The complete chloroplast genome of *Lonicera fulvotomentosa* Hsu et S. C. Cheng and its phylogenetic analysis

Zhengwen Yu, Yin Yi and Lei Gu

School of Life Science, Guizhou Normal University, Guiyang, China

**ABSTRACT**

*Lonicera fulvotomentosa* Hsu et S. C. Cheng is widely used as an edible and medicinal food in China and also displays excellent pharmacological activities. The phylogenetic relationship between *L. fulvotomentosa* and other family members remains unclear. In this work, we assembled the cp genome of *L. fulvotomentosa* using the high-throughput Illumina pair-end sequencing data. The circular cp genome is 155,102 bp in size, including a large single-copy (LSC) region of 88,906 bp and a small single-copy (SSC) region of 18,628 bp, which were separated by two inverted repeat (IR) regions (23,784 bp each). A total of 129 genes were predicted, including eight ribosomal RNAs (rRNAs), 39 transfer RNAs (tRNAs), and 82 protein-coding genes (PCGs). Furthermore, phylogenetic analysis revealed that *L. fulvotomentosa* formed a different clade from other two congeneric species (*Lonicera confuse* and *Lonicera japonica*). This study provides useful information for future genetic study of *L. fulvotomentosa*.

**KEYWORDS**

*Lonicera fulvotomentosa*; Caprifoliaceae; complete chloroplast genome; phylogenetic

**ARTICLE HISTORY**

Received 14 December 2020
Accepted 26 January 2021

**CONTACT** Yin Yi, yiyin@gznu.edu.cn; Lei Gu, leigu1216@nwafu.edu.cn School of Life Science, Guizhou Normal University, Guiyang, China

**ARTICLE INFORMATION**

MITOGENOME ANNOUNCEMENT

**OPEN ACCESS**

**MITOCHONDRIAL DNA PART B**

**VOL. 6, NO. 3, 842–843**

**https://doi.org/10.1080/23802359.2021.1884027**
trees through maximum-likelihood (ML) analysis. The ML tree was performed using RAxML (Version 8.0.19, GTRGAMMA) (Stamatakis 2014) with 1000 bootstrap replicates. The phylogenetic tree indicated that _L. fulvotomentosa_ belongs to genus _Lonicera_ (Figure 1) and formed a different clade from _Lonicera confuse_ and _Lonicera japonica_ (Figure 1).

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

**Funding**

This study was supported by the National Natural Science Foundation of China under Grant [Nos. U1812401 and 32060068] and the Guizhou Provincial Science and Technology Foundation under Grant [No. 2020-1Y096].

**Data availability statement**

The annotated chloroplast genome data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov](https://www.ncbi.nlm.nih.gov) under the accession number MW186760. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA674956, SRX9460984, and SAMN16684233, respectively.

**References**

Jin JJ, Yu WB, Yang JB, Song Y, dePamphilis CW, Yi TS, Li DZ. 2019. GetOrganelle: a fast and versatile toolkit for accurate de novo assembly of organelle genomes. bioRxiv.256479.

Kong D, Li Y, Bai M, Deng Y, Liang G, Wu H. 2017. A comparative study of the dynamic accumulation of polyphenol components and the changes in their antioxidant activities in diploid and tetraploid _Lonicera japonica_. Plant Physiol Biochem. 112:87–96.

Lin LM, Zhang XG, Zhu JJ, Gao HM, Wang ZM, Wang WH. 2008. Two new triterpenoid saponins from the flowers and buds of _Lonicera japonica_. J Asian Nat Prod Res. 10(9–10):925–929.

Peng LY, Mei SX, Jiang B, Zhou H, Sun HD. 2000. Constituents from _Lonicera japonica_. Fitoterapia. 71(6):713–715.

Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics. 30(9):1312–1313.

Tillich M, Lehwark P, Pellizzer T, Ulbricht-Jones ES, Fischer A, Bock R, Greiner S. 2017. GeSeq- versatile and accurate annotation of organelle genomes. Nucleic Acids Res. 45(W1):W6–W11.

Xiong J, Li S, Wang W, Hong Y, Tang K, Luo Q. 2013. Screening and identification of the antibacterial bioactive compounds from _Lonicera japonica_ Thunb. leaves. Food Chem. 138(1):327–333.

Xu Y, Oliverson BG, Simmons DL. 2007. Trifunctional inhibition of COX-2 by extracts of _Lonicera japonica:_ direct inhibition, transcriptional and post-transcriptional down regulation. J Ethnopharmacol. 111(3):667–670.

Yu Y, Jiang Z, Song W, Yang Y, Li Y, Jiang J, Shi J. 2015. Glucosylated caffeoylquinic acid derivatives from the flower buds of _Lonicera japonica_. Acta Pharm Sin B. 5(3):210–214.

Zheng ZF, Zhang QJ, Chen RY, Yu DQ. 2012. Four new N-contained iridoid glycosides from flower buds of _Lonicera japonica_. J Asian Nat Prod Res. 14(8):729–737.

**Figure 1.** Maximum-likelihood tree based on the complete cp genome sequences of 20 species from the Caprifoliaceae family. GenBank accession numbers are described in the figure. Shown next to the nodes are bootstrap support values based on 1000 replicates.