

MITOGENOME ANNOUNCEMENT



## The complete chloroplast genome sequence of *Phalaenopsis wilsonii* (Orchidaceae)

Keke Xia<sup>a</sup>, Ding-Kun Liu<sup>b</sup> and Jie-Yu Wang<sup>c,d</sup>

<sup>a</sup>BGI-Shenzhen, Shenzhen, China; <sup>b</sup>Key Laboratory of National Forestry and Grassland Administration for Orchid Conservation and Utilization at College of Landscape Architecture, Fujian Agriculture and Forestry University, Fuzhou, China; <sup>c</sup>Key Laboratory of Plant Resources Conservation and Sustainable Utilization, South China Botanical Garden, Chinese Academy of Sciences, Guangzhou, China; <sup>d</sup>Laboratory for Orchid Conservation and Utilization, The Orchid Conservation and Research Center of Shenzhen, The National Orchid Conservation Center of China, Shenzhen, China

### ABSTRACT

In the present study, we reported and characterized the complete chloroplast genome of a moth orchid, *Phalaenopsis wilsonii*, which is endemic to South China. Its plastid genome size is 145,373 bp, consisting of a large single copy (LSC) region (84,996 bp), a small single-copy region (10,668 bp), and two inverted repeats (IRs) regions (24,855 bp). A total of 122 plastid genes were annotated, comprising 76 protein-coding genes, 38 tRNA genes, and 8 rRNA genes. The phylogenetic tree further revealed that *P. wilsonii* showed a sister relationship with *P. lowii* within subgenus *Parishianae*.

### ARTICLE HISTORY

Received 1 April 2021  
Accepted 13 October 2021

### KEYWORDS



Orchidaceae; Parishianae;  
moth orchid;  
plastid genome

Moth orchid (*Phalaenopsis* Blume) is widely used in gardening around the world, and also occupies a large proportion of orchid industry (Van Huylenbroeck 2018). Previously phylogenetic analyses revealed that *Phalaenopsis* can be divided into four subgenera, subgen. *Phalaenopsis*, *Parishianae*, *Hygrochilus* and *Ornithochilus* (Kocyan and Schuiteman 2014; Li et al. 2014, 2016). Although Subgen. *Parishianae* constitutes more than a half of the species richness in *Phalaenopsis*, only one complete chloroplast genome of this subgenus can be found in NCBI (Wang et al. 2019). *P. wilsonii* is an endemic species in China, and is also a typical deciduous *Phalaenopsis* belonging to subgen. *Parishianae*. Here, we provide a complete chloroplast genome of *P. wilsonii*, aiming to facilitate our understanding on *Phalaenopsis* as well as to expand orchid resources in wild.

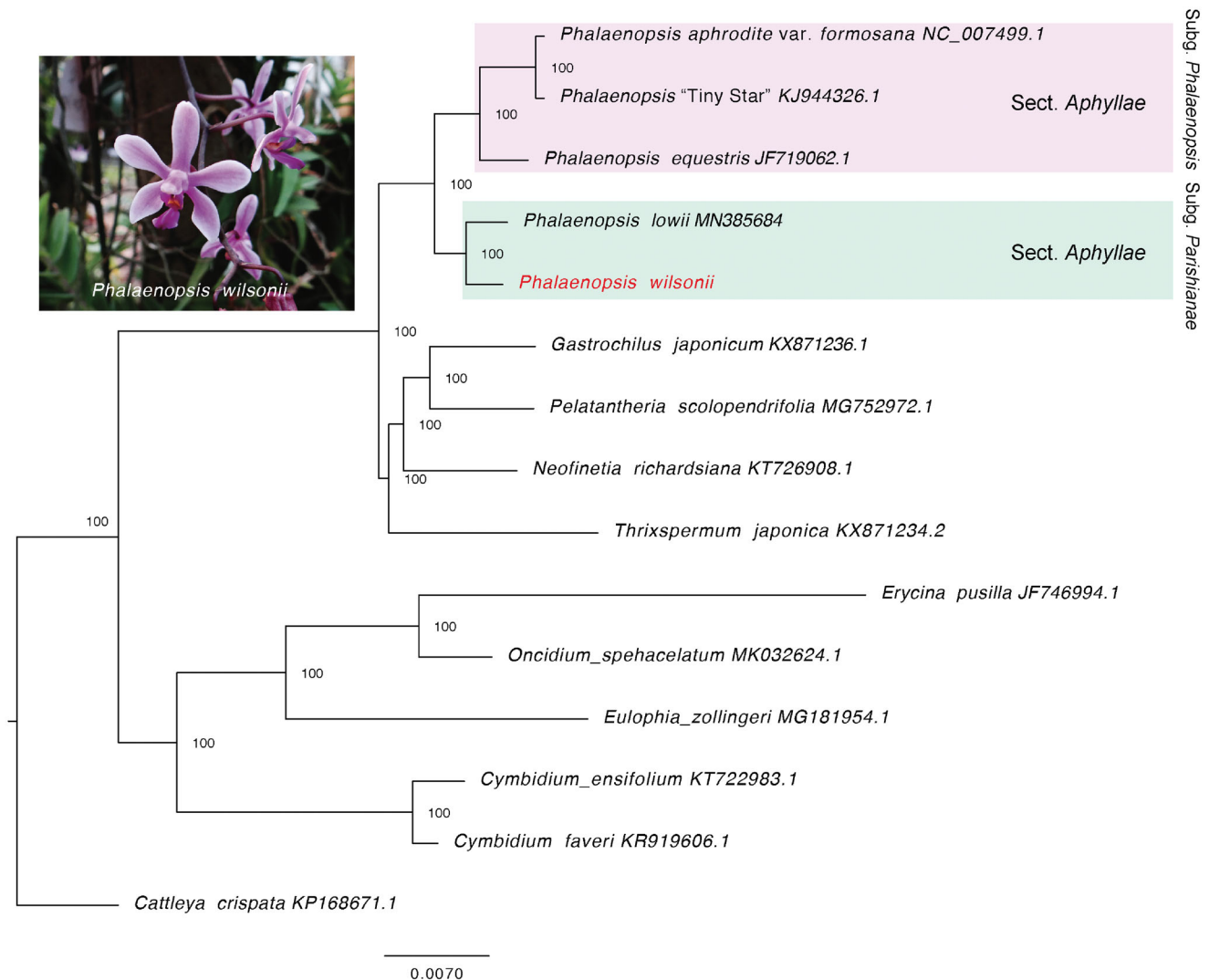
The sampling individual of *Phalaenopsis wilsonii* is cultivated in National Orchid Conservation Center in Guangdong province of China (114°19'01"E, 22°60'34"N), and a voucher specimen (noccphal031n) was also deposited in the Herbarium of National Orchid Conservation Center, Shenzhen, China. We extracted the total DNA from the young leaf of the voucher specimen and conducted high throughput sequencing at Illumina HiSeq 2000 platform (Illumina, San Diego, CA). Firstly, we constructed a reference dataset with all publicly available *Phalaenopsis* plastid genomes, and then mapped the clean reads against the reference dataset to obtain the chloroplast reads for *P. wilsonii*. PLATANUS (Kajitani et al. 2014) was adopted for contig assembly and

scaffolding, resulting in the final complete genome with the artificial modification. BLAST was further used to align the reads onto the genome again to determine the IR boundaries, and the annotation was performed using Geneious 2019.0.3 (Kearse et al. 2012). The resulting complete chloroplast genome of *P. wilsonii* was submitted to GenBank under the accession number of MW218959. The total length of *P. wilsonii* chloroplast genome is 145,373 bp, with the GC content being 36.9%. The chloroplast genome we identified here is slightly shorter than other published moth orchids (from 146,834 bp for *P. lowii* to 148,964 bp for *P. aphrodite* subsp. *formosana*). As with other orchids, the chloroplast genome of *P. wilsonii* consists of a large single copy (LSC) region (84,995 bp) and a small single-copy region (10,668 bp), which are segmented by two inverted repeat (IRs) regions (24,855 bp). Overall, 122 genes (containing repeat region gene) were annotated, including 76 protein-coding genes, 8 rRNAs, and 38 tRNAs. Similar to a former study (Chang et al. 2006), all *ndh* genes of *P. wilsonii* are nonfunctional, and the *ndhE* was also missing.

To infer the phylogenetic relationship for *P. wilsonii*, we used RAXML v.8 (Stamatakis 2014) to reconstruct the maximum-likelihood phylogenetic tree based on the whole plastid genomes of *P. wilsonii*, four moth orchids, and also the other ten orchids. *Cattleya crispate* was applied as an out-group according to the topology from Givnish et al. (2015). The TIM1 + I + G model was applied by jModelTest (Posada 2008), and the reliability of topology was supported with

**CONTACT** J.-Y. Wang ✉ [jywang@scbg.ac.cn](mailto:jywang@scbg.ac.cn)  Key Laboratory of Plant Resources Conservation and Sustainable Utilization, South China Botanical Garden, Chinese Academy of Sciences, Guangzhou, China;  Laboratory for Orchid Conservation and Utilization, The Orchid Conservation and Research Center of Shenzhen, The National Orchid Conservation Center of China, Shenzhen, China

© 2021 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.



**Figure 1.** Maximum-likelihood tree reconstructed by RAxML based on complete chloroplast genome sequences from *P. wilsonii*, four *Phalaenopsis* species, and ten other orchids. *Cattleya crispata* was selected as an outgroup. Numbers on branches are bootstrap support values.

1000 bootstrap replicates. Consistent with Givnish's study Givnish et al. (2015), the phylogenetic tree showed that Vandeae presented a sister relationship to Cymbidieae. Besides, *P. wilsonii* was sister to *P. lowii*, both of which belong to the subgen. *Parishianae* that are grouped into a single clade (Figure 1). This complete chloroplast genome of *P. wilsonii* will be helpful for future phylogenetic studies and conservation in *Phalaenopsis*.

## Disclosure statement

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

## Funding

This work was supported by the Science, Technology and Innovation Commission of Shenzhen Municipality under Grant No. JCYJ20170817151501595.

## Authors' contributions

J.Y.W. and K.K.X. conceived the study; J.Y.W. and K.K.X. obtained the molecular data; J.Y.W. and D.K.L. conducted the data analysis; K.K.X.

drafted the manuscript; J.Y.W. and D.K.L. revised the manuscript. All authors provided comments and final approval.

## Data availability statement

The data that newly obtained at this study are available in the NCBI under accession number of MW218959 (<https://www.ncbi.nlm.nih.gov/nuccore/MW218959>). The sequencing reads are available under the SRA accession number of SAMN18924765.

## References

- Chang C-C, Lin H-C, Lin I-P, Chow T-Y, Chen H-H, Chen W-H, Cheng C-H, Lin C-Y, Liu S-M, Chang C-C, et al. 2006. The chloroplast genome of *Phalaenopsis aphrodite* (Orchidaceae): comparative analysis of evolutionary rate with that of grasses and its phylogenetic implications. *Mol Biol Evol.* 23 (2):279–291.
- Givnish TJ, Spalink D, Ames M, Lyon SP, Hunter SJ, Zuluaga A, Iles WJD, Clements MA, Arroyo MTK, Leebens-Mack J, et al. 2015. Orchid phylogenomics and multiple drivers of their extraordinary diversification. *Proc R Soc B.* 282(1814):20151553.
- Kajitani R, Toshimoto K, Noguchi H, Toyoda A, Ogura Y, Okuno M, Yabana M, Harada M, Nagayasu E, Maruyama H, et al. 2014. Efficient

- de novo assembly of highly heterozygous genomes from whole-genome shotgun short reads. *Genome Res.* 24(8):1384–1395.
- 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.
- Kocyan A, Schuiteman A. 2014. New combinations in Aseridinae (Orchidaceae). *Phytotaxa.* 161 (1):61–85.
- Li M-H, Gruss O, Liu Z-J. 2016. Nomenclature changes in *Phalaenopsis* subgen. *Hygrochilus* (Orchidaceae; Epidendroideae; Vandeeae) based on DNA evidence. *Phytotaxa.* 275(1):55–61.
- Li M-H, Zhang G-Q, Liu Z-J, Lan S-R. 2014. Revision of *Hygrochilus* (Orchidaceae: Epidendroideae: Aseridinae) and a molecular phylogenetic analysis. *Phytotaxa.* 159(4):256.
- Posada D. 2008. jModelTest: phylogenetic model averaging. *Mol Biol Evol.* 25(7):1253–1256.
- Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics.* 30(9):1312–1313.
- Van Huylbroeck J. 2018. Ornamental crops. Springer.
- Wang J-Y, Liu Z-J, Zhang G-Q, Peng C-C. 2019. The complete chloroplast genome sequence of *Phalaenopsis lowii* (Orchidaceae). *Mitochondrial DNA B Resour.* 4(2):3569–3570.