

MITOGENOME ANNOUNCEMENT



## Complete plastid genome sequence of *Neolitsea aciculata* (Laurales: Lauraceae), an evergreen broad-leaved tree endemic to East Asia

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### ABSTRACT

In this study, we sequenced the complete plastid genome (plastome) of *Neolitsea aciculata*, an evergreen broad-leaved tree endemic to East Asia, a woody component of East Asian warm-temperate and subtropical forests across China, Korea, and Japan. The plastome of *N. aciculata* is assembled as a single contig (152,722 bp). A large and a small single copy (93,785 and 18,795 bp, respectively) of the genome are separated by a pair of inverted repeats (20,071 bp). The genome consists of 126 genes, including 80 protein-coding, eight ribosomal RNA, and 36 transfer RNA genes. Two genes in the IR region (*ycf1* and *ycf2*) are pseudogenized. Our phylogenetic analysis revealed the phylogenetic position of *N. aciculata* in a highly supported clade of the genus *Neolitsea* along with other two congeners, *N. pallens* and *N. sericea*.

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The family Lauraceae consists of approximately 50 genera and 2,500–3,000 species worldwide (Chanderbali et al. 2001). *Neolitsea* (Benth.) Merr., a major genus of the family comprises ca. 100 species widely distributed throughout the tropical and subtropical habitats in Asia, including China, Korea, and Japan (Gentry 1988; van der Werff 2001; Lee 2003; Ohba 2006; Huang and van der Werff 2008). Its high species diversity is of considerable evolutionary importance as a core genus of Laureae, *Litsea* complex (Li et al. 2004, 2007). However, their phylogenetic relationships are still poorly understood.

To date, only two *Neolitsea* plastid genomes (plastomes) have been sequenced. A study on the woody plants, *N. pallens* (D. Don) Momiyama and H. Hara and *N. sericea* (Blume) Koidz., has provided powerful phylogenetic utilities, regarding the *Litsea* complex in particular (Xiao et al. 2020). However, given their high species diversity, such deficiency in the plastome sequence resources on the genus level is a hindrance to improving our understanding of the woody plant-related evolutionary processes in tropical and subtropical forests. *Neolitsea aciculata* (Blume) Koidz. 1918 is a woody plant of East Asian warm-temperate and subtropical forests across China, Korea, and Japan. In this study, we sequenced and characterized a complete plastome from *N. aciculata*, endemic to East Asia.

*N. aciculata* samples were collected from the Jeju Island, South Korea (33°18'26.7"N, 126°27'09.9"E). The voucher specimen (Lee-Na200529) was stored in the department of

Biology Education, Chonnam National University (BEC: [quercus@jnu.ac.kr](mailto:quercus@jnu.ac.kr)). The DNA library was constructed and sequenced using an MGI-seq 2000 platform (LAS, Seoul, Republic of Korea) following the manufacturer's protocol. It generated 75,078,260 raw reads (150 bp paired-end). The *N. aciculata* plastome was assembled using NOVOPlasty 4.1 (Dierckxsens et al. 2017), using the *N. pallens* *matK* gene sequence (Xiao et al. 2020; MN428466) as the seed. The assembled plastome was verified using Geneious 11.0.5 (Kearse et al. 2012) by reference mapping 381,661 reads, resulting in a coverage of 150×. The annotation was separately performed using Geneious 11.0.5 and manually corrected for the start and stop codons, as well as the intron-exon boundaries. The annotated plastome sequence was deposited in the GenBank (accession number: MW845678). To construct the phylogenetic tree, plastomes of 10 Lauraceae species (*Neolitsea*, *Lindera*, and *Litsea*: two species each, and *Cinnamomum*, *Laurus*, *Actinodaphne*, and *Machilus*: one species each, respectively) were downloaded from the NCBI database. The alignments were performed using MAFFT (Kato and Toh 2010). The maximum likelihood (ML) analysis was performed with RAXML v.8.0 (Stamatakis 2014) using default parameters and 1000 bootstrap replicates. For the RAXML tree, the general time-reversible (GTR) model of nucleotide substitution was used with the Gamma model of rate heterogeneity.

Our results showed that the *N. aciculata* plastome is 152,722 bp long, with two inverted repeat (IR) regions

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The ML phylogenetic tree shows that *N. aciculata* is closely related to *N. pallens* and *N. sericea* with strong (100%) bootstrap support. The genus *Neolitsea* was distinguished from the *Lindera*-related *Litsea* complex, forming a sister clade with *Actinodaphne obovata* (Figure 1). The complete plastome sequenced in this study represents valuable genomic resource data of the Lauraceae, and this new phylogenetic information could be used in future evolutionary studies of the Lauraceae.

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

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