The Complete chloroplast genome of *Geodorum densiflorum* (Orchidaceae)

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**ABSTRACT**

*Geodorum densiflorum* is a popular terrestrial orchid in the Southeast Asia. It has high medicinal and ornamental value. In this study, the chloroplast genome of *G. densiflorum* was determined from BGISEQ-500 sequencing data. The total chloroplast genome was 149,468 bp in length, consisting of a large single copy region (LSC 85,070 bp), a small single copy region (SSC 13,290 bp), and two inverted repeat regions (IRA and IRB 25,554 bp). The complete chloroplast genome contains 132 genes, including 76 protein-coding genes, 36 tRNA genes, and 8 rRNA genes. In addition, the phylogenetic analysis indicates that *G. densiflorum* was sister to *Eulophia zollingeri*. The chloroplast genome will contribute to the research and conservation of *G. densiflorum*.

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*Geodorum densiflorum* is a perennial terrestrial orchid distributed in the Southeast Asia. It usually grows on grassy slopes, streamside or in forests at altitudes of 300–2,400 m (Chen and Stephan 2009). *G. densiflorum* has a high ornamental value with white flowers and its pseudobulb has anti-diabetic effect (Li et al. 2012). Since the discovery and naming of this plant by German scientist Schlechter in 1921, the species has not been found in the wild, and it was not until 2004 that a population of less than 400 individuals of *Geodorum eulophioides* was found in the Yachang Orchidaceae National Nature Reserve (Feng et al. 2012). Unfortunately, with the over-excavation of *Geodorum densiflorum*, their habitats have been broken up and the wild resources have decreased significantly over the last decades. Therefore, the *G. densiflorum* is listed as an endangered species in the China Species Red List (Wang and Xie 2004). Therefore, we report the complete chloroplast genome of *G. densiflorum*, in order to better understand the relationship between *G. densiflorum* and related genera, and contribute to the effective conservation strategy of *G. densiflorum*.

In this study, the complete genomic DNA was extracted from fresh leaves using a modified CTAB method (Doyle and Doyle 1987) and sequenced by the BGISEQ-500 platform. The samples were collected from Yachang Orchidaceae National Nature Reserve, Guangxi, China (24°44′N, 106°15′E) and the voucher specimen deposited at Herbarium of Guangxi Institute of Botany, Guangxi Zhuang Autonomous Region and Chinese Academy of Sciences (specimen code Densiflorum_GX).

The clean reads were used to assemble the complete chloroplast genome by the GetOrganelle pipeline (Jin et al. 2018), with the chloroplast genome of *Eulophia zollingeri* (NC_037212) as the reference sequences. The assembled chloroplast genome was annotated using the Geneious R11.15 (Kearse et al. 2012). The physical map of the chloroplast genome was generated using the online tool OGDRAW (Lohse et al. 2013). Finally, we obtained a complete chloroplast genome of *G. densiflorum* and submitted to GenBank with accession number MT_153204.

The total chloroplast genome of *G. densiflorum* was 149,468 bp in length, consisting of a large single copy region (LSC 85,070 bp), a small single copy region (SSC 13,290 bp), and two inverted repeat regions (IRA and IRB 25,554 bp). The complete chloroplast genome contains 132 genes, including 76 protein-coding genes, 36 transfer RNA (tRNA) genes, and 8 ribosomal RNA (rRNA) genes. The GC content of the chloroplast genome of *G. densiflorum* is 37%.

To investigate the phylogenetic position of *G. densiflorum*, a phylogenetic analysis was performed based on 17 complete chloroplast genome sequences of Orchidaceae. All sequences were aligned with the HomBlock pipeline (Bi et al. 2018) and subsequently checked manually in Bioedit v5.0.9 (Hall 1999). Then, the phylogenetic tree constructed by RaxML (Stamatakis 2014) with 1000 ultrafast bootstrap (UFBoot) replicates (Minh et al. 2013; Chernomor et al. 2016). The results showed that *G. densiflorum* was sister to *Eulophia zollingeri* with 100% bootstrap support (Figure 1).

ARTICLE HISTORY

Received 18 April 2020
Accepted 25 April 2020

KEYWORDS

Geodorum densiflorum; orchid; chloroplast genome; phylogenetic analysis
Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was financially supported by Fund of National Natural Science Foundation of China [31760085]; Special Fund of Guangxi Key Laboratory of Functional Phytochemical Research and Utilization [ZRRJ2018-9]; Special Fund of Guangxi Talent Highlands [2020].

Data availability

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 [National Center for Biotechnology Information] at [https://www.ncbi.nlm.nih.gov/], reference number [MT153204].

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