

## Next-generation sequencing yields the complete chloroplast genome of *Abies kawakamii*

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### ABSTRACT

*Abies kawakamii* is endemic to the island of Taiwan and has been listed as a threatened species in the Red List. In present study, we reported the complete chloroplast genome of *A. kawakamii*. The chloroplast genome is 121,290 bp in size. It was composed of 114 genes and they were 68 peptide-encoding genes, 35 tRNA genes, four rRNA genes, six open reading frames and one pseudogene. Loss of *ndh* genes was identified in the genome of *A. kawakamii*. Inverted repeat sequences include *trnS-psaM-ycf12-trnG* and *trnG-ycf12-psaM-trnS* were recognized in 52-kb inversion points. The phylogenetic analysis confirms that the *Abies* species are strongly supported as monophyletic. The complete plastome of *A. kawakamii* will provide potential genetic resources for further conservation and management strategies.

### ARTICLE HISTORY

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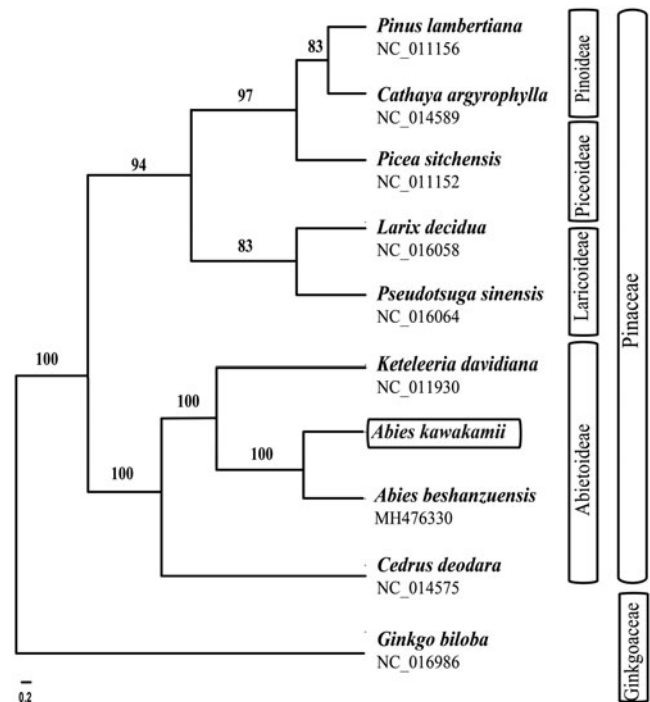
### KEYWORDS

*Abies kawakamii*;  
chloroplast genome;  
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*Abies kawakamii* (Hay.) Ito is endemic to the island of Taiwan and has been listed as a threatened species in the Red List (IUCN 2018). It is one of the southernmost firs (together with *A. fansipanensis*, native to Vietnam, and *A. guatemalensis*, from Mexico and Guatemala) (Liu 1971; Farjon 2001; Xiang et al. 2015). The Taiwan fir adapted to a cold, humid environment at high elevations and typically occurs in sheltered to windswept sites (Huang 2002). In the present study, we assembled and characterized the complete plastome of *A. kawakamii*. It will be fundamental to formulate conservation and management strategies for this threatened species.

We collected the plant material from the Hehuan Mountain of Taiwan. The voucher specimen (Chen C.-J., No. 9471) was deposited at the herbarium of Institute of Botany, CAS (PE). Complete chloroplast (cp) genome of *Abies kawakamii* was sequenced by HiSeq4000 of Illumina. Totally 10.3 million high-quality clean reads (150 bp PE read length) were obtained. In total, ca. 10.1 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 (Schattner et al. 2005) were used to align, assemble, and annotate the plastome.

The complete chloroplast genome consists of 121,290 bp for *Abies kawakamii* (GenBank: MH706726). The circle genome was comprised of a large single copy region (LSC with 65,646 bp), a small single copy region (SSC with 55,116 bp), and two inverted repeat regions (IR with 264 bp). The overall GC content of the *A. kawakamii* cp genome was 38.3%. It was composed of 114 genes and they were 68



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

peptide-encoding genes, 35 tRNA genes, four rRNA genes, six open reading frames and one pseudogene. All *ndh* genes have been lost in the genome of *A. kawakamii*. Short inverted repeat sequences were detected in 52-kb inversion

points of the cp genome, which consist of trnS-psaM-ycf12-trnG and trnG-ycf12-psaM-trnS (1183 bp). Interestingly, such inverted repeats had been reported in several members of the genus *Abies* (*A. koreana* and *A. ziyuanensis*) (Yi et al. 2015; Shao et al. 2018).

To infer the phylogenetic position of *Abies kawakamii*, nine chloroplast genomes were selected in Pinaceae with *Ginkgo biloba* (Ginkgoaceae) as the outgroup. These sequences were fully aligned with MAFFT v7.3 (Suita, 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 two *Abies* species (*A. kawakamii* and *A. beshanzenzensis*) were found to be a monophyletic group (Figure 1).

### Disclosure statement

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

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