The complete plastid genome sequence of *Ilex suaveolens* (H. Lév.) Loes, the most abundant medicinal holly in Mount Huangshan

Lige Yuan\*\*, Han Wu\*\*, Can Zhang\*\*, Ying Wang\*, Qi Huang\*, Shiming Fan\* and Tao Su\*\*,\*\*

\*Co-Innovation Center for Sustainable Forestry in Southern China, College of Biology and the Environment, Nanjing Forestry University, Nanjing, China; \*Key Laboratory of State Forestry Administration on Subtropical Forest Biodiversity Conservation, Nanjing Forestry University, Nanjing, China

ABSTRACT

Holly (*Ilex* L.) is a woody dioecious genus cultivated as pharmaceutical, ornamentals, and industrial materials. *Ilex suaveolens* (H. Lév.) Loes is an endemic medicinal holly with a predominant distribution in Mount Huangshan, China. In the present work, the complete plastid genome of *I. suaveolens* was de novo sequenced by high-throughput sequencing technology. The newly-assembled plastid genome holds 37.6% of the overall GC content and a length of 157,857 bp, comprising a large single-copy (LSC, 87,255 bp), a small single-copy (SSC, 18,398 bp), and a pair of inverted repeat (IRs, 26,102 bp) regions. The plastid genome annotation suggested the presence of a total of 89 protein-encoding genes, 37 transfer RNA (tRNA) genes, and eight ribosomal RNA (rRNA) genes. The plastome-mediated phylogenetic topology revealed that *I. suaveolens* clustered together with *I. szechwanensis* and *I. viridis* in the same clade, and a strong relationship between clades and biogeography was found. These data contribute to the understanding of genetic diversity and conservation study of *Ilex* in Mount Huangshan.
15 *Ilex* species were aligned (Katoh et al. 2019). The plastid topology of phylogenies was reconstructed using the software MEGA X, showing that *I. suaveolens* is mostly related to *I. szechwanensis* and *I. viridis* in the clade III (Figure 1). In summary, the plastid phylogenetic tree displayed superior resolution for species discrimination and a better indication of the phylogeographic distribution in *Ilex*.

**Disclosure statement**

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

**Funding**

This research was supported by the National Natural Science Foundation of China [31700525]; The Scientific Research Foundation for High-Level Talents of Nanjing Forestry University [GXL2017011; GXL2017012]; The Undergraduate Innovation and Entrepreneurship Training Programs [201910298115Y; 2020NFUSPITP0819].

**Data availability statement**

The complete plastid genome data that support the findings of this study are openly available in the GenBank of NCBI (https://www.ncbi.nlm.nih.gov/) under the accession number of MN830249. The raw sequence reads have been deposited in GSA database (https://bigd.big.ac.cn/gsa/) associated with the accession number of CRR147931.

**References**

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.

Ding H, Fang Y, Yang X, Yuan F, He L, Yao J, Wu J, Chi B, Li Y, Chen S, et al. 2016. Community characteristics of a subtropical evergreen broad-leaved forest in Huangshan, Anhui Province, East China. Biodivers Sci. 24(8):875–887.

Hao D, Gu X, Xiao P, Liang Z, Xu L, Peng Y. 2013. Research progress in the phytochemistry and biology of *Ilex* pharmaceutical resources. Acta Pharm Sin B. 3(1):8–19.

Katoh K, Rozewicki J, Yamada KD. 2019. MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Brief Bioinform. 20(4):1160–1166.

Manen JF, Boulter MC, Naciri-Graven Y. 2002. The complex history of the genus *Ilex* L. (Aquifoliaceae): evidence from the comparison of plastid and nuclear DNA sequences and from fossil data. Plant Syst Evol. 235(1):79–98.

Nock CJ, Waters DLE, Edwards MA, Bowen SG, Rice N, Cordeiro GM, Henry RJ. 2011. Chloroplast genome sequences from total DNA for plant identification. Plant Biotechnol J. 9(3):328–333.

Qian Y, Tian R. 2016. Research advance of *Ilex* germplasm resources and their application to landscape. World Forest Res. 29:40–45.

Su T, Han M, Min J, Cao D, Pan H, Liu Y. 2019. The complete chloroplast genome sequence of *Populus deltoides* ‘Siyang-2’. Mitochondrial DNA Part B. 5(1):283–285.

Wyman SK, Jansen RK, Boore JL. 2004. Automatic annotation of organellar genomes with DOGMA. Bioinformatics. 20(17):3252–3255.

Yao X, Song Y, Yang J, Tan Y, Corlett RT. 2020. Phylogeny and biogeography of the hollies (*Ilex* L., Aquifoliaceae). J Syst Evol. 00(0):1–10.

Yao X, Tan Y-H, Liu Y-Y, Song Y, Yang J-B, Corlett RT. 2016. Chloroplast genome structure in *Ilex* (Aquifoliaceae). Sci Rep. 6:28539.

Yi F, Zhao X, Peng Y, Xiao P. 2016. Genus *Ilex* L. phytochemistry, ethnopharmacology, and pharmacology. Chinese Herb Med. 8(3):209–230.

Zong D, Gan P, Zhou A, Zhang Y, Zou X, Duan A, Song Y, He C. 2019. Plastome sequences help to resolve deep-level relationships of *Populus* in the family Salicaceae. Front Plant Sci. 10:5.