

MITOGENOME ANNOUNCEMENT



The complete chloroplast genome of *Tainia dunnii* (Orchidaceae): genome structure and evolution

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ABSTRACT

Tainia dunnii is a terrestrial orchid with high ornamental value. Herein, we assembled the complete chloroplast genome of *Tainia dunnii* by next-generation sequencing technologies. The complete chloroplast genome sequence of *Tainia dunnii* is 158,305 base pairs (bp) in length, including a pair of inverted repeat regions (IRs, 25,244 bp), one large single-copy region (LSC, 86,819 bp), one small single-copy region (SSC, 20,998 bp). Besides, the complete chloroplast genome contains 136 genes in total, including 88 protein-coding genes, 38 tRNA genes, and 8 rRNA genes. Phylogenetic analysis showed that *Tainia dunnii* has the closest relationship with *Calanthe davidii* and *Calanthe triplicata*. Our study lay a foundation for further research of *Tainia dunnii*.

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Tainia, a genus, belongs to the Orchidaceae family, contains approximately 32 species, distributed north to China and Japan, and south to New Guinea and the Pacific Islands (Wu and Raven 2009). *Tainia dunnii* is a terrestrial orchid widely distributed in southern part of China, such as Jiangxi, Fujian, and Guangdong Province (Wu and Raven 2009). *Tainia dunnii* is often planted as potted plants and has high ornamental value with beautiful flowers and long inflorescences. However, there are very few studies on the *Tainia dunnii*, which greatly limit the development and utilization of *Tainia dunnii*. In this study, we assembled the complete chloroplast genome of *Tainia dunnii*, hoping to lay a foundation for further research.

The samples of *Tainia dunnii* were collected from Qinglong waterfall scenic area (25°46'22.18"N, 118°57'50.14"E), in Yongtai city, Fujian province, China, and the specimens are kept in the Herbarium of Fujian Agriculture and Forestry University (specimen code FAFU01867).

High-quality genomic DNA of *Tainia dunnii* was extracted from leaves by TIANGEN plant genomic DNA kit, and sequenced by the BGISEQ-500 platform. With the chloroplast genome of *Calanthe davidii* (GenBank accession number NC.037438) as the reference sequences, we assembled the complete chloroplast genome from the clean reads by the GetOrganelle pipe-line (Jin et al. 2018), and then annotated

the new sequences using the Geneious R11.15 (Kearse et al. 2012). Finally, a complete chloroplast genome of *Tainia dunnii* was obtained and submitted to Genbank (accession number MN641754).

The complete chloroplast genome of *Tainia dunnii* was 158,305 bp in length, consisting of two inverted repeat (IR) regions of 25,244 bp, a large single-copy (LSC) region of 86,819 bp, a small single-copy (SSC) region of 20,998 bp. Besides, the complete chloroplast genome has 136 genes in total, including 88 protein-coding genes, 38 tRNA genes, and 8 rRNA genes. In addition, the overall GC content of the genome was 37.2%.

In order to confirm the phylogenetic position of *Tainia dunnii*, a maximum likelihood analysis was performed by MEGA 6.0 (Tamura et al. 2013) with 1000 bootstrap replicates (Minh et al. 2013; Chernomor et al. 2016) based on 12 complete chloroplast genomes of Orchidaceae species, including *Cattleya crispata* (NC.026568), *Cattleya liliputana* (NC.032083), *Masdevallia picturata* (NC.026777), *Corallorhiza odontorhiza* (NC.025664), *Oncidium Gower Ramsey* (NC.014056), *Erycina pusilla* (NC.018114), *Cymbidium tortisepalum* (NC.021431), *Calanthe davidii* (NC.037438), *Calanthe triplicata* (NC.024544), *Dendrobium salaccense* (NC.035332), and *Oberonia japonica* (NC.035832). The results showed that *Tainia dunnii* was related to *Calanthe davidii* and *Calanthe triplicata* (Figure 1).

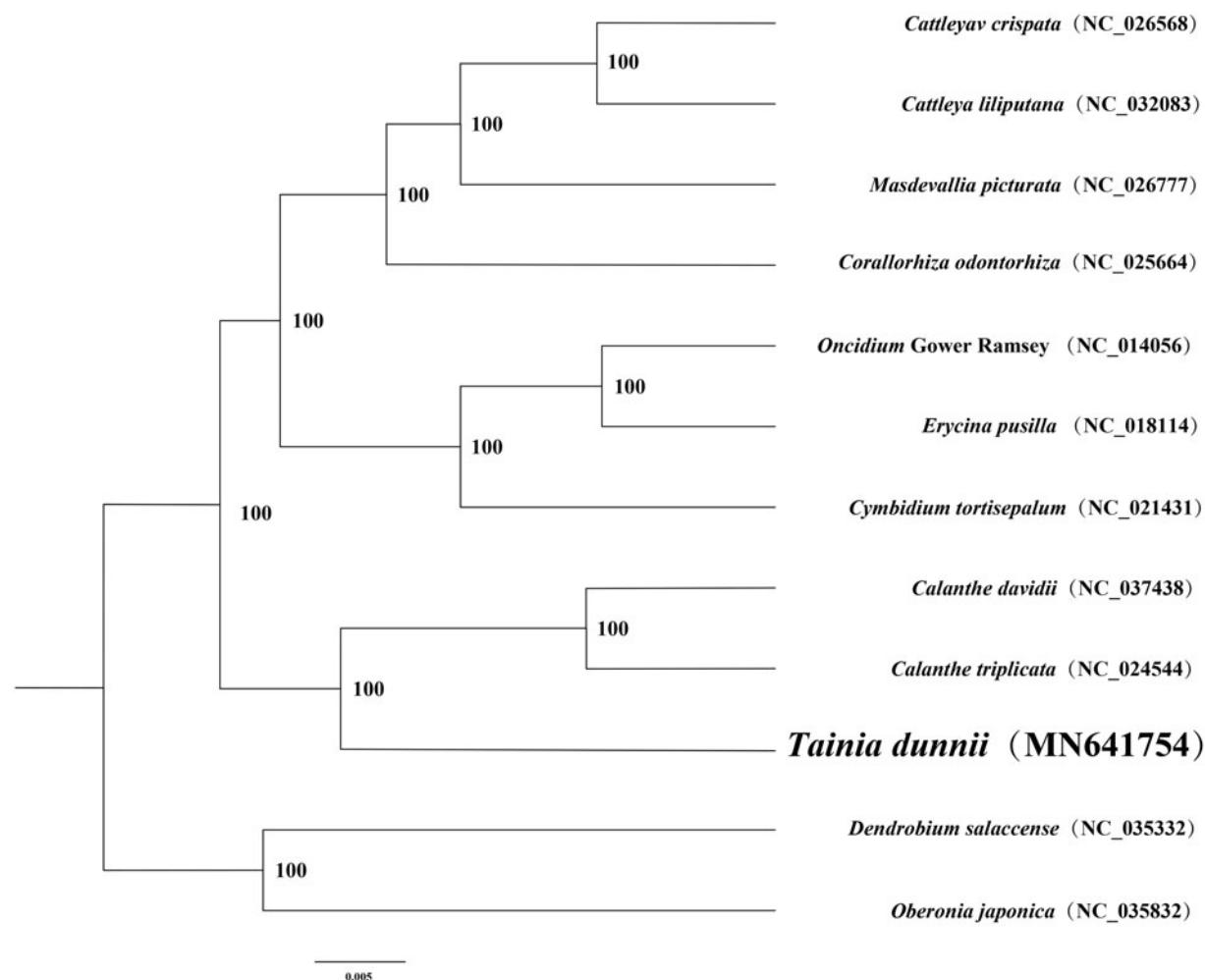


Figure 1. A phylogenetic tree was constructed based on 12 complete chloroplast genome sequences of Orchidaceae. All the sequences were downloaded from NCBI GenBank.

Disclosure statement

No potential conflict of interest was reported by the authors.

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