


The complete plastid genome sequence of *Ilex micrococca* Maxim

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ABSTRACT

Ilex micrococca Maxim. is a widely distributed species of Aquifoliaceae in Eastern Asia. In this study, the complete chloroplast (cp) genome sequence of *I. micrococca* was assembled and characterized by high-throughput sequencing data. The entire cp genome was 157,782 bp in length, containing a large single-copy region (LSC) of 87,200 bp, and a small single-copy region (SSC) of 18,434 bp, which were separated by a pair of 26,074 bp inverted repeat (IR) regions. The cp genome contained 134 genes, including 89 protein-coding genes, 37 tRNA genes, and 8 ribosomal RNA genes. Eighteen genes occur in double copies. The overall GC content is 37.6%. The phylogenetic tree reconstructed by 13 chloroplast genomes reveals that *I. micrococca* is most related with *Ilex wilsonii*. The complete cp genome provides valuable information for further phylogenetic and cp genetic engineering studies of this important *Ilex* species *I. micrococca*.

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Ilex is the largest woody dioecious genus in the angiosperms containing approximately 600 species within the monogeneric family of Aquifoliaceae (Manen et al. 2010). Among them, *Ilex micrococca* Maxim. is a deciduous species with wide distributions in Eastern Asia. The holly family plants have been cultivated as ornamentals, herbal medicine, and industrial resources. *I. micrococci* is used as a dye owing to the abundance of tannin, protocatechuic acid, and volatile oil in the bark (Hao et al. 2013). *I. micrococca* also exhibits superior wood qualities prompting them to be used for furniture, agriculture tools, and printing papers. The roots and leaves show potential clinical functions for scavenging heat, detoxication, and analgesia (Li et al. 2013; Yi et al. 2016). Besides, the fancy red fruits produced in autumn make *I. micrococca* as one of the most popular garden tree species (Yao et al. 2016). Hitherto, the cp genome of *I. micrococca* remains undocumented. In this work, using the next-generation sequencing and in combination with *de novo* and reference-guided assembly, the complete cp genome of *I. micrococca* constructed provides informatics data for the evolution and phylogenies of Aquifoliaceae.

The fresh leaves of *I. micrococca* were sampled from Yangmeiqian, Xingcun Town, Wuyishan City, Nanping City, Fujian Province, China (117.770°E 27.598°N) and the altitude is 418 m. The voucher specimen (accession number YL20190417016) was preserved at the Herbarium of Nanjing Forestry University (HNFU). The DNA was extracted according to the previous report (Su et al. 2020). The whole-genome

sequencing was implemented by Hefei Biodata Biotechnologies Inc. (Hefei, China) on the BGISEQ-500 platform. In total, 40.8 MB high-quality clean reads were obtained. The filtered sequences were assembled by the program SPAdes assembler 3.10.0 (Bankevich et al. 2012). Annotation was performed using the DOGMA (Wyman et al. 2004) and BLAST searches.

The complete cp genome sequence of *I. micrococci*, together with gene annotations, was submitted to GenBank (accession no: MN830251). The cp genome contains double-stranded, circular DNA of 157,782 bp, including two IR regions of 26,074 bp each, separated by LSC and SSC region of 87,200 and 18,434 bp, respectively. The genome contained 134 genes, including 89 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. Most of the genes occurred as a single-copy, while eight protein-coding genes, four rRNA genes, and six tRNA genes had two copies, respectively. Besides, four protein-coding genes had three exons each. Twelve protein-coding genes and seven tRNA genes contained two exons. The overall GC content is 37.6%, and the corresponding values in LSC, SSC, and IR regions are 35.7%, 31.9%, 43.0%, respectively.

The phylogenetic relationships of *I. micrococci* with other eleven species in the *Ilex* genus and one outgroup species *Helwingia himalaica* were analyzed by MAFFT v7.307 (Katoh and Standley 2013). The ML phylogenetic tree was constructed by FastTree version 2.1.10 (Price et al. 2010), showing that *I. micrococci* was closely related to *Ilex wilsonii*

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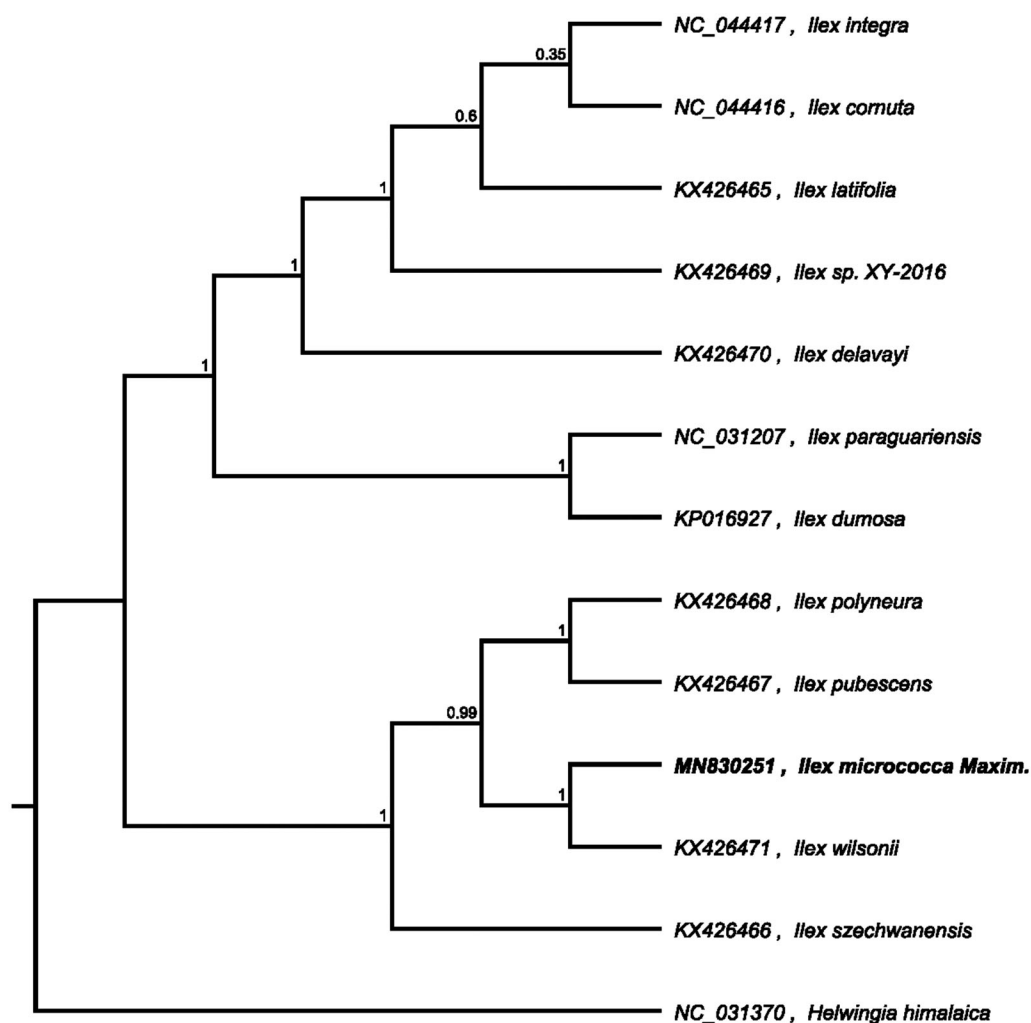


Figure 1. Phylogenetic tree inferred by Maximum Likelihood (ML) method based on the complete chloroplast genome of *I. micrococci* and other twelve species (eleven *Ilex* genus and one outgroup species *H. himalaica*). The bootstrap values are shown on the branches.

(Figure 1). The cp genome provides valuable information for further population, phylogeny and cp genetic engineering of *I. micrococci*.

Disclosure statement

No potential conflict of interest was reported by the authors.

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