The complete chloroplast genome of Lonicera hypoglauca Miq (Caprifoliaceae: Dipsacales) from Guangxi, China

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**ABSTRACT**

*Lonicera hypoglauca* Miq, which is widely distributed in south China, is an important Chinese plant used in traditional medicine. Here we report the first complete chloroplast (cp) genome sequence of this species. The circular cp genome is 154,581 bp in size, including a large single-copy (LSC) region of 88,379 bp and a small single-copy (SSC) region of 18,646 bp, which was separated by two inverted repeat (IR) regions (IRA and IRB, 23,778 bp each). A total of 121 genes were annotated, including 8 ribosomal RNAs (rRNAs), 33 transfer RNAs (tRNAs) and 80 protein-coding genes (PCGs). Phylogenetic analysis of 20 representative members within the Caprifoliaceae showed that *L. hypoglauca* is closely related to the *Lonicera macranthoides*. This study provides important genetic information for future systematic and evolutionary studies of *L. hypoglauca*.

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fully resolved in a clade with *L. macranthoides*, sister to two other species of *Lonicera*, *L. confusa* and *L. japonica* (Figure 1). Compared to other Flos Lonicerae members, *L. hypoglauca* was also fully resolved in a clade with *L. macranthoides* according to *rbcL* gene sequence analysis (Li et al. 2012). Because of the closely evolutionary relationship between *L. macranthoides* and *L. hypoglauca*, in comparison with other DNA barcodes, only the *psbA-trnH* intergenic spacer sequence had appropriate mutation sites to distinguish *L. macranthoides* and *L. hypoglauca* (Sun et al. 2011).

**Disclosure statement**

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

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**Data availability statement**

The complete 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 MW186761. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA674956, SRX9460983, and SAMN16684231, respectively.

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**Figure 1.** Maximum likelihood tree based on the complete cp genome sequences of 20 species from the Caprifoliaceae. GenBank accession numbers follow the binomials included in the figure. Shown next to the nodes are bootstrap support values based on 1,000 replicates.