



Plant Biodiversity Study of Cunningham Park and Juniper Valley Park

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Abstract

Our experiment sought to better understand the plant biodiversity between two city parks located in Queens—Juniper Valley Park and Cunningham Park. Additionally, we tested the accuracy of PlantSnap, a plant species identification app, by comparing it to traditional DNA barcoding techniques. Many of our samples were unsuccessfully sequenced, so we were unable to draw concrete conclusions surrounding the biodiversity of the two parks. We did observe some overlap of species between Cunningham and Juniper Valley Park. PlantSnap was imperfect with species identification—with a genus identification accuracy rate of 42%. However, we believe that plant identification apps can still serve as a useful supplement to traditional techniques.

Introduction

Juniper Valley Park and Cunningham Park are 55.64 acres and 358.00 acres large respectively around 5.60 miles apart. Parks are believed to be vital in preserving biodiversity in urban settings and have major effects on the organisms within those ecosystems, such as birds and also the quality of life for residents (Savard et al., 2000). Due to the parks' close proximity, we hypothesize that there would be relatively high similarity between the plant species in both parks. Our experiment also aims to assess the accuracy of the PlantSnap app, which utilizes photos of plants to identify species. The specific goals of this experiment are to evaluate the biodiversity of the plant life in Juniper Valley Park and Cunningham Park, and to compare the similarities and differences between the predicted species using the Plantnet app and traditional DNA sequencing.

Materials & Methods

In the early spring, we visited Juniper Valley Park and Cunningham Park to collect samples. Leaf tissue samples were collected through the parks by extensively surveying the flora on the ground, as well as a few leaf samples from trees. Before each sample collection, we took a photo of the plant using the PlantSnap app and recorded the identified species. In total, 81 samples were collected, with 39 from Juniper Valley Park and 42 from Cunningham Park. Tissue samples were stored in freezers to preserve them before DNA sequencing. DNA isolation was performed through the Chelex Isolation protocol using 3mm tissue samples. After isolating the DNA, we performed a PCR using matK primers and then sent the samples for DNA sequencing. Finally, DNA Subway was utilized to analyze sequencing data for species identification.

TABLE 1

Cunningham Park PlantSnap identification and BLASTn results (abridged)

Specimen ID	PlantSnap identification	BLASTn results
C1	<i>Allium sativum</i>	<i>Allium sativum</i>
C4	<i>Trifolium pratense</i>	<i>Trifolium repens</i>
C7	<i>Elymus repens</i>	<i>Festuca arundinacea</i>
C8	<i>Pisum sativum</i>	<i>Stellaria crassipes</i>
C16	<i>Narcissus 'jetfire'</i>	<i>Narcissus munozii-garmendiae</i>
C18	<i>Lycoris radiata</i>	<i>Crocus banaticus</i>
C21	<i>Furcraea foetida</i>	<i>Yucca queretaroensis</i>
C23	<i>Cotyledon orbiculata</i>	<i>Hylotelephium spectabile</i>
C26	<i>Stellaria media</i>	<i>Stellaria crassipes</i>
C26b	<i>Lavandula angustifolia</i>	<i>Lavandula angustifolia</i> subsp. <i>angustifolia</i>
C27	<i>Saponaria officinalis</i>	<i>Capsella bursa-pastoris</i>
C33	<i>Skimmia reevesinana</i>	<i>Skimmia japonica</i>
C39	<i>Viola hirta</i>	<i>Viola pedatifida</i>
C41	<i>Valeriana alliariifolia</i>	<i>Alliaria petiolata</i>

Results

For the samples that were successfully sequenced, we found the PlantSnap results to be imperfect. Overall, we observed an accuracy rate of 42% in genus identification through the PlantSnap app (with 10 out of 24 samples having the same genus between the PlantSnap results and BLASTn result). It should be noted that many of our sequenced samples had comparable bit scores between species of the same genus, adding to the difficulty of receiving the same species result. For example, sample J20 was identified as *Vinca major* by the PlantSnap app; our BLASTn results came back as *Vinca minor* with a bit score of 1548, *Vinca major* with a bit score of 1526, and another sample of *Vinca minor* in the database with a bit score of 1521. Within successfully sequenced samples, we also observed some overlap in species between the parks; for instance, C16 and J17 were both identified as *Narcissus munozii-garmendiae* after running BLASTn.

TABLE 2

Juniper Valley Park PlantSnap and BLASTn results (abridged)

Specimen ID	PlantSnap identification	BLASTn results
J4	<i>Muhlenbergia schreberi</i>	<i>Poa sieberiana</i>
J7	<i>Dracaena fragrans</i>	<i>Narcissus munozii-garmendiae</i> / <i>Narcissus blancoi</i> (similar bit scores)
J8	<i>Crocus vernus</i>	<i>Tulipa systola</i>
J18	<i>Helleborus X Hybridus</i>	<i>Lepidium meyenii</i>
J20	<i>Vinca major</i>	<i>Vinca major</i> / <i>Vinca minor</i> (similar bit scores)
J22	<i>Tradescantia virginiana</i>	<i>Scilla siberica</i>
J25	<i>Fallopia convolvulus</i>	<i>Viola pedatifida</i>
J26	<i>Lespedeza procumbens</i>	<i>Persicaria posumbu</i>
J30	<i>Lupinus polyphyllus</i>	<i>Lupinus polyphyllus</i>
J33	<i>Begonia cucullata</i>	<i>Begonia radicans</i>

Discussion

Given the time constraints of our project, we were unable to gather many tree leaf samples for our experiment nor perform DNA barcoding again for the samples that failed to be sequenced. As a result, this study can only serve as a preliminary assessment of the biodiversity of Cunningham Park and Juniper Valley Park. Overall, both parks were planned with purposeful and diverse plantings that thrive in an urban Northeast setting, and they provide New Yorkers a good amount of biodiversity in plant life to enjoy. Based on our study, while PlantSnap should not be exclusively relied on for species identification, it can still serve as a valuable tool, especially for genus identification. Traditional barcoding has its own shortcomings, as it requires species that have clear, distinguishable barcoding patterns and is inaccurate when dealing with hybrid species (Besse et al., 2021). PlantSnap and other similar species identification apps may assist traditional barcoding techniques to help distinguish species, especially for similar species within the genus.

References

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Acknowledgements

- The Urban Barcoding Research Program
- Allison Mayle, PhD
- Marianne Williams, PhD
- The Pinkerton Foundation