The complete chloroplast genome of *Cephalotaxus lanceolata* (Taxaceae), a plant species with extremely small populations

Jia Ge\(^\text{a,b}\), Yun Xiong\(^\text{c}\) and Guifen Luo\(^\text{a,b}\)

\(^\text{a}\)Yunnan Key Laboratory for Integrative Conservation of Plant Species with Extremely Small Populations, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, P. R China; \(^\text{b}\)Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, P. R China; \(^\text{c}\)Gongshan Administrative Sub-Bureau of Gaoligongshan National Nature Reserve, Nujiang, P. R China

**ABSTRACT**

*Cephalotaxus lanceolata* K. M. Feng ex C. Y. Cheng W. C. Cheng and L. K. Fu (Taxaceae) is a threatened plant species and a typical plant species with extremely small populations (PSESP) with only four individuals found in Gaoligong Mountain. With the aim of providing data for future conservation efforts, we sequenced the whole chloroplast (cp) genome of *C. lanceolata*. The results showed that the plastid genome is 136,404 bp in size. In total, 116 unique genes were annotated, including 83 protein-coding genes, 29 tRNA genes, and 4 rRNA genes. The total GC content was 35.1%. We performed phylogenetic analyses based on 12 cp genomes of Taxaceae, and we determined that the genus *Cephalotaxus* forms a sister group to *Taxus* and *Pseudotaxus*.

The genus *Cephalotaxus* (Taxaceae) is endemic to southern and eastern Asia comprising nine species according to the Plant List (http://www.plantlist.org). Phytochemical research indicated that the constituents identified from this genus such as the cephalotaxin-type alkaloids and flavonoids were found to have remarkable anticancer activities (Chen et al. 2017). Owing to the medical value, the *Cephalotaxus* genus has been overharvesting for decades. Unfortunately, there is few conservation action or conservation biology research conduct on this species. *Cephalotaxus lanceolata* K. M. Feng ex C. Y. Cheng W. C. Cheng and L. K. Fu is restrict distributed along the upper reaches of Dulong River in Gongshan County, northwestern Yunnan, only four individuals have been found so far. According to the literature, it is also distributed in Myanmar, but it is deficient in the distributional data. It was categorized as Endangered (EN) in the Red List (Yang and Liao 2013), and it is a typical plant species with extremely small populations (PSESP) (Sun et al. 2019). The only four *C. lanceolata* individuals need an urgent conservation attention. At this point, we report and characterized the complete plastome of *C. lanceolata* for the further conservation efforts.

In August 2020, we collected the fresh leave material of *C. lanceolata* from Gaoligong Mountain, Yunnan Province of China (27.68°N, 93.30°E). The voucher herbarium specimen was stored in the herbarium of Gongshan Administrative Sub-Bureau of Gaoligongshan National Nature Reserve (voucher: XY2020091). The complete chloroplast (cp) genome sequencing was performed on the Illumina Hiseq X platform (Illumina Inc., San Diego, CA, USA), assembled into contigs using the de novo assembler SPAdes version 3.11.0 (Bankevich et al. 2012) with complete plastome of *C. sinensis* (Accession no.: NC_037245.1) as the reference. Initial annotations were made by using planteao and together form a sister group to *Taxus* and *Pseudotaxus.*

**CONTACT**

Jia Ge \(<\text{gejia@mail.kib.ac.cn}\>\); Guifen Luo \(<\text{lgf@mail.kib.ac.cn}\>\) Yunnan Key Laboratory for Integrative Conservation of Plant Species with Extremely Small Populations, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, P. R China

**ARTICLE HISTORY**

Received 5 November 2020
Accepted 8 March 2021

**KEYWORDS**

*Cephalotaxus lanceolata*; chloroplast genome; plastid genome; plant species with extremely small populations
The genus *Cephalotaxus* forms a sister group to *Taxus* and *Pseudotaxus*, and these three genus together form a sister group to *Torreya* and *Amentotaxus* (Figure 1).

**Acknowledgment**

We are grateful to Guiqi Bi for data analysis.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

**Funding**

This work was supported by the Science & Technology Basic Resources Investigation Program of China: Survey and Germplasm Conservation of Plant Species with Extremely Small Populations in Southwest China [grant No. 2017FY100100], Yunnan Provincial Natural Science Foundation Projects: Phylogenetics, evolution strategy and the taxonomy of the core Asian clade of *Buddleja* (Scrophulariaceae) [grant No. 202001AT070097], and Yunnan Provincial Wildlife Conservation Projects: Urgent Rescuing Conservation of *Amentotaxus yunnanensis*, a plant species with extremely small population.

**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (https://www.ncbi.nlm.nih.gov/) under the accession no. MW149080. The associated BioProject, SRA and Bio-Sample numbers are PRJNA6852599, SRR13254579 and SAMN17080720 respectively.

**References**

Andrew R. 2016. Fig tree: tree figure drawing tool version 1.4.3. Institute of evolutionary biology, University of Edinburgh. http://tree.bio.ed.ac.uk/software/figtree/.

Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, et al. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol. 19(5):455–477.

Bi G, Mao Y, Xing Q, Cao M. 2018. HomBlocks: a multiple-alignment construction pipeline for organelle phylogenomics based on locally collinear block searching. Genomics. 110(1):18–22.

Chen XJ, Ni L, Bao MF, Wang L, Cai XH. 2017. Abietane diterpenoids from *Cephalotaxus lanceolata*. Nat Prod Res. 31(21):2473–2478.

Ge J, Bi G, Luo G. 2019. Characterization of complete chloroplast genome of *Amentotaxus yunnanensis* (Taxaceae), a species with extremely small populations in China. Mitochondr DNA. 4(1):1765–1767.

Huang DI, Cronk QCB. 2015. Plann: a command-line application for annotating plastome sequences. Appl Plant Sci. 3: apps.1500026.

Nguyen LT, Schmidt HA, Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol. 32(1):268–274.

Qu XJ, Moore MJ, Li DZ, Yi TS. 2019. PGA: a software package for rapid, accurate, and flexible batch annotation of plastomes. Plant Methods. 15:50.

Sun WB, Yang J, Dao ZL. 2019. Study and conservation of plant species with extremely small populations (PSESP) in Yunnan province. China. Beijing: Science and Technology Press; p. 54.

Yang Y, Liao W. 2013. *Cephalotaxus lanceolata*. The IUCN red list of threatened species 2013: e.T32330A2815177. https://dx.doi.org/10.2305/IUCN.UK.2013-1.RLTS.T32330A2815177.en