The Utilization of Polymerase Chain Reaction, DNA Barcoding and Bioinformatics in Identifying Plant Species

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Abstract
Bioinformatics and DNA barcoding is a process used to identify plants, animals, and fungi. DNA barcoding in plants utilizes a key variable region in the genome, the RuBisCo large subunit (RbcL) on Chloroplast DNA. Once the DNA is extracted, Polymerase Chain Reaction (PCR) amplifies that region and that sample is sent off for sequencing. Bioinformatics and DNA barcoding helps taxonomists determine the sequence of the RbcL gene as well as obtain a unique barcode that can be used to identify plants.

Methods

- Collect Sample
- Isolation of DNA
- PCR
- Gel Electrophoresis
- DNA Sequencing
- Bioinformatic Analysis
- DNA Barcoding

Background Information

There are about 400,000 known plant species in the world. Nearly all coniferous plants have been identified, however one-fifth of all vascular plants and an unknown amount of algae remains unnamed.

DNA barcoding and bioinformatics lets scientist identify the species. DNA barcodes are cataloged on the Barcode of Life Database (BOLD), as well as Basic Local Alignment Search Tool (BLAST), which helps analyze, store, and publish records. Using the DNA sequence extracted and these databases we could verify the names of the sample species.

Goals:
- Master the processes of Polymerase Chain Reaction, DNA barcoding and bioinformatics
- Determine whether the Carolina genomic protocol or the Wizard genomic protocol is more efficient
- Use the processes mentioned above to identify campus plant biodiversity.

Discussion
- The Carolina genomic protocol was more efficient than the Wizard genomic protocol.
- If a plant’s DNA wasn’t extracted using one protocol, the other was sufficient to extract the DNA.
- The RbcL gene varied enough across species to identify them.
- A variety of plants were identified across the Northwest Nazarene University campus.
- LT05 was not identified as the DNA was not extracted.

Results

<table>
<thead>
<tr>
<th>Sequence Number</th>
<th>Barcode</th>
<th>Latin Name</th>
<th>Common Name</th>
<th>QR Code</th>
</tr>
</thead>
<tbody>
<tr>
<td>RF01</td>
<td>Ulmus Minor</td>
<td>Field Elm</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RF02</td>
<td>Amelanchier Alnifolia</td>
<td>Western Juneberry</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RF03</td>
<td>Fraxinus Pennsylvanica</td>
<td>Green Ash</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RF04</td>
<td>Acer Pseudoplatanus</td>
<td>Sycamore Maple</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RF05</td>
<td>Malus Pumila</td>
<td>Paradise Apple</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RF06</td>
<td>Acer Platanoides</td>
<td>Norway Maple</td>
<td></td>
<td></td>
</tr>
<tr>
<td>LT01</td>
<td>Symphoricarpos occidentalis</td>
<td>Western Snowberry</td>
<td></td>
<td></td>
</tr>
<tr>
<td>LT02</td>
<td>Berberis thunbergii</td>
<td>Japanese Barberry</td>
<td></td>
<td></td>
</tr>
<tr>
<td>LT03</td>
<td>Populus tremuloides</td>
<td>Quaking Aspen Tree</td>
<td></td>
<td></td>
</tr>
<tr>
<td>LT04</td>
<td>Arctostaphylos uva-ursi</td>
<td>Pinemat Manzanita Bearberry</td>
<td></td>
<td></td>
</tr>
<tr>
<td>LT06</td>
<td>Koelreuteria elegans</td>
<td>Goldenrain Tree</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Conclusion
- The DNA barcoding with the use of RuBisCo large subunit from the Chloroplast gene was highly successful.
- The DNA barcodes received could be matched with previous submissions on the BOLD and BLAST databases allowing us to confirm plant species.
- Further research can help Northwest Nazarene University identify more plant species on campus.

References


Bio-Rad Barcode Generator

Gibson. How DNA barcoding can boost quality control for medical plant products. 2015.

Acknowledgments
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