa	763
Salt Marsh	Ulva compressa	726
Salt Marsh	Unsuccessful	N/A

Figure 2: Results of DNA sequencing

Figure 3: Untrimmed Multiple
Alignment Created by MUSCLE. This
image shows 600 bp of sequence
conservation, with the color
demonstrating different nucleotides. In
both the sequence conservation bar
and the sequence variation bar,
conservation is represented by gray
and variation by white.



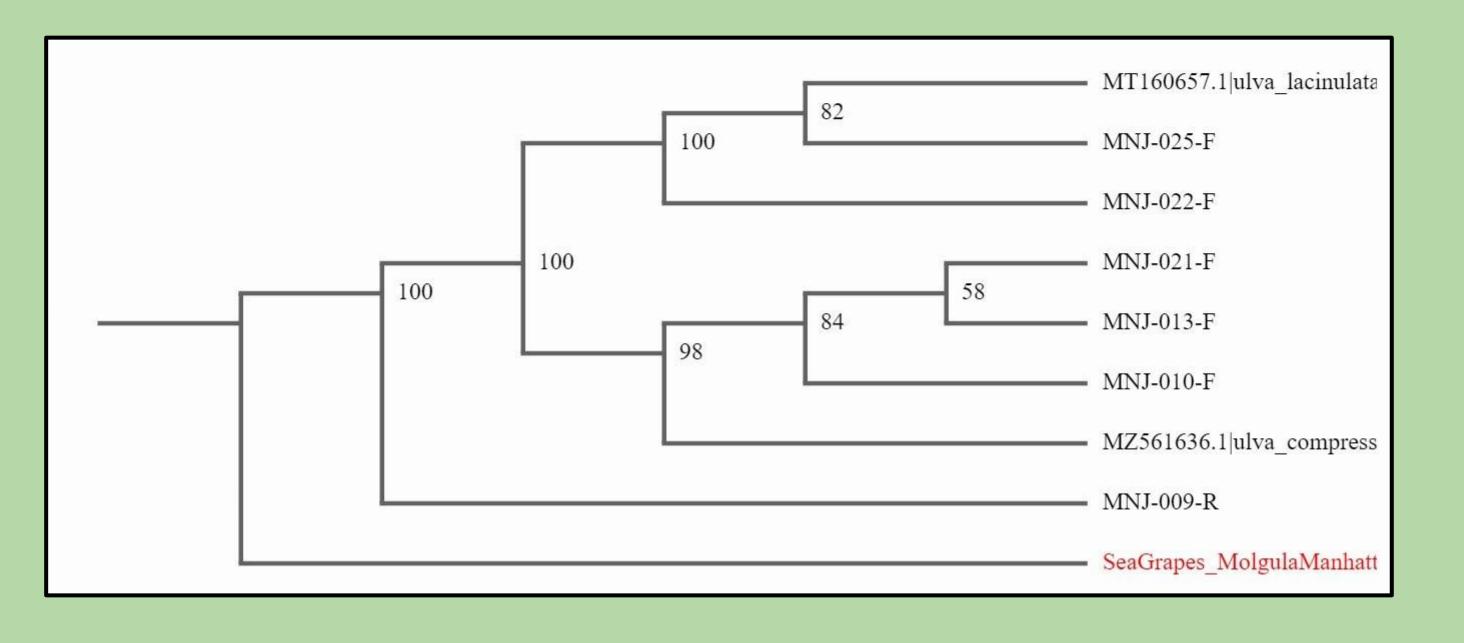


Figure 4: Phylogenetic Tree of Sequencing Results. Neighbor Joining (NJ) phylogenetic tree displaying the evolutionary relationships between the identified species. The species highlighted in red has the least genetic commonalities with the rest of the species.

Discussion

- The results we obtained contradicted our hypothesis
- Hypothesis: the salt marsh will contain more species than the East River
 - increased rocks to attach to, slow-moving water, and less pollution
- One found species in the salt marsh and two found species in the East River
- These results do not support a specific conclusion due to a small sample size
- MUSCLE ⇒ high similarities between samples found to be the same species
- PHYLIP ⇒ high similarities between
 Ulva compressa, similarities between
 Ulva lacinulata
- No red algae was sequenced successfully likely due to the an incorrect primer
 - The tufA primer used is intended for green algae, it may not be as effective with red algae
- The school laboratory had never processed algae samples of any kind

References

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Hewitt, S. J. (2018, November 12). Seaweeds of NYC. INaturalist. https://www.inaturalist.org/posts/19785-marine-macroalgae-of-nyc REFERENCES CONTINUED ON BACK OF POSTER

Acknowledgements

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