

Complete chloroplast genome of sympetalous plant from Central China

June 10 2021

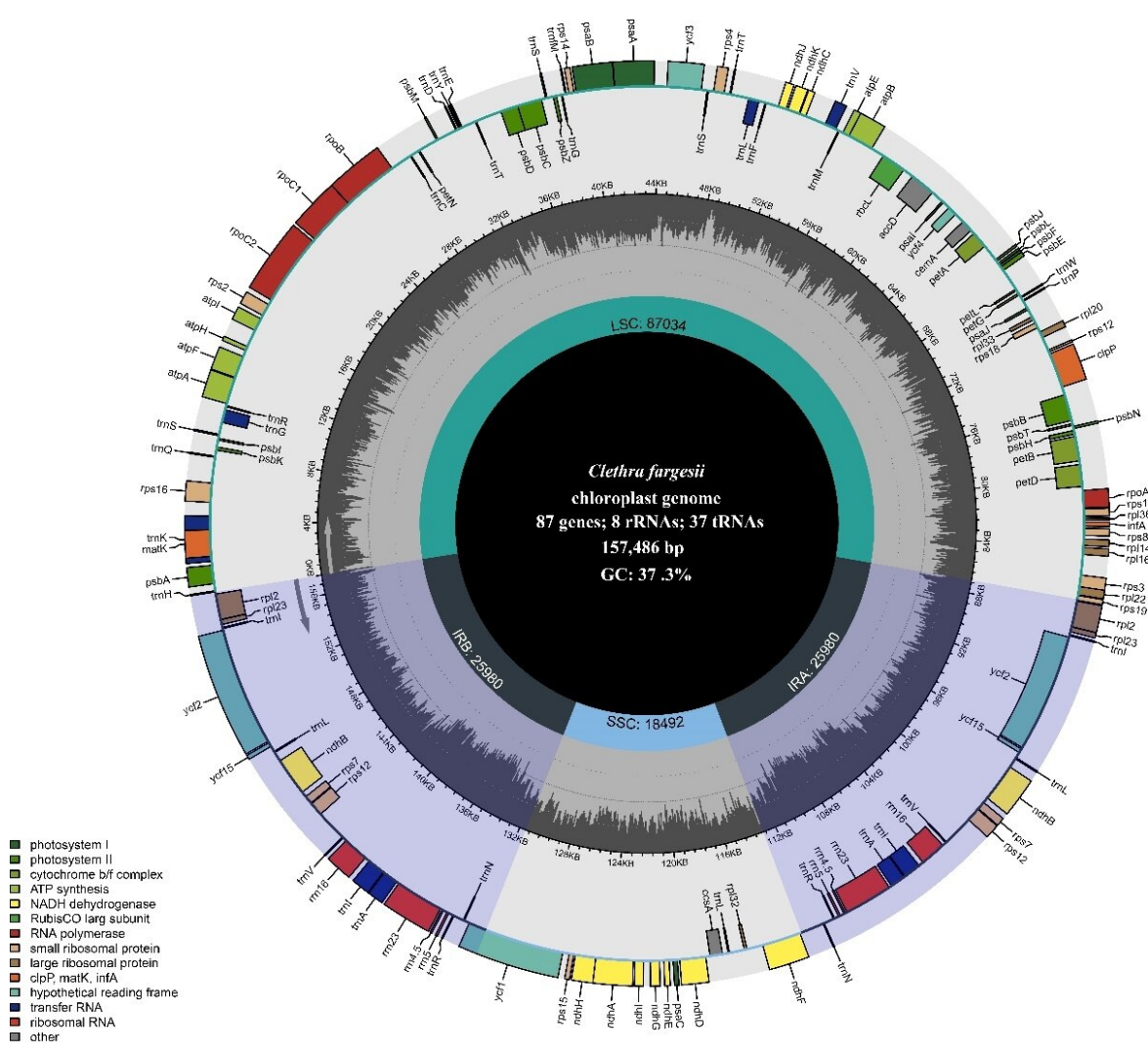


Figure 1. The chloroplast genome map of *Clethra fargesii*. Credit: DING Shixiong

Clethra fargesii Franch., in the family Clethraceae, is an important plant with ornamental value and environmental adaptability that widely distributed in mountainous areas of Central China. So far, *Clethra delavayi* Franch. is the only complete chloroplast genome that has been sequenced with paucity in the available DNA fragments of *Clethra*. Therefore, there is a need to sequence more chloroplast genomes of *Clethra* species for further study for the family.

The East African Flora and Taxonomy Research Group from the Wuhan Botanical Garden reported the complete chloroplast [genome](#) of *C. fargesii* and [comparative analysis](#) for the genome features of *Clethra* species with the closely related species in Ericales.

The complete chloroplast genome of *C. fargesii* is 157,486 bp in length, annotated with 112 single-copy genes, including 80 protein-coding genes, 30 tRNA genes, and four rRNA genes.

The number of genes, GC content and codon usage bias of *C. fargesii*, are highly similar to the other family species in the order Ericales. Also, the chloroplast genome is highly conserved in some aspects by alignment and rearrangement, selection pressure, and nucleotide diversity analysis.

Seventy-three microsatellite sequences (SSR) and seven regions with high nucleotide diversity are identified in this genome, which could be used as potential markers for the identification and phylogeny of *Clethra* species. The [phylogenetic tree](#) in Ericales is reconstructed based on the 75 protein-coding sequences of the chloroplast genome, which supports *Clethra* and Ericaceae are the sister groups.

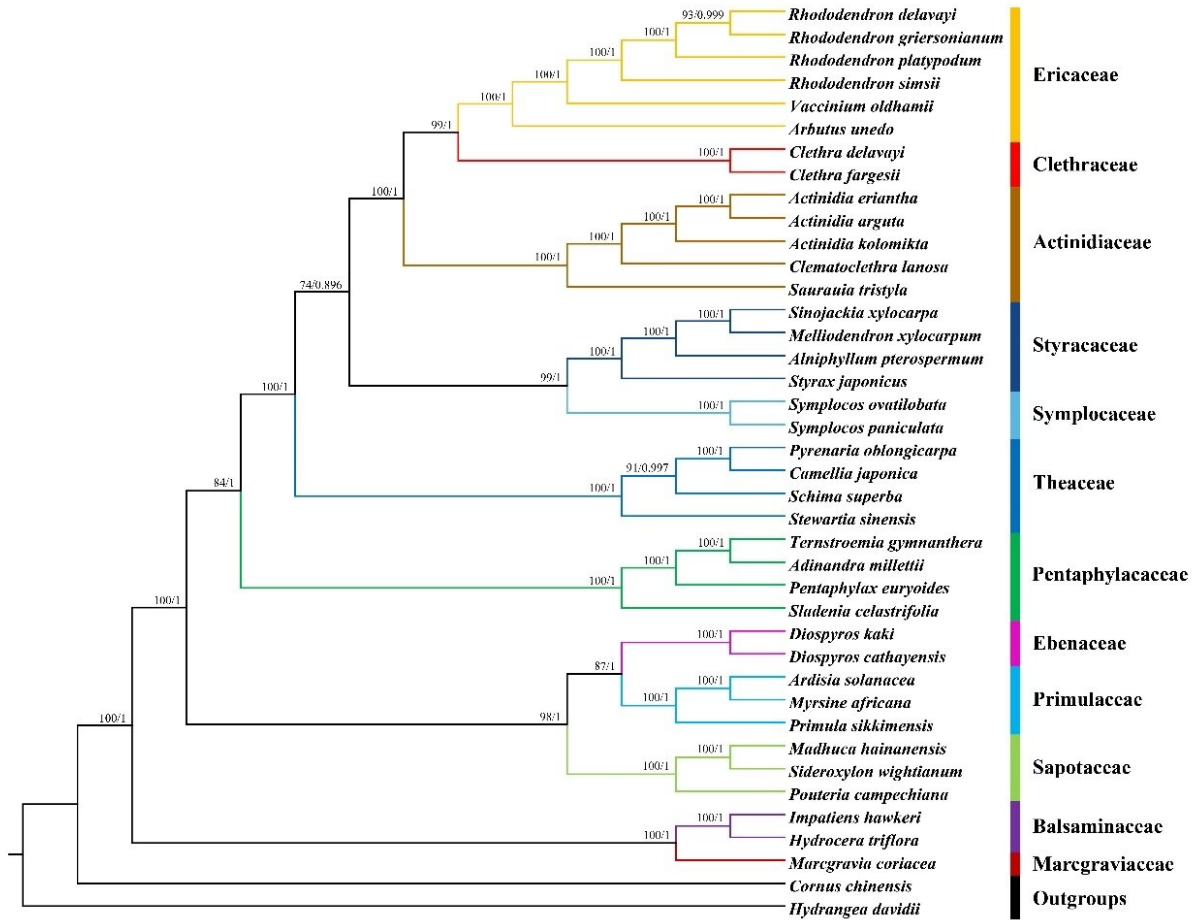


Figure 2. The phylogenetic tree is based on the 75 protein-coding sequences of chloroplast genomes of 40 Ericales species using maximum likelihood and Bayesian methods. Credit: DING Shixiong

This study provides important data for the study of [chloroplast](#) genomes of *Clethra* and will be of great significance for the phylogenetic study and species evolution of this genus.

The study, titled "Complete Chloroplast Genome of *Clethra fargesii* Franch., an Original Sympetalous Plant from Central China: Comparative Analysis, Adaptive Evolution, and Phylogenetic

Relationships," was published in *Forests*.

More information: Shixiong Ding et al, Complete Chloroplast Genome of *Clethra fargesii* Franch., an Original Sympetalous Plant from Central China: Comparative Analysis, Adaptive Evolution, and Phylogenetic Relationships, *Forests* (2021). [DOI: 10.3390/f12040441](https://doi.org/10.3390/f12040441)

Provided by Chinese Academy of Sciences

Citation: Complete chloroplast genome of sympetalous plant from Central China (2021, June 10) retrieved 25 April 2024 from <https://phys.org/news/2021-06-chloroplast-genome-sympetalous-central-china.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.