The complete chloroplast genome sequence of *Trigonotis peduncularis* (Boraginaceae)

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**ABSTRACT**

*Trigonotis peduncularis* (Boraginaceae) is an annual or biannual herb widely distributed in temperate Asia and East Europe. The complete chloroplast genome of *T. peduncularis* was sequenced by high-throughput technologies and assembled for the first time. The complete chloroplast genome of *T. peduncularis* was 147,508 bp in length with a GC content of 37.6%, which includes a large single-copy region (80,546 bp), a pair of inverted repeats (24,877 bp), and a small single copy (17,208 bp). GC content of IR regions (43.3%) were higher than LSC (35.5%) and SSC (31.1%) regions. The genome was predicted to encode 130 genes, of which 114 were unique, including 80 protein-coding genes, 30 tRNA genes, and four rRNA genes. Result from phylogenetic analysis showed that *T. peduncularis* was sister to *Plagiobothrys nothofulvus*, and the intergeneric relationships among the six genera sampled in Boraginaceae were well resolved and strongly supported.

The genus *Trigonotis* Steven (Boraginaceae) consists of approximately 60 species of herbs, mainly distributed in Asia and East Europe (Zhu et al. 1995; Weigend et al. 2016). There are ca. 40 *Trigonotis* species recorded in China, and more than 30 are endemic (Zhu et al. 1995). *Trigonotis peduncularis* (Trevis.) Benth. ex Baker & S. Moore 1879 is the most widely distributed species in China, which is also widely distributed in temperate Asia and East Europe. This species has been used as a medical plant for treating stomachache, bleeding, and fracture (Yao et al. 2012). Several new compounds have also been discovered in *T. peduncularis* (Song et al. 2008; Otsuka et al. 2008).

So far, there is no complete chloroplast genome sequence of *Trigonotis* available in GenBank. In this study, we reported the complete chloroplast genome sequence of *T. peduncularis*, which could provide a basis for further study on its genetic diversity, phylogeeny, and evolution.

The fresh leaves of *T. peduncularis* were collected from Nanjing Botanical Garden Mem. Sun Yat-Sen, Nanjing, Jiangsu Province, China (118°49′49″N, 32°3′32″E) with the permission from the garden. The voucher specimen (*H.M. Li & B. Xue 345*) was deposited in the herbaria of the South China Botanical Garden, Chinese Academy of Sciences (IBSC, http://herbarium.scbg.cas.cn/), Feiyan Zeng, zengfeiy@scbg.ac.cn). Total genomic DNA of *T. peduncularis* was extracted using the modified CTAB method (Doyle and Doyle 1987). Library construction and sequencing were performed by BGI-Shenzhen (Shenzhen, China), using an Illumina HisSeq 2500 Sequencing System following the manufacturer’s instructions. About 3 G data were obtained. The pair-end reads were assembled into a circular contig using NOVOPlasty v.4.2 (Dierckxsens et al. 2017). The genome was then annotated using PGA (Plastid Genome Annotator) (Qu et al. 2019), and manually corrected in the Geneious v.2020.0.5 (Kearse et al. 2012).

The annotated chloroplast genome of *T. peduncularis* was submitted to GenBank with the accession number MZ911745. The complete chloroplast genome was 147,508 bp in length, which include a large single-copy region, a pair of inverted repeats, and a small single copy, and the sequence lengths were 80,546 bp, 24,877 bp, and 17,208 bp, respectively. The overall GC content is 37.6%, and GC contents of IR regions (43.3%) were higher than that of LSC (35.5%) and SSC (31.1%) regions. The genome was predicted to encode 130 genes, of which 114 were unique, including 80 protein-coding genes, 30 transfer RNA genes, and four ribosomal RNA genes.

To investigate the phylogenetic position of *T. peduncularis*, seven chloroplast genome sequences of species from Boraginaceae were downloaded from Genbank for phylogenetic analysis. Chloroplast genome sequences of *Tiquilia plicata* (Torr.) A.T.Richardson (MG573056) from Ehretiaceae and *Isodon serra* (Maximowicz) Kudo (MT317099) from Lamiaeae were also downloaded and selected as outgroups. The total
ten complete chloroplast genome sequences were aligned using MAFFT v.7.471 (Katoh and Standley 2013). A maximum-likelihood analysis was performed by RAxML v. 8.2.12 (Stamatakis 2014) under GTR+G model with 1000 bootstrap replicates. Result from phylogenetic analysis showed that *T. peduncularis* was sister to *Plagiobothrys nothofulvus* with strong support, and the intergeneric relationships among the six genera sampled in Boraginaceae were also well resolved and strongly supported (Figure 1).

**Authors’ contributions**

Jian-hua Wu and Hui-min Li conceived the study and drafted the paper. Jin-man Lei analyzed and interpreted the data. Ze-rui Liang prepared the figure. All authors revised the draft and approved the final draft. All authors agree to be accountable for all aspects of the work.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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**Data availability statement**

The genome sequence data that obtained at this study are openly available in GenBank of NCBI [https://www.ncbi.nlm.nih.gov/] under the accession number of MZ911745. The associated BioProject, Bio-Sample and SRA, numbers are PRJNA767254, SAMN21895048 and SRR16146713, respectively.

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