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Characterization of the complete chloroplast genome of *Homalocladium platycladum* (Polygonaceae) and its phylogenetic analysis

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ABSTRACT

Homalocladium platycladum is a fascinating ornamental plant that has long been used in Chinese medicine. Here, we characterize the complete chloroplast genome sequence of this plant (GenBank: NC_062330). This circular genome has a total length of 163,202 bp containing a large single-copy region (87,820bp), a small single-copy region (13,538bp), and a pair of inverted repeat regions (30,922bp). A total of 130 predicted genes were identified, including 85 protein-coding genes, 37 transfer RNA genes, and 8 ribosomal RNA genes. Phylogenetic analysis demonstrated that *H. platycladum* belongs to the Polygonaceae family and is highly analogous with *Homalocladium* and *Muehlenbeckia* families.

Homalocladium platycladum (F. Muell.) L.H. Bailey [syn. *Muehlenbeckia platyclada* (F. Muell.) Meisn.], as the only species of *Homalocladium*, Polygonaceae, originates in the Solomon Islands in the South Pacific (Jørgensen et al. 2015), F.J.H. von Mueller published *Polygonum platycladum* F. Muell. as a basionym in 1858 (Victoria 1858). In Southern China, *H. platycladum* is widely planted for its horticultural benefit as well as its therapeutic effects in the treatment of snake bites and fractures (Yen et al. 2009). Chloroplast genomes are often employed in various scientific pursuits, including plant phylogenetic analysis (Refulio-Rodriguez and Olmstead 2014) and plant identification (Nock et al. 2011). However, the chloroplast genome of *H. platycladum* has not been formally analyzed and reported in the literature. Here, for the first time, we report the complete chloroplast genome sequence of *H. platycladum* and its phylogenetic analysis.

Samples of *H. platycladum* used for this study were collected at the Institute of Botany, Chinese Academy of Sciences (IBCAS), Beijing(116° 21′ N, 39° 99′ E), and the specimen was identified by Wei Zhai. A specimen was deposited at the Herbarium of Anqing Normal University (contact person: Wei Zhai, email: weizhai@aqnu.edu.cn) under the voucher number ZW2901. The experimental material is not an endangered species and is cultivated by individuals, and no approval is required for the collection of specimens. The chloroplast genome DNA library was constructed and sequenced on the Illumina NovaSeq 6000 (Novogene Co. Ltd, Beijing, China) according to the manufacturer's instructions. Run reports detailed a total of ~11.5 GB of clean reads which were then assembled using SPAdes v3.15.3 (Bankevich et al. 2012) and Bandage (Wick

et al. 2015). Total coverage of the sequencing was evaluated using BWA (Li and Durbin 2009) after initial *de novo* assembly of the chloroplast genome sequence, and the mean genome coverage: was 1435.2×. Assembled chloroplast genome sequences were annotated using PGA (Qu et al. 2019). Finally, annotated results were manually corrected using Geneious R11.1 software (Kearse et al. 2012) to ensure correctness. The annotated chloroplast genome sequence of *H. platycladum* has been submitted to GenBank and received the accession number NC_062330.

The total length of the *H. platycladum* chloroplast genome is 163,202 bp, containing a large single-copy (LSC) region of 87,820 bp, a small single-copy (SSC) region of 13,538 bp, and a pair of inverted repeat regions (IRa and IRb) of 30,922 bp each. The overall GC content of the genome was 37.3%. A total of 130 predicted genes were identified, including 85 protein-coding genes (CDS), 37 transfer RNA genes (tRNA), and 8 ribosomal RNA (rRNA) genes. Among the annotated genes, 6 protein-coding, 7 tRNA, and 4 rRNA genes were duplicated in the inverted repeat regions. Fifteen genes (*atpF*, *ndhA*, *ndhB*, *petB*, *petD*, *rpl16*, *rpoC1*, *rps12*, *rps16*, *trnA-UGC*, *trnG-UCC*, *trnI-GAU*, *trnK-UUU*, *trnL-UAA*, and *trnV-UAC*) contained only a single intron, while four genes (*ycf3*, *clpP*, and two *rps12*) possess two introns.

Fifteen available complete chloroplast genomes from Polygonaceae were selected based on annotation quality and sequence homology to indicate the phylogenetic position of *H. platycladum* and *Limonium sinense* (MN599096) from Plumbaginaceae, the sister family of Polygonaceae (Group et al. 2016), was selected as an outgroup. Chloroplast sequences from the different species were aligned by MAFFT
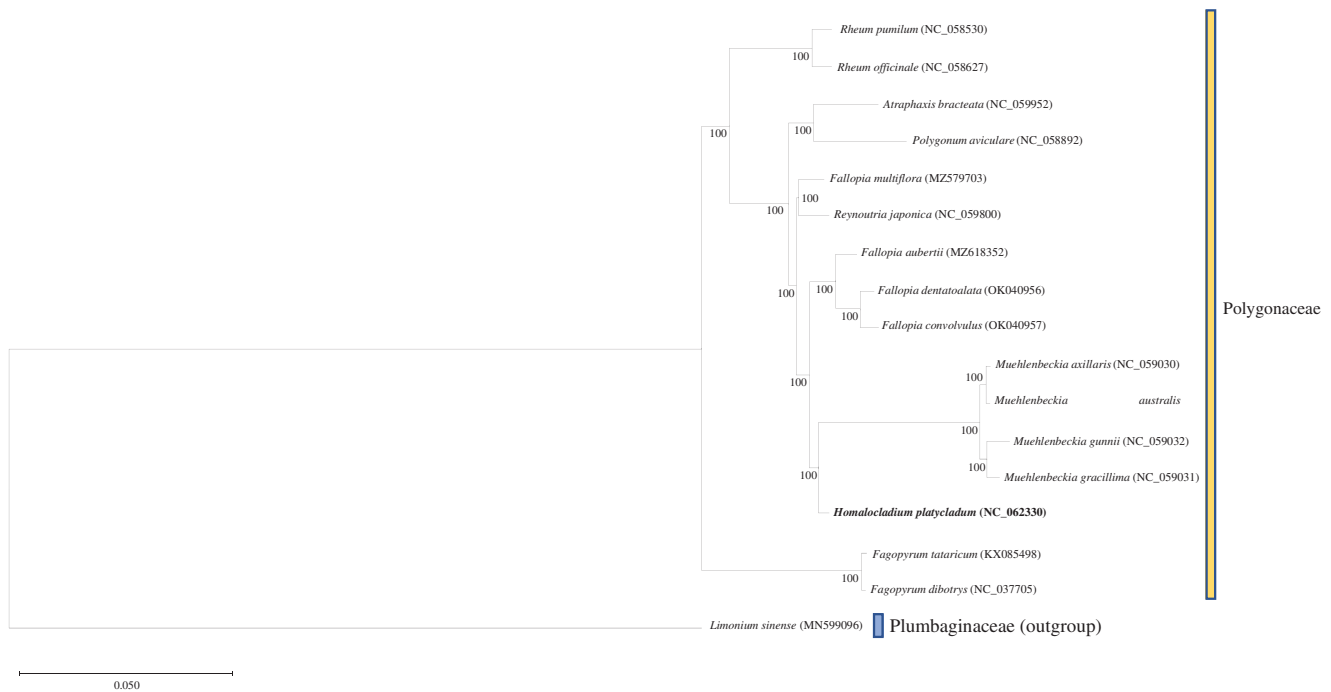
Figure 1. The number adjacent to the node shows the bootstrap value in this ML phylogenetic tree based on 17 complete chloroplast genome sequences. The bolded font represents the chloroplast genome of *H. platycladum* in this study.

v7.490 (Katoh and Standley 2013), and the maximum-likelihood (ML) phylogenetic tree was constructed in IQ-TREE v1.6.12 (Nguyen et al. 2015), with 1000 bootstrap replicates. The phylogenetic tree indicates that *H. platycladum* belongs to the Polygonaceae family and supports a sister relationship between *Homalocladium* and *Muehlenbeckia* with high bootstrap value (Figure 1). In total, this study illustrates the chloroplast genome structure of *H. platycladum* and gives crucial information for understanding its evolutionary development.

Ethical approval

We did not need permission to use these samples because this research does not include ethical research and all experimental materials were personally grown by Wei Zhai.

Author contributions

Zijie Chen: assembly and analysis of chloroplast genome data and Original draft preparation; Wei Zhai and Kai Zhao: formulation of overarching research goals and preparation of experimental materials and apparatus; Qingxiang Fu and Changrui Tai: critical review, commentary and revision; All authors agree to be accountable for all aspects of the work.

Disclosure statement

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

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Data availability statement

The genome sequence data of *H. platycladum* that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov under the accession no. NC_062330. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA824631, SRS12542718, and SAMN27409548, respectively.

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