Plant Diversity in Randall's Island

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Introduction

- Object of the study was to answer the question: **How does biodiversity of plants differ between a meadow and a salt marsh?**
- **Hypothesis: We hypothesized that there would be species endemic to each site as well as grasses, shrubs, and flowers common in both the salt marsh and meadow biomes**
- Biodiversity measured by **species richness**
- We **collected** different plants from the meadows and salt marsh, DNA **sequenced** them, and **compared** them
- The meadows of Randall's Island are the habitat for **native species** Switchgrass, Seaside Goldenrod, New York Aster, Milkweed, and more
- New York salt marshes are the habitat for **native plants** such as Saltgrass, and Butterfly milkweed
- Meadows and salt marshes are vital ecosystems that **provide habitats** for wildlife
- Salt marshes are defined as ecosystems between open water and land
- Salt marshes are especially important in our changing environment because they serve as **flood protection** and help **stabilize shores**
- Meadows are also uniquely important because they **absorb storm runoff**

Materials & Methods

- **Collection:** 11 plant samples from **salt marsh** and **meadow** and filled tubes with **ethanol**. Identified them with the *Seek* app
- **Extraction:** Added **300μL** of lysis buffer & **grounded** samples. Then added **3μL** of silica resin and **rinsed** the DNA with **500μL** of cool wash buffer **three** times. Finally, added **100μL** of distilled water
- **Amplification:** We used *rbc*I primers and added **23μL** of *rbc*L primer with **2μL** of the homogenous DNA solution. Then, corresponding procedure for **PCR**
- **Gel Electrophoresis: 5μL** of each sample with **2% agarose** solution
- **DNA Analysis:** DNA Subway to create MUSCLE and phylogenetic tree figures
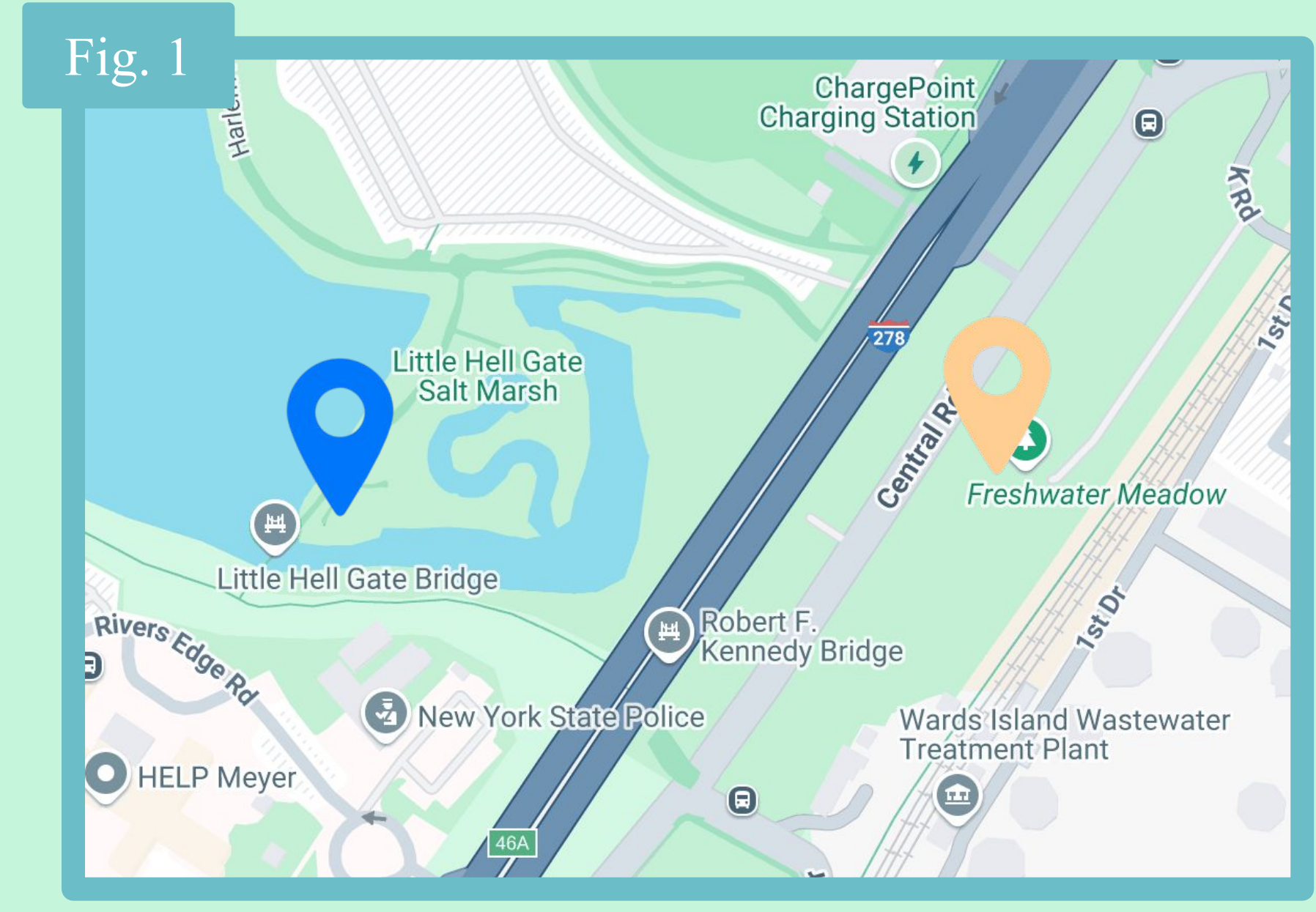
Results

Figure 1: Sample Collection Location - Randall's Island
The pins indicate locations where samples were collected. The blue pin is the first site where samples were collected. This area is near Little Hell Gate bridge, a salt marsh and brackish water. The orange pin is the second site, Freshwater Meadow. This area is a freshwater meadow that was curated to grow native plants.
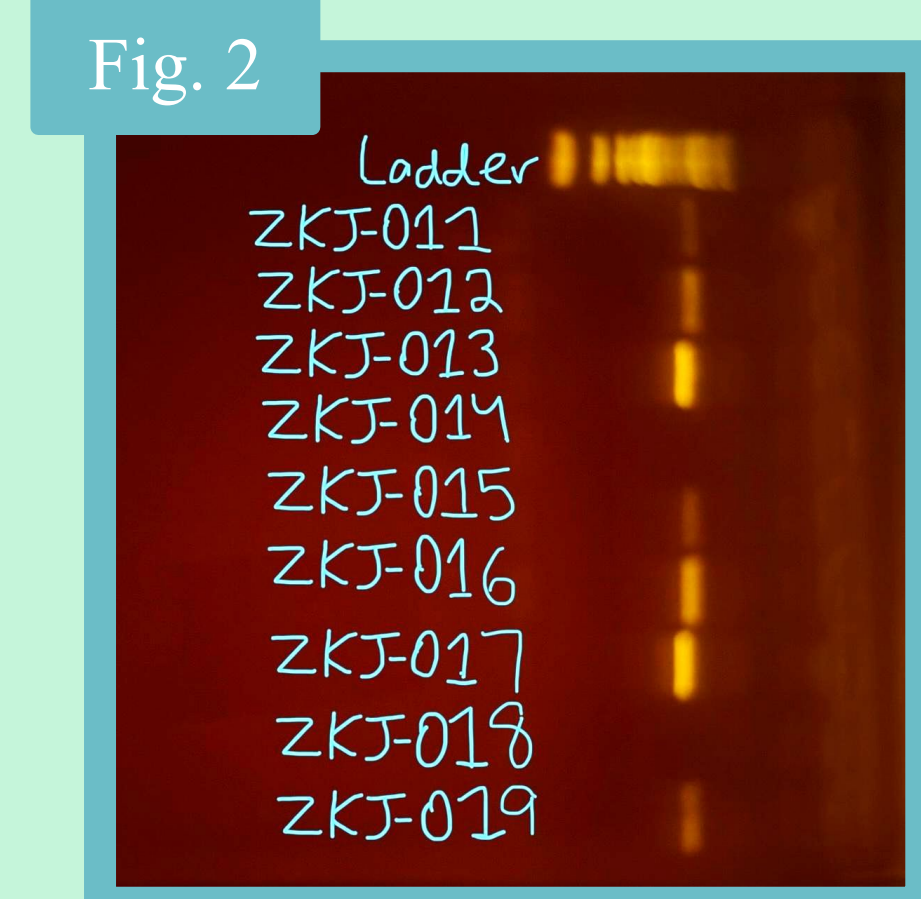

Figure 2: Gel Electrophoresis of Samples 011-019 (04/08)
The yellow lines to the write of the labels indicate the presence of DNA found in the sample. The absence of a yellow line suggests that DNA could not be found in the sample, likely due to an extraction error.

Figure 3: Phylogenetic Tree of Sequencing Results
The phylogenetic tree, using Neighbor Joining (NJ), consists of 12 plant samples with the outgroup *Arabidopsis Brassicaceae*. The numbers shown represent the bootstrap value. This shows the evolutionary similarities between species and how closely they are related.
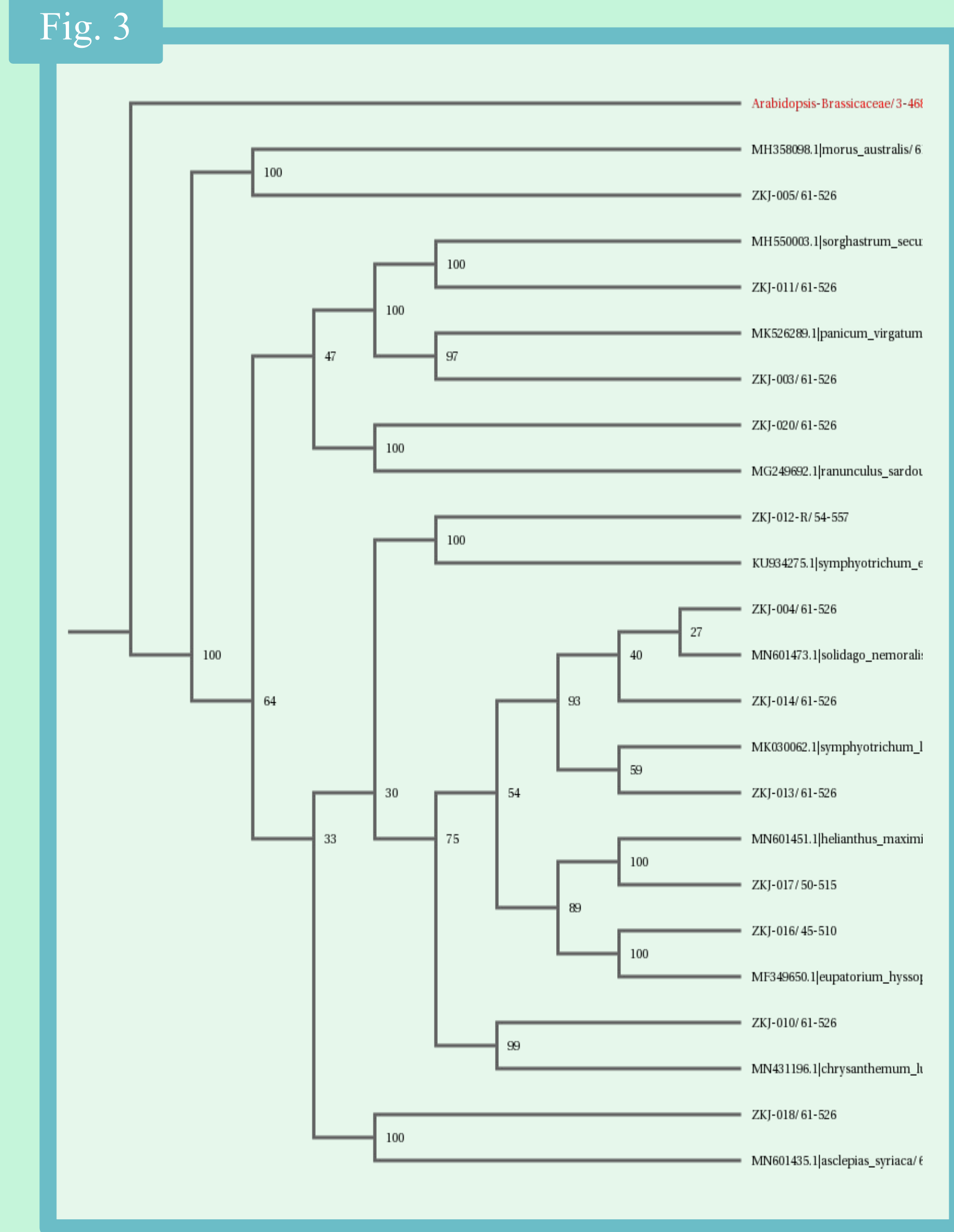

Sample Number	Site Number	Seek ID	BLASTIN ID	Aln. Length	Bit Score	e	Mismatches
ZKJ-003	1	Grasses	1. Panicum virgatum	535	966	0	0
ZKJ-004	1	Goldenrods	1. Solidago nemoralis 2. Solidago canadensis 3. Solidago tortifolia 4. Solidago stricta 5. Solidago leavenworthii	534	964	0	0
ZKJ-005	1	Dicots	1. Morus australis 2. Morus alba	539	973	0	0
ZKJ-010	1	Dicots	1. Chrysanthemum lucidum 2. Artemisia sp. 3. Asteraceae sp.	534	964	0	0
ZKJ-011	1	Grasses	1. Sorghastrum secundum 2. Sorghastrum nutans 3. Trachypogon spicatus 4. Sorghastrum nutans	537	969	0	0
ZKJ-012	2	American Asters	1. Symphyotrichum eatonii	570	1029	0	0
ZKJ-013	2	American Asters	1. Symphyotrichum lateriflorum 2. Eclipta prostrata 3. Symphyotrichum dumosum 4. Symphyotrichum cordifolium	534	964	0	0
ZKJ-014	2	Goldenrods	1. Solidago nemoralis 2. Solidago canadensis 3. Solidago tortifolia 4. Solidago stricta 5. Solidago leavenworthii	534	964	0	0
ZKJ-016	2	Bonesets	1. Eupatorium hyssopifolium	511	922	0	0
ZKJ-017	2	Sunflowers	1. Helianthus maximiliani 2. Helianthus petiolaris 3. Helianthus pauciflorus 4. Helianthus hirsutus 5. Helianthus grosseserratus	522	939	0	1
ZKJ-018	2	Milkweed	1. Asclepias syriaca 2. Asclepias exaltata	536	967	0	0
ZKJ-020	2	Buttercups	1. Ranunculus sardous 2. Ranunculus macranthus	536	967	0	0

Table 1: Results from DNA Sequencing and Seek ID
This table indicates the BLASTIN ID, Alignment length, bit score, e-score, and mismatches for each sample. For many of our samples, there were multiple possible species matches with the exact same e-score, bit score, alignment length, and mismatches. Therefore, we cannot definitively identify some samples as one species.

Figure 4: Multiple Sequence Comparison by Log-Expectation (MUSCLE)
DNA Sequences from samples of plants were compared using MUSCLE. Each colored vertical line represents a base pair from the DNA sequence and lines with the same color in the same location indicate similarities in sequences and vice versa. Grey shaded areas indicate missing data, sequence conservation refers to the frequency of a certain nucleotide in the given sequences, and sequence variation refers to the variation in that column from the consensus.
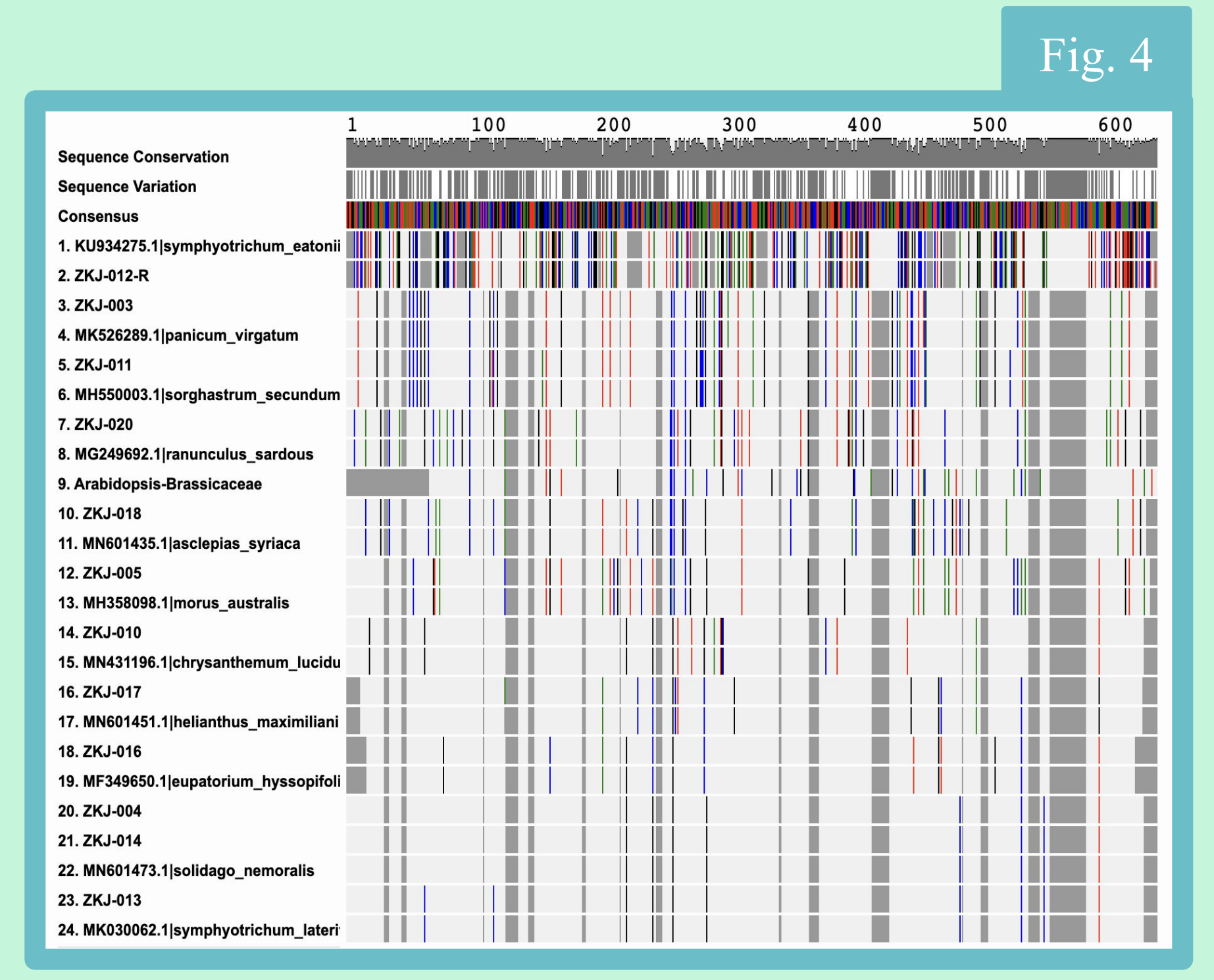
Discussion

- Out of the **22 samples** collected, we identified **five** different species in site 1 and **seven** in site 2
- We **cannot definitively identify** the species for samples with **multiple possible species matches** (same bit score, e, and number of mismatches)
- Samples from both sites had the same species matches, under the genus *Solidago*, so there may have been **endemic *Solidago* species**
- Asters were found in both sites, but not necessarily the same species of Asters, so there is a **possibility** of an **endemic species**
- Surprisingly, *Chrysanthemum lucidum* (one of the matches for ZKJ-010) is **native to Korea**
- The rest of the species we found were **unique to their respective habitats**
- **Errors** during the isolation and amplification of DNA may have **impacted the results** of gel electrophoresis and sequencing
- If this study were replicated in the future
  - Spend more time **carefully extracting DNA**
  - Collect a **larger sample size**
  - Use a **different measure** of biodiversity
- Since our data set was limited, **we cannot draw many conclusions on the difference in biodiversity between the salt marsh and meadow habitats**

References

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Acknowledgements

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