

## Characterization of the complete chloroplast genome of *Dendrobium christyanum* and its phylogenetic analysis

Feng-Ping Zhang\*, Zi-Li Yin\* and Hong-Ping He

Yunnan Key Laboratory of Dai and Yi Medicines, College of Traditional Chinese Medicine, Yunnan University of Chinese Medicine, Kunming, Yunnan, China

### ABSTRACT

*Dendrobium christyanum* H.G. Reichenbach (Orchidaceae) is used as a source of the Chinese traditional medicine. Here, we report that the complete chloroplast (cp) genome sequence of *D. christyanum* is 157972 bp in length with 134 genes, of which 114 are unique genes (80 protein-coding genes, 30 tRNAs, and 4 rRNAs). Phylogenetic analysis indicated that *D. christyanum* was closely related to *D. strongylanthum*, and *D. longicornu*. The newly sequenced cp genome will be useful for the phylogenetic and genetic conservation studies of *Dendrobium*.

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The orchid genus *Dendrobium* Sw. (Epidendroideae, Orchidaceae) is one of the largest genera in flowering plants, over 1450 species that are mainly distributed in Asia and Oceania (Cribb and Govaerts 2005; Xiang et al. 2016). Approximately 90 species of *Dendrobium* are found in China (Zhu et al. 2009; Zhang and Feng 2018). Most members of this genus have a high ornamental value (Teixeira da Silva et al. 2016), and some *Dendrobium* species have also the medicinal and pharmaceutical values (Teixeira da Silva et al. 2015). *Dendrobium christyanum* H. G. Reichenbach (1882) is an medicinal orchid plant, its short fleshy stems are very suitable for processing into Fengdous (Fengdous, fresh stems of *Dendrobium* species are processed into the dry products, which have the effects of stimulating saliva, tonifying stomach, and relieving the cough, etc.) (Bao et al. 2005). In this study, we sequenced and assembled the complete chloroplast (cp) genome sequence of *D. christyanum*, and assessed phylogenetic position within *Dendrobium*, and it could provide useful genomic resources for future studies on identification, phylogeny and evolution of *Dendrobium* species.

The plants of *D. christyanum* were collected from Jiangcheng County, Puer City, Yunnan Province, China (101° 51'44"E, 22°35'6"N) and grow in the green house in the Kunming Institute of Botany, Chinese Academy of Sciences. A specimen was deposited at the Herbarium of Kunming Institute of Botany, Chinese Academy of Sciences (KUN, <http://www.kun.ac.cn/>, contact person: Feng-Ping Zhang, email: [zhangfengping8008@163.com](mailto:zhangfengping8008@163.com)) under the voucher number 1511669). Fresh leaves of *D. christyanum* were harvested for the total genomic DNA extraction using the modified CTAB procedure (Doyle and Doyle 1987) and sequenced on Illumina Novaseq 6000 platform (Illumina, San Diego, CA, USA). The complete chloroplast

genome was assembled with SPAdes (Bankevich et al. 2012, version: 3.13.0) referencing cp genome of closely related *Dendrobium* species and the genome was annotated with CpGAVAS2 (Liu et al. 2012). Finally, we submitted the complete cp genome sequence to the GenBank with accession number MZ241112.

The cp genome sequence of *D. christyanum* is 157972 bp in length, which presented a typical quadripartite structure, containing a large single-copy region (LSC, 87,717 bp), a small single-copy region (SSC, 18,313 bp), and two inverted repeat regions (IRA and IRB, 25,971 bp). Besides, the cp encoded 134 genes, of which 114 are unique genes (80 protein-coding genes, 30 tRNAs, and 4 rRNAs). In addition, the overall GC content of the whole plastome is 37.23%, whereas the corresponding values of the LSC, SSC, and IRs regions are 34.92, 30.74 and 43.42%, respectively.

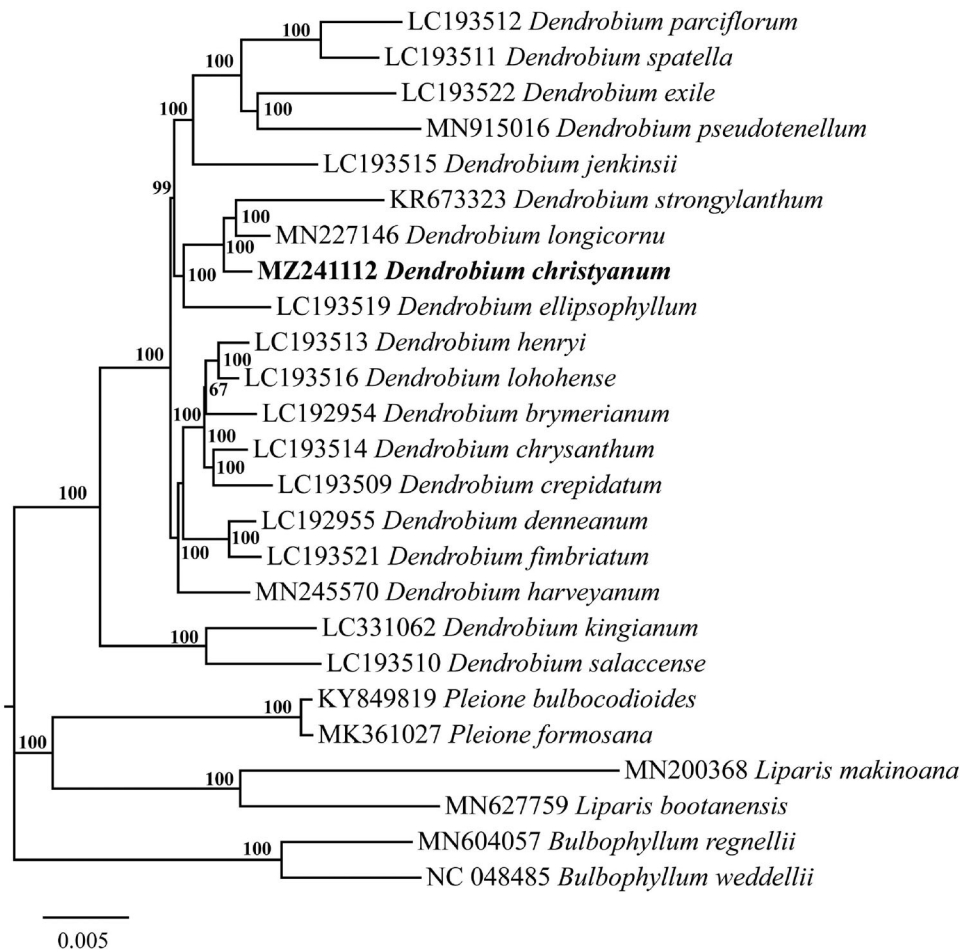
To detect its phylogenetic position, the sequences of *D. christyanum* and other 18 *Dendrobium* species (downloaded from NCBI GenBank) were aligned by MAFFT v7.450 software (Katoh and Standley 2013), and two *Pleione* species, two *Bulbophyllum* species, two *Liparis* species were selected as outgroup. The phylogenetic tree was constructed by IQ-tree (v2.1.3, <http://www.iqtree.org/>) with the maximum-likelihood (ML) method. The model GTR+G+I was selected for ML analyses with 5000 ultrafast bootstraps replicates. As expected, *D. christyanum* was more closely related to *D. strongylanthum*, and *D. longicornu* with 100% bootstrap support (Figure 1), which was consistent with the topology based on molecular analyses of the ITS of the nuclear ribosomal and plastid DNA (*rbcl*, *matK-trnK*, *trnH-psbA*, and *trnL-F*) in Chen et al. (2016). This newly reported cp genome of *D. christyanum* is of great benefit to further investigation on its phylogeny and conservation in *Dendrobium*.

**CONTACT** Hong-Ping He  [hehongping@yahoo.com](mailto:hehongping@yahoo.com)  Yunnan Key Laboratory of Dai and Yi Medicines, College of Traditional Chinese Medicine, Yunnan University of Chinese Medicine, Kunming, Yunnan, China

\*These authors have contributed equally to this work.

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**Figure 1.** Phylogenetic position of *Dendrobium christyanum* inferred by maximum likelihood (ML) of complete cp genome. The bootstrap values are shown next to the nodes.

## 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> under the accession no. MZ241112. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA739017, SRR14859971, and SAMN19769087, respectively.

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