The complete chloroplast genome of *Primula odontocalyx*, a heterostyloous species

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**ABSTRACT**

*Primula odontocalyx* (Franch.) Pax (1905) is a perennial herb of the genus *Primula* in Primulaceae with heterostyly and ornamental value. Here, the chloroplast genome of *P. odontocalyx* was sequenced, assembled, and annotated. The complete chloroplast genome was a closed-circular molecule of 151,738 bp in length, containing a large single-copy region (LSC) of 83,817 bp, a small single-copy region (SSC) of 17,529 bp, and two inverted repeat (IR) regions of 25,196 bp. A total of 115 unique genes were annotated in the whole cp genome, including 81 protein-coding genes, 4 rRNA genes, and 30 tRNA genes. Phylogenetic analysis confirmed the close relationship between *P. odontocalyx* and *Primula moupinensis*, and both species belong to Sect. Petiolares Pax.

**KEYWORDS**

Chloroplast genome; *Primula odontocalyx*; phylogenomic analysis

*Primula odontocalyx* (Franch.) Pax (1905) is a perennial herb of Sect. Petiolares Pax in the genus *Primula* (Primulaceae) (Hu and Kelso 1996). *Primula odontocalyx* was placed in Sect. Davidii by Smith and Fletcher (1944). But now it was placed in Sect. Petiolares due to the absence of long hairs and basal bud scales at an early stage as shown by most specimens of this species (Richards 2003). *Primula odontocalyx* is mainly distributed in thickets and forest margins at an altitude of 900–3400 m in southern Gansu, western Hubei, southern Shanxi, Henan, and Sichuan Provinces of China (Hu and Kelso 1996). The flower of *P. odontocalyx* has 1–3 or rarely as many as 8 pink or lilac-rose corollas (Hu and Kelso 1996), this species, therefore, exhibits high ornamental value. In this study, we reported the first chloroplast genome of *P. odontocalyx*, which is useful for its taxonomic, systematics, and evolutionary studies.

Fresh leaf of *P. odontocalyx* was collected from Chengkou of Sichuan Province, China (31.948°N, 108.665°E), and the corresponding voucher specimens were deposited in the Herbarium of Yunnan Normal University (Kunming, China; Jianlin Hang, hjlyun@163.com) under the accession number HY-24. Total genomic DNA was extracted using a modified CTAB method (Porebski et al. 1997) and 300 bp short-insert libraries were constructed following the manufacturer’s protocol (Illumina Inc., USA), and then paired-end sequenced on Illumina HiSeq X Ten sequencer platform. We obtained 14,914,454 filtered reads and then assembled the plastid genome using software NOVOPlasty v4.3.1 (Dierckxsens et al. 2017) with *Primula sinensis* Sabine ex Lindley as reference genome (GenBank accession No: NC_030609). The assembled genome was annotated using Geneious v2020.1.1 (Kearse et al. 2012), with *Primula moupinensis* (GenBank accession No. NC_050244) as the reference genome.

The complete plastid genome of *Primula chionantha* was assembled into a circular molecule with a length of 151,738 bp (Figure 2), average coverage of 506.5, and GC content of 37.0%, respectively, the NCBI accession number of the plastid genome is ON416872. The plastid genome of this species has a large single-copy region of 83,817 bp and a
small single-copy region of 17,529 bp, which are separated by a pair of inverted repeats of 25,196 bp. In total, the plastid genome has 134 genes, 89 protein-coding genes (CDS), 37 tRNA genes, and 8 rRNA genes are annotated in the plastome, of which 115 genes, 81 protein-coding genes, 30 tRNA genes, and 4 rRNA genes are unique, respectively.

In order to further determine the phylogenetic position of *P. odontocalyx* within the genus *Primula*, we downloaded 39 *Primula* plastomes and two *Androsace* species, two *Lysimachia* species, and *Glaux maritima* (Liu et al. 2021) as outgroups. A total of 45 chloroplast genome sequences were aligned using MAFFT v7.47 (Katoh and Standley 2013). A maximum-likelihood phylogenetic tree was constructed using IQ-TREE v1.6.10 (Nguyen et al. 2015), and the best-fitted model is TVM + F + R2 using ModelFinder according to Bayesian information criterion (Kalyaanamoorthy et al. 2017). Branch supports were tested using ultrafast bootstrap (UFBoot) (Hoang et al. 2018) and SH-like approximate likelihood ratio test (SH-aLRT) (Guindon et al. 2010) with 10,000 replicates. The ML tree showed that *P. odontocalyx* was highly supported to be a sister species to *P. moupinensis*, forming a monophyletic clade with the rest species of Sect. *Petiolares* (Figure 3). This result supports that *P. odontocalyx* belongs to Sect. *Petiolares*, rather than Sect. *Davidii*. Additionally, the topologic structure of the phylogenetic tree showed that the relationships between *Primula, Androsace, Lysimachia*, and *Glaux* are consistent with previous phylogenetic studies (Mast et al. 2001).
Ethical approval

This study does not involve ethical issues. The sample of this study is not a protected plant, and specimens are collected in accordance with the laws and regulations of the country where we are located.

Authors’ contributions

Yuan Huang designed the study. Yunqi Liu, Li Zhang, Shubao Wang, and Rui Li collected materials and performed the experiments and analysis. Yunqi Liu drafted the original manuscript.

Disclosure statement

No potential conflict of interest was reported by the author(s). All authors revised and approved the manuscript.

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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 accession no. ON416872. The associated BioProject, SRA, and BioSample numbers are PRJNA834967, SRR19141931, and SAMN28088246, respectively.
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