The chloroplast genome of an endangered tree *Artocarpus nanchuanensis* (Moraceae)

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**ABSTRACT**

The complete chloroplast genome sequence of *Artocarpus nanchuanensis* was determined, an Endangered species of *Artocarpus* in the family Moraceae. The plastome is 160,752 bp in length, exhibiting a characteristic quadripartite structure with a pair of inverted repeat regions (IRs) of 25,693 bp, separated by a large single-copy region (LSC) and a small single-copy region (SSC) of 89,345 bp and 20,021 bp, respectively. Further, the maximum likelihood phylogenetic analysis was conducted using 24 complete plastomes of the Moraceae and Cannabaceae, which supports the close relationship between *Artocarpus* and *Morus*.

*Artocarpus nanchuanensis* S.S. Chang is a member of the genus *Artocarpus* (Moraceae), which includes approximately 70 species mostly native to the hot regions of South and Southeast Asia and Oceania (William et al. 2017). *A. nanchuanensis* is unique as the northernmost species of *Artocarpus*, distributing at low elevations in Chongqing of SW China (Wu and Zhang 1989). In spite of its potential edible, medical, and industrial value, the few *A. nanchuanensis* communities in the field are facing a hard situation due to their rare seedlings in the understory (Sun 2011). In 2004, *A. nanchuanensis* was classified as a Critically Endangered species on the China Species Red List (Wang 2004). However, rare genomic data was reported about *A. nanchuanensis*, even the genus of *Artocarpus*. Here, we determined the complete chloroplast genome of *A. nanchuanensis*.

About 5 g leaf tissue of *A. nanchuanensis* was used from the specimen, which was collected from Nanchuan District, Chongqing, China (29°15′N, 107°11′E, 994.59 m) to extract genomic DNA using the modified CTAB method (Doyle and Dickson 1987). The voucher specimen was deposited at the Herbarium of Xishuangbanna Tropical Botanical Garden (Accession Number: XTBG-BRG-SY34421). The whole plastome genome was sequenced following Zhang et al. (2016) and their 15 universal primer pairs were used to perform long-range PCR for next-generation sequencing. The contigs were aligned using the publicly available chloroplast genome of *Morus indica* (GenBank accession number DQ226511) and then annotated in Geneious 4.8.

The chloroplast genome of *A. nanchuanensis* is 160,752 bp in length, exhibiting a characteristic quadripartite structure with a pair of inverted repeat regions (IRs) of 25,693 bp, separated by a large single-copy region (LSC) and a small single-copy region (SSC) of 89,345 bp and 20,021 bp, respectively. The G + C content is 35.8%. The plastome contains a total of 122 genes (108 unique genes), among which 20 genes have one intron and three genes have two introns.

The complete plastid genome sequence of *A. nanchuanensis* and the other sequenced Moraceae and Cannabaceae taxa including *Morus cathayana*, *M. alba var. atropurpurea*, *M. mongolica*, *M. alba var. multicaulis*, *M. notabilis*, *M. indica*, *Artocarpus heterophyllus*, *Ficus racemosa*, *F. religiosa*, *F. carica*, *Broussonetia papyrifera*, *Parasponia rugosa*, *P. rigidia*, *P. andersonii*, *Trema levigata*, *T. orientalis*, *T. tomentosa*, *Cannabis sativa*, *Humulus lupulus*, *Chaetacme aristata*, *Gironniera celtidifolia* and *Aphananthe aspera*, formed the base to perform a phylogenetic analysis, with *Zelkova serrata* and *Ulmus changii* as outgroup. A maximum likelihood analysis yielded a tree topology with 87–100% bootstrap (BS) values at each node based on GTR model in the RAXML version 8 program with 1000 bootstrap replicates (Darriba et al. 2012; Stamatakis 2014). The data supports the close relationship between *Artocarpus* and *Morus* and the robust monophyly of the Moraceae and Cannabaceae (Figure 1). In the family Moraceae, *Artocarpus* and *Morus* formed a strong supported clade which was sister to the clade including *Ficus*.
and Broussonetia, consisting of previous phylogenies (Zerega et al. 2005; Liu et al. 2018).

**Data archiving statement**

The plastome data of the *A. nanchuanensis* will be submitted to Genebank of NCBI through the revision process. The accession numbers from Genebank must be supplied before the final acceptance of the manuscript.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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**References**

Darriba D, Taboada GL, Doallo R, Posada D. 2012. jModelTest 2: more models, new heuristics and parallel computing. Nature Methods. 9:772.

Doyle JJ, Dickson EE. 1987. Preservation of plant samples for DNA restriction endonuclease analysis. Taxon. 36:715–722.

Liu J, Niu YF, Ni SB, Liu ZY, Zheng C, Shi C. 2018. The complete chloroplast genome of *Artocarpus heterophyllus* (Moraceae). Mitochondrial DNA B. 3:13–14.

Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics. 30:1312–1313.

Sun R. 2011. Genetic resource conservation and development and utilization countermeasure of *Artocarpus nanchuanensis*. J Green Sci Technol. 09:20.

Wang S. 2004. The China species Red List. Beijing: Higher Education Press.

Zerega NJC, Clement WL, Datwyler SL, Weiblen GD. 2005. Biogeography and divergence times in the mulberry family (Moraceae). Mol Phylogenet Evol. 37:402–416.