

MITOGENOME ANNOUNCEMENT



# The complete chloroplast genome sequence of *Firmina danxiaensis*

Xiao-Yu Lin, Zhi-Hui Chen, Yun-Yuan Yang, She-Qin Mo and Dong-Lin Li

College of Ying-Tong Agricultural Science and Engineering, Shaoguan University, Shaoguan, China

## ABSTRACT

The complete chloroplast genome of *Firmina danxiaensis*, an important deciduous tree, was identified and sequenced in this study. The genome size is 161,205 bp, the GC content is 36.88%. A total of 129 genes were identified, including 84 protein-coding genes, 8 rRNA genes, and 37 tRNA genes. 10 plastome accessions from Sterculiaceae were selected to assess the phylogenetic placement of genus and the result showed that *F. danxiaensis* is most closely related to *F. simplex*.

## ARTICLE HISTORY

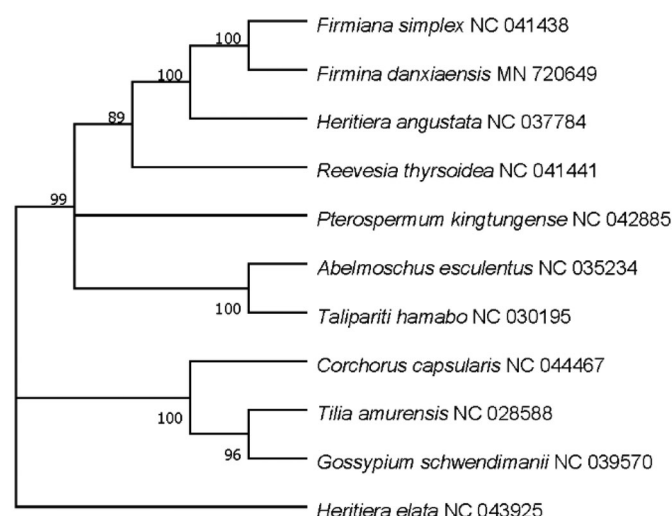
Received 24 December 2019  
Accepted 7 January 2020

## KEYWORDS

*Firmina danxiaensis*; *Firmina*; chloroplast genome; phylogenomic tree

Danxia Mountain is located in a special geographical location of the Nanling Mountains, which is the natural boundary between the north and south of vegetation (He et al. 1991). A large number of rare and endemic species have been preserved in the area, such as *Firmina danxiaensis*, *Chiritopsis danxiaensis* and *Spiradiclis danxiashanensis*. *F. danxiaensis*, Sterculiaceae, is a small deciduous tree characterized by beautiful tree shape, flower colors, and golden autumn leaves (Xu et al. 1987). It is an endemic species in Guangdong Province, and only distributed in Danxia Mountain and Cangshi Village in Shaoguan. Additionally, it was listed as a critically dangerous (CR) grade in the assessment of the first volume of the Chinese Red List of Species (Wang and Xie 2004). Previous research reports on *F. danxiaensis* mainly focus on the analysis of the geographical flora of its community (Luo et al. 2015), the spatial distribution of micro-geomorphic environmental features (Ouyang et al. 2017), and genetic diversity (Fan et al. 2013; Chen et al. 2014), no chloroplast genome resource is available so far for this important tree. In this study, the first complete chloroplast genome of *F. danxiaensis* is reported.

The fresh leaves of *F. danxiaensis* was collected from Xiafu village (25°0'04"N, 113°41'44"E) in Shaoguan, Guangdong, China, and the Voucher specimens were deposited in the Herbarium of Shaoguan university, the accession number is Li-201905. Total genomic DNA was extracted from the fresh mature leaves using the Plants Genomic DNA Kit (DP305, Tiangen Biotech Co., Ltd., Beijing, China). The plastome sequences was generated using Illumina HiSeq 2500 platform (Illumina Inc., San Diego, CA, USA). In total, 6.5Gb raw reads were obtained. The filtered reads were assembled with the program NOVOPlasty 3.1 (Dierckxsens et al. 2017) with a part of



**Figure 1.** Maximum likelihood tree based on the sequences of ten complete chloroplast genomes. Numbers in the nodes were bootstrap values from 1000 replicates. Scale in substitutions per site.

*rbcl* gene of *Antiaris toxicaria* (NC 042884), and then the sequence of *F. danxiaensis* was annotated using DOGMA (Wyman et al. 2004). The annotated sequence was submitted to NCBI, the accession number is MN720649.

The full length of *F. danxiaensis* chloroplast genome was 161,205 bp. It is made up of a large single-copy region (LSC with 90,114 bp), a small single-copy region (SSC with 20,057 bp) and two inverted repeat regions (IRs with 25,517 bp). Total GC content is 36.88%. A total of 129 genes are successfully annotated, including 84 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. The tRNA genes

are distributed throughout the whole genome with 21 in the LSC, 3 in the SSC, and 9 in the IR regions, while rRNAs are only situated in the IR regions.

To further investigate the phylogenetic position of *F. danxiaensis* in Sterculiaceae family, 10 of complete chloroplast genomes in Sterculiaceae family was download from NCBI, and then the maximum-likelihood (ML) phylogenetic tree was generated by MEGA 7.0 (Kumar et al. 2016), with *Heritiera eleta* as outgroup. The results in Figure 1 shows that *F. danxiaensis* is closed to *F. simplex*. This newly reported chloroplast genome will provide valuable information for genetic evolution and molecular breeding studies of *Firmiana*.

### Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

### Funding

This study was supported by PhD research startup foundation of Shaoguan University [99000612] and the National Science Foundation of Hainan Province [319QN214].

### References

- Chen S, Li M, Hou R, Liao W, Zhou R, Fan Q. 2014. Low genetic diversity and weak population differentiation in *Firmiana danxiaensis*, a tree species endemic to Danxia landform in northern Guangdong, China. *Biochem Syst Ecol.* 55:66–72.
- Dierckx N, Mardulyn P, Smits G. 2017. NOVOPlasty: de novo assembly of organelle genomes from whole genome data. *Nucleic Acids Res.* 45(4):e18.
- Fan Q, Chen S, Li M, He S, Zhou R, Liao W. 2013. Development and characterization of microsatellite markers from the transcriptome of *Firmiana danxiaensis*. *Appl Plant Sci.* 1(12):1300047–1300047.
- He DQ, Ao HX, Wu HM. 1991. The vegetation and its conservation in the Danxia Mountains. *Trop Geogr.* 11(3):261–270.
- Kumar S, Stecher G, Tamura K. 2016. MEGA7: molecular evolutionary genetics analysis Version 7.0 for bigger datasets. *Mol Biol Evol.* 33: 1870–1874.
- Luo XY, Chen QH, Cai CR, et al. 2015. Analysis on geographical elements of the community of plant species with extremely small populations *Firmiana danxiaensis*. *J Shaoguan Univ Nat Sci.* 36(12):28–31.
- Ouyang J, Peng H, Luo XY, et al. 2017. Environmental features of the micro - landforms of the spatial distribution of the National Rare Species of *Firmiana danxiaensis* on the Danxiashan Mountain. *Sci Geogr Sinica.* 37(10):1585–1592.
- Wang S, Xie Y. 2004. China species red list (Vol. 1). Beijing: Higher Education Press. p. 35–36.
- Wyman SK, Jansen RK, Boore JL. 2004. Automatic annotation of organellar genomes with DOGMA. *Bioinformatics.* 20(17):3252–3255.
- Xu XH, Qiu HX, Xu SJ. 1987. New species and variety of Sterculiaceae from China. *J South China Agric Univ.* 8(3):1–5.