

MITOGENOME ANNOUNCEMENT



Characterization of the complete chloroplast genome of a common Chinese medicinal herb, *Eriocaulon buergerianum* (Eriocaulaceae: *Eriocaulon*)

Mingliang Shan^{a*}, Tianyi Cao^{b*}, Wenhao Xing^a and Chengwei Guo^c

^aShandong University of Traditional Chinese Medicine, Jinan, PR China; ^bIntegrated Traditional Chinese and Western Medicine Hospital, Hangzhou, PR China; ^cAffiliated Hospital, Shandong University of TCM, Jinan, PR China

ABSTRACT

Eriocaulon buergerianum is a common Chinese medicinal herb and belongs to the family Eriocaulaceae genus *Eriocaulon* the annual herbs. In this study, the complete chloroplast genome of *E. buergerianum* was assembled and reported. The complete chloroplast genome of *E. buergerianum* is 157,016 bp in length as the circular, which harbours a large single-copy region (LSC) of 81,534 bp, a small single-copy region (SSC) of 17,114 bp, and two inverted-repeat regions (IRs) of 26,393 bp each one. The overall nucleotide content of the chloroplast genome: A of 31.8%, T of 32.4%, C of 18.2% G of 17.6%, and 35.8% GC content. The chloroplast genome of *E. buergerianum* contains 133 genes, which includes 88 protein-coding genes (PCGs), 37 transfer RNA (tRNAs), and 8 ribosome RNA (rRNAs). The evolutionary analysis used neighbour-joining (NJ) method and the result showed that *E. buergerianum* was closely related to *Eriocaulon sexangulare* in the family Eriocaulaceae. This study will be helpful for genome data and genomic resources of the family Eriocaulaceae for further.

ARTICLE HISTORY

Received 21 August 2019
Accepted 23 September 2019

KEYWORDS

Eriocaulon buergerianum;
Eriocaulaceae; Chinese
medicinal herb; chloroplast
genome; evolution-
ary analysis

Eriocaulon buergerianum is a common Chinese medicinal herb and belongs to the family Eriocaulaceae genus *Eriocaulon*, which also is the annual herb. Plant whole of *E. buergerianum* is named Gu-Jing-Cao in Chinese (Ho and Chen 2002). Thirteen genera is in the family Eriocaulaceae, which the genus *Eriocaulon* contains around 435 species distributed throughout the world (Ho and Chen 2002). Previous phytochemical research revealed *E. buergerianum* of the genus *Eriocaulon* led to the identification of flavonoids, naphthopyranones and γ -tocopheryl acetate (Santos et al. 2005). *E. buergerianum* is frequently used as anti-inflammatory and antimicrobial medicine in China. Now, we do not have knowledge about the chloroplast genome and other genome information of the *E. buergerianum*. So, in this study, the complete chloroplast genome of *E. buergerianum* was assembled, annotated, and reported, which can be valuable for genome data and genomic resources for further, also can be important for evolutionary analysis and utilization of the Eriocaulaceae family.

Plant whole of *E. buergerianum* was collected from Shandong University of Traditional Chinese Medicine in Jinan, Shandong, China (36.65°N, 117.05°E). The total genomic DNA of *E. buergerianum* was extracted from the whole plant using the modified CTAB method and stored in Shandong University of Traditional Chinese Medicine (No.SUTCM-01). The genomic DNA was purified and fragmented using the NEB Next Ultra™ II DNA Library Prep Kit

(NEB, BJ, and CN), which was sequenced. FastQC version 0.11.8 (Andrews 2015) was used to perform and remove low-quality reads and adapters for quality control. The chloroplast genome of *E. buergerianum* was assembled and annotated using the MitoZ (Meng et al. 2019). OrganellarGenomeDRAW version 1.3.1 (Greiner et al. 2019) was used to draw the physical map of the chloroplast genome of *E. buergerianum*.

The complete chloroplast genome of *E. buergerianum* is 151,434 base pairs (bp) in length which is the circular with the overall nucleotide content of the chloroplast genome: 31.8% A (Adenine), 32.4% T (Thymine), 18.2% C (Cytosine), 17.6% G (Guanine), and 35.8% GC content. It harbours a characteristic quadripartite structure with a large single-copy region (LSC) of 81,534 bp, a small single-copy region (SSC) of 17,114 bp, and two inverted repeat regions (IRs) of 26,393 bp. The chloroplast genome of *E. buergerianum* contains 133 genes, which includes 88 protein-coding genes (PCGs), 37 transfer RNA genes (tRNAs), and 8 ribosomal RNA genes (rRNAs). And 20 genes were found duplicated in IR regions at each one, which included 8 PCG genes species (*rps19*, *rpl2*, *rpl23*, *ycf2*, *ndhB*, *rps7*, *rps12*, and *ycf1*), 8 tRNA genes species (*trnH-GUG*, *trnI-CAU*, *trnL-CAA*, *trnV-GAC*, *trnI-GAU*, *trnA-UGC*, *trnR-ACG*, and *trnN-GUU*), and 4 rRNA genes species (*rnn16*, *rnn23*, *rnn4.5*, and *rnn5*). The complete chloroplast genome of *E. buergerianum* has submitted to the GenBank that NCBI accession No.MH9677841.

CONTACT Guo Chengwei  guocw12009@163.com  Affiliated Hospital, Shandong University of TCM, Jinan Shandong 250011, PR China

*These authors equally contributed to this work.

© 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.

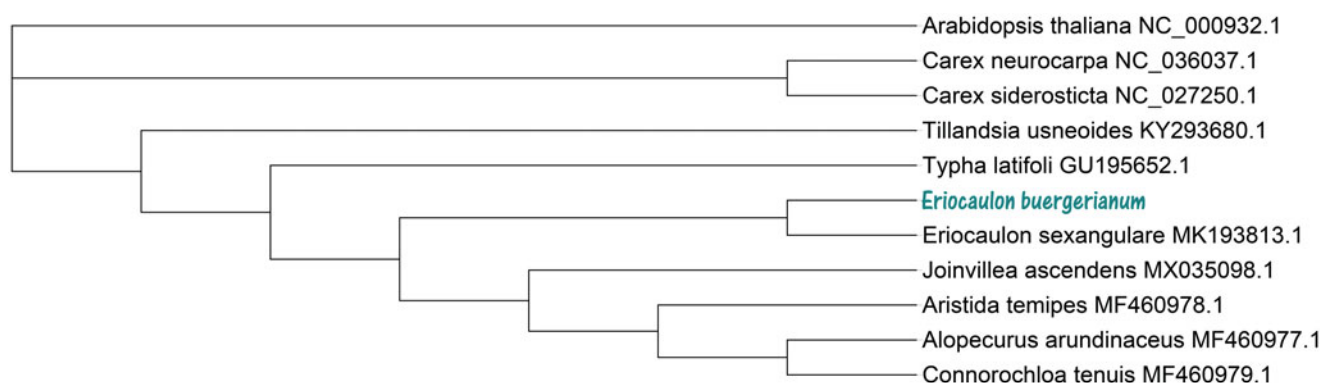


Figure 1. Phylogenetic relationships of 11 species chloroplast genome sequences based on the neighbour-joining (NJ) method analysis using 2000 bootstrap replicates. Bootstrap support is indicated for each branch.

To further investigate *E. buergerianum* evolutionary and phylogenetic position, the neighbour-joining (NJ) tree was constructed based on the chloroplast genome sequences of 10 other species using MEGA X (Kumar et al. 2018). NJ tree analysis used NJ method and performed using 2000 bootstrap values replicate at each node. All of the nodes were inferred with strong support by the NJ methods. The final NJ evolutionary tree was edited using the iTOL version 4.0 online web (<https://itol.embl.de/>) (Letunic and Bork 2016). The evolutionary tree analysis result showed that *E. buergerianum* was closely related to *Eriocaulon sexangulare* (MK193813.1) in the family Eriocaulaceae (Figure 1). In a word, the complete chloroplast genome of *E. buergerianum* is very important for Chinese medicinal herb research value and clinical drug development for further.

Disclosure statement

The authors have declared that no competing interests exist.

References

- Andrews S. 2015. FastQC: a quality control tool for high throughput sequence data. <http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>.
- Greiner S, Lehwark P, Bock R. 2019. OrganellarGenomeDRAW (OGDRAW) version 1.3.1: expanded toolkit for the graphical visualization of organellar genomes. Nucleic Acids Res. 47:W59–W64.
- Ho JC, Chen CM. 2002. Flavonoids from the aquatic plant *Eriocaulon buergerianum*. Phytochemistry. 61:405–408.
- Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol. 35:1547–1549.
- Letunic I, Bork P. 2016. Interactive tree of life (iTOL) v4: an online tool for the display and annotation of phylogenetic and other trees. Nucleic Acids Res. 44:W242–W245.
- Meng GL, Li YY, Yang CT, Liu SL. 2019. MitoZ: a toolkit for animal mitochondrial genome assembly, annotation and visualization. Nucleic Acids Res. 47:e63.
- Santos LCD, Rodrigues CM, Silva MA, Coelho RG, Sannomiya M, Vilegas W. 2005. Chemical profile of *Eriocaulon ligulatum* (Vell.) L.B. Smith (Eriocaulaceae). Biochem Syst Ecol. 33:1159–1166.