


The complete chloroplast genome of the *Abies yuanbaoshanensis*, an endangered Pinaceae species in Southern China

Jie Yang^{a*} , Tao Ding^{b*}, Ri-Hong Jiang^a, Ya-Rong Wang^c and Xiang Qiao-Ping^a

^aInstitute of Botany, Chinese Academy of Sciences, Beijing, China; ^bGuangxi Institute of Botany, Chinese Academy of Sciences, Guilin, China; ^cHainan University, Haikou, China

ABSTRACT

Abies yuanbaoshanensis is critically endangered and endemic to Guangxi province of China, with no more than 900 surviving individuals. In this study, we reported the complete chloroplast (cp) genome of *A. yuanbaoshanensis*. The complete chloroplast genome is 121897 bp in size. In total, 112 genes were identified, including 74 protein-coding genes, 34 tRNA genes, and four rRNA genes. In phylogenetic analysis, the tree supported the monophyly of the genus *Abies*. The complete plastome of *A. yuanbaoshanensis* will provide potential genetic resources for further conservation and evolutionary studies of this highly endangered species.

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Abies consists of around 50 species, which are widely distributed in the Northern Hemisphere with major centres of distribution in North America and eastern Asia. (Liu 1971; Farjon 2001). *Abies* are ecologically crucial for water and soil restoration in areas where they occur (Liu 1971). However, many fir species have been listed as endangered species (Xiang et al. 2015). *Abies yuanbaoshanensis* is listed as highly endangered species in the Red List (IUCN 2018). Now *A. yuanbaoshanensis* is endemic to Guangxi province of China with less than 900 surviving individuals (Li et al. 2002). Here, we assembled and characterized the complete plastome of *A. yuanbaoshanensis*. It will provide potential genetic resources for further conservation and evolutionary studies of *A. yuanbaoshanensis*.

The plant material of *A. yuanbaoshanensis* was collected from a single individual that lives in the natural forest habitat of Mt. Yuanbaoshan (Guangxi, China; 25.43°N, 109.18°E). Voucher specimen (YBS20190711) and DNA sample were deposited in the herbarium of Institute of Botany, CAS (PE). In total, 6 G high-quality clean reads (150 bp PE read length) were generated with adaptors trimmed. The GetOrganelle (Jin et al. 2018), Bandage (Wick et al. 2015), Geneious R11

(Biomatters Ltd., Auckland, New Zealand), were used to align, assemble, and annotate the plastome.

The full length of *A. yuanbaoshanensis* chloroplast genome (GenBank Accession No. MN399749) was 121897 bp and comprised of a large single copy region (LSC with 67152 bp), a small single copy region (SSC with 54467 bp), and two inverted repeat regions (IR with 139 bp). The overall GC content of the *A. yuanbaoshanensis* cp genome was 38.30%. A total of 112 genes were contained in the cp genome (74 protein-coding genes, 34 tRNA genes, and four rRNA genes). Only one tRNA gene (trnI-CAU) is duplicated and located on the IR regions.

Fourteen chloroplast genomes were selected to infer the phylogenetic relationships among the main representative species of Pinaceae with *Ginkgo biloba* (Ginkgoaceae) as the outgroup. All of these 14 complete chloroplast sequences were aligned by the MAFFT version 7 software (Katoh and Standley 2013). A maximum-likelihood (ML) tree was inferred by Ultrafast bootstrapping with 1000 replicates through IQ-TREE 1.5.5 (Nguyen et al. 2015) based on the GTR+F+R3 nucleotide substitution model, which was selected by Model Finder (Kalyaanamoorthy et al. 2017).

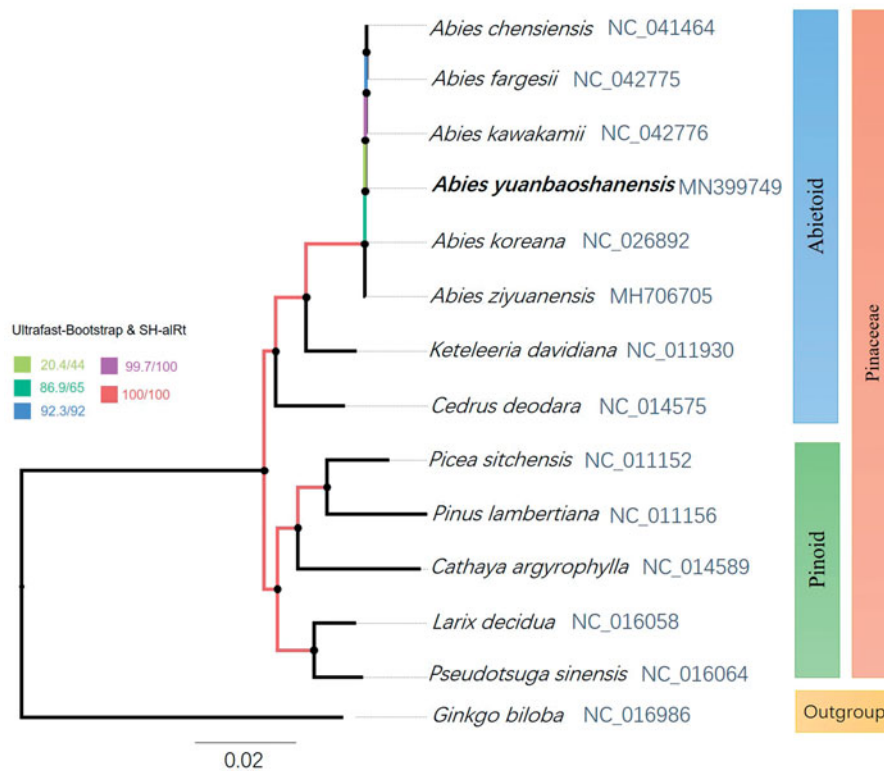


Figure 1. The ML phylogeny result from 14 complete plastome sequences by IQ-TREE. Accession numbers: *Abies chensiensis* NC_041464, *A. fargesii* NC_042775, *A. kawakamii* NC_042776, *A. yuanbaoshanensis* MN399749, *A. koreana* NC_026892, *A. ziyuanensis* MH706705, *Keteleeria davidiana* NC_011930, *Cedrus deodara* NC_014575, *Picea sitchensis* NC_011152, *Pinus lambertiana* NC_011156, *Cathaya argyrophylla* NC_014589, *Larix decidua* NC_016058, *Pseudotsuga sinensis* NC_016064, and *Ginkgo biloba* NC_016986.

The result revealed that the five *Abies* species (*A. yuanbaoshanensis*, *A. koreana*, *A. kawakami*, *A. fargesii*, *A. chensiensis*, and *A. ziyuanensis*) are strongly supported as monophyletic (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the authors.

Data availability

The complete chloroplast genome sequence of *Abies yuanbaoshanensis* in this study was submitted to the NCBI database under the accession number MN399749.

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ORCID

Jie Yang  <http://orcid.org/0000-0003-4528-1048>

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