Leaf it to Us

Amelia Citron, Ruby Davies, Hazel Christensen, Miranda Gluck

Ethical Culture Fieldston School

Introduction

- The Field(ston) Ecology independent study aims to create a fully developed field guide of the Fieldston campus. For trees we are unfamiliar with and cannot identify the species, we will use DNA barcoding determine the species.
- The observable characteristics of plants are susceptible to the influence of their environment, causing plants of the same species to look very different, simply because of location.
- Luckily, DNA barcoding can be used to fill in the gaps and provide very accurate species identification.
- Our project will use amplification and sequencing across multiple samples to improve areas of our campus identification that are made difficult by environmental impacts on plant development.
- Our general goal in working with Urban Barcode is to expand our understanding of the species of trees on Fieldston's campus.

Materials and Methods

1. Our team collected 16 leaves in total
2. We placed each leaf in a labeled bag, and stored them in the -20°C freezer.
3. We followed the UBP protocol to isolate and extract the DNA from our samples.
4. We attached DNA to silica resin, washed it down, and put it in the PCR machine to be amplified.
5. After, we used gel-electrophoresis to see which of our samples contained enough DNA to be sent off for sequencing.(*Using DNA Barcodes to Identify and Classify Living Things*, 2024).

Results

Sample #	Prediction	Top species results	Bit Score	e Score
7	Magnolia	magnolia (species), magnolia x soulangeana, *Magnolia cylindrica*	881	0.0
8	Elm/Slippery elm	*Ulmus americana, Ulmus parvifolia, Ulmus glabra*	948	0.0
10	White/Green ash	*Fraxinus pennsylvanica, Fraxinus profunda, Fraxinus americana*	946	0.0
11	Elm	*Rhamnus cathartica,* magnoliophyta, *Rhamnus leptophylla, Rhamnus davurica, Rhamnus globosa, Rhamnus parvifolia, Rhamnus tangutica, Rhamnus utilis, Rhamnus dumetorum*	939	0.0
12	Red Oak	*Lithocarpus edulis, Quercus velutina, Quercus rubra, Quercus palustris, Quercus laevis, Quercus myrtifolia, Quercus incana, Quercus nigra, Quercus hemisphaerica, Quercus velutina, Quercus shumardii, and Quercus ilicifolia*	946	0.0
14	Birch	*Rhamnus cathartica,* magnoliophyta, *Rhamnus leptophylla, Rhamnus davurica, Rhamnus globosa, Rhamnus parvifolia, Rhamnus tangutica, Rhamnus utilis, Rhamnus dumetorum*	939	0.0
15	Dogwood	*Rhamnus cathartica,* magnoliophyta, *Rhamnus leptophylla*	936	0.0
16	Birch	*Lonicera maackii, Lonicera periclymenum, Lonicera xylosteum, Lonicera demissa, Lonicera chrysantha*	940	0.0

Table 1. Every sample with its sample number, predicted species, species result, bit score, and e score. Mis-matches were excluded because they are indicated in the paper

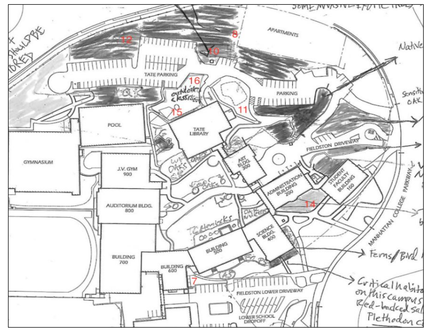

Fig. 1 Map of campus with sample collection locations.

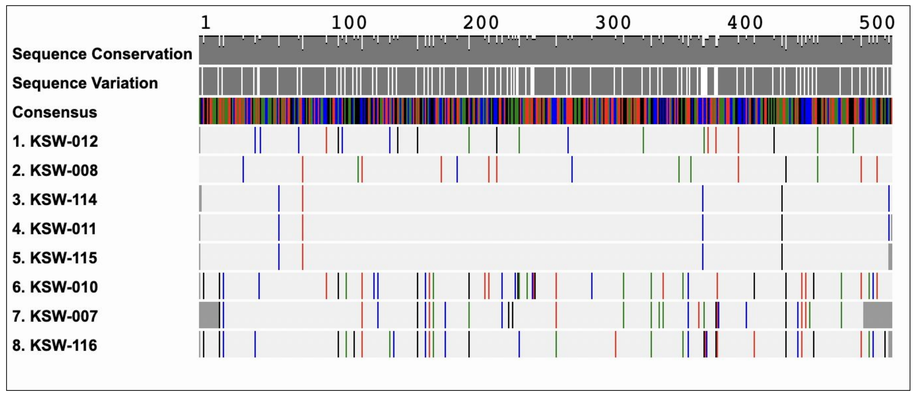

Fig. 4 Every sample's genome mismatches to a consensus genome comprised of the most common base pair for each sample.

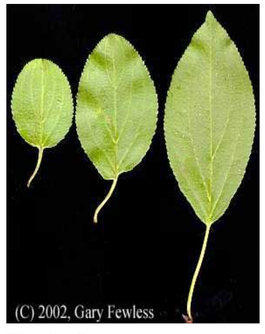

Fig 2. *Rhamnus cathartica*

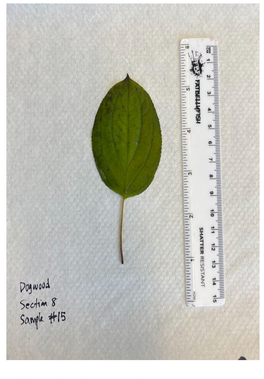

Fig 3. Sample 15

Discussion

- Out of our 16 samples, DNA was extracted and sequenced for samples 7, 8, 10, 11, 12, 14, 15, and 16.
- Each sample's sequencing showed multiple possible species with the same bit score, E score, and number of mismatches.
- Figure 4 represents similarities between the genomes of each species. The consensus alignment represents each genome of each sample combined. The lines underneath the consensus correspond to a sample, and each line represents an inaccuracy between the consensus and the sample genome. Samples with matching inaccuracies are closely related and contain similar/the same genomes.
- More samples need to be collected and identified to confirm the identity of tree species on campus in the future to complete a field guide of the Fieldston campus.

References

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