

The complete chloroplast genome sequence of *Docynia indica* (Wall.) Decne

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ABSTRACT

Docynia indica (Wall.) Decne. (Duo-Yi) is a high economic value for exploitation and utilization wild fruit tree species with edible and medicinal values in southwest China. We have sequenced the chloroplast genome to facilitate genetic improvement of this species and to assess phylogenetic relationships among major lineages. The result showed that the total chloroplast genome size of Duo-Yi was 159,546 bp in length, containing a pair of inverted repeats (IRs) of 26,369 bp, which were separated by a large single copy (LSC) and small single copy (SSC) of 87,650 bp and 19,158 bp, respectively. The overall guanine-cytosine (GC) content of the chloroplast genome was 36.6%. There were 125 genes in the chloroplast genome, which including 82 protein-coding genes, 35 transfer RNA genes, and 8 ribosomal RNA genes. Among these genes, there were 14 genes with one intron and 3 genes have two introns. The result of phylogenetic analysis indicated that the Duo-Yi was closely related to the genera of *Malus doumeri*.

ARTICLE HISTORY

Received 19 June 2019
Accepted 1 August 2019

KEYWORDS

Docynia indica (Wall.)
Decne.; chloroplast genome;
phylogenetic analysis

Docynia indica (Wall.) Decne., also called Duo-Yi in China, is an evergreen wild fruit tree species belonging to the Rosaceae family, which widely distributed from East Asia to China (Rymbai et al. 2016). Its leaves are rich in polyphenols and flavonoids, extracts from the leaves have several pharmacological actions such as anti-obesity (Nguyen et al. 2011), antifungal (Zhang et al. 2018a), antioxidant (Sharma et al. 2015), which were widely used as a medicine for the healing of empyrosis, fracture and fever by the local ethnic minorities in China (Lin et al. 2003; Zhang et al. 2018b). The fruits contain high levels of biologically active components including anti-oxidants, tannins and flavonoids, which were used as natural remedy to treat digestive problems and infectious diseases (Tiep et al. 2018). Recent studies have shown that the extracts of fruits have hypoglycemic, hypolipidemic, lipid-lowering and weight-loss effects (Vivek et al. 2017). Generally, Duo-Yi is a high economic value for exploitation and utilization wild fruit tree species with edible and medicinal values in southwest China.

Chloroplast genetic engineering had become a powerful tool for basic research in biogenesis and function of this organelle (Bausher et al. 2006). The complete chloroplast genomes have extensively been used in resolution of phylogenetic relationships, study of DNA barcoding and genome evolution (Leseberg and Duvall 2009; Dong et al. 2012; Zong et al. 2019). Currently, complete chloroplast genomes

of several species from the Rosaceae family have been studied and deposited at the GenBank database (Gichira et al. 2017). These studies have greatly boosted our understanding of phylogenetic relationships in Rosaceae. However, the plastome of Duo-Yi has not been reported. In this paper, we reported the complete chloroplast genome sequence of Duo-Yi employing the high-throughput sequencing approaches. The phylogenetic analysis will provide an examination of relationships among several major clades of Rosaceae family.

Leaf samples of Duo-Yi were obtained from the Puer city (Yunnan, China; geospatial coordinates: 100°17'19"E, 22°59'74"N; Altitude: 1694 m). The total genome DNA was isolated using the Ezup plant genomic DNA kit (Sangon Biotech, Shanghai, China), and DNA samples (Duo-Yi 1-5) were stored at the Key Laboratory for Forest Resources Conservation and Utilization in the Southwest Mountains of China Ministry of Education, Southwest Forestry University, Kunming, China. After DNA extraction, a library with the insertion size of 350 bp was constructed using procedures described by Zong et al. There were approximately 7 G raw data generated from the high-throughput sequencing. Then the soft-ware of Get Organelle (Jin et al. 2018) was employed to assemble the complete chloroplast genome. The assembled chloroplast genome sequence was then annotated using the program Geneious R8 (Biomatters Ltd, Auckland,

The neighbour-joining tree showed that the position of Duo-Yi was closely related to the genera of *Malus doumeri* (Figure 1). The result provided vital molecular information to phylogenetic and evolutionary study.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

The study was supported by the Forestry Science and Technology Development Project of National Forestry and Grassland Administration of China under Grant Number [KJZXSA2019036].

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