

## The complete chloroplast genome sequence of *Abies beshanzuensis*, a highly endangered fir species from south China

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### ABSTRACT

*Abies beshanzuensis* is critically endangered and endemic to Zhengjiang province of China, with only three surviving individuals. In present study, we reported the complete chloroplast (cp) genome of *Abies beshanzuensis*. The complete chloroplast genome size is 121,399 bp. In total, 114 genes were identified, including 68 peptide-encoding genes, 35 tRNA genes, four rRNA genes, six open reading frames and one pseudogene. Loss of *ndh* genes was also identified in the genome of *A. beshanzuensis* like other genomes in the family Pinaceae. Thirteen genes contain one (11 genes) or two (*rps12* and *ycf3* genes) introns. Inverted repeat sequences located in 42-kb inversion points (1186 bp) include *trnS-psaM-ycf12-trnG* genes. In phylogenetic analysis, the tree confirms that the four *Abies* species are strongly supported as monophyletic. The complete plastome of *A. beshanzuensis* will provide potential genetic resources for further conservation and evolutionary studies of this highly endangered species.

### ARTICLE HISTORY

Received 6 July 2018  
Accepted 8 July 2018

### KEYWORDS





*Abies beshanzuensis*;  
Chloroplast genome;  
Endangered; Phylogenetic

*Abies* is the second largest genus of family Pinaceae (after *Pinus*), comprising about 50 species (Liu 1971; Farjon 2001). Due to extensive habitat loss by climate change and human activities, many economically and ecologically valuable firs are listed as Threatened or Endangered (Xiang 2015). *Abies beshanzuensis* M.H. Wu is one of the highly endangered fir species, with only three surviving individuals endemic to Mt. Baishanzu of China. Here, we assembled and characterized the complete plastome of *A. beshanzuensis*. It will provide potential genetic resources for further conservation and evolutionary studies of *A. beshanzuensis*.

The plant material of *Abies beshanzuensis* was collected from a single individual that lives in the natural forest habitat of Mt. Baishanzu in Zhejiang, China. Voucher specimen and DNA sample (Wang X.-Q. 04039) were deposited in the herbarium of Institute of Botany, CAS (PE). In total, ca. 10.4 million high-quality clean reads (150 bp PE read length) were generated with adaptors trimmed. The CLC de novo assembler (CLC Bio, Aarhus, Denmark), BLAST, GeSeq (Tillich et al. 2017), and tRNAscan-SE v1.3.1 (Santa Cruz, USA) (Schattner et al. 2005) were used to align, assemble, and annotate the plastome.

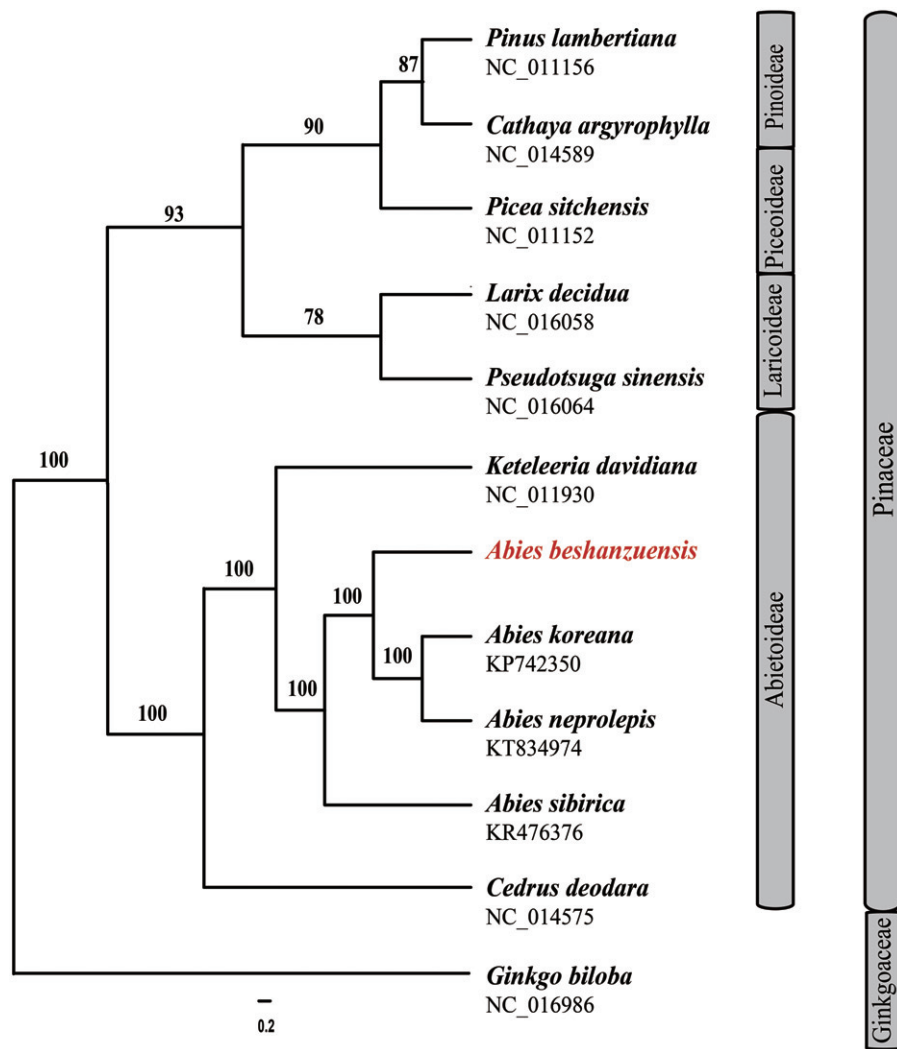
The full length of *Abies beshanzuensis* chloroplast genome (GenBank Accession No. MH476330) was 121,399 bp and comprised of a large single copy region (LSC with 66,657 bp), a small single copy region (SSC with 54,214 bp), and two inverted repeat regions (IR with 264 bp). The overall GC

content of the *A. beshanzuensis* cp genome was 38.3% and the GC content in the LSC, SSC, and IR regions are 37.4, 39.3, and 39.0%, respectively. A total of 114 genes were contained in the cp genome (68 peptide-encoding genes, 35 tRNA genes, four rRNA genes, six open reading frames and one pseudogene). Fifty-three protein coding, 16 tRNA genes, three open reading frames and one pseudogene are located in the LSC region, while 15 protein-coding, 17 tRNA genes, 4 rRNA and 3 open reading frames are located in the SSC region, respectively. Only one tRNA gene (*trnI*-CAU) is duplicated and located on the IR regions. All *ndh* genes have been lost in the genome of *A. beshanzuensis* like other cp genomes of family Pinaceae. Among the protein-coding genes, two genes (*rps12* and *ycf3*) contained two introns, and other eleven genes (*trnK*-UUU, *trnV*-UAC, *rpoC1*, *atpF*, *trnG*-GCC, *petB*, *petD*, *rpl16*, *rpl2*, *trnL*-UAA, *trnA*-UGC) had one intron each. In previous studies, short inverted repeat sequences which consist of *trnS-psaM-ycf12-trnG* and *trnG-ycf12-psaM-trnS* (1186 bp) are located in the cp genome of *A. beshanzuensis*. Length and sequence of inverted repeats from *A. beshanzuensis* is identical with those of *A. koreana* (Yi et al. 2015). Twelve chloroplast genomes of Pinaceae and Ginkgoaceae were fully aligned with MAFFT v7.3 (Saito, Osaka, Japan) (Kato and Standley 2013), and the maximum likelihood (ML) inference was performed using GTR $\Gamma$ 4 model with RAxML v.8.2.1 (Karlsruhe, Germany) (Stamatakis 2014) on the CIPRES cluster service (Miller et al. 2010). The

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**Figure 1.** The best Maximum likelihood (ML) phylogram inferred from 12 chloroplast genomes in Pinaceae and Ginkgoaceae (bootstrap value are indicated on the branches).

result revealed that the four *Abies* species (*A. beshanzenensis*, *A. koreana*, *A. neprolepis* and *A. sibirica*) are strongly supported as monophyletic (Figure 1).

### Disclosure statement

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

### Funding

This work was supported by the National Natural Science Foundation of China [31600163].

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