Investigating Algal Biodiversity in Little Hell Gate Salt Marsh

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Introduction

- Algae are diverse photosynthetic organisms that range from unicellular to multicellular forms and thrive in both freshwater and marine environments.
- Because they rely on sunlight, algae are typically found near the waters surface and act as primary producers that support aquatic food webs.
- Algal abundance and diversity are strongly influenced by environmental conditions, making them effective indicators of water quality.
- Excessive algal growth often signals nutrient pollution within an ecosystem.
- This study examines algal diversity and abundance to identify variation among microhabitats in a salt marsh ecosystem.
- The marsh also provides important environmental benefits, including flood protection, storm surge reduction, sediment stabilization, and erosion control.
- The purpose of this study is to analyze algal communities as biological indicators of environmental variation within salt marsh microhabitats.
- It is hypothesized that microhabitats will show slight differences in algal diversity and abundance, while overall community composition will remain relatively consistent due to shared environmental conditions.
- The independent variable is the microhabitat location, and the dependent is the species of algae found

Methods

- Thirty environmental samples were collected from open-water, rocky, and plant dense microenvironments at the Little Hell Gate Salt Marsh.
- DNA was extracted from each sample using a centrifuge with lysis solution, silica resin, and an ice-cold wash buffer to isolate genetic material.
- The isolated DNA was amplified through polymerase chain reaction (PCR) using UBP-issued TUFA primer, which specifically targeted algal DNA.
- The PCR products were analyzed using gel electrophoresis, and four positive samples were identified and submitted to Azenta for DNA sequencing.
- The resulting DNA sequences were uploaded to the DNA Subway BLAST database for species identification, aligned using the MUSCLE program, and used to generate a maximum likelihood phylogenetic tree with NJ PHYLIP to analyze evolutionary relationships among the algae species.

Results

Sample	Species	Bit Value	E Value	Aln. Length	Mismatches
KKW-06	N/A				
KKW-07	N/A				
KKW-09	*Blidingia minima*	1611	0	939	7
KKW-15	*Ulva flexuosa*	1478	0	879	23

Table 1: Results of DNA Sequencing

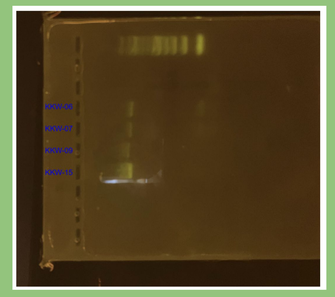

Figure 2: Gel Electrophoresis Photograph showing bands for KKW-06, KKW-07, KKW-09, KKW-15.

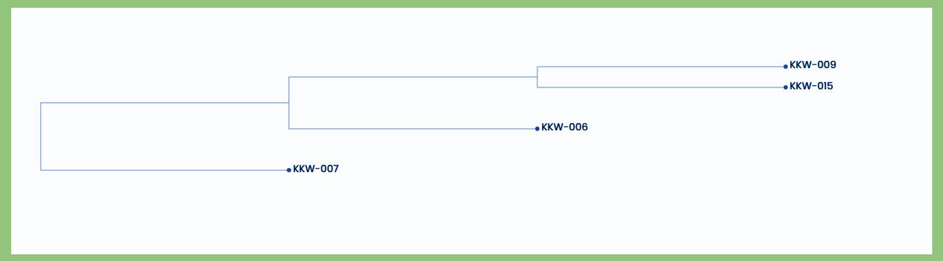

Figure 3: Neighbor Joining Phylogenetic Tree

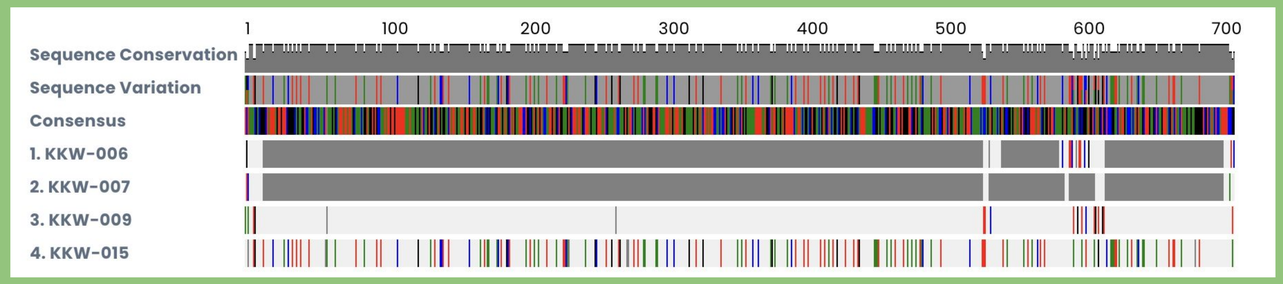

Figure 4: MUSCLE Alignment

Figure 5: *Ulva Flexuosa*

Figure 6: *Blidingia Minima*

Discussion

- The results obtained provided no conclusive data to confirm our hypothesis.
- We hypothesized that there would be a slight discrepancy in each microhabitat, but overall, the community composition would remain relatively consistent across the salt marsh due to shared environmental conditions.
- Under technicality, our results illustrated very different community compositions in each microhabitat; however, due to our low identification rate, these results do not support a specific conclusion.
- We have surmised that our low identification rate is largely due to a high sediment concentration within each sample. During our procedure, we did not have a method to sieve out the sediment. This likely disrupted the PCR and gel electrophoresis.
- A potential solution to this is to filter out the sediment from the algae.

References

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