INTRODUCTION

The book, Weeds: the Story of Outlaw Plants [1], inspired us to study the weeds in the garden, to better understand biological invasion and the influence of human activities on environment. We used DNA barcoding to determine the species and their origins. DNA barcoding is a taxonomic method that uses a short genetic marker in an organism’s DNA to identify it as belonging to a particular species.[2]

METHODS

1. Specimen collection: We chose plants that grew in the sidewalks, because they were not grown on purpose. *
2. DNA Extraction: To test DNA extraction methods, we use both silica and whatman for DNA purification.
3. PCR: We used 2 primer sets that had M13F-M13R tails: matK- expected size 888 bp, rbcl- expected size 671bp.
4. Gel Electrophoresis
5. DNA sequencing
6. Upload the sequence and analyse data with dnasubway.dnalcasia.org

RESULT

To test DNA extraction methods, we use both silica and whatman for DNA purification. In trial 1, the success rate of silica outweighed that of whatman. Based on this result, we used silica for trial 2.

Figure 1, 2 & 3: Images of gel electrophoresis; Table 1, 2 & 3: The result of PCR and analysis of figure 1, 2 & 3; The identification numbers on figure 1, 2 & 3 match the numbers in Column A in table 1, 2 & 3; √ means expected bands were shown on the images. * These data are from dnasubway.dnalcasia.org. * based on the results of group 1.

<table>
<thead>
<tr>
<th>#</th>
<th>Species [3]</th>
<th>Aligned bp</th>
<th>Mismatches</th>
<th>% similar</th>
</tr>
</thead>
<tbody>
<tr>
<td>1-1</td>
<td>Euphorbia serpillifolia</td>
<td>573</td>
<td>*2</td>
<td>99.96%</td>
</tr>
<tr>
<td>1-2</td>
<td>Acalypha australis</td>
<td>573</td>
<td>*0</td>
<td>100.0%</td>
</tr>
<tr>
<td>1-4</td>
<td>Typha angustifolia</td>
<td>581</td>
<td>*0</td>
<td>100.0%</td>
</tr>
<tr>
<td>1-5</td>
<td>Hieracium bifidum</td>
<td>594</td>
<td>*4</td>
<td>99.33%</td>
</tr>
<tr>
<td>1-6</td>
<td>Sonchus oleraceus</td>
<td>581</td>
<td>*2</td>
<td>99.96%</td>
</tr>
<tr>
<td>1-8</td>
<td>Cynodon transvaalensis</td>
<td>580</td>
<td>*0</td>
<td>100.0%</td>
</tr>
</tbody>
</table>

For sample 1-5, the results are different. The result of matK is more credible with 0 mismatches. For sample 1-6, we got the same species with different mismatches.

DISCUSSION

1. There are only 4 mismatches between persea floccosa and sample 1-6, even though they are in different orders. Two possible explanations:
   • rbcl genes are conservative.
   • That sequence was mistakenly named as persea floccosa.
2. Plants within a family might have highly different features, for example leaves and sizes. Asterenace plants have similar leaves, so we could not distinguish sample 1-5 and 1-6 solely with pictures of leaves.

CONCLUSIONS

1. Many weeds in this region are exotic or invasive plants.
   • Euphorbia serpillifolia - native to a large part of North America from Canada to Mexico [4]
   • Sonchus oleraceus - native to Europe and western Asia. [4]
   • Cynodon transvaalensis - native to South Africa, Lesotho [4]
2. Some plants acclimated successfully and are often regarded as local plants, for example Euphorbia serpillifolia and Cynodon transvaalensis.

FUTURE DIRECTION

In the future, we would test different gene markers and PCR primers to get more information. We would analyze shared features of invasive plants that account for their tolerance and adaptability.

DNA barcoding can be used to determine the candidate genes for understanding those features. With these data, we can find better method to control weeds and invasive plants.