MITOGENOME ANNOUNCEMENT

The complete chloroplast genome sequences of an endangered orchid species *Paphiopedilum parishii* (Orchidaceae)

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**ABSTRACT**

*Paphiopedilum parishii* (Rchb. f.) Stein is an endangered and rare species with highly ornamental value. In this study, we report the complete chloroplast genome of *P. parishii* using the Illumina sequencing data. The total genome of *P. parishii* is 154,689 bp in length and the GC content is 35.9%, with a pair of inverted repeats (IRs) regions of 32,690 bp each, a large single-copy region (LSC) of 86,863 bp and a small single-copy region (SSC) of 2,446 bp. The chloroplast genome encoded 127 genes, including 82 protein-coding genes (PCGs), 8 rRNA genes and 37 tRNA genes. The phylogenetic tree showed that *P. parishii* was clustered with other species in *Paphiopedilum* with strong support based on the complete chloroplast genome.

**ARTICLE HISTORY**

Received 24 March 2021
Accepted 16 July 2021

**KEYWORDS**

Paphiopedilum parishii; complete chloroplast genome; endangered species; Orchidaceae; phylogenomics

*Paphiopedilum parishii* (Rchb. f.) Stein grows on tree trunks or forks in broad-leaved forests at an altitude of 1,000-1,100 m in China, Laos, Myanmar and Thailand (Chen et al. 2009). *P. parishii* has high ornamental value, since its drooping and curly linear petals have won the favor of many people. However, due to the destruction of habitat, the number and size of its populations are drastically reduced. It has been listed in the Red List of Threatened Species (The International Union for Conservation of Nature, IUCN 2015). To better protect *P. parishii* and provide significant genomic resources in the further study of Orchidaceae, we reported its chloroplast (cp) genome firstly and a neighbour-joining (NJ) phylogenetic tree was constructed for phylogenomic analysis.

We sampled the fresh leaf material from a living individual in the greenhouse of Beijing Forestry University, which was obtained from Guwen village, Jingxi county, Guangxi Zhuang Autonomous Region, China (23.047602°N, 106.316139°E). The specimen was deposited at the herbarium of Plant Biology Department, Beijing Forestry University (Wu Qi. e-mail: wuqi9907@163.com) under the voucher number BFU-ORCHID-201701. The total genomic DNA was extracted using CTAB method (Doyle and Doyle 1987). Then, the next-generation sequencing was performed with an Illumina HiSeq Xten platform at oebiotech (https://www.oebiotech.com/, China). The clean reads were assembled to published cp genomes of *Paphiopedilum* using the GetOrganelle pipeline (Jin et al. 2018). Finally, we got the complete cp genome of *P. parishii* and annotated it using PGA (Qu et al. 2019). The complete cp genome sequence was submitted to GenBank with the accession number MW528213.

The complete cp genome of *P. parishii* is 154,689 bp in length, which harbors a typical quadripartite structure with a pair of inverted repeats (IRs) regions of 32,690 bp each, a large single-copy region (LSC) of 86,863 bp and a small single-copy region (SSC) of 2,446 bp. The base composition of the genome is 31.7% A, 18.2% C, 17.7% G, 32.4% T, and the total GC content is 35.9%. The cp genome consists of 127 functional genes, including 82 protein-coding genes (PCGs), 8 rRNA genes and 37 tRNA genes. Among them, 6 tRNA genes (trnK-UUU, trnG-GCC, trnL-UAA, trnV-UAC, trnL-GAU, trnA-UGC) and 11 protein-coding genes (psp16, atpF, rpcP1, ycf3, clpP, rps12, petB, petD, rpl16, ndhB, rpl2) have introns.

To confirm the phylogenetic position of *P. parishii*, a molecular phylogenetic tree was constructed with the CDS extracted from the complete cp genome sequence of *P. parishii* and other 14 complete cp genome sequences (9 species from Orchidaceae and 5 species from other families as out-group) downloaded from GenBank. All sequences were alignment using the MAFFT (Katoh and Standley 2013). The neighbour-joining (NJ) phylogenetic tree was constructed using MEGA X (Kumar et al. 2018) with 1000 bootstrap replicates. The results showed that *P. parishii* was clustered with other species in *Paphiopedilum* with strong support (Figure 1). The data of the complete cp genome of *P. parishii*...
provided an essential clue for better understanding the phylogeny and biodiversity of *Paphiopedilum*.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

**Funding**

This work was supported by the [111 Project # 1] under Grant [No.B13007]; National Natural Science Foundation of China # 2] under Grant [No.32001348]; and [Research Fund from China Urban and Rural Holding Group Co., LTD # 3] under Grant [No.2020-Q7-KJB-005].

**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI (https://www.ncbi.nlm.nih.gov/) under the accession no. MW528213. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA741068, SUB9894385, and SAMN19844049 respectively.

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**Figure 1.** Phylogenetic relationships of 15 species based on complete chloroplast genome using the neighbour-joining methods. The bootstrap values were based on 1000 replicates and shown next to the branches.