The complete chloroplast genome of an endangered endemic herb species in China, Primula filchnerae (Primulaceae)

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ABSTRACT

Primula filchnerae (Primulaceae) is an endangered endemic herb species in China. In this study, we characterized the complete chloroplast genome of P. filchnerae based on next generation sequencing (NGS). The chloroplast genome of P. filchnerae was 151,547 bp in size, containing a large single-copy (LSC) region of 82,662 bp and a small single-copy (SSC) region of 17,749 bp. These two regions were separated by a pair of inverted repeat regions (IRs), each of 25,568 bp. A total of 130 functional genes were encoded, consisted of 86 protein-coding genes, 36 tRNA genes, and eight rRNA genes. The complete plastome could provide valuable genomic information for the conservation and restoration of this relict species.

Fresh leaves tissues of P. filchnerae were collected from a wild population (109°31′58″E, 32°19′20.49″N) in Zhuxi County. The voucher specimen was deposited in the herbaria of Kunming Institute of Botany (KUN 1444082). We isolated total genomic DNA following a modified CTAB protocol (Doyle 1991). The purified genomic DNA was sheared into c. 500 bp fragments to construct a paired-end (PE) library according to the Nextera XT sample preparation procedures (Illumina, San Diego, CA). We generated the PE reads of 150 bp using HiSeq X-Ten sequencer (Illumina, San Diego, California, USA).

In all, 3.3 Gb of raw sequence data were obtained. Reads were assembled into contigs using program CLC Genomics Workbench version 8.5.1 (CLC Inc, Arhus, Denmark). We annotated the complete plastome using the DOGMA pipeline (Wyman et al. 2004) and validated by comparing with the chloroplast genome of P. sinensis Sabine ex Lindl. (KU321892) (Liu et al. 2016). We determined transfer RNAs using tRNAscan-SE (Schattner et al. 2005), and a circular map of annotated genome was generated by using OGDRAW (http://ogdrew.mpimp-golm.mpg.de/) (Lohse et al. 2013). The annotated chloroplast genome of P. filchnerae was deposited into GenBank with the accession number MK888698.

The complete chloroplast genome of P. filchnerae was 151,547 bp in size with a typical quadripartite structure, containing a large single-copy (LSC) region of 82,662 bp and a small single-copy (SSC) region of 17,749 bp. These two regions were separated by a pair of inverted repeat regions (IRs), each of 25,568 bp. A total of 130 functional genes were encoded, consisted of 86 protein-coding genes (PCG), 36 tRNA genes, and eight ribosomal RNA (rRNA) genes. Of these genes, 18 genes were duplicated in the IR region, including seven protein-coding genes, seven tRNA genes, and four rRNA genes. Eighteen genes contain one or two introns. The overall GC content of the chloroplast genome was 37.2%, whereas the corresponding values of the LSC, SSC, and IR regions were 35.2, 30.5, and 42.8%, respectively.

Phylogenetic tree was reconstructed using RAxML (Stamatakis 2014) based on 11 complete chloroplast genomes of Primula and Androsace laxa as outgroup. The phylogenetic results indicated that the sampled Primula species clustered as a monophyletic clade with high support (100%), and P. filchnerae formed a clade with P. sinensis, with 100% bootstrap values (Figure 1). This published P. filchnerae chloroplast genome will provide useful information for phylogenetic and evolutionary studies in Primula.
Disclosure statement

No potential conflict of interest was reported by the authors.

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References

Doyle J. 1991. DNA protocols for plants: CTAB total DNA isolation. In: Hewitt GM, Johnston A, editors. Molecular techniques in taxonomy. Berlin: Springer-Verlag Press; p. 283–293.

Gan QL, Li XW. 2015. Neotypification of Primula filchnerae (Primulaceae). Novon. 24:155–158.

Hu CM. 1990. Primulaceae. In: Chen FW, Hu CM, editors. Flora Reipublicae Popularis Sinicae, Vol 59. Beijing: Science Press; p. 111–128.

Liu TJ, Zhang CY, Yan HF, Zhang L, Ge XJ, Hao G. 2016. Complete plastid genome sequence of Primula sinensis (Primulaceae): structure comparison, sequence variation and evidence for accD transfer to nucleus. PeerJ. 4:e2101.

Lohse M, Drechsel O, Kahlau S, Bock R. 2013. OrganellarGenomeDRAW: a suite of tools for generating physical maps of plastid and mitochondrial genomes and visualizing expression data sets. Nucleic Acids Res. 41:W575–W581.

Schattner P, Brooks AN, Lowe TM. 2005. The tRNAscan-SE, snoscan and snoGPS web servers for the detection of tRNAs and snoRNAs. Nucleic Acids Res. 33:W686–W689.

Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics. 30:1312–1313.

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