

MITOGENOME ANNOUNCEMENT



The complete chloroplast genome of *Edgeworthia chrysantha* (Thymelaeaceae)

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ABSTRACT

Edgeworthia chrysantha is a subtropical plant with significant medicinal value. Herein, we assembled and characterized the complete chloroplast genome of *E. chrysantha* as genomic resource for future study. The genome consisted a total length of 172,446 bp, comprising of a large single-copy (LSC) region of 85,527 bp, a small single-copy (SSC) region of 2871 bp, separated by two inverted repeat (IR) regions of 42,024 bp each; a total of 139 genes were predicted for the chloroplast genome. Phylogenetic analysis showed that *E. chrysantha* is placed at the base of the Daphne group of tribe Daphneae, within the family Thymelaeaceae.

ARTICLE HISTORY

Received 31 August 2020
Accepted 30 September 2020

KEYWORDS

Daphneae; genomic resources; illumina sequencing; traditional medicine; phylogenomics

Edgeworthia chrysantha Lindl., from the family Thymelaeaceae, is naturally distributed in the eastern Asian region. The traditional usage of *E. chrysantha* stem includes as raw material for paper-making, while its flowers, barks, and roots are used as folk medicine due to its anti-bacterial properties, detumescence and acesodyne effects (Xu and Cai 2011). Due to its medicinal value, studies that focus on its phytochemical properties and bioactivities often overshadow the genetic information of this species. In this study, we aimed to characterize the complete chloroplast (cp) genome sequence of *E. chrysantha* to serve as a valuable genomic resource for this important medicinal plant species.

Total genomic DNA was extracted using DN15 Plant DNA Mini Kit (Aidlab Biotechnologies, China), according to the manufacturer's protocol, from fresh leaves of *E. chrysantha* planted in the Germplasm Resource Nursery of Ornamental Plants, Guangzhou Institute of Forestry and Landscape Architecture, Guangdong province of China (N113°20'25", E23°13'47"). Additional dried leaf specimens were kept in the Herbarium of SYSU (SYS) under the collection number LSY-THY-5001. A genomic library consisting of an insert size of 300 bp was constructed using TruSeq DNA Sample Prep Kit (Illumina, USA) and sequencing was conducted on an

Illumina Novaseq platform. Approximately 6 Gb of raw data of 150-bp paired-ends reads were generated and genome assembly was conducted using NOVOPlasty (Dierckxsens et al. 2017). The *rbcl* sequence of *E. chrysantha* (Genbank accession number: MF349726) was selected as the seed sequence. Gene annotation was conducted using GeSeq (Tillich et al. 2017) and manually corrected.

The complete cp genome sequence of *E. chrysantha* (GenBank accession number: MT135125) was 172,446 bp in length, including a large single-copy (LSC) region of 85,527 bp, a small single-copy (SSC) region of 2871 bp, separated by a pair of inverted repeat (IR) regions of 42,024 bp each. A total of 139 genes were predicted, consisting of 93 protein-coding genes, 38 tRNA genes, and 8 rRNA genes. The overall GC content was 36.6%.

To understand the relationship of *E. chrysantha* within the family Thymelaeaceae, nine complete cp genome sequences from the family Thymelaeaceae were included in a phylogenetic analysis. The sequences were aligned using MAFFT (Katoh and Standley 2013), and a maximum-likelihood (ML) tree was constructed using RAxML (Stamatakis 2014). Two species, *Gossypium hirsutum* (Malvaceae) and *Eucalyptus grandis* (Myrtaceae), were included as outgroups. The ML tree

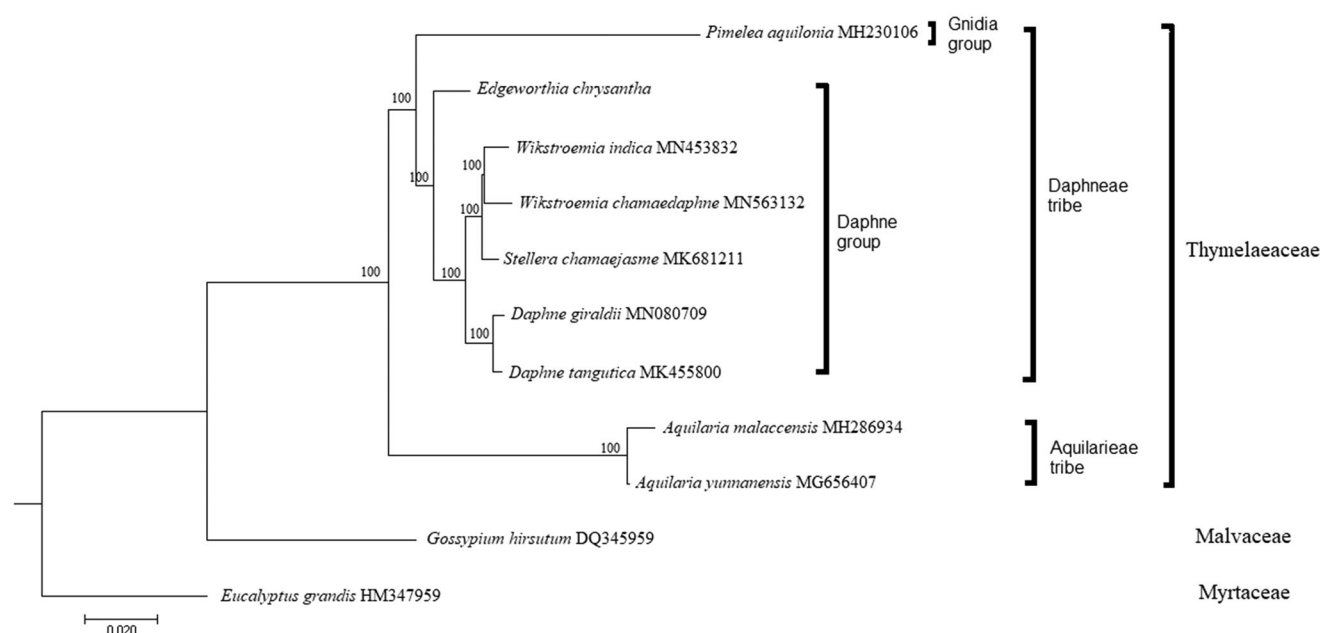


Figure 1. Maximum likelihood tree constructed based on the complete chloroplast genome sequences of nine species from the family Thymelaeaceae, with *Gossypium hirsutum* (Malvaceae) and *Eucalyptus grandis* (Myrtaceae) as outgroup. All branch nodes are indicated with bootstrap support values based on 1000 replicates.

showed that *E. chrysantha* is placed at the base of the Daphne group (including *Daphne*, *Stelleria*, and *Wikstroemia*) with strong bootstrap support (Figure 1).

Data availability statement

The data that support the findings of this study are openly available in the NCBI GenBank at <http://www.ncbi.nlm.nih.gov>, accession number MT135125.

Disclosure statement

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

Funding

This work was supported by the Fundamental Research Funds for the Central Universities [33000-31611215], Shenzhen Dapeng Peninsula National Geopark Horizontal Research Grant [33000-71021140] as well as Guangdong Basic and Applied Basic Research Foundation [2018B 030320001].

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