

The Complete Chloroplast Genome of *Ardisia Japonica* Thunb. Blume

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Abstract

Ardisia japonica Thunb. Blume is a small shrub or sub-shrub of the genus *Taurus* in the *Taurus* family. The whole plant and root of *A. japonica* are used for medicinal purposes. It is a common Chinese herbal medicine and a common flower. To study its complete chloroplast genome, we collected leaves and obtained chloroplast genome information through next-generation sequencing. The results showed that the length of the genome is 155,996 bp, and the GC content ratio is 37.0%. The large single-copy region (LSC) is 86803 bp, the small single-copy region (SSC) is 18080 bp, and the inverted repeat region (IR) is 25507 bp. The chloroplast genome encodes 130 genes, including 85 protein genes, 8 rRNA genes, and 37 tRNA genes. By analyzing the phylogeny of *A. japonica*, it is found that *A. japonica* and other *Ardisia* species are closely related.

Full Text

Ardisia japonica is an evergreen small shrub or subshrub of *A. japonica* in the *Ardisia* family. It is widely distributed in China. The whole plant and roots can be used for medicinal purposes (Lin et al., 2012). However, the information about its chloroplast genome is still unclear. To solve this problem, we extracted the chloroplast genome DNA, and after sequencing, annotated the characteristics of the chloroplast genome.

Fresh leaves were collected from Kunming City, Yunnan Province (102°10'–103°40' east longitude, 24°23'–26°22' north latitude, 1928m). A specimen was deposited at the (bbg.swfu.edu.cn, Dr. Yao and bbg01@swfu.edu.cn) under the voucher number: SWFU-AAP-DAJ 3638. Chloroplast genomic DNA fragments were extracted from fresh leaves. Sequencing was performed on the Illumina NovaSeq 6000 platform of Annuoyouda Biotechnology Co., Ltd. (Zhejiang, China) and by adjusting the adapter, high-quality clean reading of about 5.0GB was generated. Then we used Get Organelle v1.6.2 to assemble the complete chloroplast genome (Jin et al. 2020), select sauerkraut (NC045098) annotated the complete chloroplast genome as a reference, used Geneious to annotate, and manually adjusted (Kearse et al. 2012). The annotated complete chloroplast genome of *A. japonica* was submitted to the Genbank under the registration number MZ666385.1.

Through the analysis of the whole genome of *A. japonica* chloroplast, we discovered its full length is 155996bp, GC ratio of 37.0%. In addition, it also contains 130 genes, including 85 protein genes, 8 rRNA, and 37 tRNA genes. The length of the large-single copy region (LSC) is 86803bp, the small single-copy region (SSC) is 18080bp, and the inverted repeat (IR) is 25507bp.

The available chloroplast genome information is limited. We selected 17 related species, used MEGA-X, combined with the bootstrap method (1000 replicates) to obtain an alignment and a maximum likelihood (ML) tree. The Tamura-Nei surrogate model was used in ML analysis (Kumar et al., 2018). According to the phylogenetic tree, the *A. japonica* (underlined) is compared with other taxa related (Figure 1).

Declarations

Disclosure statement

No potential conflict of interest was reported by the authors.

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Data availability statement

The voucher specimens of *Ardisia japonica* was deposited at the Herbarium of South west Forestry University, Kunming, Yunnan, China (accession number: SWFU-AAP-DAJ-3638).

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (<https://www.ncbi.nlm.nih.gov/>) under the accession no. MZ666385.1. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA764454, SRR, and SAMN21503434, respectively.

Declare

The collection of plant material in the article have been carried out in accordance with the guidelines provided by Southwest Forestry University and national or international regulations. The article does not include field research and research on plants without ethical approval.

Ethics approval and consent to participate

The experiment materials do not include a human being or animal. Hence, ethics approval and consent to participate is not applicable.

Author contribution description

Ruyou Deng, Shujin Ding, Sujie Wang participated in the concept and design of the article, Ruyou Deng was responsible for the drafting of the article, Hanyao Zhang was responsible for the revision of the article, and finally approved the published version. All authors agreed to be responsible for all aspects of the work.

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Figures

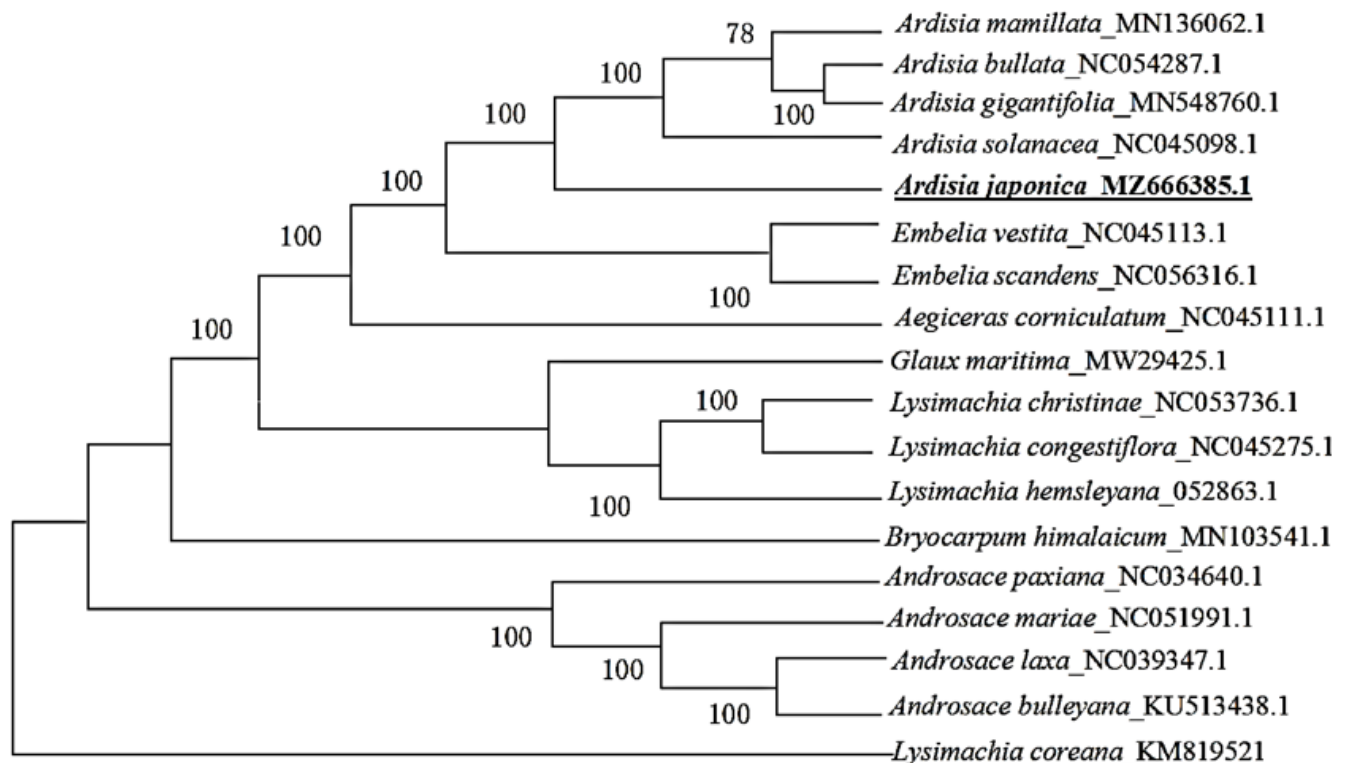


Figure 1

Maximum likelihood phylogenetic tree based on the chloroplast genome sequences from 17 related species. Values along branches refer to the percentage of replicate trees where the associated taxa clustered together.

Supplementary Files

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