The complete chloroplast genome of the newly recorded species *Tainia acuminata* Averyanov (Orchidaceae) from China

Xia-lian Ou\(^a\), Ying Qin\(^b\), Li-guo Zhang\(^c\), Ting-guang Sun\(^d\) and Xin-mei Qin\(^b\)

\(^a\)College of Life Science, Guangxi Normal University, Guilin, China; \(^b\)Guangxi Key Laboratory of Plant Conservation and Restoration Ecology in Karst Terrain, Guangxi Institute of Botany, Guangxi Zhuang Autonomous Region and Chinese Academy of Sciences, Guilin, China; \(^c\)Guangxi Key Laboratory of Watershed Ecosystem Change and Biodiversity, Institute of Life Science and School of Life Sciences, Nanchang University, Nanchang, China; \(^d\)Department of Medicine, Guangxi University of Science and Technology, Liuzhou, China

**ABSTRACT**

The complete chloroplast genome sequence of *Tainia acuminata* Averyanov was assembled and the phylogenetic relationship of the species to other taxa in Subtribe Bletilinae was inferred in this study. The length of the complete chloroplast sequence is 157,603 bp, and it contains a large single-copy (LSC) region of 86,336 bp, a small single-copy (SSC) region of 18,129 bp, and two inverted repeat (IRA and IRB) regions of 26,569 bp. A total of 134 genes were annotated including 89 protein-coding genes, 37 tRNA, and eight rRNA. Phylogenetic analysis showed that *T. acuminata* was closely related to *T. cordifolia*, and the genus was closely related to a clade consisting of *Calanthe*, *Phaius*, and *Cephalantheropsis*.

*Averyanov* 2013, a plant of Orchidaceae, is distributed in China and Vietnam (Averyanov 2013; Yuan et al. 2020). The genus was most closely related to *Calanthe*, *Phaius*, and *Cephalantheropsis*. It has high ornamental value owing to its characteristic leaf shape and large beautiful flowers. *T. acuminata* has not been sequenced yet according to our knowledge, and the phylogenetic placement, species identification, genetic diversity, and conservation situation, etc. of the species remain unknown. The chloroplast sequences or genomes have been widely used in the studies of these areas (Daniell et al. 2016; Li et al. 2021). Here, we report the complete chloroplast genome of *T. acuminata* and its phylogenetic position in Subtribe Bletilinae.

A sample of *T. acuminata* was collected from Jiuwanshan National Nature Reserve in Guangxi, China (25°11′26″ N, 108°47′31″ E), and the voucher specimen was deposited at the Herbarium of Guangxi Institute of Botany (http://www.gxib.cn/spIBK/, contact person: Chun-Rui Lin, Email: chunrui@tom.com) under the voucher number QY20190410027. The total DNA was extracted from silica-gel dried leaves by the CTAB method (Doyle and Doyle 1987). The genomic paired ends (PE150) sequencing was performed on NovaSeq 6000 (in Novogenecorp, Tianjin, China). Approximately, 1.6 Gb of clean data were gained after quality filtering using fastp (Chen et al. 2018). The complete chloroplast genome was de novo assembled using GetOrganelle (Jin et al. 2020), and annotated using PGA (Qu et al. 2019) and the online tool GeSeq (Tillich et al. 2017) with reference to the chloroplast genome of *T. dunnii* (NC_045862). The sequence was submitted to the GenBank (accession number: OL489753).

The complete chloroplast genome of *T. acuminata* has a length of 157,603 bp, consisting of a large single-copy (LSC region of 86,336 bp) region, a small single-copy (SSC 18,129 bp) region, and two inverted repeat (IRA and IRB 26,569 bp) regions. The overall GC content of the complete chloroplast genome is 37.3%. It contains 134 genes, including 89 protein-coding genes, 37 tRNA, and eight rRNA.

To investigate the phylogenetic position of *T. acuminata*, maximum-likelihood (ML) phylogenetic tree was reconstructed using RAxML (Stamatakis 2014) based on 17 chloroplast genomes using *Eria lasiopetala* as the outgroup. The phylogenetic tree indicated that *T. acuminata* was most closely related to *T. cordifolia* (BS = 100%) (Figure 1), which was consistent with morphological observation (Averyanov 2013; Yuan et al. 2020). The genus was most closely related to a clade consisting of *Calanthe*, *Phaius*, and *Cephalantheropsis*.

**Ethics statement**

The sample collection was approved by Guangxi Jiuwanshan National Nature Reserve Administration.
Author contributions

Xia-lian Ou: analyzed data and wrote the manuscript. Ying Qin: collected materials and identified species. Li-guo Zhang: collected materials and analyzed data. Ting-guang Sun: identified and sent samples for sequencing. Xin-mei Qin: designed of the work and guided the analysis and modified the manuscript. All authors have read and agreed to publish the manuscript.

Disclosure statement

No potential conflict of interest was reported by the authors.

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Data availability statement

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. OL489753. The associated BioProject, SRA, and BioSample numbers are PRJNA781090, SRR16964329, and SAMN23235068, respectively.

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