# Effect of Meadow versus Forest Environment on Grass Height and Biodiversity on Randall's Island

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## Introduction

- Grass samples collected on Randall's Island, a 516-acre NYC park (Margolies, 2017).
- Grass purifies air by absorbing $CO_2$, preventing soil erosion, supporting biodiversity, and filtering groundwater (Sloat, Lindsey et. al, 2025).
- Meadowlands have more species due to sunlight, open conditions, and diverse pollinators (Frenne et. al, 2021).
- Patterns are influenced by water-table depth and soil redox potential (USDA Forest Service, 2006).
- This demand results in high plant diversity in meadowlands, with varied species attracting a variety of pollinators (Kiviat, McDonald, 2002).
- Forests in the northeast have shaded understories and woody vegetation with less grass growth (New York Flora Atlas, 2025).
- This experiment aims to determine if light availability and soil conditions produce taller, more diverse grasses in meadows vs. forests.
- Field observations and DNA barcoding allowed confirmation of the hypothesis.
- Temperature and soil moisture are used to understand how abiotic factors affect vegetation productivity.

## Materials and Methods

1) **Collect Samples →**
- Grass was collected from two environments: forest and meadowland
- 15-meter transect was run and grass samples were collected each meter
  - Each blade of grass was put into a 1.5ml test tube with 70% ethanol
- Below was also collected every meter:
  - Temperature, soil humidity and height measured for each sample

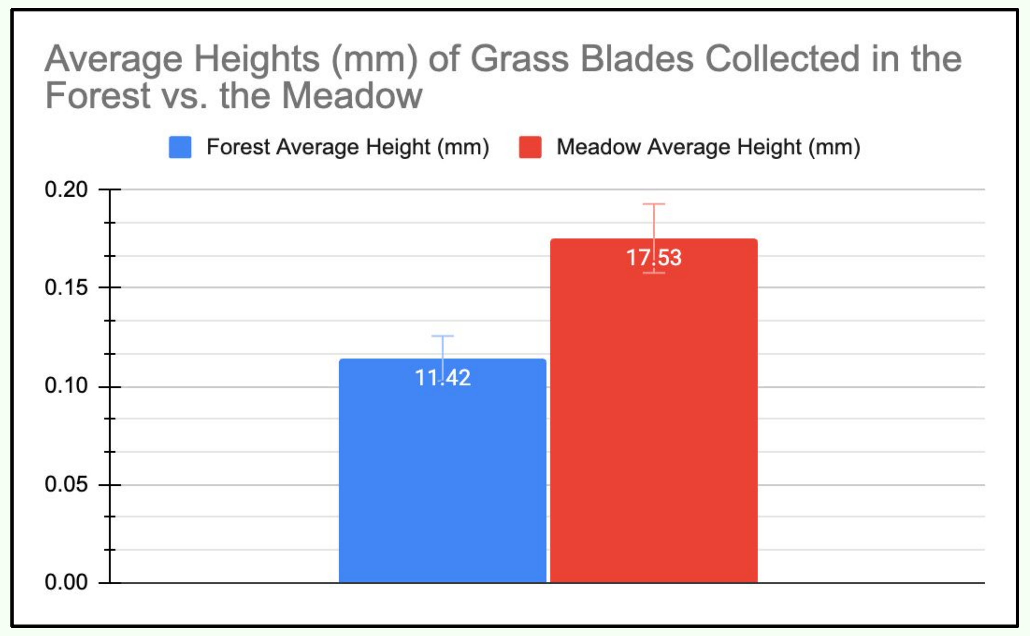
2) **DNA Extraction →**
- Samples were ground with a mortar and pestle with lysis solution
  - Silica method was performed

3) **DNA Amplification →**
- The DNA samples were mixed with rbcL primer and then amplified using PCR

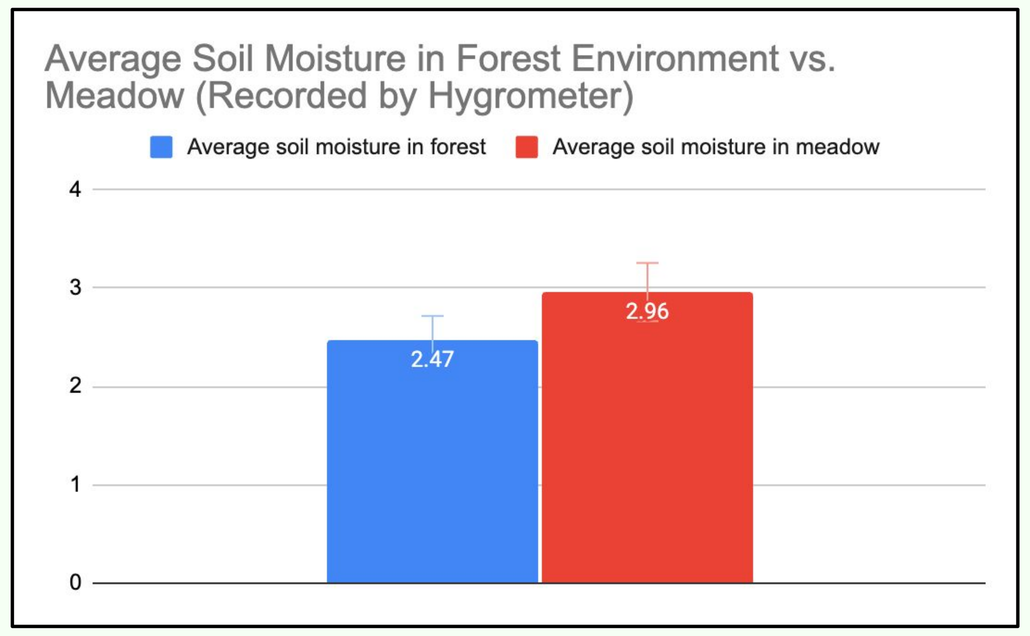
4) **DNA Confirmation →**
- Gel electrophoresis is performed to ensure that DNA was collected

5) **DNA Sequencing and Analyzing →**
- The DNA samples are then sent to the lab
- Upon return, DNA Subway was used with the samples to determine how many species were collected (Cold Spring Harbor Laboratory, 2018)

## Results




**Graph 1:** The average height of grass blades in the forest and meadow measured by a ruler. The average height of grass blades was higher in the meadow than the forest which supported the hypothesis. The average of the three individual height blades per meter on the transect (in the forest) ranged from 6.17nm-20.67nm. The average height of all of the blades of grass extracted in the forest was 11.42 mm +- 1.65mm. The average of the three individual height blades in the meadow per meter on the transect ranged from 9.17mm-24.83mm. The average height of all of the blades of grass extracted from the meadow was 17.53mm +/-1.19mm.




**Graph 2:** The average of soil moisture in forest vs. meadow environment measured by a soil hygrometer (unitless on this device). The average soil moisture was higher in the meadow compared to the forest which opposes our hypothesis. The moisture content in the soil was recorded three times at each meter on the 15-meter transect. In the forest, the average moisture readings ranged from 1.67-3.33 in the forest. The average moisture for all of the locations recorded in the forest was 2.47 +/- 0.42. In the meadow, the average moisture in the meadow ranged from 1.6-5.6. The average moisture in the meadow was 2.95 +- 1.46.

| Sample # | Common Name | Genus/ Species | Common Name (DNA Subway) |
|---|---|---|---|
| 1M | Bermuda grass | Bromus japonicus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Japanese Brome |
| 2M | Fragaria vesca | Bromus japonicus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Japanese Brome |
| 3M | Yorkshire Fog | Bromus japonicus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Japanese Brome |
| 4M | Green dragon | Symphyotrichum lanceolatum ribulose 1,5-bisphosphate carboxylaseoxygenase large subunit (rbcL) gene, partial cds; chloroplast | Panicled Aster |
| 6M | Tall Fescue | Lolium multiflorum voucher NSMK-PI20190070 ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Italian ryegrass/annual ryegrass |
| 7M | Bahiagrass | Allium stellatum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Autumn onion/cliff onion/grade onion |
| 8M | Great brome | Allium stellatum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Autumn onion/cliff onion/grade onion |
| 9M | Orchard grass | Allium stellatum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Autumn onion/cliff onion/grade onion |
| 11M | Loblolly pine | Poa pratensis voucher NSMK-PI201900100 ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Kentucky Bluegrass |
| 12M | Smooth crabgrass | Poa pratensis voucher NSMK-PI201900100 ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Kentucky Bluegrass |
| 13M | Wild garlic | Poa pratensis voucher NSMK-PI201900100 ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Kentucky Bluegrass |
| 14M | Smooth brome | Lolium multiflorum voucher NSMK-PI20190070 ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Italian ryegrass/annual ryegrass |
| 15M | Yorkshire Fog | Poa pratensis voucher NSMK-PI201900100 ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Kentucky Bluegrass |

**Table 1 and 2:** The species in the forest and meadow with their predicted species name in the field using *Picture This*, their scientific name and the common name of the scientific name. The scientific names were given from DNA Subway.

| Sample # | Common Name | Genus/ Species | Common Name (DNA Subway) |
|---|---|---|---|
| 1F | Orchard grass | Dactylis glomerata ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Orchard Grass |
| 2F | Virginia Wild rye | Elymus wiegandii ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Wiegand's wild-rye |
| 3F | Slender false brome | Bromus erectus voucher NSMK-Pl2019000235 ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Erect Brome/upright brome/ meadow brome |
| 4F | Common chickweed | Achillea millefolium ribulose 1,5-bisphosphate carboxylaseoxygenase large subunit (rbcL) gene, partial cds; chloroplast | Common yarrow |
| 7F | Smooth brome | Elymus wiegandii ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Wiegand's Wild Rye |
| 9F | Lilyturf | Carex vaginata voucher NMW7951 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Sheathed sedge |
| 12F | Eastern woodland sedge | Carex vaginata voucher NMW7951 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Sheathed sedge |
| 13F | Cabbage tree | Carex gracilescens voucher JK 010 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Slender Loose-Flowered Sedge |
| 15F | Eastern star sedge | Carex appalachica voucher B0086 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast | Appalachian Sedge |

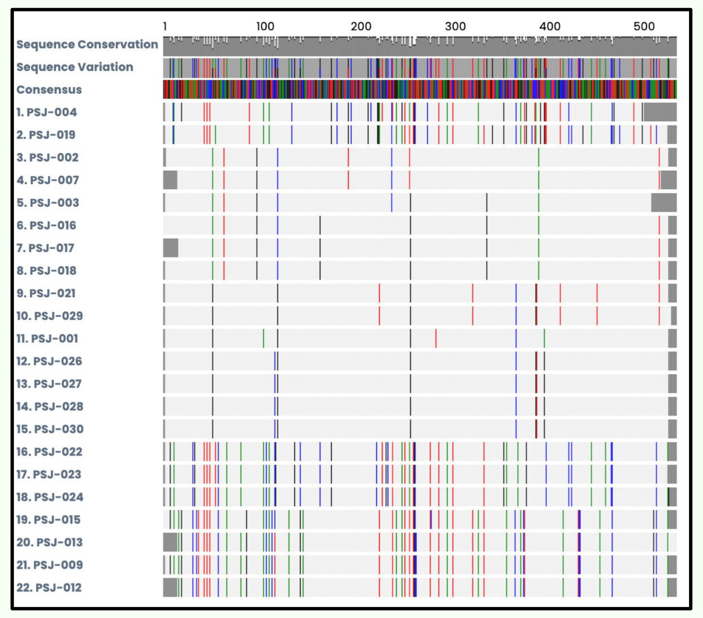



**Figure 1:** Multiple sequence alignment of rbcL DNA sequences from all successfully barcoded grass samples, each generated through DNA Subway. Each row represents one sample and the colored bars represent nucleotide variation relative to the consensus sequence. Samples with fewer color marks show great similarity to consensus while samples with less represent more related species.

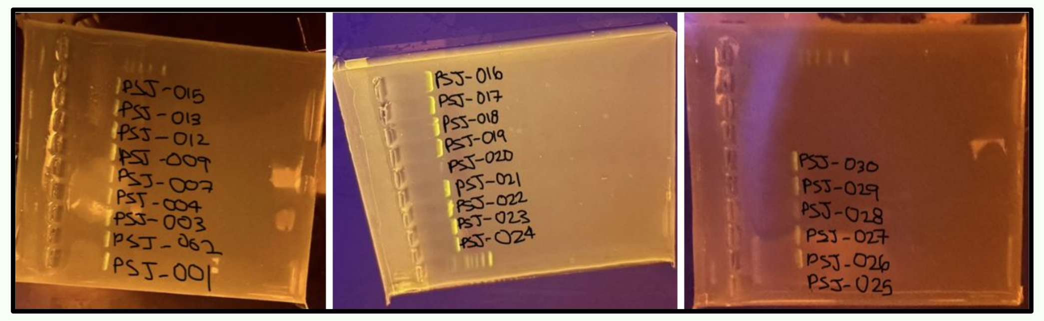


**Figure 2:** Results from the gel electrophoresis confirmation (yellow bands show where DNA was correctly extracted). This step occurs to confirm there is DNA in the samples before they are sent to the lab.

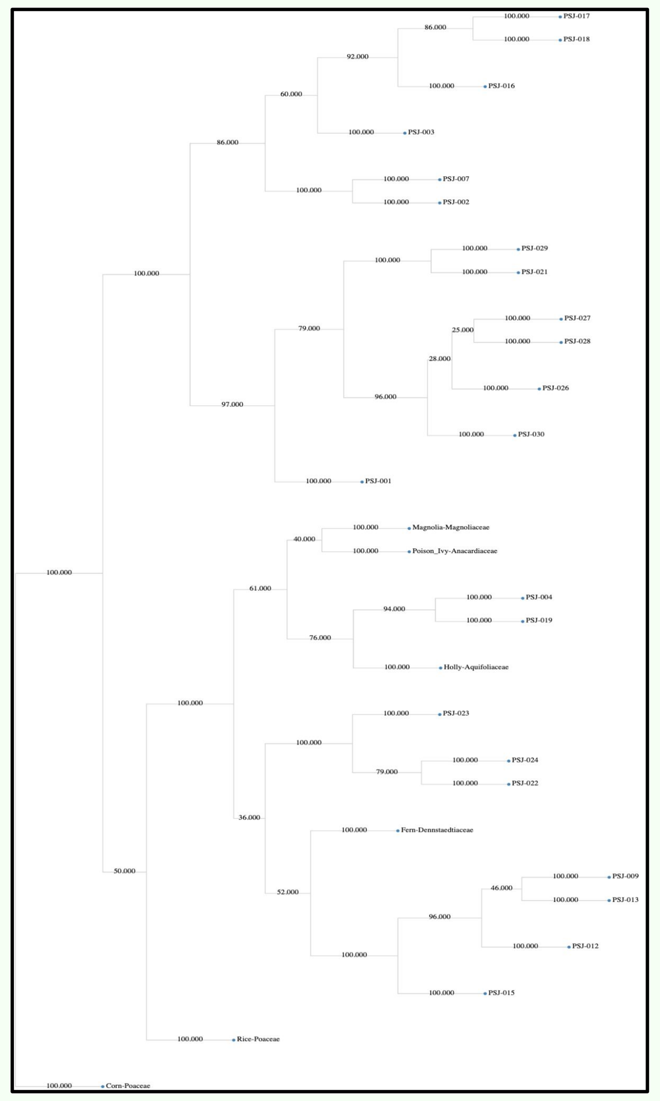


**Figure 3:** This graph represents an analysis performed on the DNA samples using Neighbor Joining (NJ) through software named PHYLIP. It depicts the relationship between 22 specimens collected in either meadow or forest ecosystems. The numerical values on each node indicate bootstrap probabilities as confidence intervals. The control group corn-poaceae is used as an outgroup for the purpose of rooting the tree.

## Discussion

- Hypotheses Outcomes:
  - Our results supported our hypothesis that meadowland grasses would have a greater species diversity.
  - The hypothesis that the forest would be more moist was contradictory to the results; however, this could be due to heavy precipitation during data collection.
  - Results supported the hypothesis that the meadow would have a greater soil temperature, but differed by a 1 degree Celsius spread, possibly due to a lack of sunlight that day.
  - The average height measurements supported the hypothesis that the height of grass in the meadow was higher than that in the forest.
- Species Overlap: The smooth brome and orchard grass in both sites suggest that there are species that overlap between the two regions.
- Future Research: Further studies should use a longitudinal approach to determine how weather changes influence soil moisture, temperature and growth across all four seasons.

Sources of Error:

- Using only one transect on a single day makes results susceptible to weather anomalies.
- Five unidentified forest samples may have skewed diversity comparisons.
- Foot traffic on Randall's Island, affect grass height and soil compaction.
- DNA breakdown or PCR contamination in the lab may have caused misidentification.
- Human error in measuring grass height may have led to inaccurate measurements.

## References

## Acknowledgements

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