

Complete plastome sequence of *Tetrataenium Candicans* (tribe Tordylieae, Apiaceae): a medicinal plant

Qun-Ying Xiao^a, Tu Feng^a, Yan Yu^b , Qiang Luo^a and Xing-Jin He^b 

^aSchool of Ecological Engineering, Key Laboratory of Biological Resources and Ecological Remediation of Guizhou Province, Collaborative Innovation Center of Wetland Eco-engineering of Guizhou Province, Guizhou University of Engineering Science, Bijie, P. R. China; ^bKey Laboratory of Bio-Resources and EcoEnvironment of Ministry of Education, College of Life Sciences, Sichuan University, Chengdu, P. R. China

ABSTRACT

Tetrataenium candicans is a Himalayan native medicinal plant species. In this study, we report and characterize the complete plastid genome sequence of *T. candicans* in order to provide genomic resources helpful for promoting its systematics research and conservation. The complete chloroplast (cp) genome is a circular structure and 147,335 bp in length, composing of one large single-copy (LSC) region of 92,996 bp, one small single-copy (SSC) region of 17,473 bp, and separated by a pair of inverted repeat (IR) regions of 18,433 bp each. It encodes 129 genes, including 85 protein-coding genes, 36 tRNA genes, and 8 rRNA genes. The GC content is 37.5%. Phylogenetic analysis of 31 representative plastomes indicated that the *T. candicans* was close to *Semenovia gyirongensis*.

ARTICLE HISTORY

Received 11 September 2019
Accepted 25 September 2019

KEYWORDS

Tetrataenium candicans;
complete chloroplast
genome; phylogenetic
analysis





Tetrataenium candicans (Wallich ex de Candolle) Mandenova is a widespread species of the Himalayan in the family Apiaceae. It grows in the sparse forests, coniferous forests margin, scrub on arid slopes and in abandoned fields, streamsides with altitudes ranging from 1800 to 4500 m (Pu and Watson 2005). It is a native medicinal herb being a potential source of Xanthotoxin and has constant demand in pharmaceutical industries (BCIL 1996). Over-collecting coupled with other biotic pressures posed a severe threat to its existence in natural habitats and thus, enlisted as Endangered species of the Himalayan region (CAMP 2003).

The species was first described by Candolle (1830) as *Heracleum candicans* Wall. ex DC. within *Heracleum* L. section *Tetrataenium*. Later, *Tetrataenium* was elevated to generic rank (Mandenova 1959) and it was also transferred to *Tetrataenium* as *T. candicans* (Wallich ex de Candolle) Mandenova. Paik (2008) recognized that *T. candicans* may represent a new genus. Recent researches proved that *Tetrataenium* was not monophyletic including *Tetrataenium* sensu stricto and *Candicans* clade (Downie et al. 2010; Logacheva et al. 2010; Yu et al. 2011; Liu and Downie 2017). Consequently, the genetic and genomic information is urgently needed to promote its systematic research and the development of the conservation value of *T. candicans*. Here, we determined to report the complete plastid genome sequence of *T. candicans* (GenBank accession number: MN419228) to provide genetic and genomic information to promote its systematics research and conservation.

The mature leaves of *T. candicans* were obtained from a scrub on arid slope near Tiantuo town (29°53'33.52''N, 97°38'13.05''E, altitude 4074 m), Zuogong County, Xizang, China. Voucher specimens (voucher number: xqy201408260101) were deposited in the herbarium of Natural History Museum of Sichuan University (SZ). The experiment procedure is as reported in Xiao et al. (2019). Around 5 Gb raw data were assembled against the plastome of *Semenovia gyirongensis* (MK757488) (Xiao et al. 2019) using Geneious version 11.0.4 (Kearse et al. 2012). The plastome was annotated using Geneious version 11.0.4 against the plastome of *S. gyirongensis* (MK757488) coupled with manual check and adjustment.

The plastome of *T. candicans* was found to possess a total length 147,335 bp with the typical quadripartite structure of angiosperms, containing a large single-copy region (LSC) of 92,996 bp and a small single-copy region (SSC) of 17,473 bp joined by two identical inverted repeat regions (IRa and IRb, 18,433 bp each). A total of 129 genes are successfully annotated, consisting of 85 protein-coding genes, 8 rRNA genes, and 36 tRNA genes were annotated. Among them, 15 gene duplicates in the inverted repeat (IR) regions include six tRNA, four rRNA, and five protein-coding genes. Total GC content is 37.5%.

We used RAXML (Stamatakis 2014) with 1000 bootstraps under the GTRGAMMAI substitution model to reconstruct a maximum likelihood (ML) phylogeny of 31 published complete plastomes of Apiaceae, using *Bupleurum latissimum*, *B.*

CONTACT Tu Feng  fengtu@gues.edu.cn  School of Ecological Engineering, Key Laboratory of Biological Resources and Ecological Remediation of Guizhou Province, Collaborative Innovation Center of Wetland Eco-engineering of Guizhou Province, Guizhou University of Engineering Science, Bijie, P. R. China; Xing-Jin He  xjhe@scu.edu.cn  Key Laboratory of Bio-Resources and EcoEnvironment of Ministry of Education, College of Life Sciences, Sichuan University, Chengdu, P. R. China

© 2019 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

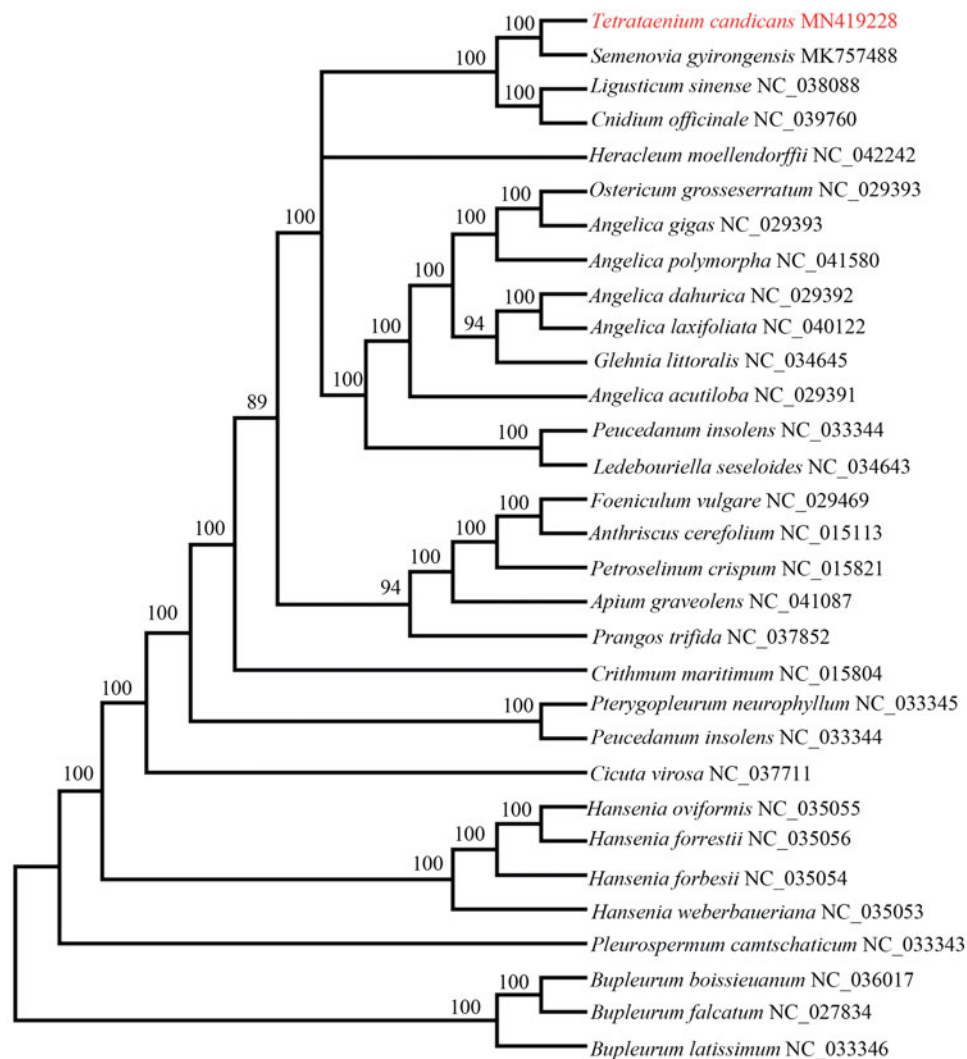


Figure 1. The best ML phylogeny recovered from 31 complete plastome sequences by RAxML. The number on each node indicates bootstrap support value.

boissieuanum, and *B. falcatum* as outgroups. The phylogenetic tree (Figure 1) indicated that *T. candicans* was closely related to *S. gyirongensis*. This published *T. candicans* chloroplast genome will provide useful information for phylogenetic studies and conservation genetics.

Ethical approval

Research involving human participants and/or animals, this article does not contain any studies with human participants or animals performed by any of the authors.

Disclosure statement

The authors report no conflicts of interest.

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 Key Laboratory of Biological Resources and Ecological Remediation of Guizhou Province ([2012]012, The Key Discipline of Ecology of Guizhou

Province [ZDXK[2013]11], The Collaborative Innovation Centre of Wetland Ecological Engineering of Guizhou Province [2015XT003], High-level Innovative Talents Project in Guizhou Province [No.[2016]4], Talents Research Project of Guizhou Provincial Department of Education [No.KY[2018]072], and the National Natural Science Foundation of China, [No. 31560059].

ORCID

Yan Yu  <http://orcid.org/0000-0001-7177-7552>
Xing-Jin He  <http://orcid.org/0000-0003-2064-0112>

References

- BCIL. 1996. Sectoral study of Indian medicinal plants- status, perspective and strategy for growth. New Delhi, India: Biotech Consortium India Ltd.
- CAMP. 2003. CAMP report: conservation assessment and management prioritisation for the medicinal plants of Jammu and Kashmir, Himachal Pradesh and Uttaranchal, Workshop, Shimla, Himachal Pradesh. Vol. 206. Bangalore, India: FRLHT.
- Candolle D. 1830. Umbelliferae. In: De Candolle AP, editor. Prodrromus systematis naturalis regni vegetabilis. Vol. 4. Paris: Treüttel and Würtz; p. 55–220.
- Downie SR, Spalik K, Katzdownie DS, Reduron JP. 2010. Major clades within *Apiaceae* subfamily *Apioidae* as inferred by phylogenetic analysis of nrDNA ITS sequences. *Plant Divers Evol.* 128:111–136.

- Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics*. 28: 1647–1649.
- Liu M, Downie SR. 2017. The phylogenetic significance of fruit anatomical and micromorphological structures in Chinese *Heracleum* species and related taxa (*Apiaceae*). *Syst Bot*. 42:313–325.
- Logacheva MD, Valiejoroman CM, Degtjareva GV, Stratton JM, Downie SR, Samigullin TH, Pimenov MG. 2010. A comparison of nrDNA ITS and ETS loci for phylogenetic inference in the Umbelliferae: an example from tribe Tordylieae. *Mol Phylogenet Evol*. 57:471–476.
- Mandenova IP. 1959. Materialy po sistematike triby Pastinaceae K.-Pol. emend. Manden. (Umbelliferae –*Apioidae*) (Materials to systematics of tribe of Pastinaceae K.-Pol. bracts and bracteoles). *Trudy Tbilissk Bot Inst*. 20:3–57.
- Paik JH. 2008. Systematic studies of *Heracleum* L. (Umbelliferae) and related genera in the Sino-Himalayan region [doctor thesis]. Edinburgh, UK: University of Edinburgh.
- Pu FD, Watson MF. 2005. *Heracleum* L., *Semenovia* regel & herder and *Tordyliopsis* de candolle. *Apiaceae*. In: Wu ZY, Raven PH, editors. *Flora of China*. Vol. 14. Saint Louis, China: Science Press; Beijing: Missouri Botanical Garden Press; p. 201.
- Stamatakis A. 2014. RAXML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics*. 30:1312–1313.
- Xiao QY, Feng T, Yu Y, Luo Q, He XJ. 2019. The complete chloroplast genome of *Semenovia gyirongensis* (Tribe Tordylieae, *Apiaceae*). *Mitochondr DNA B*. 4:1863–1864.
- Yu Y, Downie SR, He XJ, Deng XL, Yan L. 2011. Phylogeny and biogeography of Chinese *Heracleum* (*Apiaceae* tribe Tordylieae) with comments on their fruit morphology. *Plant Syst Evol*. 296:179–203.