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Characterization of the complete chloroplast genome of *Corallodiscus flabellatus* (Gesneriaceae), a medicinal plant in southwest of China

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ABSTRACT

Corallodiscus flabellatus is a medicinal plant commonly used in southwest of China. In this study, we sequenced the complete chloroplast (cp) genome sequence of *C. flabellatus* to investigate its phylogenetic relationship in the family Gesneriaceae. The chloroplast genome of *C. flabellatus* was 156,614 bp in length with 43.2% overall GC content, including a large single copy (LSC) region of 87,429 bp, a small single copy (SSC) region of 17,871 bp and a pair of inverted repeats (IRs) of 25,657 bp. The cp genome contained 112 genes, including 79 protein coding genes, 29 tRNA genes, and 4 rRNA genes. The phylogenetic analysis indicated *C. flabellatus* was closely related to *Oreocharis mileensis*.

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Corallodiscus flabellatus;
chloroplast; Illumina
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Corallodiscus is a great genus of the Gesneriaceae family, which includes 11 species in the world. Most of them are widely distributed in China, Sikkim, Bhutan, Nepal and Northern India. There are nine species in China (Li and Ian 1994). Plants of this genus have been widely used in traditional Chinese medicine for thousands of years (Jiangsu New Medical College 1977). Among these species, *C. flabellatus* is widely distributed in southwest China which have been used in ethnic medicine as activating blood, bleeding and analgesia (Minru and Yi 2016). However, up to now for such medicinal plant, many studies have mainly focused on describing its chemical compositions (Xiao-Ke et al. 2002; Yao et al. 2012), with little involvement in its molecular biology, so that no comprehensive genomic resource is conducted for it. Here, we report the chloroplast genome sequence of *C. flabellatus* and find its internal relationships within the family Gesneriaceae.

Fresh and clean leave materials of *C. flabellatus* were collected from Li Jiang city, Yunnan, China (N26°55'37.55", E100°14'16.35"), and the plant materials and a voucher specimen (No. TC35) were deposited at Tourism and Culture College of Yunnan University (Lijiang). Total genomic DNA was extracted using the improved CTAB method (Doyle 1987; Yang et al. 2014), and sequenced with Illumina HiSeq 2500 (Novogene, Tianjin, China) platform with pair-end (2 × 300 bp) library. The raw data was filtered using Trimmomatic v.0.32 with default settings (Bolger et al. 2014). Then paired-end reads of clean data were assembled into circular contigs using GetOrganelle.py (Jin et al. 2018) with *Oreocharis*

mileensis (MK342624) as reference. Finally, the cpDNA was annotated by the Dual Organellar Genome Annotator (DOGMA; <http://dogma.cccb.utexas.edu/>) (Wyman et al. 2004) and tRNAscan-SE (Lowe and Chan 2016) with manual adjustment using Geneious v. 7.1.3 (Kearse et al. 2012).

The circular genome map was generated with OGDRAW v.1.3.1 (Greiner et al. 2019). Then the annotated chloroplast genome was submitted to the GenBank under the accession number MT012414. The total length of the chloroplast genome was 156,614 bp, with 43.2% overall GC content. With typical quadripartite structure, a pair of IRs (inverted repeats) of 25,657 bp was separated by a small single copy (SSC) region of 17,871 bp and a large single copy (LSC) region of 87,429 bp. The cp genome contained 112 genes, including 79 protein coding genes, 29 tRNA genes, and 4 rRNA genes.

To investigate its taxonomic status, a total of 8 cp genome sequences of Gesneriaceae species were downloaded from the NCBI database used for phylogenetic analysis. After using MAFFT V.7.149 for aligning (Kato and Standley 2013), a neighbor-joining (NJ) tree was constructed in MEGA v.7.0.26 (Kumar et al. 2016) with 1000 bootstrap replicates and three Orchidaceae species *Bletilla ochracea*(KT695602; NC 029483), *Bletilla formosana*(MN526744), *Bletilla striata*(KT588924; NC 028422) were used as outgroups. The results showed that *C. flabellatus* was closely related to *Oreocharis mileensis* (Figure 1). Meanwhile, the phylogenetic relationship in Gesneriaceae was consistent with previous studies and this will be useful data for developing markers for further studies.

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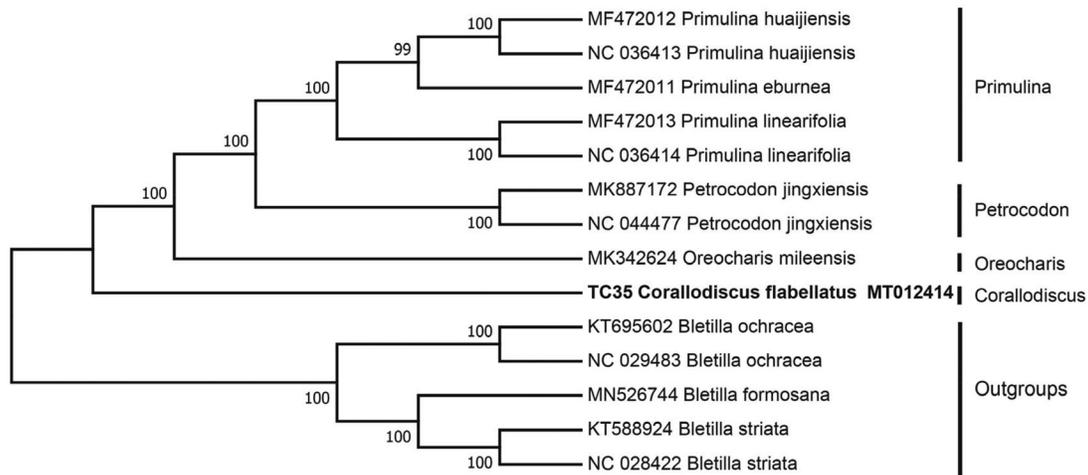


Figure 1. Neighbor-joining (NJ) tree of 26 species within the family Gesneriaceae based on the plastomes using five Orchidaceae species as outgroups.

Disclosure statement

The authors are highly grateful to the published genome data in the public database. The authors declare no conflicts of interest and are responsible for the content.

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