The Effect of Biological Nitrogen Fixation on Plant Biodiversity on Randall's Island

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Introduction

- Biological nitrogen fixation (BNF) — diazotrophic bacteria converts atmospheric nitrogen into ammonia
- BNF is essential for synthesis of amino acids, nucleic acids, amino sugars and vitamin B coenzymes (Lee, 2023), and is beneficial for soil health, plant nutrient content, and ecosystem function (Mahmud et al. 2020)
- Clovers and Black Locust trees are nitrogen-fixing plants on Randall's Island, host nitrogen-fixing (Rhizobia) bacteria on their root nodules (Jennings, n.d.)
- The purpose of this experiment is to determine how the presence of nitrogen-fixing plants impacts biodiversity
- We hypothesize that areas with nitrogen-fixing plants will have increased species richness compared to those without because of soil nitrogen's beneficial effects
- We will be sampling from three different sites in the Freshwater Meadow with various nitrogen-fixing clover densities, and from two sites in the Urban Forest near a Black Locust tree

Methods

- 30 samples were collected from the Freshwater Meadow and Urban Forest using 2mx2m transects, then stored in ethanol and refrigerated at -20°C.
- DNA was isolated using a centrifuge, lysis solution, silica resin, and wash buffer.
- Isolated DNA was amplified using PCR and an rbcL primer.
- PCR products were analyzed by gel electrophoresis.
- DNA Subway 2.0 was used to identify species using BLAST, create a MUSCLE alignment, and generate an NJ PHYLIP tree.

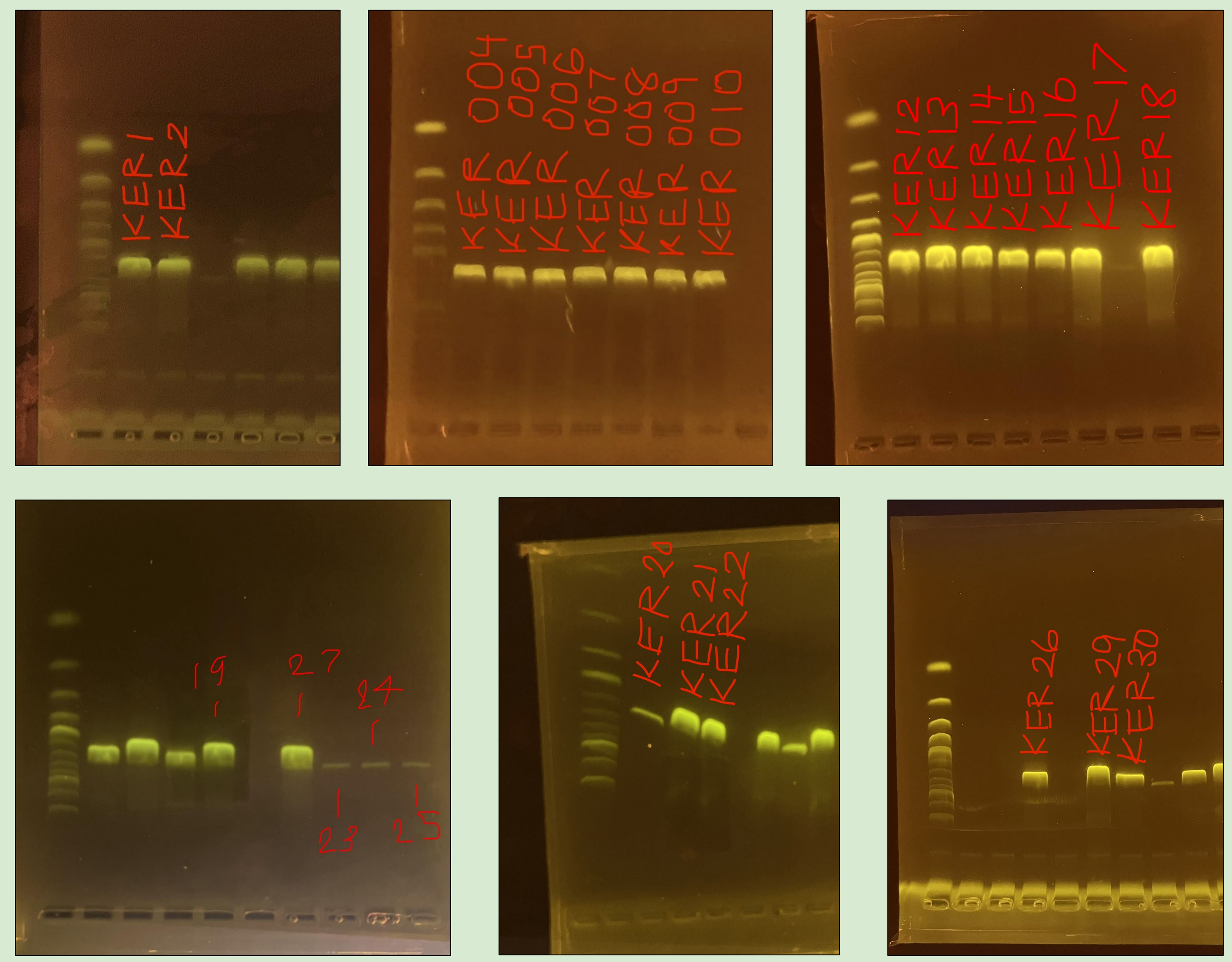

Figure 1a/1b/1c/1d/1e/1f Gel Electrophoresis results
Results of all gel electrophoresis tests. Fig. 1a was taken on January 12th, Fig. 1b on February 11th, Fig. 1c on April 20th, Fig. 1d on April 8th, Fig. 1e on April 20th, Fig. 1f on April 20th

Figure 2: Untrimmed Multiple Alignment Created by MUSCLE. These are sequences of results illustrated by the MUSCLE program. This image shows ~350 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.

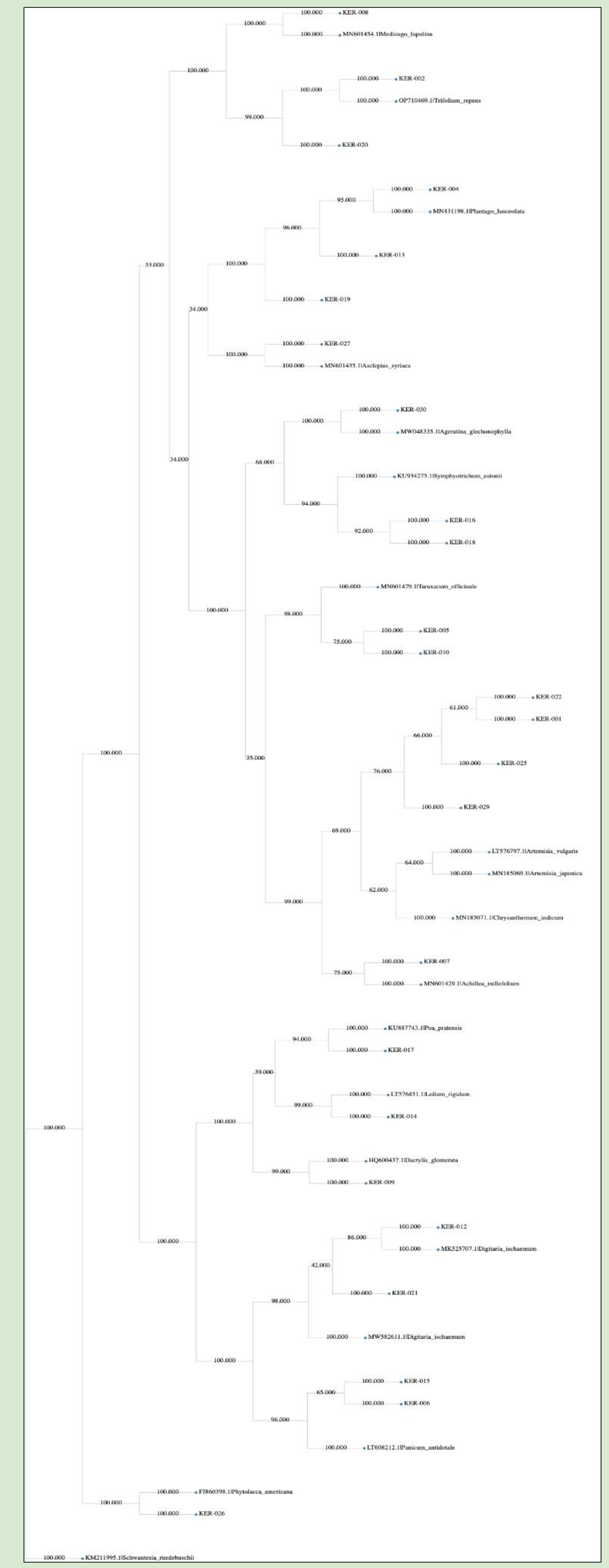

Figure 3: Phylogenetic Tree of Sequencing Results. Maximum likelihood phylogenetic tree displaying the evolutionary relationships between the identified species. The species Schwantesia ruedebuschii is the outgroup.

Discussion

- Our results contradicted our hypothesis
  - We hypothesized that areas with higher clover density would have a higher diversity of species; however, we found that the area with the lowest clover density had the largest range in species diversity
- We collected a small sample size and we collected a different amount of samples at each site
  - For these reasons, we cannot accurately compare the biodiversity from each site
- The MUSCLE program shows similar sequences between most samples and their BLAST matches
  - Samples 001, 022, 025, and 029 are not as closely related to their BLAST matches, insinuating that they may have been misidentified
- Further research could be improved by collecting a larger sample size and by collecting samples from multiple sites with and without nitrogen fixing species

References

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