Analysis of *Poncirus polyandra* (Rutaceae) chloroplast genome and its phylogenetic implications

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**ABSTRACT**

*Poncirus polyandra* is a threatened plant in China. Now, the complete chloroplast (cp) genome of *P. polyandra* was assembled. The cp genome of *P. polyandra* was 160,212 bp in length, it consists of a pair of inverted repeats ([IRa and IRb] regions (27,016 bp) separated by the large single-copy (LSC, 87,407 bp) and small single-copy (SSC, 18,775 bp) regions. The cp genome encodes 105 unique genes, including 70 protein-coding genes, 30 transfer RNA genes, 4 ribosomal RNA genes, and 1 pseudogene. The phylogenetic tree of Rutaceae showed that *P. polyandra* was clustered together with genus *Citrus* and *Poncirus*. The complete cp genome sequence was submitted to the GenBank to get the accession number MK764539 and was 160,212 bp in length. It was the typical quadripartite structure and contained two short inverted repeat (IRa and IRb) regions (27,016 bp) which were separated by a single copy (SSC) region (18,775 bp) and a large single copy (LSC) region (87,407 bp). The cp genome encodes 105 unique genes, including 70 protein-coding genes, 30 transfer RNA (tRNA) genes, 4 ribosomal RNA (rRNA) genes, and 1 pseudogene. Twenty-one gene species are partially or completely duplicated, including nine PCG (ndhB, ndhF, rpl2, rps12, rpoC2, rps7, rps12, rps19, ycf1, and ycf2), seven tRNA (trnL-GAU, trnA-UGC, trnL-CAA, trnI-CAU, trnR-ACG, trnV-GAC, and trnN-GUU), all four rRNA (4.5S, 5S, 16S, and 23S rRNA), and one pseudogene (*Yrpl22*). The AT content of the cp genome was 61.6%, while the corresponding values for LSC, SSC, and IR regions were 63.2, 64.8, and 57.1%, respectively.

The chloroplast genome sequences of Rutaceae were downloaded from GenBank and aligned with *P. polyandra* using MAFFT (Katoh and Standley 2013) in Geneious R11.0.2 (Auckland, New Zealand). To resolve its phylogenetic placement within the family Rutaceae, the maximum-likelihood (ML) phylogeny tree was reconstructed using RAxML version 8.1.1179 (Stamatakis 2014). *Commiphora wightii* (NC036978, Burseraceae) was selected as an outgroup. The topology of the phylogenetic tree showed that the species of *P. polyandra* was clustered together with genus *Citrus* and *Poncirus*. The complete cp genome sequence was submitted to the GenBank to get the accession number MK764539 and was 160,212 bp in length. It was the typical quadripartite structure and contained two short inverted repeat (IRa and IRb) regions (27,016 bp) which were separated by a single copy (SSC) region (18,775 bp) and a large single copy (LSC) region (87,407 bp). The cp genome encodes 105 unique genes, including 70 protein-coding genes, 30 transfer RNA (tRNA) genes, 4 ribosomal RNA (rRNA) genes, and 1 pseudogene. Twenty-one gene species are partially or completely duplicated, including nine PCG (ndhB, ndhF, rpl2, rps12, rpoC2, rps7, rps12, rps19, ycf1, and ycf2), seven tRNA (trnL-GAU, trnA-UGC, trnL-CAA, trnI-CAU, trnR-ACG, trnV-GAC, and trnN-GUU), all four rRNA (4.5S, 5S, 16S, and 23S rRNA), and one pseudogene (*Yrpl22*). The AT content of the cp genome was 61.6%, while the corresponding values for LSC, SSC, and IR regions were 63.2, 64.8, and 57.1%, respectively.

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Figure 1. The complete cp genome information reported in this study will be a valuable resource for future studies of the species’ genetic diversity, and the conservation of this highly endangered species.

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No potential conflict of interest was reported by the authors.

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