

The complete chloroplast genome sequence of *Euscaphis japonica* (Staphyleaceae)

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ABSTRACT

Euscaphis japonica is not only an ideal ornamental plant, but also a traditional medicinal plant, which is an extremely valuable species to study. We determined the complete chloroplast genome sequence for *E. japonica* using Illumina sequencing technology. The complete chloroplast sequence is 160,467 bp in length, including a large single-copy (LSC) region of 88,716 bp, a small single-copy (SSC) region of 18,614 bp, and a pair of invert repeats (IR) regions of 26,568 bp. Plastid genome contains 142 genes, 46 protein-coding genes, 39 tRNA genes, and eight rRNA genes. Phylogenetic analysis based on 14 chloroplast genomes indicates that *E. japonica* forms an isolated clade and sisters to *Glycosmis-Gossypium* clade with strong support.

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Euscaphis japonica is a species of Staphyleaceae, which is widely distributed in southern China, Japan, and Korea (Li et al. 2008). As an ideal landscape tree species, it has very high ornamental value, especially in the flowering and fruiting stage (Yuan et al. 2018). *Euscaphis japonica* is also a traditional medicinal plant, of which the chemical component has good use on anti-cancer, anti-inflammation, etc. (Liang et al. 2018). While previous studies on *E. japonica* mainly focused on cultivation techniques, chemical components and medicinal activities, but molecular research was limited. Since phenotypic variation of *E. japonica* is abundant in different areas, and the biological characteristics vary with populations at different altitudes (Cheng et al. 2010). Therefore, the complete chloroplast genomic data will be helpful to study the origin, evolution and the relationship between the phenotype and environment of *E. japonica*. In this study, we report the complete chloroplast genome (cp) of *E. japonica* based on Illumina pair-end sequencing data

The plant material of *E. japonica* was collected from Shiniu Mountains, Quanzhou City, Fujian province, China (119°38'93.20"E, 26°05'24.03"N). The voucher specimen is kept at the Herbarium of College of Forestry, Fujian Agriculture and Forestry University (specimen code FAFU08180).

DNA extraction from fresh leaf tissue, with 500 bp randomly interrupted by the Covaris ultrasonic breaker for library construction. The constructed library was sequenced PE150 by Illumina HiSeq Xten platform, approximately 2GB data generated. Illumina data were filtered by script in the

cluster (default parameter: -L 5, -p 0.5, -N 0.1). Complete plastid genome of *Gossypium darwinii* (GeneBank accession: NC_016670) is used as reference and the plastid genome of *E. japonica* was assembled by GetOrganelle pipe-line (<https://github.com/Kinggerm/GetOrganelle>): it can get the plastid-like reads, and the reads were viewed and edited by Bandage (Wick et al. 2015). Assembled chloroplast genome annotation was based on the comparison with *G. arboreum* by Geneious v 11.1.5 (Biomatters Ltd, Auckland, New Zealand) (Kearse et al. 2012). The annotation result was drawn with the online tool OGDRAW (<http://ogdraw.mpimgolm.mpg.de/>) (Lohse et al. 2013).

The complete plastid genome sequence of *E. japonica* (GenBank accession: MN159078) was 160,467 bp in length, with a large single-copy (LSC) region of 88,716 bp, a small single-copy (SSC) region of 18,614 bp, and a pair of inverted repeats (IR) regions of 26,568 bp. Complete chloroplast genome contains 142 genes, there were 46 protein-coding genes, 39 tRNA genes, and eight rRNA genes. The complete genome GC content was 37.4%. In order to reveal the phylogenetic position of *E. japonica*, a phylogenetic analysis was performed based on 14 complete cp genomes. They were all downloaded from NCBI GenBank. The sequences were aligned by MAFFT v7.307 (Katoh and Standley 2013), and phylogenetic tree was constructed by RAxML (Stamatakis 2014). The phylogenetic tree showed that *E. japonica* formed an isolated clade and sister to *Glycosmis-Gossypium* clade with strong support (Figure 1).

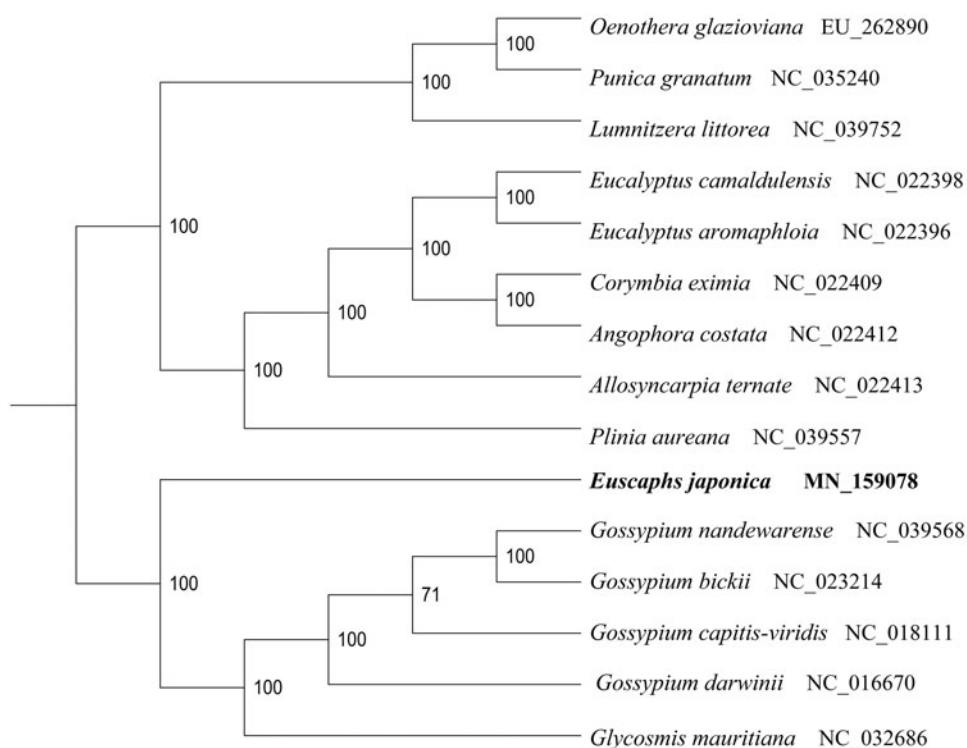


Figure 1. Phylogenetic analysis of 14 species based on plastid genome sequences by RAxML, bootstrap support value near the branch.

Disclosure statement

No potential conflict of interest was reported by the authors.

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