Complete plastome sequence of *Tetrataenium yunnanense* (tribe Tordylieae, Apiaceae) with anti-tumor activity

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**ABSTRACT**

The species *Tetrataenium yunnanense* is a medicinal herb exhibiting excellent anti-tumor activity in vitro and mainly distributed in northwest Yunnan, China. The assembled genome is 142,739 base-pairs (bp) in size, with one large single-copy region of 99,975 bp and one small single-copy region of 17,375 bp separated by two inverted repeats of 25,386 bp. The genome contains a total of 121 genes, including 78 protein-coding genes, 8 rRNAs and 35 tRNAs. Furthermore, phylogenomic estimation indicated that two individuals of *T. yunnanense* could be clustered into an obvious lineage and failed to recover the two *Tetrataenium* species (*T. yunnanense* and *T. candicans*) as a monophyletic group.

*Tetrataenium* has been widely accepted by taxonomists as a separate genus (Logacheva et al. 2010; Yu et al. 2011; Pimenov 2017; Xiao et al. 2018), but non-monophyletic, including *Tetrataenium* sensu stricto clade and *Candicans* clade (Downie et al. 2010; Logacheva et al. 2010; Yu et al. 2011; Liu and Downie 2017). *Tetrataenium yunnanense* (Franch.) Manden. ex Q. Y. Xiao & X. J. He. (Apiaceae, Apioideae), is a perennial herb endemic to northwest Yunnan (Dali County, Deqin County, Eryuan County, Ertyuan County, Fugong County and Gongshan County), China, growing in alpine meadows at 3200–4300 m (Xiao et al. 2018). In the previous researches, the species was attributed to multiple genera and described as multiple taxa, i.e. *Heracleum yunnanense* Franch., *Angelica oncostepala* Hand.-Mazz., *Heracleum oncosepulum* (Hand.-Mazz.) Pimenov & Kljuykov. (Franchet 1894; Handel-Mazzetti 1933; Pimenov and Kljuykov 2003). *Heracleum yunnanense* is recorded as incompletely known species only from a few collections. In the *Flora of China*, the roots of *A. oncostepala* are recorded as having reputed medicinal value (Pan and Watson 2005). Li et al. (2012) reported further that *A. oncostepala* exhibit excellent anti-tumor activity in vitro and may be a good resource for new anti-tumor compounds. Here, we assembled the complete chloroplast genome of *T. yunnanense* to explore the reasonably systematic position and conservation of this taxon.

The mature leaves of *T. yunnanense* were obtained from among shrubs in grassland at coniferous forest margins Luoping Shan (26°0′56.21″N, 99°53′25.92″E, altitude 3200 m), Eryuan County, Yunnan Province, China. Voucher specimens (voucher number: xqy-2016082201) were deposited in the herbarium of the Natural History Museum of Sichuan University (SZ). The total genomic DNA was isolated from dry leaves using the TIANGEN plant genomic DNA extraction kit, following the manufacturer’s instructions and sequenced at Novogene (Novogene BioTech, Inc. Beijing, China) by Illumina Hiseq 2500 platform (Illumina, San Diego, CA). Around 5 Gb raw data were assembled against the plastome of *H. yunnanense* (MN365275) (Kang et al. 2019) and the genome obtained was annotated using software Geneious version 11.0.4 (Kearse et al. 2012). The annotated plastid genome sequence has been deposited into the GenBank with the accession number MN935165.

The whole plastid genome of *T. yunnanense* was 142,739 bp in length, with a large single-copy (LSC) region (99,975 bp), a small single-copy (SSC) region (17,375 bp), and a pair of inverted repeats (IRa and IRb: 25,386 bp). The overall GC content was 37.3%. The genome consisted of 121 genes, including 78 protein-coding genes, 35 distinct tRNA genes, and 8 rRNA genes.

To further investigate the phylogenetic position of *T. yunnanense* and *T. candidans*, 38 cp genome sequences of Apiaceae were downloaded from the NCBI database, aligned by MAFFT (Katoh et al. 2017), and trimmed properly by trimAl v1.4 (Capella-Gutierrez et al. 2009). RAxML-HPC2 on XSEDE version 8.2.10 (Stamatakis 2014) was used to construct a maximum likelihood tree. As a result, phylogenetic analysis indicated that two individuals of *T. yunnanense* could be clustered into an obvious lineage and failed to recover the two *Tetrataenium* species (*T. yunnanense* and *T. candidans*) as a monophyletic group, while *T. candidans* is closely related to *Semenovia* (Figure 1), supporting the separation of *T. candidans* from *Tetrataenium* sensu stricto clade to establish as a...
new genus (Paik 2008). The whole chloroplast genome sequences provided sufficient genetic information for phylogenetic reconstruction of the genus *Tetrataenium*.

**Ethical approval**
This article does not contain any studies with human participants or animals performed by any of the authors.

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

**Funding**
This work was supported by the National Specimen Information Infrastructure, specimen platform of China, teaching specimens sub-platform [Web, http://mnh.scu.edu.cn/, 2005DKA21403-JK]: The Science and
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