MITOGENOME ANNOUNCEMENT

The complete chloroplast genome of Gymnospermium kiangnanense (Berberidaceae): an endangered species endemic to Eastern China

Zhaoping Yang^a,b*, Zhengkang Peng^a*, Hongwei Zhang^c, Joongku Lee^d, Xuelian Liu^e and Chengxin Fu^b

^aKey Laboratory of Conservation Biology for Endangered Wildlife of the Ministry of Education, Laboratory of Systematic & Evolutionary Botany and Biodiversity, College of Life Sciences, Zhejiang University, Hangzhou, China; ^bCollege of Life Sciences, Tarim University, Alaer, China; ^cAdministration of Zhejiang Qingshitan National Natural Reserve, Hangzhou, China; ^dDepartment of Environment and Forest Resources, Chungnam National University, Daejeon, South Korea; ^eCollege of Life Science, Tonghua Normal University, Tonghua, China

ABSTRACT

Gymnospermium kiangnanense is an endangered species in the family Berberidaceae. In this study, we assembled the chloroplast (cp) genome of G. kiangnanense and reconstructed the phylogenetic tree of Berberidaceae based on the complete cp genome. The cp genome of G. kiangnanense is 160,136 bp in length, comprising a pair of inverted repeat (IR) regions (26,424 bp) separated by a large single-copy (LSC) region (87,580 bp) and a small single-copy (SSC) region (19,709 bp). The genome encodes 111 unique genes, consisting of 77 different protein-coding genes, 30 transfer RNA, and 4 ribosomal RNA genes, with 18 duplicated genes in the inverted repeats. Phylogenetic analysis indicates that G. kiangnanense is sister to G. microrrhynchum, and the Gymnospermium clade is closely related with Nandina.

CONTACT Chengxin Fu cxfu@zju.edu.cn College of Life Sciences, Tarim University, Alaer, 843300, China

These authors contributed equally to this work.

The complete chloroplast genome of Gymnospermium kiangnanense (approximately 1.37 Gb) was filtered by quality with Phred score <30 and all remaining sequences were assembled into contigs using CLC Genomic Workbench 10.1.1 (QIAGEN Bioinformatics, Aarhus, Denmark). All the contigs were aligned according to the reference chloroplast genome. The representative chloroplast contigs were ordered and oriented according to the reference chloroplast genome. Finally, clean reads re-mapped to the draft genome and yielded the complete chloroplast genome sequences. The phylogenetic tree was reconstructed based on the complete cp genome sequences of 15 Berberidaceae species and one outgroup, using maximum likelihood (ML) method. ML analysis was implemented in RAxML-HPC v8.2.10 (Stamatakis 2014) on the CIPRES cluster (Miller et al. 2010). The complete chloroplast genome of G. kiangnanense is 160,136 bp in length and shares the common feature of comprising two copies of IR (26,424 bp each) that divide the genome into two single-copy regions (LSC 87,579 bp; SSC 19,709 bp). The whole GC content of the total length, LSC, SSC, and IR regions is 37.8%, 36.1%, 31.0%, and 43.1%, respectively, which is similar to that of the chloroplast genomes reported for the other Berberidaceae species (Zhang et al. 2016; Meng et al. 2017). Within the cp genome of G. kiangnanense, there are 111 unique genes, including 77 protein coding genes, 30 tRNA genes, and four rRNA genes, with 18 genes duplicated in the IR regions.

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CONTACT Chengxin Fu cxfu@zju.edu.cn College of Life Sciences, Tarim University, Alaer, 843300, China

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tree showed that *G. kiangnanense* was sister to *G. microrrhynchum*, and the *Gymnospermium* clade was closely related with *Nandina domestica* (Figure 1).

In conclusion, this is the first report of the complete chloroplast genome of *G. kiangnanense*. It will provide useful genetic resources for future conservation of this endangered species, and also shed light on the evolution of the family Berberidaceae.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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**Figure 1.** Phylogenetic tree reconstruction based on complete chloroplast genome sequences of 15 Berberidaceae taxa and one outgroup, using maximum likelihood (ML) method.