



Mitochondrial DNA Part B Resources

ISSN: (Print) 2380-2359 (Online) Journal homepage: <https://www.tandfonline.com/loi/tmdn20>

Complete plastid genome sequence of *Erigeron breviscapus* (Asteraceae), an endemic traditional Chinese herbal medicine

Jing Meng, Linna Zhang, Zhiyuan Dong & Jun He

To cite this article: Jing Meng, Linna Zhang, Zhiyuan Dong & Jun He (2019) Complete plastid genome sequence of *Erigeron breviscapus* (Asteraceae), an endemic traditional Chinese herbal medicine, *Mitochondrial DNA Part B*, 4:2, 4077-4078, DOI: [10.1080/23802359.2019.1605854](https://doi.org/10.1080/23802359.2019.1605854)

To link to this article: <https://doi.org/10.1080/23802359.2019.1605854>



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



Published online: 18 Nov 2019.



Submit your article to this journal [↗](#)



Article views: 181



View related articles [↗](#)



View Crossmark data [↗](#)

Complete plastid genome sequence of *Erigeron breviscapus* (Asteraceae), an endemic traditional Chinese herbal medicine

Jing Meng^a, Linna Zhang^a, Zhiyuan Dong^b and Jun He^c

^aCollege of Horticulture and Landscape, Yunnan Agricultural University, Kunming, China; ^bInstitute of Medicinal Plant, Yunnan Academy of Agricultural Sciences, Kunming, China; ^cKunming Institute of Botany, Chinese Academy of Sciences, Kunming, China

ABSTRACT

Erigeron breviscapus is an important traditional Chinese herb endemic to China for cardiovascular and cerebral vessel diseases. Here, the complete plastid genome of *E. breviscapus* was sequenced using Illumina sequencing technology. The complete chloroplast genome size is 152,183 bp, including a large single-copy region of 84,705 bp, a small single-copy region of 18,112 bp and a pair of inverted repeat regions of 24,683 bp. The total GC content is 37.2%. The genome contains 113 genes, including 80 protein-coding genes, 29 tRNA genes, and four rRNA genes. Phylogenetic analysis showed that *E. breviscapus*, *Aster altaicus*, and *Eschenbachia blinii* formed a clade with 100% bootstrap support.

ARTICLE HISTORY

Received 18 March 2019
Accepted 6 April 2019

KEYWORDS





Erigeron breviscapus; plastid genome; traditional Chinese herb; endemic species

Erigeron breviscapus (Vaniot) Hand.-Mazz., also called ‘Duan Ting Fei Peng’ or ‘Deng Zhan Xi Xin’ in Chinese, is a perennial herb endemic to China, distributed in Yunnan, Sichuan, Guangxi, Guizhou, Xizang and Hunan provinces (Wu et al. 2011). *Erigeron breviscapus* is an important traditional Chinese herb, which has been listed in the updated version Chinese Pharmacopeia (China Pharmacopeia Committee 2015), and widely used for the treatment of stroke hemiplegia, retinal vein occlusion, promoting cerebral circulation, and reducing platelet destruction (Chen et al. 2018; Li et al. 1998). Scutellarin, the main chemical active component of *E. breviscapus*, is the natural specific drug for treatment of obdurate cerebrovascular disease and sequela of cerebral hemorrhage (Li et al. 2017). Unfortunately, due to overexploitation of wild resources, the wild populations of *E. breviscapus* have been severely destroyed (Yu and Chen 2002). To date, there is no report about the complete plastid genome of genus *Erigeron* including this important traditional Chinese medicine plant, *E. breviscapus*.

For the first time, we sequenced and characterized the complete plastid genome of *E. breviscapus*. The material was obtained from Gejiu’s Lianhua Mountain of Yunnan province (103°13′00.92″E, 23°20′06.14″N), and voucher specimen was deposited in the herbarium of KUN. Total genomic DNA was extracted using a modified CTAB method (Doyle and Doyle 1987). A paired-end library was constructed, and paired reads were then sequenced on Illumina Miseq platform (Illumina, San Diego, CA, USA). We assembled the reads through CLC Genomic Workbench v10 (CLC Bio., Aarhus, Denmark). All the contigs were checked against the reference genome of

Eschenbachia blinii (KX 085421) using BLAST (<https://blast.ncbi.nlm.nih.gov/>). The web program DOGMA (<http://dogma.cccb.utexas.edu/>) (Wyman et al. 2004) and Geneious v8.0.2 (Kearse et al. 2012) were utilized to annotate and construct a complete sequence, respectively. To determine the phylogenetic position of *E. breviscapus*, the whole chloroplast genome sequences of 13 species from Asteraceae were aligned by MAFFT v7 (Katoh et al. 2017), then a maximum likelihood (ML) phylogenetic tree was constructed using MEGA v 7.0 (Kumar et al. 2016).

The plastid genome of *E. breviscapus* is a circular DNA with 152,183 bp in length, and the genome sequence has been deposited in GenBank under accession number MK414770. Total genome contains a pair of inverted repeat (IRs) regions of 24,683 bp each separated by a large single-copy (LSC) region of 84,705 bp and a small single-copy (SSC) region of 18,112 bp. The overall GC content of *E. breviscapus* plastid genome is 37.2%, and GC content (43.1%) in IRs regions is higher than those of LSC and SSC regions (35.0% and 31.0%, respectively). The complete chloroplast genome contains 113 genes, including 80 protein-coding (PCGs) genes, 29 transfer RNA (tRNA) genes, and four ribosomal RNA (rRNA) genes. Among them, 18 intron-containing genes were investigated: three of which (*ycf3*, *clpP*, and *rps12*) contained two introns, other 15 genes had one intron. Eight PCG genes, seven tRNA genes, and all four rRNA genes are duplicated in IR regions. The phylogenetic analysis indicated that *E. breviscapus* formed a monophyletic group with *Aster altaicus* and *Eschenbachia blinii*, with bootstrap support values of 100% (Figure 1).

CONTACT Zhiyuan Dong  yndongzhiyuan@126.com  Institute of Medicinal Plant, Yunnan Academy of Agricultural Sciences, Kunming, Yunnan 650204, China; Jun He  hejuna@mail.kib.ac.cn  Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650204, 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.

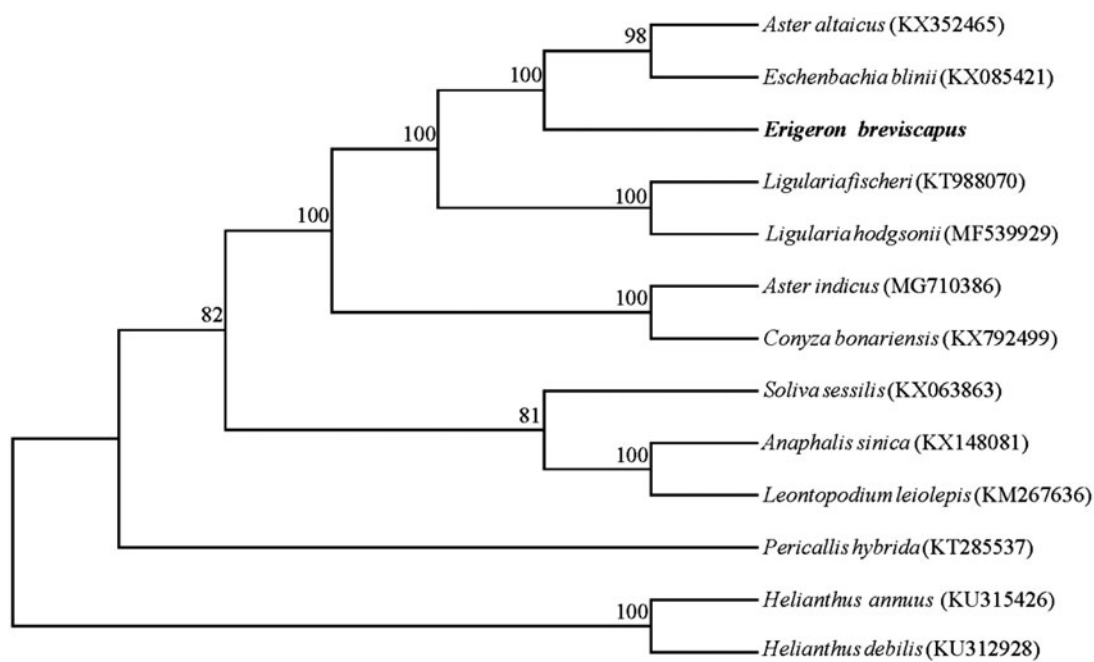


Figure 1. Maximum likelihood (ML) phylogenetic tree based on 13 complete plastid genome sequences. Bootstrap support values are shown on each node based on 1000 replicates.

Acknowledgements

We appreciate the Laboratory of Molecular Biology in the Germplasm Bank of Wild Species in Southwest China, Kunming Institute of Botany, Chinese Academy of Sciences for providing experimental platform.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was supported by the National Natural Science Foundation of China [No. 31660422].

References

- Chen SY, Li M, Li YT, Hu HJ, Li Y, Huang Y, Zheng L, Lu Y, Hu J, Lan YY. 2018. A UPLC-ESI-MS/MS method for simultaneous quantitation of chlorogenic acid, scutellarin, and scutellarein in rat plasma: application to a comparative pharmacokinetic study in sham-operated and MCAO rats after oral administration of *Erigeron breviscapus* extract. *Molecules*. 23:1808.
- China Pharmacopoeia Committee. 2015. Pharmacopoeia of the people's republic of China (the first division). Beijing: Chinese Medical Science and Technology Press.
- Doyle JJ, Doyle JL. 1987. A rapid DNA isolation procedure for small amounts of fresh leaf tissue. *Phytochem Bull*. 19:11–15.
- Katoh K, Rozewicki J, Yamada KD. 2017. MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. *Brief Bioinform*.
- 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.
- Kumar S, Stecher G, Tamura K. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol Biol Evol*. 33:1870.
- Li JG, Wang LQ, Yang XY, Chen Z, Lai LYW, Xu H, Liu JP. 2017. Chinese herbal medicine Dengzhan Xixin injection for acute ischemic stroke: a systematic review and meta-analysis of randomised controlled trials. *Complement Ther Med*. 34:74–85.
- Li NG, Liang FZ, Zhang JR, Xu SX, Mao XC, Wang Y, Li XH. 1998. Effect of *Erigeron breviscapus* hand on hemorheology and microcirculation of acute cerebral infarction. *Chin J Hemor*. 8:42–44.
- Wu ZY, Raven P, Hong DY. 2011. Flora of China volume 20–21. St. Louis: Beijing Science Press and Missouri Botanical Garden Press.
- Wyman SK, Jansen RK, Boore JL. 2004. Automatic annotation of organellar genomes with DOGMA. *Bioinformatics*. 20:3252–3255.
- Yu HY, Chen ZL. 2002. Studies on artificial culture of *Erigeron breviscapus*. *Acta Botanica Yunnanica*. 24:115–120.