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

Dawei Wang, Chen Shi, Hongyan Tang, Chengzhong He, Anan Duan, and Hede Gong

**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; chloroplast genome; phylogenetic analysis

*Docynia indica* (Wall.) Decne., also called Duo-Yi in China, is an evergreen wild fruit tree belonging to the Rosaceae family, which wildly 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, hypolipidodemic, 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,
New Zealand) and manually corrected. The chloroplast DNA sequence with complete annotation information was deposited at GenBank database under the accession number MN088849.

The total length of Duo-Yi chloroplast genome was determined to be 159,564 bp with the circular quadripartite structure similar to major angiosperms chloroplast genomes. The genome contained a small single-copy (SSC) region of 19,158 bp and a large single-copy (LSC) region of 87,650 bp, separated by two copies of an inverted repeat (IR) of 26,369 bp. The overall guanine-cytosine (GC) content of the chloroplast genome was 36.6%. The genome was structured with 111 unique genes including 82 distinct protein-coding genes, eight distinct rRNA genes and 35 distinct tRNA genes. There were 6 tRNA genes, 4 rRNA genes and 4 CDS duplicated in the IR regions, making a total number of 125 genes. Among these genes, there were 14 genes (atpF, ndhA, ndhB, petB, petD, rpl2 and rpl16; trnA-UGC, trnI-GAU, trnK-UUU, trnL-CAA; trnV-UAC) with one intron and three genes (clp P, rps12 and ycf3) with two introns Figure 1.

To analyze the Duo-Yi phylogenetic position within Rosaceae lineage, we performed a phylogenetic tree using other 25 chloroplast genome sequences (P. rupicola, M. hupehensis, M. transitoria, M. micromalus, M. baccata, M. doumeri, P. hopeiensis, E. japonica, M. florentina, M. triloba, P. pyrifolia, P. pashia, P. spinosa, C. japonica, C. sinensis, C. speciosa, S. torminalis, P. fortuneana, C. kansuensis, S. ulleungensis, C. oblonga, D. delavayi, P. yedoensis, P. pedunculata, P. utilis) in Rosaceae family by the MAFFT version 7 software (Katoh and Standley 2013). The maximum likelihood method for phylogenetic analysis was performed by Zong et al. (2019).

Figure 1. Phylogenetic relationships among 25 complete chloroplast genomes of Rosaceae. Bootstrap support values are given at the nodes. Chloroplast genome accession number used in this phylogeny analysis: Pentactina rupicola: JQ041763; Malus hupehensis: MK020147; Malus transitoria: MK098838; Malus micromalus: MF062434; Malus baccata: KX499859; Malus doumeri: KX499861; Pyrus hopeiensis: MF521826; Eriobotrya japonica: KT633951; Malus florentina: KX499862; Malus triloba: KX499858; Pyrus pyrifolia: AP012207.1; Pyrus pashia: KY626169; Pyrus spinosa: HG737342; Chaenomeles japonica: KT932966; Chaenomeles sinensis: KT932967; Chaenomeles speciosa: KT932965; Sorbus torminalis: KY457242; Pyracantha fortuneana: MH890570; Crataegus kansuensis: MF784433; Sorbus ulleungensis: MG011706; Cydonia oblonga: KX499857; Docynia delavayi: KX499860; Prunus yedoensis: KU985054; Prunus pedunculata: MG869261; Prinsepia utilis: KC571835.
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 evolutional 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].

**References**

Bausher MG, Singh ND, Lee SB, Jansen RK, Daniell H. 2006. The complete chloroplast genome sequence of *Citrus sinensis* (L.) Osbeck var ‘Ridge Pineapple’: organization and phylogenetic relationships to other angiosperms. BMC Plant Biol. 6:21.

Dong W, Liu J, Yu J, Wang L, Zhou S. 2012. Highly variable chloroplast markers for evaluating plant phylogeny at low taxonomic levels and for DNA barcoding. PLoS One. 7:e35071.

Gichira AW, Li Z, Saina JK, Long Z, Hu G, Gituru RW, Wang Q, Chen J. 2017. The complete chloroplast genome sequence of an endemic monotypic genus *Hagenia* (rosaceae): structural comparative analysis, gene content and microsatellite detection. Peer J. 5:e2846.

Jin JJ, Yu WB, Yang JB, Song Y, Yi TS, Li DZ. 2018. GetOrganelle: a simple and fast pipeline for de novo assembly of a complete circular chloroplast genome using genome skimming data. BioRxiv.

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 30:772–780.

Leseberg CH, Duvall MR. 2009. The complete chloroplast genome of Coix lacryma-jobi and a comparative molecular evolutionary analysis of plastomes in cereals. J Mol Evol. 69:311–318.

Lin YF, Yi Z, Zhao YH. 2003. Chinese Dai medicine colorful illustrations. Kunming:Yunnan National Press.

Nguyen TTL, Hoang TMT, Vu THT, Chu LL, Le MH, Do NL. 2011. Anti-obesity and body weight reducing effect of *Docynia indica* (Wall.) Decne fruit extract fractions in experimentally obese mice. VNU J Sci Nat Tech. 27:125–133.

Rymbai H, Roy AR, Deshmukh NA, Jha AK, Shimray W, War GF, Ngachan SV. 2016. Analysis study on potential underutilized edible fruit genetic resources of the foothills track of Eastern Himalayas, India. Genet Resour Crop Evol. 63:125–139.

Sharma PB, Handique PJ, Devi HS. 2015. Antioxidant properties, physicochemical characteristics and proximate composition of five wild fruits of Manipur, India. J Food Sci Technol. 52:894–902.

Tiep HV, Thuong PH, Nguyen L, Lua HT, Thuan VV, Kieu LT, Carsan S, Degrande A, Catucan D, Harwood C. 2018. Domestication of *Docynia indica* in Vietnam. Forests Trees Livelihoods. 27:230–242.

Vivek K, Mishra S, Sasikumar R. 2017. Effect of ultra-sonication on post-harvest quality parameters and microbial load on *Docynia indica*. Sci Hortic. 225:163–170.

Zhang XY, Mei XR, Wang ZG, Wu J, Liu G, Hu HL, Li QJ. 2018a. Chemical fingerprint and quantitative analysis for the quality evaluation of *Docynia dens* leaves by high-performance liquid chromatography coupled with chemometrics analysis. J Chromatograph Sci. 56: 575–581.

Zhang XY, Yi K, Chen J, Li RP, Xie J, Jin Y, Wei XR, Li YJ, Liu G, Wang ZG. 2018b. Purified phlorizin from *Docynia Indica* (Wall.) Decne by HSCCC, compared with whole extract, phlorizin and non-phlorizin fragment ameliorate obesity, insulin resistance, and improves intestinal barrier function in high-fat-diet-fed mice. Molecules. 23:2701.

Zong D, Zhou AP, Li D, He CZ. 2019. The complete chloroplast genome of *Populus xiangchengensis*, an endemic species in Southwest China. Mitochondrial DNA Part B. 4:70–71.