MITOGENOME ANNOUNCEMENT

The complete chloroplast genome sequence of Flacourtia jangomas

Xiaoyan Zhang*, Shuyu Liu*, Yang Tian*, Yi Li*, Jianguo Zhang* and Zhaoshan Wang*

*State Key Laboratory of Tree Genetics and Breeding, Key Laboratory of Silviculture of the State Forestry Administration, Research Institute of Forestry, Chinese Academy of Forestry, Beijing, China; #Collaborative Innovation Center of Sustainable Forestry in Southern China, Nanjing Forestry University, Nanjing, China

ABSTRACT

In this study, the complete chloroplast genome sequence of Flacourtia jangomas was featured from Illumina pair-end sequencing. In F. jangomas, its length was 156,223 bp, consisting of a large single copy (LSC) region of 84,233 bp, two inverted repeat (IR) copies 27,649 bp and a small single copy (SSC) region of 16,693 bp. The entire GC contents were 37%, and in the LSC, SSC, and IR regions were 35, 31, and 42%, respectively. Flacourtia jangomas has 130 unique genes, including 86 protein-coding genes, 36 tRNA genes, and 8 rRNA genes. The chloroplast genomes of 12 species of Salicaceae and 1 species of Euphorbiaceae were used to construct the maximum-likelihood phylogenetic tree. It indicated that F. jangomas belongs to Salicaceae and is clustered with Flacourtia indica as sisters.

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Introduction

Flacourtia jangomas (Lour.) Rauschel, a species of Flacourtia (Salicaceae), with varying names such as coffee plum, East Indian plum, Indian plum, and Manila cherry among others. It mainly distributed in the southeast of China and Vietnam, which is a shrub or small tree (Ishikawa et al. 2004). As a medicinal plant, it plays an important role in the economy and ecology. But wild F. jangomas are facing serious damage because of overexploitation. In this study, we characterized the whole chloroplast genome of F. jangomas and comprehended more about genetic information of this species, which can contribute to the conservation, and supply useful help for population genetics studies of F. jangomas.

The leaf samples of F. jangomas were collected from Jinhong (Yunnan, China; 21°54′N,102°32′E), and stored the voucher specimen (FJ20180622-4) at the herbarium of Research Institute of Forestry, Chinese Academy of Forestry. A modified CTAB method was used to isolate total genomic DNA from silica gel-dried leaves (Doyle and Doyle 1987). The isolated DNA stored in the −80°C refrigerator at the herbarium of Research Institute of Forestry. Sequencing was carried out on the Illumina HiSeq 2000 platform (Illumina, San Diego, CA). We used MITObim 1.8 (University of Oslo, Oslo, Norway; Kaiseraugst, Switzerland) to package the chloroplast genome (Hahn et al. 2013) and use Flacourtia indica (GenBank: MG262341) as the reference. We annotated the complete chloroplast genome using DOGMA software (Wyman et al. 2004) and then submitted by Sequin 15.50 (http://www.ncbi.nlm.nih.gov/Sequin/).

The chloroplast genome of F. jangomas (GenBank accession MK572740) has a total length of 156,223 bp and is composed of a large single copy (LSC) region of 84,233 bp, two inverted repeat (IR) copies 27,649 bp and a small single copy (SSC) region of 16,693 bp. The entire GC contents were 37%, and in the LSC, SSC, and IR regions were 35, 31, and 42%, respectively. The proportion of coding sequences including all RNA regions is 59.5%. A total of 130 unique genes, including 86 protein-coding genes, 36 tRNA genes, and 8 rRNA genes. Seventeen genes contain introns, and three of these genes, rps12, and ycf3, exhibit two introns. The 5′-end exon of the rps12 gene was located in the LSC region, and the 3′-end exons, as well as the introne of the gene, were situated in the IR region. A total of 19 of these genes were duplicated in the IR regions including 7 tRNAs (trnA-UGC, trnI-CAU, trnL-GAU, trnL-CAC, trnN-GUU, trnR-ACG, and trnV-GAC), 8 protein genes (psp7, rpl2, rpl23, rps12, rps19, ndhB, ycf1, ycf2, and ycf15) and 4 rRNAs (4.5S, 5S, 16S, and 23S rRNA). Also, partial of ycf1 duplicated in IR region is formed as one pseudogene.

We used MEGA 7.0 (Kearse et al. 2012) by the MAFFT (Katoh and Standley 2013) to construct a maximum-likelihood
phylogenetic tree (with 1000 bootstrap replicates), and the phylogenetic tree including 10 related species of Salicaceae, and *Hevea brasiliensis* (Euphorbiaceae) as the outgroup. The results meant that *F. jangomas* and *F. indica* were as close as sisters, and suggested that *F. jangomas* belongs to Salicaceae as observed in the phylogenetic tree (Figure 1). In conclusion, the complete chloroplast genome in this study promotes the phylogenetic studies of the Salicaceae family.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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**ORCID**

Shuyu Liu [http://orcid.org/0000-0002-6411-685X](http://orcid.org/0000-0002-6411-685X)

**References**

Doyle JJ, Doyle JL. 1987. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochem Bull*. 19:11–15.

Hahn C, Bachmann L, Chevreux B. 2013. Reconstructing mitochondrial genomes directly from genomic next-generation sequencing reads—a baiting and iterative mapping approach. *Nucleic Acids Res.* 41:e129.

Ishikawa T, Nishigaya K, Takami K, Uchikoshi H, Chen IS, Tsai IL. 2004. Isolation of salicin derivatives from *Homalium cochinchinensis* and their antiviral activities. *J Nat Prod.* 67:659–663.

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

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics*. 28: 1647–1649.

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