The complete chloroplast genome sequence of *Poncirus polyandra* (Rutaceae), an endangered species endemic to Yunnan Province, China

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**ABSTRACT**

*Poncirus polyandra*, a plant species with extremely small populations endemic to Fumin county of Yunnan province, has been classified as a national second-class protected wild plant. In this study, we assembled its complete chloroplast genome. The total genome size of *P. polyandra* was 160,211 bp in length, containing a large single-copy region of 87,406 bp, a small single-copy region of 18,771 bp, and a pair of inverted repeat regions of 27,017 bp. The all GC content of *P. polyandra* chloroplast genome was 38.4%. It contains 137 function genes, including 92 protein-coding genes, 37 tRNA genes, and eight rRNA ribosomal genes, 14 genes contain a single intron, and three genes have two introns. Phylogenetic analysis results strongly supported that *P. polyandra* was closely related to the genera of *Citrus*.

*Poncirus* Raf. is a genus in the Rutaceae of only two species: *P. trifoliate* Raf. and *P. polyandra* S. Q. Ding (Fang 1993; Fang et al. 1999). Of them, *P. polyandra*, also known as wild orange and used as a dwarf stock of *Citrus reticulate*, with extremely small populations endemic to Fumin county of Yunnan province, had been classified as a national second-class protected wild plant in the Information System of Chinese Rare and Endangered Plants (ISCRPE) (http://rep.iplant.cn/protlist). However, it has been extinct in the wild due to the drastic changes in the natural environment (Li et al. 2010) and the excessive excavation of human beings (Gao et al. 2017). So it is necessary to protect *P. polyandra* germplasm resources.

Chloroplast genomes are widely used for phylogeny (Xue et al. 2012), DNA barcoding (Dong et al. 2012, 2014), genome evolution and species conservation (Dong et al. 2013). So far, the chloroplast genome such as *Clauseneae tribe* (Shivakumar et al. 2017), genus *Citrus* (Bausher et al. 2006; Yang et al. 2016; Liu and Shi 2017), *Phellodendron amurense* (Chen 2018) and *Zanthoxylum bungeanum* (Liu and Wei 2017) within the family of Rutaceae have been reported, while the plastome of *P. polyandra* has not been reported. Here, we reported the complete chloroplast genome sequence of *P. polyandra* based on the next-generation sequencing, and the annotated genomic sequence was submitted to GenBank under accession number MK250977.

The fresh leaves of *P. polyandra* were collected from three-year-old seedling planted in the greenhouse of Southwest Forestry University, Kunming, China. Total genome DNA was extracted with the Ezup plant genomic DNA prep kit (Sangon Biotech, Shanghai, China), and DNA samples were properly stored at the Key Laboratory of State Forestry Administration on Biodiversity Conservation in Southwest China, Southwest Forestry University, Kunming, China.

Total DNA was used to generate libraries with an average insert size of 350 bp, which were sequenced using the Illumina HiSeq X platform. Approximately 14.0 GB of raw data were generated with 150 bp paired-end read lengths. Then, the raw data were used to assemble the complete cp genome using GetOrganelle software (Jin et al. 2018) with *Citrus aurantifolia* as the reference. Genome annotation was performed with the program Geneious R8 (Biomatters Ltd, Auckland, New Zealand) by comparing the sequences with the cp genome of *Citrus aurantifolia*. The tRNA genes were further confirmed through online tRNAscan-SE web servers (Schattner et al. 2005). A gene map of the annotated *P. polyandra* cp genome was drawn by OGdraw online (Lohse et al. 2013).

The complete chloroplast genome of *P. polyandra* is a circular molecule of 160,211 bp in length comprising a large single copy (LSC) region of 87,406 bp and a small single copy (SSC) region of 18,771 bp separated by a pair of inverted repeats (IRs), each 27,017 bp in length. The all GC content of *P. polyandra* chloroplast genome was 38.4%, while the GC

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The chloroplast genome of *P. polyandra* contains 137 function genes, including 92 protein-coding genes, 37 tRNA genes, and eight rRNA ribosomal genes. Ten protein-coding genes, 7 tRNA genes, and all rRNA genes were duplicated in the IR regions. Among 116 unique genes, 14 genes (atpF, ndhA, ndhB, petB, petD, rpl2, rpoC1, rps16, trnA-UGC, trnG-GCC, trnL-GAU, trnK-UUU, trnL-UAA, and trnV-UAC) contain a single intron, and three genes (clpP, rps12, and ycf3) have two introns.

To confirm the phylogenetic location of *P. polyandra* within the family of Rutaceae, a total of 16 complete cp genomes of Rutaceae were obtained from GenBank, and two species, *Dimocarpus longan* and *Acer buergerianum* in the family of Sapindaceae were used as out-groups. The 19 complete chloroplast sequences were aligned by the MAFFT version 7 software (Katoh and Standley 2013). Phylogenetic analysis was conducted based on maximum likelihood (ML) analyses were implemented in IQ-TREE 1.5.5 (Nguyen et al. 2015) under the GTR+F+R3 nucleotide substitution model, which was selected by ModelFinder (Kalyaanamoorthy et al. 2017). Support for the inferred ML tree was inferred by bootstrapping with 1000 replicates. Phylogenetic analysis results strongly supported that *P. polyandra* was closely related to the genera of *Citrus* (Figure 1). The chloroplast genome of *P. polyandra* will provide useful genetic information for further study on genetic diversity and conservation of *Poncirus* species.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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