The complete chloroplast genome of *Cymbidium maguanense* (Orchidaceae)

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**ABSTRACT**

*Cymbidium maguanense* is a valuable orchid endemic to China, with delicate smelling, ivory white flower, and showy yellow labellum. Herein, we reported the complete chloroplast genome of *C. maguanense*. This chloroplast genome was 156,530 bp in length. It presented a typical structure including a large single-copy region (LSC, 85,112 bp), a small single-copy region (SSC, 17,874 bp), and two inverted repeat regions (IRs, 26,772 bp). It contained 138 genes, 37 tRNA, and 8 rRNA with an average GC content of 36.8%. Besides, the phylogenetic analysis showed that *C. maguanense* displayed a closer kinship to *C. eburneum* in the section *Eburnea* under subgenus *Cymbidium*. This chloroplast genome will provide a reference for future studies on species evolution, germplasm resources utilization, and genetic engineering of genus *Cymbidium*.

**ARTICLE HISTORY**

Received 22 January 2020
Accepted 11 February 2020

**KEYWORDS**

*Cymbidium maguanense*; chloroplast genome; phylogenetics

*Cymbidium* is one of the ornamental genus in Orchidaceae, including 3 subgenera and 11 sections in China (Liu et al. 2009). *Cymbidium maguanense* is an epiphytic orchid in *Cymbidium* Sw. sect. *Eburnea* under subgenus *Cymbidium*, distributed in southeast Yunnan at an altitude of 1000–1800 m (Liu 2006). It is very valuable in ornament applications with delicate smelling, ivory white flower, and showy yellow labellum (Chen 2011). *Cymbidium maguanense* is originally described by F. Y. Liu based on a cultivated plant. Its morphology is intermediate between the sympatric species *C. mastersii* and *C. eburneum*, whether it is a natural hybrid is still controversial. Morphological similarity also makes it difficult to be distinguished from related taxa in terms of species identification. The origin and classification of *C. maguanense* 

![Figure 1](https://example.com/figure1.png)

*Figure 1.* Maximum parsimony (MP) phylogenetic tree of 18 chloroplast sequences in *Cymbidium*, with *Pleione bulbocodioides* and *Pleione formosana* as outgroup. *Cymbidium maguanense* was marked with a red circle. Bootstrap support values are shown next to the nodes.

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are unclear. Besides, related genetic information and relationship based on it have not been clearly formulated. Therefore, we reported the complete chloroplast genome of *C. maguanense* to obtain a better understanding of the relationship between *C. maguanense* and its related taxa, and provide a foundation to species evolution, identification, and germplasm diversity of genus *Cymbidium*.

Cultivated plant samples of *C. maguanense* were acquired from Yunnan and preserved at Fujian Agriculture and Forestry University (Voucher specimen: JL-FJ2019-11A, FAFU, 26°20′21.3″ N, 113°12′39.6″ E). DNA from fresh leaves was extracted using a modified CTAB method and sequenced on the BGI-500 platform (BGI, Wuhan, China). Approximately, 6 GB data were generated after removing adapters and unqualified reads by fastp software. Genome sequences were assembled with SPAdes 3.13.1, then annotated for genes and tRNA using Dual Organellar GenoMe Annotator (DOGMA) (Wyman et al. 2004) and Geneious ver. 2020.0.4 (Li et al. 2019), to adjust the starting position by comparing with the complete chloroplast genome of *C. ensifolium* (NC028525).

The complete chloroplast genome of *C. maguanense* (GenBank accession MN885494) was 156,530 bp in length with an average GC content of 36.8%. This plastid genome presented a typical structure, including a length of 85,112 bp large single-copy (LSC) region, a 17,874 bp small single-copy (SSC) region, and two conserved 26,772 bp inverted repeat (IRs). Every part showed unequal GC contents, respectively, LSC-34.3%, SSC-29.6%, and IR-43.1%. The complete chloroplast genome contained 138 genes, 37 tRNA, and 8 rRNA.

*Cymbidium maguanense*, *C. mastersii*, and *C. eburneum* are similar in morphological characters. The classification relationship among them is controversial (Liu et al. 2009; Liu 2006). To determine the phylogenetic position of *C. maguanense*, the complete chloroplast genome of *C. maguanense* was aligned with 17 accessions of *Cymbidium* and 2 other genera (*Pleione bulbocodioides*, *Pleione formosana*) as outgroups using HomBlocks pipeline (Bi et al. 2018). A molecular phylogenetic tree was constructed with the maximum parsimony (MP) in PAUP v4.0b10 (Cummings 2004). The result indicated that *C. maguanense* displayed a more close kinship to *C. eburneum* in the section *Eburnea*, while *C. mastersii* was sister to *C. changningense* and *C. erythryeum* in section *Iridorchis* (Figure 1). These information would provide genomic resources for the evolutionary status, taxonomy, and germplasm resources utilization in genus *Cymbidium*.

**Disclosure statement**

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

**Funding**

This work was supported by Project of National Key R & D Program [No. 2018YFD000401].

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