Complete chloroplast genome of *Paphiopedilum emersonii* (Orchidaceae)

Feng-Luan Tang, Li-Li Deng, Hui-Zhen Qin and Yan-Cai Shi

Guangxi Key Laboratory of Functional Phytochemicals Research and Utilization, Guangxi Institute of Botany, Guangxi Zhuang Autonomous Region and Chinese Academy of Sciences, Guilin, China

**ABSTRACT**

*Paphiopedilum emersonii* is an endemic terrestrial orchid in China. In this study, the chloroplast genome of *P. emersonii* was determined from BGISEQ-500 sequencing data. The total chloroplast genome was 162,590 bp in length, consisting of a large single-copy region (LSC, 87,852 bp), a small single-copy region (SSC, 870 bp), and two inverted repeat regions (IRA and IRB, 36,934 bp, each). The complete chloroplast genome contains 131 genes, including 81 protein-coding genes, 38 transfer RNA (tRNA) genes, and 8 ribosomal RNA (rRNA) genes. In addition, the phylogenetic analysis indicates that *P. emersonii* was sister to *Paphiopedilum micranthum*. The chloroplast genome will contribute to the research and conservation of *P. emersonii*.

**KEYWORDS**
Paphiopedilum emersonii; orchid; chloroplast genome; phylogenetic analysis

**ARTICLE HISTORY**

Received 29 August 2020
Accepted 17 September 2020

**CONTACT**

Yan-Cai Shi SYC@gxib.cn
Guangxi Key Laboratory of Functional Phytochemicals Research and Utilization, Guangxi Institute of Botany, Guangxi Zhuang Autonomous Region and Chinese Academy of Sciences, No. 85 Yanshan Street, Yanshan Town, Guilin 541006, China

© 2020 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.
This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.
showed that *P. emersonii* was sister to *P. micranthum* with 100% bootstrap support (Figure 1).

**Disclosure statement**

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

**Funding**

This work was financially supported by Fund of National Natural Science Foundation of China [31760085]; Fund of Chinese Academy of Sciences 'Light of West China' Program (2018); Science and Technology Project of Guangxi [AD18281077].

**Data availability statement**

Data openly available in a public repository that does not issue DOIs. The data that support the findings of this study are openly available in the National Center for Biotechnology Information (https://www.ncbi.nlm.nih.gov/), reference number (MT648789).

**References**

Averyanov LV, Hiep N, Loc P. 2005. Two relatives of different ecology: a field study of *Paphiopedilum emersonii* and *Paphiopedilum hangianum*. Am Orchid Soc Mag. Orchids. 74:208–215.

Bi G, Mao Y, Xing Q, Cao M. 2018. HomBlocks: a multiple-alignment construction pipeline for organelle phylogenomics based on locally collinear block searching. Genomics. 110(1):18–22.

Chen XQ, Stephan W. 2009. Flora of China. Vol.25. Orchidaceae. Beijing (China): Science Press; St. Louis (MO): Botanical Garden Press. p. 36–37.

Chernomor O, von Haeseler A, Minh BQ. 2016. Terrace aware data structure for phylogenomic inference from supermatrices. Syst Biol. 65(6): 997–1008.

Doyle JJ, Doyle JL. 1987. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. Phytochem Bull. 19:11–15.

Hall TA. 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symposium Series. 41:95–98.

Jin JJ, Yu WB, Yng JB, Song Y, Yi TS, Li DZ. 2018. GetOrganelle: a simple and fast pipeline for de novo assembly of a complete circular chloroplast genome using genome skimming data. bioRxiv. 256479.

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Kalkau 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.

Lohse M, Drechsel O, Kahlau S, Bock R. 2013. OrganellarGenomeDRAW—a suite of tools for generating physical maps of plastid and mitochondrial genomes and visualizing expression data sets. Nucleic Acids Res. 41:W575–W581.

Zeng SJ, Tian RX, Chen ZL, Wu KL, Duan J. 2010. Research progress on cross breeding of *Paphiopedilum*. J Tropical Subtropical Bot. 018(004): 459–468.