The complete chloroplast genome of *Lonicera pampaninii* Levl. and its phylogenetic analysis

Chunyan Jiang, Shaoxiong Wu, Xiayu Feng, Chenju Yang and Zhengwen Yu

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

**ABSTRACT**

*Lonicera pampaninii* Levl, a Chinese herbal medicine widely used in the folk, has the effect of clearing away heat and detoxifying similar to other plants of the *Lonicera*. However, its genetic relationship with these plants is unclear. In this work, the cp genome of *Lonicera pampaninii* Levl. was assembled by the high-throughput Illumina pair-end sequencing data. The circular cp genome is 155,249 bp in size, including a large single-copy (LSC) region of 89,068 bp and a small single-copy (SSC) region of 18,635 bp, which were separated by two inverted repeat (IR) regions (23,773 bp each). A total of 120 genes were predicted, including eight ribosomal RNAs (rRNAs), 33 transfer RNAs (tRNAs), and 79 protein-coding genes (PCGs). Furthermore, phylogenetic analysis revealed a strong sister relationship between *L. pampaninii* and other two congeneric species (*Lonicera confusa* and *Lonicera japonica*). This study provides useful information for future genetic study of *L. pampaninii*.

**CONTACT**

Zhengwen Yu, yuzhengwen2001@126.com, School of Life Sciences, Guizhou Normal University, Guiyang, China

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The length of the complete cp genome sequence of *L. pampaninii* is 155,249 bp, consisting of a large single-copy (LSC, 89,068 bp) region, a small single-copy (SSC, 18,635 bp) region, and two inverted repeat (IRA and IRB) regions of 23,773 bp respectively. Totally, 120 genes were predicted, including 79 protein-coding genes (PCGs), eight ribosomal RNA (rRNA) genes, and 33 transfer RNA (tRNA) genes. Among these assembled genes, all rRNAs, three PCGs (rps7, rps12, ndhB, ycf2, and ycf15) and seven tRNAs (trnH-GUG, trnL-CAA, trnV-GAC, trnL-GAU, trnA-UGC, trnR-ACG, and trnN-GUU) were with double copies. Intron-exon analysis showed the majority (103 genes, 86%) genes with no introns, whereas 17 genes (14%) contain introns.

To further understand the cp genome of *L. pampaninii*, 21 cp genome sequences of Caprifoliaceae family (one *Triosteum* species, 13 *Lonicera* species, one *Weigela* species, two species from *Dipelta* genus, one *Heptacodium* species, and three species from *Patrinia* genus,) were downloaded from GenBank to construct the phylogenetic trees through maximum-likelihood (ML) analysis. The ML tree based on GTR + gamma + I model was performed using RAxML (Version 8.0.19) with 1000 bootstrap replicates (Stamatakis 2014). The phylogenetic tree indicated that *L. pampaninii* belongs to *Lonicera* genus (Figure 1), and showed a strong sister relationship between *L. pampaninii* and other two congeneric species (*Lonicera confusa* and *Lonicera japonica*).

**Disclosure statement**

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

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**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov, reference number MZ241298. The associated BioProject, SRA, and Bio-Sample numbers are PRJAN752821, SUB10196548, and SAMN20608006 respectively.

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