

## Complete plastome sequence of *Ilex asprella* (Hooker and Arnott) Champion ex Bentham (Aquifoliaceae), a Chinese folk herbal medicine

Yan Chen, Hua-Xu Chen, Hai-Li Li, Xia-Lan Cheng and Li-Yun Wang

Lingnan Normal University, Zhanjiang, China

### ABSTRACT

The complete chloroplast genome of *Ilex asprella*, a species of Aquifoliaceae is reported for the first time in this study. The complete chloroplast genome of *I. asprella* is 157,856 bp in length with a typical quadripartite structure, consisting of a large single-copy region (LSC, 87,258 bp), a single-copy region (SSC, 18,441 bp) and a pair of inverted repeats (IRs, 26,082 bp). There are 114 genes annotated, including 85 unique protein-coding genes, four unique ribosomal RNA genes, and 30 transfer RNA genes. To investigate the evolution status of *T. concolor*, as well as Scrophulariaceae, we build a phylogenetic tree with *I. asprella* and other eight species based on their complete chloroplast genomes. According to the phylogenetic topologies, *I. asprella* was closely related to *I. wilsonii*.

### ARTICLE HISTORY

Received 10 May 2019  
Accepted 17 May 2019

### KEYWORDS

*Ilex asprella*; plastome; phylogeny; genome structure; Aquifoliaceae

*Ilex asprella* (Hooker & Arnott) Champion ex Bentham belongs to the family Aquifoliaceae. It produces and stores a large amount of triterpenoid saponins and is widely used as a folk herbal drug in southern China (Zheng et al. 2015). *Ilex asprella* distributes mainly in eastern and southern provinces of China, Philippines, and Vietnam (China ECoFo, 2013). Chloroplast is important in phylogeny reconstruction due to carrying maternal genes. Since there is no published plastome sequences data for *I. asprella* chloroplast in the present, the genetic and genomic information is urgently needed to promote its systematics research. We report and characterize the complete plastid genome sequence of *I. asprella* (GenBank accession number: MK834323) in an effort to provide genomic resources useful for promoting its conservation and utilization.

In this study, the fresh leaves of *I. asprella* were collected from its natural habitat Pangkan village, Suixi county, China (E110°18'40.45"N21°20'07.45"). Voucher specimens (LNH180925042) were deposited in the Herbarium of Lingnan Normal University, Zhanjiang, China. The experiment procedure is as reported in Gao et al. (2017). Around 6 Gb clean data were assembled against the plastome of *I. wilsonii* (KX426471.1) using MITO bim V1.8 (Hahn et al. 2013). The plastome was annotated using Geneious R8.0.2 (Biomatters Ltd., Auckland, New Zealand) against the plastome of *I. wilsonii* (KX426471.1). The annotation was corrected with DOGMA (Wyman et al. 2004).

The plastome of *I. asprella* was found to possess a total length 157,856 bp with the typical quadripartite structure of angiosperms, containing two Inverted Repeats (IRs) of 26,082 bp, a Large Single-Copy (LSC) region of 87,258 bp and

a Small Single-Copy (SSC) region of 18,441 bp. The plastome contains 114 genes, consisting of 85 unique protein-coding genes, 30 unique tRNA genes, and four unique rRNA genes. The overall A/T content in the plastome of *I. asprella* is 62.40%, and the corresponding values for the LSC, SSC, and IR regions were 64.40%, 68.10%, and 57.00%, respectively.

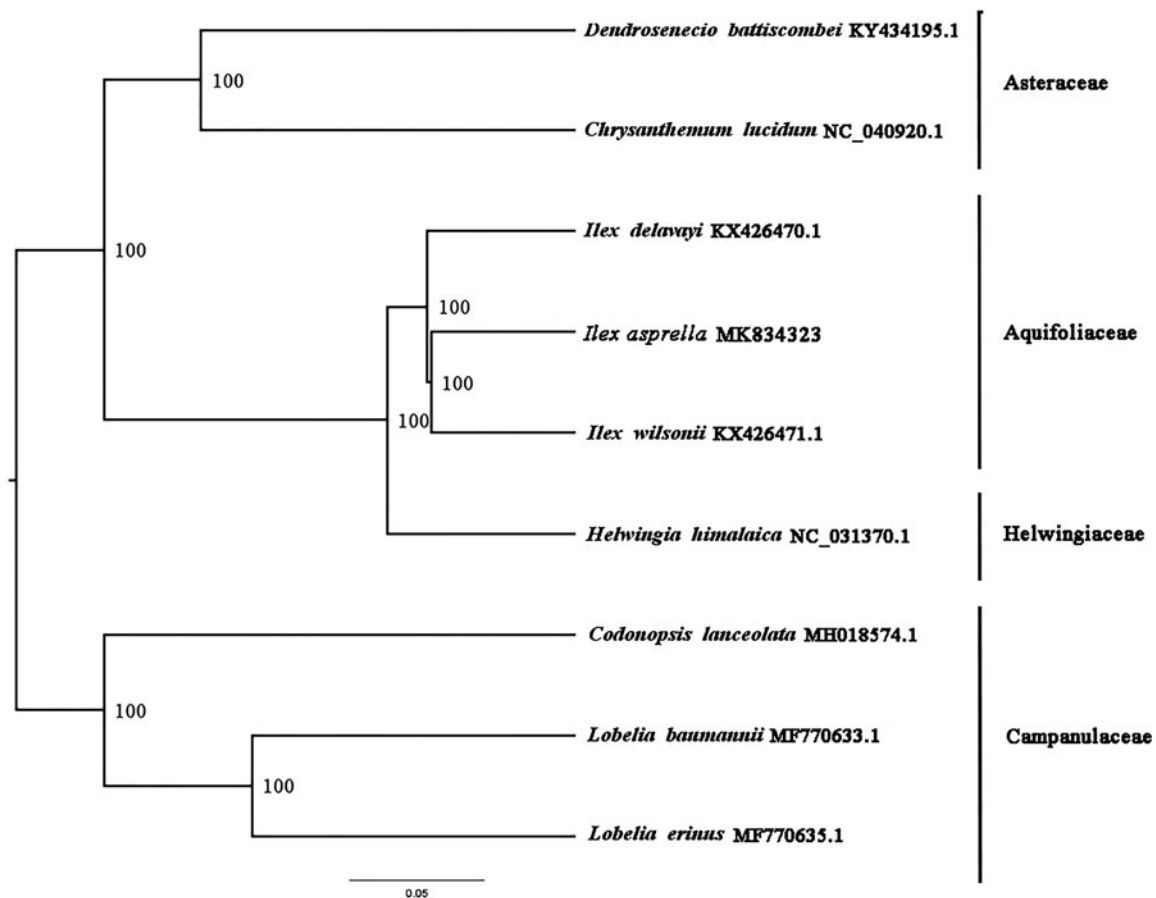
We used RAxML (Stamatakis, 2006) with 1000 bootstraps under the GTRGAMMA1 substitution model to reconstruct a maximum likelihood (ML) phylogeny of *I. asprella* and eight published complete plastomes, using *Lobelia erinus* and *Lobelia baumannii* as outgroups. According to the phylogenetic topologies, *I. asprella* was closely related to *I. wilsonii*. Most nodes in the plastome ML trees were strongly supported (Figure 1). The complete plastome sequence of *I. asprella* will provide a useful resource for the conservation genetics of this species as well as for building the phylogenetic relationships of Aquifoliaceae.

### Disclosure statement

No potential conflict of interest was reported by the authors.

### Funding

This study was supported by Nanhai Marine Biomedical Resources R&D Public Service Platform [Zhanhaichuang 2017 C8B2]; Project of State Administration of Traditional Chinese Medicine [2017-152-010]; Survey of Traditional Chinese Medicine Resources in Leizhou City, Guangdong Province [20185017].



**Figure 1.** ML phylogenetic tree of *I. wilsonii* with nine species was constructed using chloroplast genome sequences. Accession numbers: *Chrysanthemum lucidum* NC\_040920.1, *Dendrosenecio battiscombei* KY434195.1, *Ilex asprella* MK834323, *Ilex delavayi* KX426470.1, *Ilex wilsonii* KX426471.1, *Helwingia himalaica* NC\_031370.1, *Codonopsis lanceolata* MH018574.1, *Lobelia baumannii* MF770633.1, *Lobelia erinus* MF770635.1. *Lobelia erinus* and *Lobelia baumannii* were selected as outgroups.

## References

- China E. 2013. Flora of China. Beijing, China and Missouri, USA: Science Press and Missouri Botanical Garden Press.
- Gao CM, Gao YC, Liu XH. 2017. The complete genome of *Ziziphus jujube* cv. dongzao, an economic crop in Yellow River Delta of China. *Mitochondrial DNA B*. 2:692–693.
- Hahn C, Bachmann L, Chevreur B. 2013. Reconstructing mitochondrial genomes directly from genomic next-generation sequencing reads—a baiting and iterative mapping approach. *Nucleic Acids Res*. 41:e129.
- Stamatakis A. 2006. RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics*. 22:2688–2690.
- Wyman SK, Jansen RK, Boore JL. 2004. Automatic annotation of organellar genomes with DOGMA. *Bioinformatics*. 20: 3252–3255.
- Zheng XS, Luo XX, Ye GB, Chen Y, Ji XY, Wen LL, Xu YP, Xu H, Zhan RT, Chen WW. 2015. Characterisation of two oxidosqualene cyclases responsible for triterpenoid biosynthesis in *Ilex asprella*. *Int J Mol Sci*. 16:3564–3578.