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Cold Spring Harbor Laboratory
DNA LEARNING CENTER

Spilling The Tea

Investigating Unlisted Ingredients in Tea

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Abstract

Although food labeling is required for all prepared foods in the USA, products such as tea are exempt from listing all ingredients if they are determined to contain a negligible nutritional value. The aim of this project was to test commercial tea samples to identify their main ingredients.

We isolated DNA from 27 tea samples using an at-home extraction method. 22 (81%) of these samples yielded *rbcl* and/or *matK* barcodes using a standard PCR protocol. Of these 22 barcodes, 10 (45%) did not match to any listed ingredients. Our results show that since tea manufacturers are not required to list all ingredients on their labels, there may be ingredients present which are not included on the label.

Introduction

Tea is an aromatic beverage that comes from boiling water over fresh leaves of *Camellia sinensis*. For many centuries tea has been consumed for medicinal reasons, and modern research suggests that plant compounds in tea play a role in reducing the risk of chronic conditions such as cancer, obesity, diabetes, and heart illnesses (1). In 2019, Americans consumed more than 3.8 billion gallons of tea (2).

Under the Federal Food, Drug, and Cosmetic Act, food labeling is required for most prepared foods. However, coffee, tea, and spices may be exempt from FDA nutrition labeling requirements if the ingredients are deemed to contain a "negligible" nutritional content (3). Serious illness and fatalities have been known to occur after drinking herbal teas, due to causes such as allergic reactions, or substitution with toxic ingredients.

DNA barcoding is a method which can be used to identify specimens which are morphologically unidentifiable (4). The standard plant barcodes, *rbcl* and *matK* can be compared to an existing database of sequences in order to determine the identity of the unknown material.

Our study investigates whether commercially available teas contain ingredients that are not listed on their labels.

Methodology

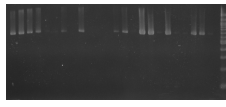
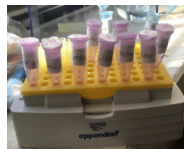
Tea bags were purchased from local stores and online.

DNA extraction from tea samples was done at home using rapid DNA extraction method which isolates DNA using chromatography paper

PCR was performed to amplify *rbcl* and *matK* barcode sequences for each sample, and gel electrophoresis was used to visualize results

Resulting sequences were trimmed and assembled using DNA Subway.

BLAST results were used to identify the main ingredient in the tea.



Clockwise from top left: Examples of commercial tea bags available for purchase online; Materials used during at-home extraction (chromatography paper discs and plastic pestles for grinding samples); Image of gel electrophoresis showing amplification of *rbcl* barcode; Extracted DNA suspended in TE buffer

Results

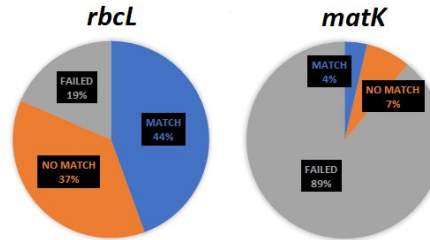


Figure A. Identification results for *rbcl* and *matK* barcodes. We considered a BLAST identification as a match if the top result was in the same genus as one of the listed ingredients. Results were considered not a match if they were a genus not listed on the label. A number of samples failed to sequence.

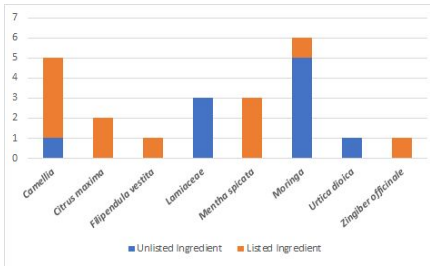


Figure B. Tea ingredients identified based on BLAST results for *rbcl* barcode.

Discussion and Conclusion

Overall, a significant percentage of our samples contained ingredients which were not listed on the label. Consumers, especially those with allergies or health concerns, should be mindful of this when consuming new teas.

This study tested the use of at-home rapid DNA extraction method, which we were able to perform at home, with minimal supplies. There may have been higher possibility of contamination between samples, as well as a presumed loss of yield compared to usual laboratory methods of DNA extraction.

However, overall this method proved to be effective for extracting amplifiable DNA.

The sequencing success rate for *rbcl* was considerably higher (20/27) than that of *matK* (3/27). This is likely due to the lower universality of *matK* primers.

The samples which failed to sequence does not indicate that there is no DNA present in those samples. Instead, it may mean that the sample contains DNA which is degraded due to processing methods, or it may be a failed extraction due to the method we used.

A major limitation of DNA barcoding is that only a single sequence can be retrieved for each sample. In a sample with multiple ingredients, we attempted to separate out distinct fragments, but this proved difficult in many samples.

References

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