The Phylogeny of *Camellia sinensis* Accessions

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Introduction

A research study at the University of Florida is working with varieties of *Camellia sinensis*, the tea plant, to assess how the plants grow in various systems. An understanding of the plant genotypes provides useful information to support observable changes in the phenotype.

Hypothesis

Construction of a molecular phylogeny using the ITSII region to ascertain its ability to differentiate accessions of *Camellia.*

Background Information

Countries such as China and Taiwan rely on *Camellia* as an important domestic cash crop. Foreign tea products often vary in quality and attempt to masquerade as higher quality Asian-produced teas. The convoluted phylogeny of *Camellia* lacks consensus on the subspecies level which creates issues of quality control, domestic tea reputation, and loss of consumer rights (Lee et al., 2017).

Methods

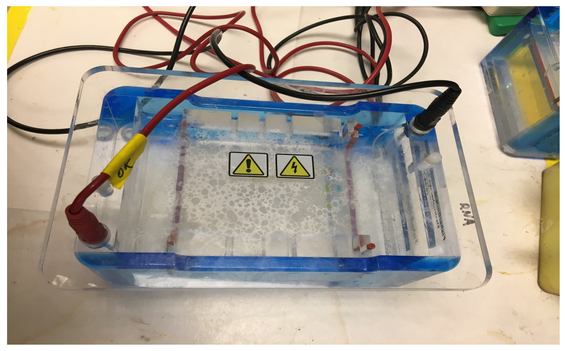
1. Obtain 2.5 cm samples of *C. sinensis var. Assamica* and *C. sinensis var. Fairhope* leaf tissue.
2. Use CTAB extraction method to isolate genomic DNA.
3. Prepare PCR solution using 2x phire plant direct PCR master mix and Bel-1 and Bel-3 primers.
4. Run PCR using conditions specified in Lee et al. paper.
5. Run a gel electrophoresis using 10 µl of PCR solutions and 100 bp ladder.
6. Elute DNA from gel and send to sequencing lab.
7. Compare sequences using MEGA X software and construct a phylogenetic tree.

Main Conclusion

Data suggest the ITSII region was amplified in both accessions.

A phylogeny comprising the UF and Lee accession data will (1) help categorize genotypes and correlate them with phenotypic responses in UF study and (2) help refine and accurately differentiate the Camellia phylogeny on the subspecies level.

Images



Results

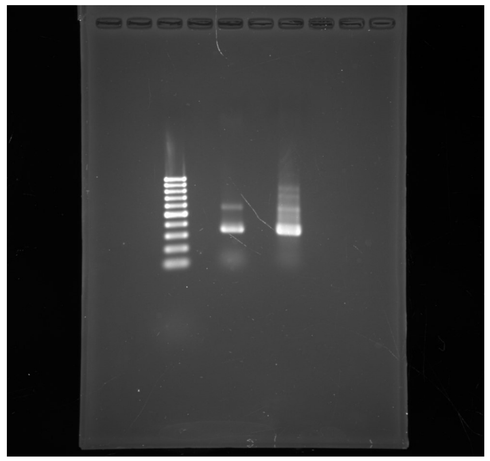


Figure 1. A gel electrophoresis showing a 100 bp ladder on the left, the *Assamica* sample in the middle, and the *Fairhope* sample on the right.

- The *Assamica* and *Fairhope* samples produced bands at approximately 360 bp.

Conclusion/Takeaway

- The data will show whether the ITSII region is capable of accurately differentiating *Camellia* on the subspecies level. The sequence data will also be useful in correlating genotypes to phenotypic responses in the UF study.
- Next steps include isolating DNA from the 18 other accessions involved in the UF study to gain a better understanding of how differences in genotypes influence phenotypic responses.

Works Cited

- Lee, Shih-Chieh, et al. “DNA Barcode and Identification of the Varieties and Provenances of Taiwan's Domestic and Imported Made Teas Using Ribosomal Internal Transcribed Spacer 2 Sequences.” *Journal of Food and Drug Analysis*, vol. 25, no. 2, 2017, pp. 260–274., doi:10.1016/j.jfda.2016.06.008.