The complete chloroplast genome sequence of *Dendrobium wangliangii* (Orchidaceae)

Shi-Cheng Shao\(^a\), Lu Tang\(^a,b\) and Yan Luo\(^a,c\)

\(^a\)Gardening and Horticulture Department, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Yunnan, P.R. China; \(^b\)College of Forestry, Shanxi Agricultural University, Shanxi, P.R. China; \(^c\)Gardening and Horticulture Department, Core Botanical Gardens, Chinese Academy of Sciences, Yunnan, P.R. China

**ABSTRACT**

*Dendrobium wangliangii* is a rare orchid species with extremely small populations, endemic to China. In this study, the complete chloroplast (cp) genome sequence and the genome features of *D. wangliangii* were analyzed. The whole cp genome sequence of *D. wangliangii* is 160,052 including a large single-copy region (LSC, 87,525 bp), a small single-copy region (SSC, 18,373 bp), and a pair of repeat regions (IRs, 27,077 bp, each). The contents of four bases in cpDNA were A (30.9%), C (18.9%), G (18.3%) and T (31.9%), respectively. The total content of GC is 37.1%. The cp genome contains 129 genes, consisting of 124 unique genes (78 protein-coding genes, 38 tRNAs, and 8 rRNAs). Phylogenetic analysis showed that *D. wangliangii* nested with other *Dendrobium* spp. and was closely related to *D. ellipsoidophyllum*, *D. wattii* and *D. longicornu*.

**KEYWORDS**

*Dendrobium wangliangii*; chloroplast genome; phylogenetic analysis; Orchidaceae

---

*Dendrobium* is one of the largest genera in the orchid family. It consists of approximately 1500 species, mainly distributed in tropical and subtropical regions of the world (Pridgeon et al. 2014). Seventy-eight species of this genus in 14 sections were recorded in China (Zhu et al. 2009). However, molecular phylogenies of the combination of partial chloroplast marks and ITS-rDNA are not always consistent to morphological sections (Xiang et al. 2016). Additional molecular marks such as complete chloroplast genome sequences are needed for phylogenetic and evolutionary analyses.

*Dendrobium wangliangii* was discovered as a new species in section *Dendrobium* in 2008 (Hu et al. 2008). *Dendrobium wangliangii* is distributed in specific habitats with narrow distributions, e.g. the Jinshajiang dry-hot valley in Luquan County, Kunming, Yunnan Province (Wang et al. 2019), and the populations are extremely small. Given the special features of morphology and the nature of drought tolerance, phylogenetic position of *D. wangliangii* is unknown. In this study, a complete chloroplast genome (cp genome) sequence of *D. wangliangii* was characterized and analyzed for its phylogenetic position.

The leave samples of *D. wangliangii* was collected in Fumin County, Yunnan, China (25°20′19″N, 102°27′26″E). Total genomic DNA from leaf was extracted using Tiangen DNA kit (TIANGEN, China), and sequenced by the Illumina Hiseq 2500 sequencing platform (Illumina, CA, USA) at Personal Biotechnology Co., Ltd (Shanghai, China). The DNA of *D. wangliangii* sample was preserved in Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences with collection number JSJSH17122018-1. The sequence data were *de novo* assembled to a complete and circular cp genome using GetOrganelle (Jin et al. 2020). Gene annotation was accomplished using GeSeq with default sets (Tillich et al. 2017), and manually checked in Geneious Primer 2020 (Kearse et al. 2012). Sequences of Coding regions (CDS) and rRNAs were extracted, aligned and concatenated in Geneious Primer 2020.

The whole cp genome sequence of *D. wangliangii* (GenBank accession no. MT798588) is totally 160,052 bp in length, in which the contents of four bases in cpDNA were A (30.9%), C (18.9%), G (18.3%) and T (31.9%), respectively. The total content of GC is 37.1%. The structure of cp genome includes a large single-copy region (LSC, 87,525 bp), a small single-copy region (SSC, 18,373 bp), and a pair of inverted repeat regions (IRs, 27,077 bp, each). Typical code ATG was used as the initiator codon and typical code TAA as the terminator codon in all the 78 protein-coding genes. The gene order and features of the *D. wangliangii* are consistent with congener species in *Dendrobium* (Niu, Xue et al. 2017; Niu, Zhu et al. 2017).

To further investigate its phylogenetic position, the complete chloroplast genomes from 22 species of subfamily Epidendroideae, e.g. 16 *Dendrobium* species, three *Bulbophyllum* species and three *Cymbidium* species, and two species of *Paphiopedilum* from subfamily Cyripedioideae as outgroup, were selected to reconstruct the phylogenetic tree. The best-fit model GTR+F+R2 using the Akaike information criterion (AIC) was applied to read the best model to construct maximum likelihood (ML) trees using IQ-TREE 1.6 (Lam-Tung...
Phylogenetic analysis showed that *D. wangliangii* nested in *Dendrobium* clade (Figure 1) and was closely related to *D. ellipsophyllum*, *D. wattii* and *D. longicornu*. The newly reported chloroplast genome of *D. wangliangii* provides important genomic information for *Dendrobium* species phylogenetic and evolutionary analyses.

**Disclosure statement**

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

**Funding**

This study was funded by the National Key R & D Program of China under grants [No. 2017YFC0505204] and the National Natural Science Foundation of China [grant No. 31870183].

**ORCID**

Shi-Cheng Shao  http://orcid.org/0000-0003-3658-5170

**Data availability statement**

The data that support the analyses and results of *Dendrobium wangliangii* in this paper are available in GenBank with accession no. MT798588 (https://www.ncbi.nlm.nih.gov/). Raw sequencing reads was deposited in SRA with BioProject accession: PRJNA659161. (https://www.ncbi.nlm.nih.gov/Traces/study/?acc=PRJNA659161).

**Acknowledgments**

The authors thank Dr. Wen-Bin Yu for help in software applications and Ms. Bi-Ying Yue for lab assistance during DNA extraction. We are also grateful to Mrs. Xiao-Yun Wang from the Wild Orchid conservation Center of Yunnan Fengchunfang Biotechnology Company for providing sample materials.

**References**

Hu GW, Long CL, Jin XH. 2008. *Dendrobium wangliangii* (Orchidaceae), a new species belonging to section *Dendrobium* from Yunnan, China. Bot J Linn Soc. 157(2):217–221.

Jin JJ, Yu WB, Yang JB, Song Y, Yi TS, Li DZ. 2020. Getorganelle: a fast and versatile toolkit for accurate de novo assembly of organelle genomes. Genome Biol. 21(1):241
Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics. 28(12):1647–1649.

Lam-Tung N, Schmidt HA, von Haeseler A, Bui Quang M. 2015.IQ-tree: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol. 32(1):268–274.

Niu Z, Xue Q, Wang H, Xie X, Zhu S, Liu W, Ding X. 2017. Mutational biases and GC-biased gene conversion affect GC content in the plastomes of Dendrobium genus. Int J Mol Sci. 18:2307.

Niu Z, Zhu S, Pan J, Li L, Sun J, Ding X. 2017. Comparative analysis of Dendrobium plastomes and utility of plastomic mutational hotspots. Sci Rep. 7:2073.

Pridgeon AM, Cribb PJ, Chase MW, Rasmussen FN. 2014. Genera Orchidacearum 6. Epidendroideae (part three). Oxford: Oxford University Press.

Tillich M, Lehward 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.

Wang Q, Shao S, Su Y, Hu X, Shen Y, Zhao D. 2019. A novel case of autogamy and cleistogamy in Dendrobium wangliangii: a rare orchid distributed in the dry-hot valley. Ecol Evol. 9(22):12906–12914.

Xiang XG, Mi XC, Zhou HL, Li JW, Chung SW, Li DZ, Huang WC, Jin WT, Li ZY, Huang LQ, Jin XH. 2016. Biogeographical diversification of mainland Asian Dendrobium (Orchidaceae) and its implications for the historical dynamics of evergreen broad-leaved forests. J Biogeogr. 43(7):1310–1323.

Zhu GH, Ji ZH, Wood JJ, Wood HP. 2009. Dendrobium. In: Wu CY, Raven PH, Hong DY, editors. Flora of China. Beijing & St. Louis: Science Press & Missouri Botanical Garden Press; p. 367–397.