Toddalia asiatica (L.) Lam. belongs to family Rutaceae and mainly distributes in dry areas of bushes in tropical Africa, Asia, and Swaziland. Sometimes it can be used as fodder for goats, but it has been used as herbs in traditional medical treatment for 1000 years (Oketch-Rabah et al. 2000). The root and bark of T. asiatica have been used in traditional medicine to treat malaria, diarrhea, cholera, and cough, and the leaves can be used for lung and skin diseases (Ramaraj et al. 2012). The studies about functions of T. asiatica have been continued for long time, however, the information about its chloroplast genome could not be found in NCBI. In previous studies, they used DNA markers and different methods to constructed phylogenetic trees, and results showed that T. asiatica had close relationship with genus Zanthoxylum (Morton 2017; Appelhans et al. 2018). In this study, we sequenced the complete chloroplast genome of T. asiatica and analyzed its phylogenetic relationship in Rutaceae by using complete chloroplast genome.

The sample of T. asiatica was collected from South China Botanical Garden, Tianhe District, Guangzhou, Guangdong Province (N113°22′50″, E113°11′12″). We used the fresh leaves to extract chloroplast DNA-based CTAB method (Doyle and Doyle 1987) and construct the libraries with an average length of 350bp using the NexteraXT DNA Library Preparation Kit (Illumina, San Diego, CA). Then the libraries were sequenced on Illumina Novaseq 6000 platform, over 2Gb clean data was assembled with de novo assembler SPAdes version 3.11.0 software (Bankevich et al. 2012) and annotated by GeSeq (Tillich et al. 2017) with the chloroplast genome of Zanthoxylum paniculatum (MN968552) as reference. The raw data of sequence and annotation results were submitted to NCBI, under the accession number (MW194118) and SRA number SRR13479128. Furthermore, the sample was stored at Laboratory of Molecular Biology, Liaocheng University, Liaocheng (Voucher specimen: TA20200701LP) (Lusha Ji, Email: jilusha2020@163.com).

The complete chloroplast genome of T. asiatica is 158,434 bp in length and contains a large single-copy (LSC) of 86,132 bp, and two inverted repeat (IR) regions of 27,008 bp each. There were 133 genes, which includes 88 protein-coding genes, 8 rRNA, and 37 tRNA, and 38.5% overall GC content. Each of trn-K-UUU, rps16, trnG-UCC, atpF, rpoC1, trnL-UAA, trnV-UAC, petB, petD, rpl16, rpl2, ndhB, trnI-GAU, trnA-UGC, and ndhA genes contains a intron, clpP and ycf3 contains 2 intron. The phylogenetic analysis result shows that T. asiatica has the closest relationship with Zanthoxylum armatum (MT990984) and Zanthoxylum nitidum (MN508801).
supporting the phylogenetic relationship between *T. asiatica* and genus *Zanthoxylum* within *Rutaceae* from complete chloroplast genome level.

**Disclosure statement**

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

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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/](https://www.ncbi.nlm.nih.gov/) under the accession no. MW194118. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA693034, SRR13479128, and SRS8071277, respectively.

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