

PLASTOME ANNOUNCEMENT



Complete chloroplast genome of *Euphorbia micractina* Boiss (Euphorbiaceae: Euphorbia)

Dan Wang^a, Yu-Rou Dan^a, Ming Liu^{a,b} and Fu-Qiang Yin^a

^aCollege of Biological and Food Engineering, Chongqing Three Gorges University, Chongqing, China; ^bThe Chongqing Engineering Laboratory for Green Cultivation and Deep Processing of the Three Gorges Reservoir Area's Medicinal Herbs, Chongqing, China

ABSTRACT

Euphorbia micractina Boiss is a plant with high medicinal value. Yet, its molecular biology is not fully understood. In this study, we sequenced the whole chloroplast genome (CP) sequence of *E. micractina* to study its phylogenetic relationship in Euphorbiaceae. The total length of the chloroplast genome of *E. micractina* is 162,056 bp, including a large single-copy (LSC) region of 89,936 bp, a small single-copy (SSC) region of 18,376 bp, and a pair of identical inverted repeat regions (IRs) of 11,367 bp. The genome has 128 genes, including 84 protein-coding genes, 36 transfer RNA (tRNA) genes, and 8 ribosomal RNA (rRNA) genes. The overall GC content of the plastome is 35.7%. The phylogenetic analysis of *E. micractina* with 30 related species suggested a closest taxonomical relationship with *Euphorbia pekinensis* in the Euphorbiaceae family.

ARTICLE HISTORY

Received 7 February 2022
Accepted 4 June 2022

KEYWORDS

Complete chloroplast genome; *Euphorbia micractina* Boiss; Euphorbiaceae; phylogenetic analysis


Euphorbia micractina Boiss is a plant that belongs to Euphorbiaceae and *Euphorbia* genus and is mainly distributed in Gansu, Qinghai, Sichuan, and Tibet, China. It was first described by Candolle in 1862 (Candolle 1862). The plant is commonly used to remove warts (Wu et al. 1991). So far, 16 terpenoids, 7 steroids, and 15 aromatic derivatives were isolated from the ethanol extract of *Euphorbia officinalis* (Tao et al. 2015, 2016). In 2012, halberylmethyl butane found in the genus *Euphorbia peplus* was approved by the American FDA to treat solar keratosis (Keating 2012). At present, the research on *Euphorbia officinalis* mainly focuses on its chemical components and pharmacological activities, while only a few studies have reported on its molecular biology. Therefore, in this study, we sequenced the whole chloroplast genome (cp) sequence of *Euphorbia micractina*, which may further promote the genetic research and resource utilization of this plant.

Fresh leaf materials of *E. micractina* were sampled from Xiaojin County, Aba Prefecture, Sichuan Province, located at 102°01'102.59"E, 30°35'31.43"N. The specimens were kept in the herbarium of the College of Biology and Food Engineering, Chongqing Three Gorges University (<https://www.sanxiau.edu.cn/smkx/>; contact person name: Nong ZHOU, Email: erhaizn@126.com) under the voucher number ZQ311416. Total genomic DNA was extracted from 100 mg of actively growing fresh leaves using a modified CTAB (hexadecyltrimethylammonium bromide) method, in which 4% CTAB was used instead of 2% CTAB, and adding approximately 1% polyvinyl polypyrrolidone (PVP) and 0.2% DL-dithiothreitol

(DTT) (Yang et al. 2014) and sequenced with Illumina Hiseq 2500 (Novogene, Tianjing, China) platform. The cp genome was assembled using GetOrganelle (Jin et al. 2020) with *Euphorbia pekinensis* (NC_058897) as reference. Annotation was performed with the GeSeq (Tillich et al. 2017) and CpGAVAS2 (Shi et al. 2019). The complete chloroplast genome sequence of *E. micractina* was submitted to GenBank (accession number: OL622067).

The chloroplast genome of *E. micractina* has a typical quadripartite structure with a length of 162,056 bp, containing inverted repeats (IRs) of 11,367 bp separated by a large single-copy (LSC) region of 89,936 bp and a single small copy (SSC) region of 18,376 bp. The cpDNA contains 128 genes, comprising 84 protein-coding genes, 36 tRNA genes, and 8 rRNA genes. The overall GC content of the plastome is 35.7%.

To identify the phylogenetic position of *E. micractina*, phylogenetic analysis was performed based on complete cp genomes from 30 Euphorbiaceae species with *Daphniphyllum macropodum* and *Daphniphyllum oldhamii* as the outgroup species. The complete chloroplast genome sequences were aligned using MAFFT version 7 (Kato and Standley 2013). Maximum likelihood (ML) analysis was performed with RAxML (Stamatakis 2014) based on the GTRGAMMA model using 1000 replicates of bootstrap analysis. The phylogenetic analysis showed a close relationship of *E. micractina* with *Euphorbia pekinensis* in the family of Euphorbiaceae (Figure 1). These newly characterized phylogenetic analysis

CONTACT Fu-qiang Yin 765504017@qq.com  College of Biological and Food Engineering, Chongqing Three Gorges University, Chongqing, China

 Supplemental data for this article is available online at <https://doi.org/10.1080/23802359.2022.2087557>

© 2022 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.

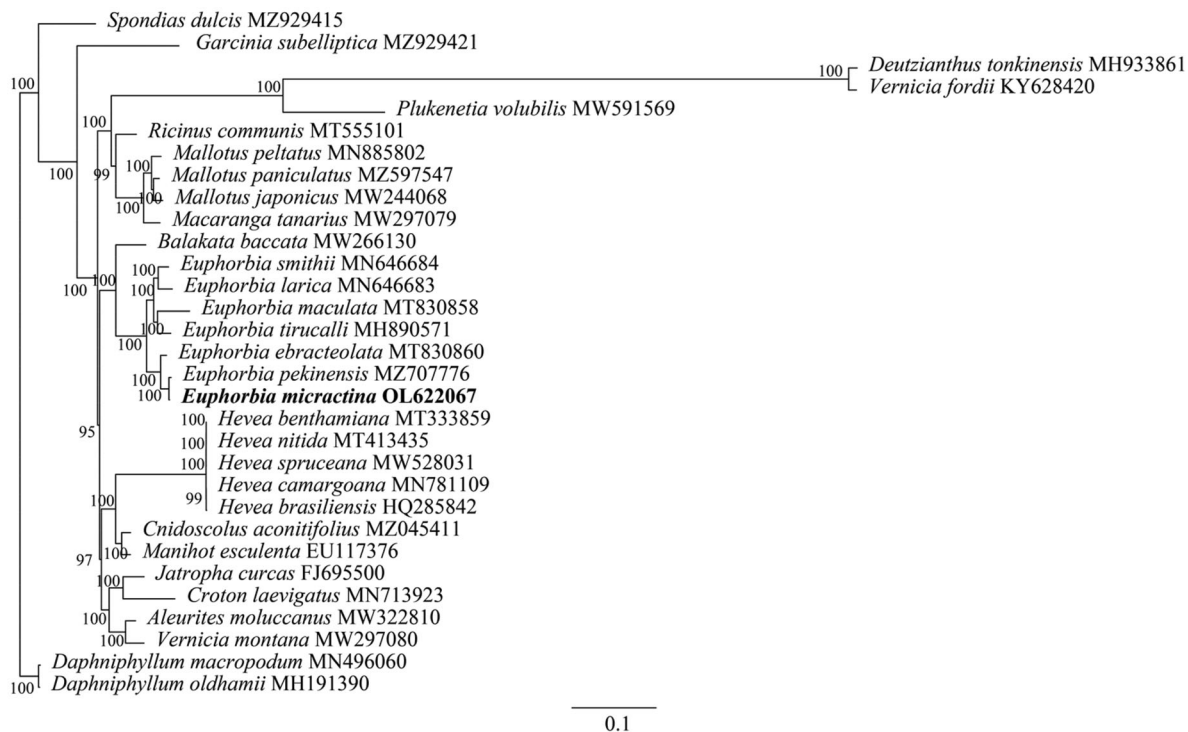


Figure 1. The construction of the phylogenetic tree performed using complete genomic sequences of 30 species and *E. micractina* based on the maximum likelihood method with a bootstrap value of 1000 replicates.

fruits can be used to develop markers for further study on the phylogeny and evolution of the genus *Euphorbia*.

Ethical approval

Euphorbia micractina Boiss is not a protected plant, and the current research will not cause any kind of damage to the population of *Euphorbia micractina* Boiss. Accordingly, no specific permissions are needed for this research.

Author contributions

Dan Wang participated in the sample assembly and annotation work, write and revise the paper; Yu-rou Dan and Ming Liu were mainly responsible for the analysis and interpretation of data; Fu-qiang Yin was mainly responsible for the design of the experiment and approved the final version of the manuscript. All authors are accountable for all aspects of the work.

Disclosure statement

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

Funding

This work was supported by the Chongqing Science and Technology Commission [cstc2018jcyjAX0639], the Scientific and Technological Research Program of Chongqing Municipal Education Commission [KJCX2020046; KJQN201901222], and the Scientific Research Startup Project of Chongqing Three Gorges University [0996061; 0996071].

Data availability statement

The data of this study are available in GenBank of NCBI at (<https://www.ncbi.nlm.nih.gov>) under accession no.OL622067. The associated BioProject, SRA, and BioSample numbers are PRJNA796732, SRR17604728, and SAMN24917951, respectively.

References

- Candolle A. 1862. *Euphorbia micractina* Boiss. Prodrum Systematis Naturalis Regni Vegetabilis. 15(2):127.
- Jin J-J, Yu W-B, Yang J-B, Song Y, dePamphilis CW, Yi T-S, Li D-Z. 2020. GetOrganelle: a fast and versatile toolkit for accurate de novo assembly of organelle genomes. *Genome Biol.* 21(1):241.
- Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol Biol Evol.* 30(4):772–780.
- Keating GMI. 2012. Mebutate gel 0.015% and 0.05%: in actinic keratosis. *Drugs.* 72(18):2397–2405.
- Shi L, Chen H, Jiang M, Wang L, Wu X, Huang L, Liu C. 2019. CPGAVA2, an integrated plastome sequence annotator and analyzer. *Nucleic Acids Res.* 47(W1):W65–W73.
- Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics.* 30(9):1312–1313.
- Tao YW, Tian Y, Xu WD. 2016. Terpenoids from *Euphorbia micractina*. *Acta Pharmaceutica Sinica.* 51(3):411–419.
- Tao Y-w, Xu W-d, Tian Y, Shi J-g. 2015. Steroids and aromatic derivatives from *Euphorbia micractina*. *Zhongguo Zhong Yao Za Zhi.* 40(23):4639–4644.
- Tillich M, Lehwark P, Pellizzer T, Ulbricht-Jones ES, Fischer A, Bock R, Greiner S. 2017. GeSeq versatile and accurate annotation of organelle genomes. *Nucleic Acids Res.* 45(W1):W6–W11.
- Wu ZY, Zhou TY, Xiao PG. 1991. *Xin Hua Ben Cao Gang Yao*. Vol. 2. Shanghai: Shanghai Science and Technology Press; p. 219.
- Yang JB, Li DZ, Li HT. 2014. Highly effective sequencing whole chloroplast genomes of angiosperms by nine novel universal primer pairs. *Mol Ecol Resour.* 14(5):1024–1031.