The complete chloroplast genome sequence of Oberonia seidenfadenii (Orchidaceae), a rare plant species endemic to China

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**ABSTRACT**

_Oberonia seidenfadenii_ is a rare and newly recorded plant species in Zhejiang province, China. In our present study, the complete chloroplast (cp) genome sequence of _O. seidenfadenii_ was assembled by using high-throughput Illumina sequencing data. The plastome is 143,062 bp in size, which contains a typical quadripartite structure with a pair of inverted repeats (IR) regions (24,278 bp) separated by a small single-copy (SSC) region (10,224 bp) and a large single-copy (LSC) region (84,282 bp). The cp genome sequence contains 127 genes, including 74 protein-coding genes, 38 tRNA genes, 8 rRNA genes, and 7 pseudogenes. Phylogenetic analysis results indicated _O. seidenfadenii_ is a sister of _Oberonia japonica_, with a support rate of 100%.

The genus _Oberonia_ belongs to the family Orchidaceae and consists of 150–200 species, and the _Oberonia_ plants are epiphytic or lithophytic (Wu et al. 2009). _Oberonia_ is a taxonomically complex genus and some species only shows slight differences in the morphology of leaves or flowers (Li et al. 2016). There are about 33 species distributed in China, and 11 of them are characterized as endemics (Wu et al. 2009). _Oberonia seidenfadenii_ is a tiny Orchidaceae plant species with distichous-equitant leaves, densely clustered inflorescences, and greenish flowers. _Oberonia seidenfadenii_ is a species native to China, and it mainly distributes in Taiwan, Guangxi, Guangdong, and Zhejiang (Huang 2000; Tian et al. 2013). In Zhejiang province, its populations are extremely small, and they are found only in some counties of Taizhou and Ningbo with less than 1000 individual plants. The information on chloroplast (cp) genome sequences of _Oberonia_ is very limited, and the complete cp genome of _O. seidenfadenii_ has not been characterized. In our present study, we assembled the cp genome of _O. seidenfadenii_ by using high-throughput sequencing data, and a phylogenetic tree was generated to reveal its relationship with other species.

Leaf samples were collected at an altitude of 36 m on Toumen Island (28'41'35'N, 121'46'14'E), Linhai County, Taizhou, Zhejiang province, China. A voucher specimen (CHS2017009) is deposited at the Molecular Biology Laboratory in Taizhou University. Total genomic DNA was extracted by using the CTAB method (Doyle and Doyle 1987), and a DNA library was constructed. The library was then sequenced on the illumina Hiseq X Ten platform (Illumina, San Diego, CA). A total of 5.5 Gb raw 150 bp paired-end reads were generated, and the filtered reads were de novo assembled by the programme NOVOPlasty (Dierckxsens et al. 2017). The cp genome was annotated by Dual Organelar GenoMe Annotator (DOGMA), tRNAscan-SE, and ARAGORN (Lohse et al. 2004; Laslett and Canback 2004; Wyman et al. 2004; Lowe and Eddy 1997). The plastome of _O. seidenfadenii_ (GenBank accession: MN414241) is 143,062 bp in size with an overall GC content of 37.1%. The cp genome consists of two inverted repeat (IR) regions, a large single-copy (LSC) region, and a small single-copy (SSC) region, and the sizes of IR, SSC, and LSC were 24,278, 10,224, and 84,282 bp, respectively. The GC contents of _O. seidenfadenii_ IR, LSC, and SSC are 43.7, 34.4, and 27.9%, respectively.

The genome encodes 127 genes, including 74 protein-coding genes, 38 tRNA genes, 8 rRNA genes, and 7 pseudogenes. Among these genes, four rRNAs (_rrn5, rrn16, rrn23_), eight tRNAs (_trnA-UGC, trnC-GAU, trnD-GAA, trnE-UUA, trnF-GAU, trnG-UAC, trnH-GUG, trnI-ACU, trnK-UGA, trnL-CAA, trnL-GAU, trnL-UGA, trnM-GAU, trnM-UGA, trnN-GUU, trnO-UGA, trnP-UCU, trnP-UCU, trnQ-UUR, trnR-ACG, trnR-ACG, trnS-UCN, trnT-AGC, trnT-UGC, trnV-GAC, trnW-GAU, trnY-UCN_), nine protein-coding genes (_ndhB, rpl2, rpl22, rpl23_, _rrn16, rps7, rps12, rps19, ycf1, ycf2_), two copies of _trnI-ACU_, two copies of _trnR-ACG_, two copies of _ndhB_ genes were identified as pseudogenes.

To understand the phylogenetic relationship with other Orchidaceae species, whole-genome sequences of 26 plants were obtained from NCBI, these included five _Dendrobium_ species (_Dendrobium officinale, Dendrobium hercoglossum, Dendrobium chrysotoxum, Dendrobium aphyllum, and Dendrobium aduncum_), three _Holcoglossum_ species (_Holcoglossum weixiense, Holcoglossum nagalandense, and Holcoglossum amesianum_), two _Neofinetia_ species (_Neofinetia..._).
falcata and Neofinetia richardsiana), as well as other 15 species from genera of Phalaenopsis, Vanda, Pelatantheria, Masdevallia, Gastrochilus, Epipactis, Oberonia, and Cephalanthera. Burmannia disticha (Burmanniaceae) was used as an outgroup. A phylogenetic tree was constructed by the maximum-likelihood method using PhyML 3.1 (Guindon et al. 2010). The results revealed that O. seidenfadenii grouped with Oberonia japonica, a morphologically similar plant species, exhibiting bootstrap support of 100% (Figure 1).

Disclosure statement
No potential conflict of interest was reported by the authors.

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References
Dierckxsens N, Mardulyn P, Smits G. 2017. NOVOPlasty: de novo assembly of organelle genomes from whole genome data. Nucleic Acids Res. 45:e118.

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

Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O. 2010. New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Syst Biol. 59:307–321.

Huang TC. 2000. Flora of Taiwan. Vol. 5. Taipei (Taiwan): Sandos Chromagraph Printing Company.

Laslett D, Canback B. 2004. ARAGORN, a program to detect tRNA genes and tmRNA genes in nucleotide sequences. Nucleic Acids Res. 32:11–15.

Li Y, Tong Y, Xing F. 2016. DNA barcoding evaluation and its taxonomic implications in the recently evolved genus Oberonia Lindl. (Orchidaceae) in China. Front Plant Sci. 7:1791.

Lohse M, Drechsel O, Kahlau S, Bock R. 2004. OrganellarGenomeDRAW— a suite of tools for generating physical maps of plastid and mitochondrial genomes and visualizing expression data sets. Nucleic Acids Res. 41:575–581.

Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in nucleic acid sequences. Nucleic Acids Res. 25:955–964.

Tian HZ, Hu C, Tong Y. 2013. Two newly recorded species of Oberonia (Orchidaceae) from China. J Trop Subtrop Bot. 21:231–233.

Wu ZY, Raven PH, Hong DY. 2009. Flora of China. Vol. 25. Beijing (China): Science Press; St. Louis (MO): Missouri Botanical Garden Press.

Wyman SK, Jansen RK, Boore JL. 2004. Automatic annotation of organelar genomes with DOGMA. Bioinformatics. 20:3252–3255.