

FONTBONNE HALL ACADEMY The Phylogeny of Lonicera Fragrantissima Alessandra Antonacci¹, Alanna McGovern¹, Gina Verrengia¹

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Abstract

Lonicera Fragrantissima is an unbarcoded species. Barcoding will allow scientists to identify the species as well as make comparisons among other species. Through this experiment, a novel sequence of *Lonicera* Fragrantissima was discovered. We are currently in the process of publishing this study to GenBank, and have been provided with a manuscript number.

Introduction

Lonicera Fragrantissima is a species of the *Caprifoliaceae,* family. The *Lonicera* family is known specifically for its ability to reduce inflammation and digestive disorders. This plant can be used to reduce inflammations caused by headaches, diabetes, arthritis, and urinary disorders. Studies show that the Lonicera is very high in disease-fighting antioxidants. The plant is said to act as an immunomodulatory agent that helps to produce natural killer cells, white blood cells, specifically lymphocytes, that have the ability to kill viruses. As a part of this *Caprifoliaceae* family, we hypothesize *Lonicera Fragrantissima* also hosts a multitude of medicinal properties.

Methods & Materials

- Extract DNA from *Lonicera Fragrantissima* leaf sample.
- Perform PCR replication and amplification
- Upload results on blue line of DNA Subway.
- Use MUSCLE BLAST Alignment to analyze differences between consensus sequence and Lonicera Fragrantissima. Find that Lonicera Fragrantissima is not the consensus.
- Use phylogenetic trees ML and NJ to analyze evolutionary relationships and common ancestors.

Results Sequence Variation Consensus 1. Ginkgo-Ginkgoaceae . Rice-Poaceae 3. Sunflower-Asteraceae 0. Coffee-Rubiacea 1. Grape-Vitacea 7. GOJ-00 30. GQ997430. 31. GO997430.1llo 32. HM228467.1|Ionicera_japonica 0. Magnolia-Magnoliaceae

The consensus sequence is derived from aligning all of the sequences of the species and determining the most frequent nucleotide similarities. On the alignment, the talvaceae Cotto consensus is indicated by the light grey space. The MUSCLE alignment shows that there are many species in the data that are under the same consensus sequence because they Ginkgo-Ginkgoaceae (outgroup) share all of the same nucleotides. The colored bars indicate Some plants, such as the *Lonicera Japonica*, appear multiple the location of the sequence where a species has a times on the alignment chart and the phylogenetic trees different nucleotide from the consensus, while the grey because there are multiple specimens within the species of bars show the nucleotides that are the same as the plant. For example, within the *Lonicera Japonica* is the consensus. Adenine is shown in green, thymine is shown in Lonicera Japonica var. Chinensis. According to the alignment red, cytosine is shown in blue, and guanine is shown in chart they share exact nucleotides, which is why they are black. Lonicera Canadensis and Lonicera Nigra share many present on the same branch under the general name of of the same nucleotide bases as Lonicera Fragrantissima, Lonicera Japonica. so they are closely related to it. The presence of the The results of the gel consensus sequence is most likely due to the plants with show the close relation to the samples the consensus sequence having the same genus- Lonicera.

Fontbonne Hall Academy, Mrs. Ashkenazy

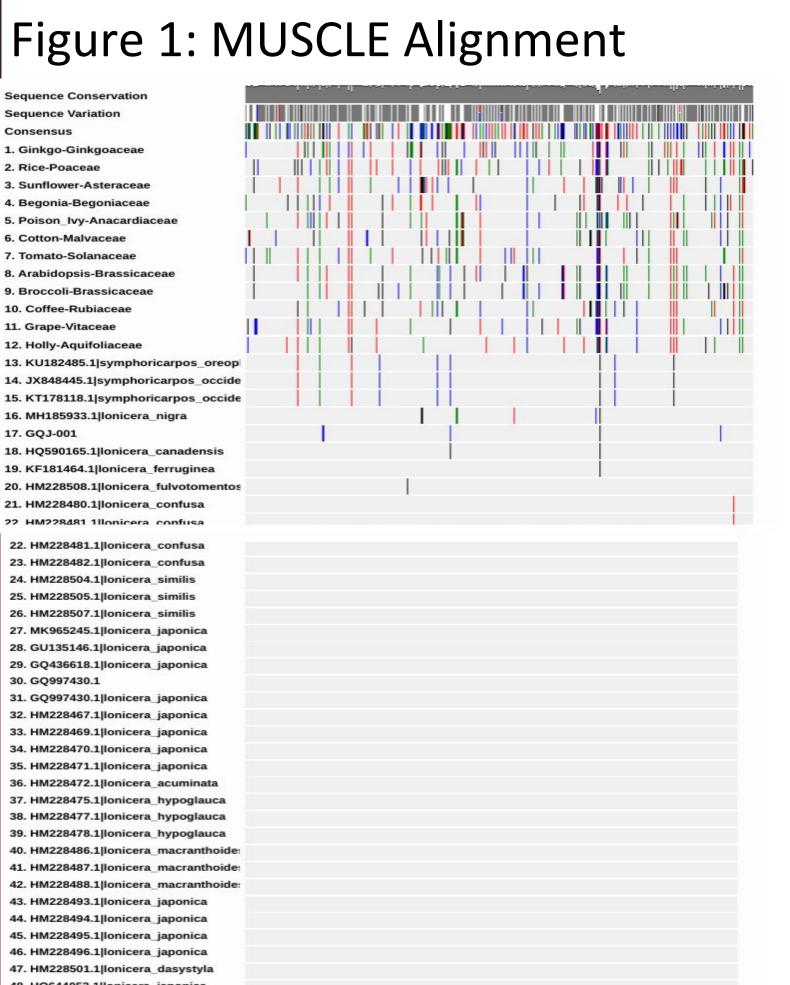
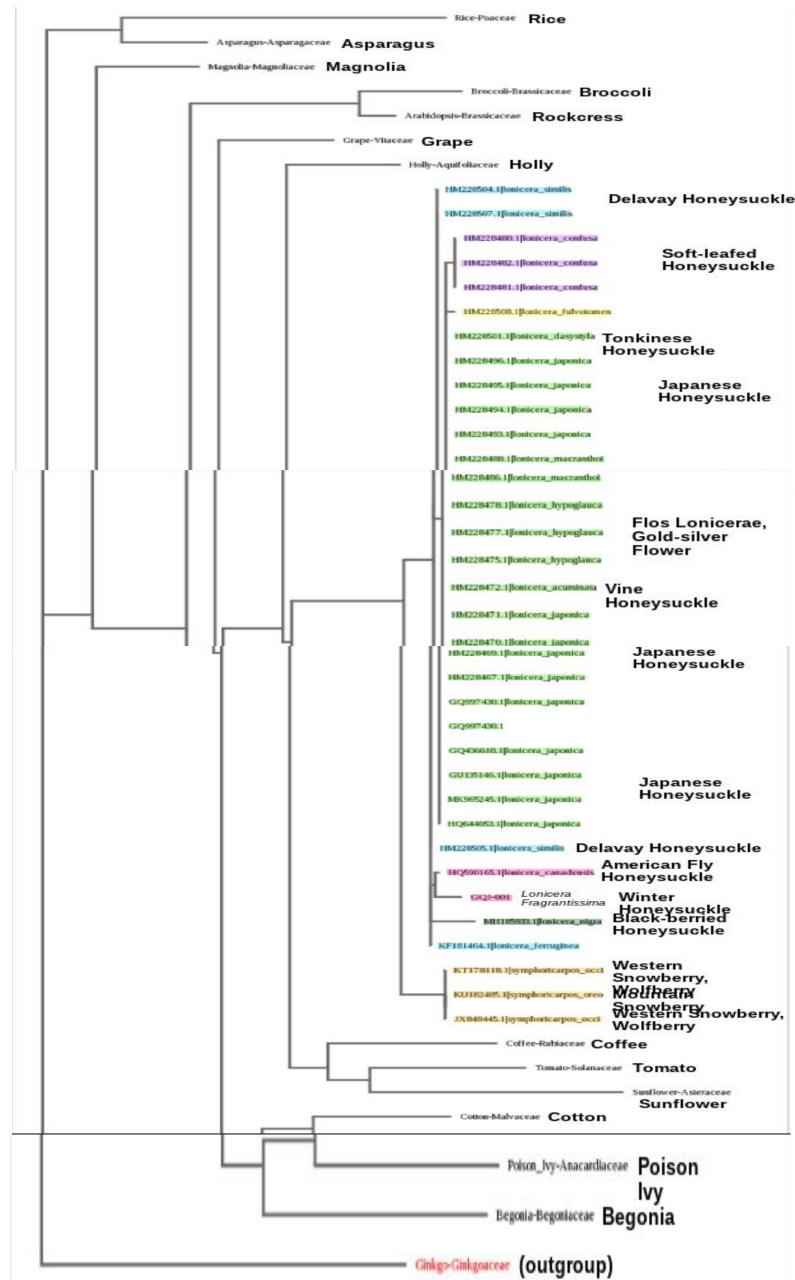
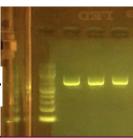


Figure 2: Phylogenetic Tree ML





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Discussion

The hypothesis of this study was that barcoding the species *Lonicera* Fragrantissima can lead to important scientific discoveries by learning new properties about the species and comparing it to other species. The gaps in understanding in this study are related to the definitive presence of these medicinal properties, as well as the presence of saponins and caffeine in the tea of Lonicera Fragrantissima.

Medicinal properties of the closely related Lonicera Japonica have been, widely researched .The nucleotide bases of *Lonicera Japonica* on the alignment were regarded by DNA Subway as the consensus sequence, as earlier stated. In the analysis of the MUSCLE chart, it is noted that few nucleotides differ between the consensus sequence and Lonicera Fragrantissima sequence. The two plants that Lonicera Fragrantissima shared the most nucleotides with on the alignment, Lonicera Nigra and Lonicera Canadensis, are also noted to share the medicinal properties of *Lonicera Japonica*. With the presence of the MUSCLE chart and the phylogenetic tree, close phylogeny may suggest that these medicinal properties are shared.

References

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