

The complete chloroplast genome sequence of *Jacobaea cannabifolia*

Xiaoyue Su^{a,b}, Huiyan Cao^a, Lianqing He^a, Jiajun He^a, Chen Qin^a, Panpan Wang^a, Lingyang Kong^a, Yu Wang^b, Weichao Ren^a and Wei Ma^a

^aSchool of Pharmacy, Heilongjiang University of Chinese Medicine, Harbin, China; ^bFirst Affiliated Hospital, Heilongjiang University of Chinese Medicine, Harbin, China

ABSTRACT

Jacobaea cannabifolia is a widely used medicinal plant. The total length of the chloroplast genome was 151,390 bp, and it comprised a large single-copy (LSC, 83,432 bp) region, a small single-copy (SSC, 18,304 bp) region, and a pair of inverted repeats (IRs, 49,654 bp). A total of 130 coding genes were annotated, including 88 protein-coding genes, 8 rRNA genes, and 34 tRNA genes. A phylogenetic tree was showed that *J. cannabifolia* and other species of the same genus clustered together.

ARTICLE HISTORY

Received 6 October 2023
Accepted 10 January 2024

KEYWORDS

Jacobaea cannabifolia;
medicinal plant; chloroplast
genome; phylogenetic
analyses

Introduction

Jacobaea cannabifolia (Less.) E.Wiebe. commonly known as Fanhuncao, is a perennial herb of the *Jacobaea* genus in the Asteraceae family and is widely distributed in China, Japan, the Korean Peninsula, and the Russian Far East. The water extract of this plant is used to prepare Feining granules, which contain flavonoids, phenolic acids, and alkaloids and are clinically used in the treatment of cough, asthma, and acute and chronic inflammation of the lungs (Yan et al. 2009; Tao et al. 2012). This genus also contains hepatotoxic pyrrolizidine alkaloids (Hongyan et al. 2011; Yang et al. 2011). Previous studies have confirmed that there are differences in the types and contents of alkaloids in *Jacobaea* plants (Zhou et al. 2010). Therefore, different plants as pharmaceutical raw materials affect the efficacy and safety of drugs. In recent years, the chloroplast genome of *Jacobaea* species has been sequenced (Doorduyn et al. 2011; Zhang and Gong 2023), but sequencing of the chloroplast genome of *J. cannabifolia* has not yet been reported. Therefore, decoding the chloroplast genome of *J. cannabifolia* and phylogenetic analysis of related species will help determine the phylogenetic relationship of *J. cannabifolia* in Asteraceae and provide a guarantee for drug safety.

Materials and methods

We collected 50 g young and healthy leaves of *J. cannabifolia* in the Botanical Garden of Heilongjiang University of Chinese Medicine, Harbin, Heilongjiang province, China (45°73'08"N, 126°65'65"E) (Figure 1). The plant samples and DNA are


stored in the Department of Pharmacy, the First Affiliated Hospital of Heilongjiang University of Chinese Medicine under voucher number FHC20230701001 (<http://www.hljzy.org.cn/index.html>; contact: Su Xiaoyue; suxiaoyue1216@163.com). Total genomic DNA was extracted from the leaf tissue using a Plant Genomic DNA Kit following the manufacturer's instructions (TIANGEN, China). The isolated genomic DNA was used to construct a paired-end library (PE) with a mean insert size of 500 bp using the NEB DNA Library Rapid Prep Kit (Ipswich, MA, USA), followed by sequencing on an Illumina HiSeq 3000 platform. The de novo assembly of the *J. cannabifolia* chloroplast genome was performed using GetOrganelle v1.7.5 (Jin et al. 2020), of which the detailed information for assembling is shown in Figure S1, and CPGAVAS2 (Shi et al. 2019) was used for the chloroplast genome annotation. Finally, the genome map was drawn using CPGView (Liu et al. 2023). The genome was deposited in the National Genomics Data Center (accession no. C_AA051578.1).

To identify the phylogenetic position of *J. cannabifolia*, a maximum likelihood phylogenetic tree was constructed based on 16 complete chloroplast genomes of Senecioneae species. All sequences were obtained from NCBI GenBank. All complete chloroplast genome nucleotide sequences were aligned in PhyloSuite v1.2.2 (Zhang et al. 2019), and used to perform ML inference in IQ-TREE v1.6.12 (Lanfear et al. 2020).

Results

The total length of *J. cannabifolia* chloroplast genome was 151,390 bp. The chloroplast genome had a circular tetrad

CONTACT Wei Ma  mawei@hljucm.edu.cn; Weichao Ren  lzyrenweichao@126.com  School of Pharmacy, Heilongjiang University of Chinese Medicine, Harbin, China

 Supplemental data for this article can be accessed online at <https://doi.org/10.1080/23802359.2024.2305714>.

© 2024 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-NonCommercial License (<http://creativecommons.org/licenses/by-nc/4.0/>), which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited. The terms on which this article has been published allow the posting of the Accepted Manuscript in a repository by the author(s) or with their consent.

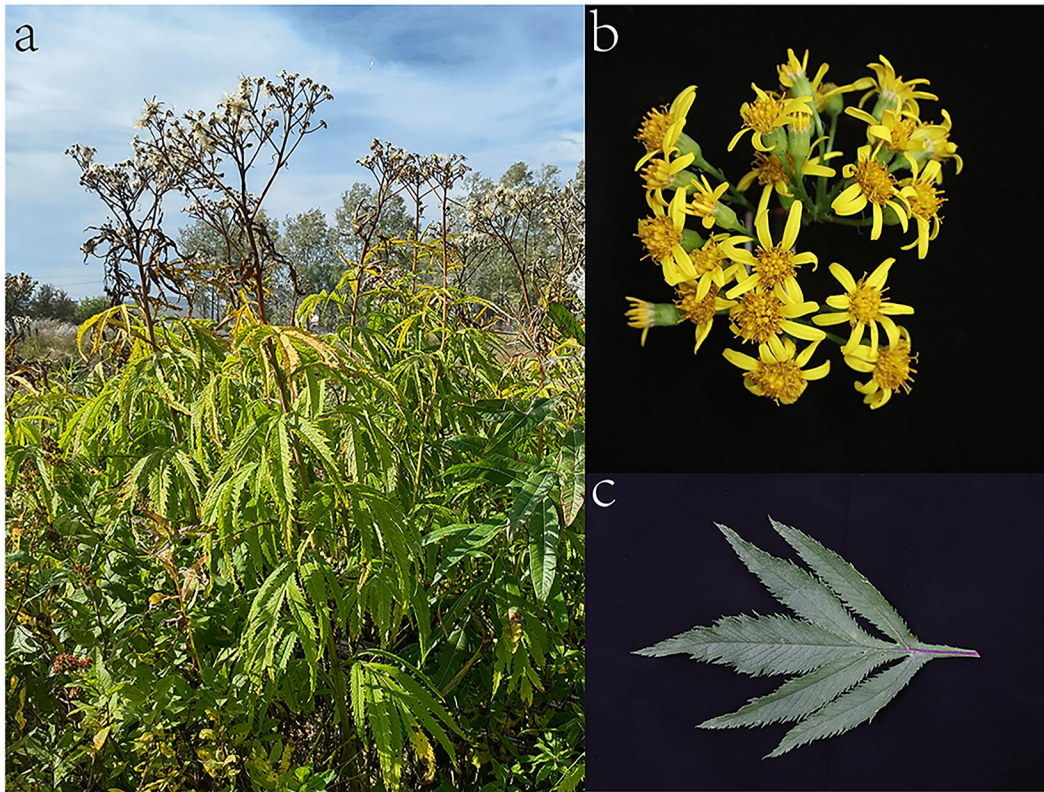


Figure 1. Image of *Jacobaea cannabifolia* (photoed by Xiaoyue Su). (a) Plant of *J. cannabifolia*. (b) Flowers. (c) Leaf structure consisting of a large single-copy region of 83,432 bp, a small single-copy region of 18,304 bp, and two

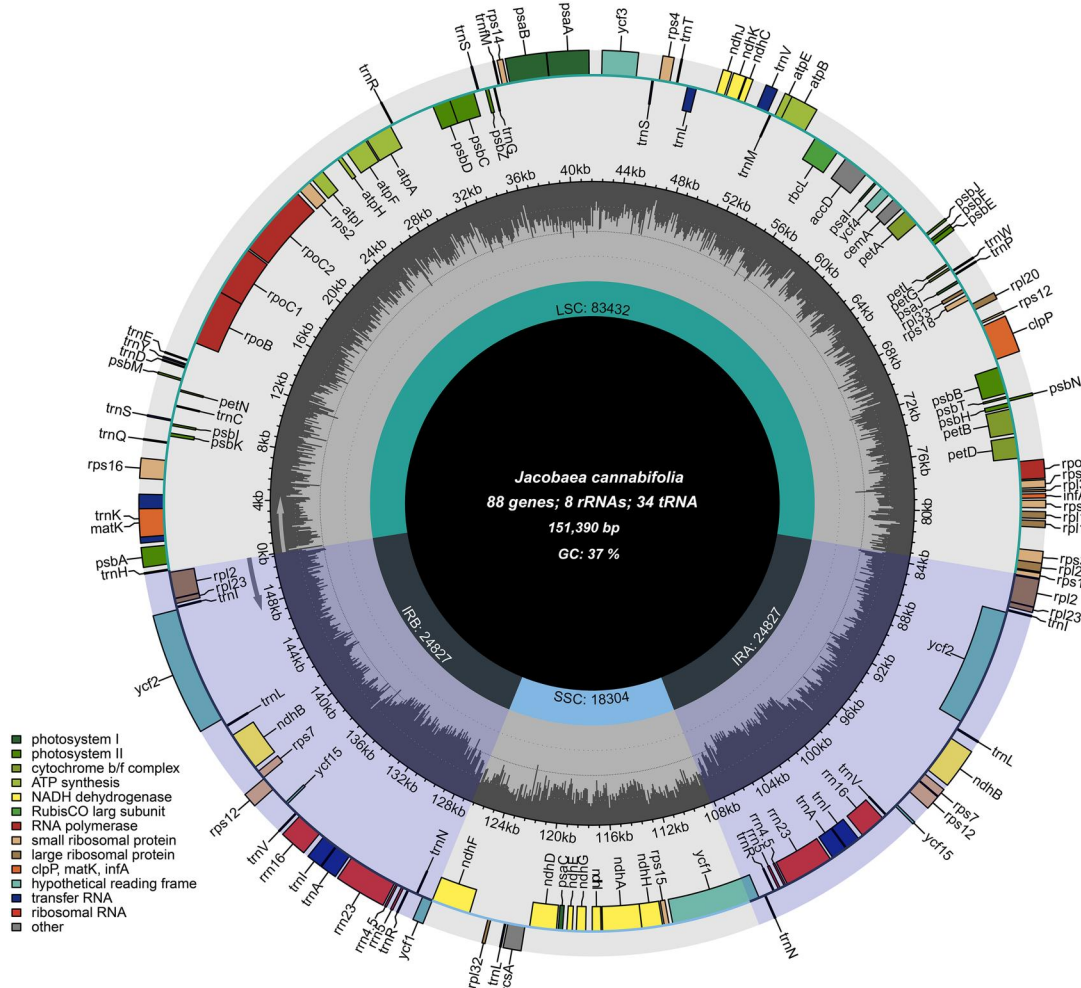


Figure 2. The *J. cannabifolia* chloroplast genome map. The map contains the core area and two tracks. The basic information of the cp genome is shown in the core area. The GC content along the genome is plotted on the inner track. The functional genes are shown on the outer circle, and different functional categories are identified by different colors.

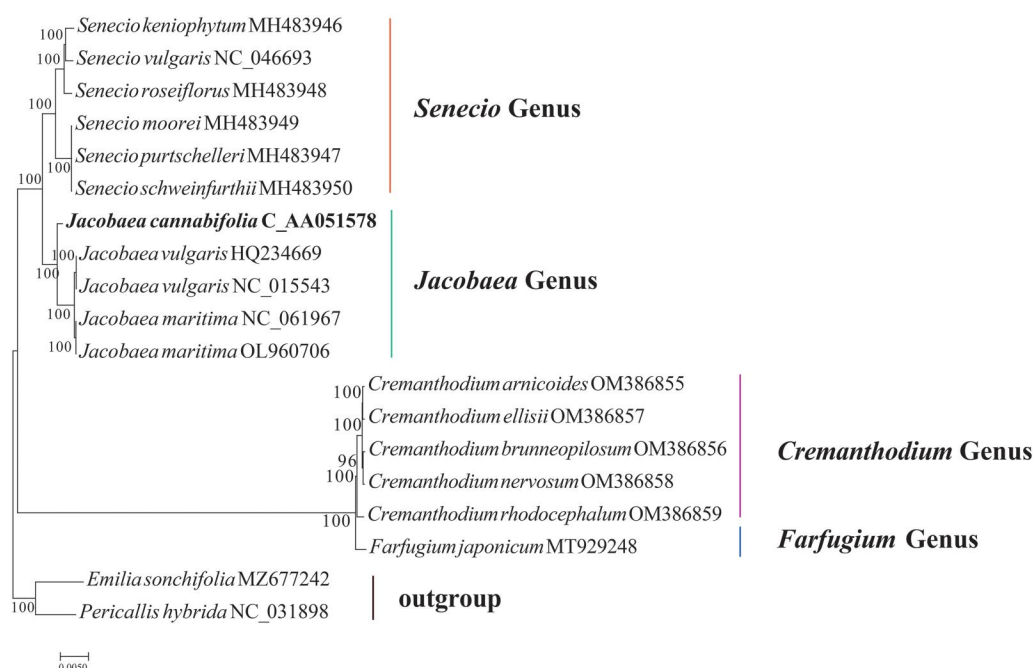


Figure 3. Maximum likelihood phylogenetic tree of *J. cannabifolia* and other 16 close plant species constructed using their complete chloroplast genome sequences. The bootstrap support value for each node is shown on the branch. The accession number of the chloroplast genome of each plant species is shown. The following sequences were used: *S. vulgaris* NC_046693 (Mei et al. 2021), *S. keniophytum* MH483946 (Gichira et al. 2019), *S. purtschelleri* MH483947 (Gichira et al. 2019), *S. roseiflorus* MH483948 (Gichira et al. 2019), *S. moorei* MH483949 (Gichira et al. 2019), *S. schweinfurthii* MH483950 (Gichira et al. 2019), *P. hybrida* NC_031898 (Wang et al. 2018), *E. sonchifolia* MZ677242 (Siu et al. 2023), *F. japonicum* MT929248 (Gu et al. 2021), *C. rhocephalum* OM386859 (Zhong et al. 2023), *C. nervosum* OM386858 (Zhong et al. 2023), *C. brunneopilosum* OM386856 (Zhong et al. 2023), *C. ellisii* OM386857 (Zhong et al. 2023), *C. arnicoides* OM386855 (Zhong et al. 2023), *J. vulgaris* HQ234669 (Doorduyn et al. 2011), *J. maritima* OL960706 (Zhang and Gong 2023), *J. vulgaris* NC_015543 (Doorduyn et al. 2011), *J. maritima* NC_061967 (Zhang and Gong 2023).

repeat regions of 49,654 bp (Figure 2). The GC content of the whole genome was 37.3%, and the GC content of the SSC, LSC, and IR regions were 30.5%, 35.4%, and 43%, respectively. The chloroplast genome encoded 130 genes, including 88 protein-coding, eight rRNAs, and 34 tRNA genes. Twenty genes contained introns, and *ycf3* and *clpP* contained two introns. Twelve cis-splicing genes and the trans-splicing gene *rps12* were identified, and their structures are shown in Figure S2 and Figure S3.

To further understand the relationship between *J. cannabifolia* and other species of the Asteraceae family, we constructed a phylogenetic tree that included 16 closely species. The results showed that *J. cannabifolia* clustered with other *Jacobaea* species and could be distinguished from related genera. Further investigation of *J. cannabifolia* at the inter- and intraspecies levels would further our understanding of the relationship between *Jacobaea* species.

Discussion and conclusion

We sequenced the chloroplast genome of *J. cannabifolia* for the first time. *J. cannabifolia* had a conserved tetrad structure with a total length of 151,390 bp, encoding 129 genes. Genome length and gene number were similar to those of other species of the same genus that have undergone chloroplast genome sequencing. The phylogenetic tree results supported that *J. cannabifolia* was more closely related to other species of *Jacobaea* genus and also proved that *Jacobaea* can be well distinguished from other genera.

Our phylogenetic findings generally concurred with the earlier research (Zhang and Gong 2023). Our results provide an essential genetic resource for taxonomic and related studies of *Jacobaea*. In the future, we will sequence the chloroplast genome of other species and investigate their evolutionary patterns, which will help in medicinal development.

Ethical approval

The authors declare that there were no ethical or legal violations when obtaining the study materials and performing the research. The species used in this study is not listed on the IUCN Red List, and the sample was legally collected in accordance with guidelines stipulated in national and international regulations. The materials were collected in a location not designated as a protected area in China.

Author contributions

Xiaoyue Su, Huiyan Cao, and Lianqing He contributed to the data analysis, interpretation, and drafting of this paper. Lingyang Kong, Chen Qin, and Yu Wang contributed to the sampling, laboratory tasks, and writing of an early version of the manuscript. Xiaoyue Su, Jiajun He, and Panpan Wang assembled and analyzed the genomic data and contributed to the writing of a draft of the manuscript. Weichao Ren and Wei Ma contributed to concept, design the project. All authors agreed on the contents of the manuscript and all 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 Heilongjiang Province traditional Chinese medicine classics popularization special topic under Grant Number [ZYW2023-093]; National Key Research and development Project, research and demonstration of collection, screening and breeding technology of ginseng and other genuine medicinal materials under Grant Number [2021YFD1600901]; Talent training project supported by the central government for the reform and development of local colleges and Universities under Grant Number [ZYRCB2021008]; and Heilongjiang Touyan Innovation Team Program under Grant Number [HLJTYTP2019001].

Data availability statement

The chloroplast genome sequence can be accessed *via* accession number C_AA051578.1 in National Genomics Data Center at <https://ngdc.cncb.ac.cn/?lang=en>. The associated BioProject, GSA, and Bio-Sample numbers are PRJCA019362, CRA012398, and SAMC3031040, respectively.

References

- Doorduyn L, Gravendeel B, Lammers Y, Ariyurek Y, Chin-A-Woeng T, Vrieling K. 2011. The complete chloroplast genome of 17 individuals of pest species *Jacobaea vulgaris*: SNPs, microsatellites and barcoding markers for population and phylogenetic studies. *DNA Res.* 18(2):93–105. doi:10.1093/dnares/dsr002.
- Gichira AW, Avoga S, Li Z, Hu G, Wang Q, Chen J. 2019. Comparative genomics of 11 complete chloroplast genomes of Senecioneae (Asteraceae) species: DNA barcodes and phylogenetics. *Bot Stud.* 60(1):17. doi:10.1186/s40529-019-0265-y.
- Gu Y, Ma Q, Lu Y. 2021. Characterization of the complete chloroplast genome of *Farfugium japonicum* (Asteraceae). *Mitochondrial DNA B Resour.* 6(2):678–679. doi:10.1080/23802359.2021.1881928.
- Hongyan M, Li Y, Changhong W, Zhengtao W. 2011. Pyrrolizidine alkaloids of *Senecio cannabifolius* var. *integrilifolius*. *Chin J Chin Mater Med.* 36(2):166–168.
- 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. doi:10.1186/s13059-020-02154-5.
- Lanfear R, von Haeseler A, Woodhams MD, Schrempf D, Chernomor O, Schmidt HA, Minh BQ, Emma T. 2020. IQ-TREE 2: new models and efficient methods for phylogenetic inference in the genomic era. *Mol Biol Evol.* 37(5):1530–1534. doi:10.1093/molbev/msaa015.
- Liu S, Ni Y, Li J, Zhang X, Yang H, Chen H, Liu C. 2023. CPGView: a package for visualizing detailed chloroplast genome structures. *Mol Ecol Resour.* 23(3):694–704. doi:10.1111/1755-0998.13729.
- Mei L, Zhu Y, Fu W, Kang Y, Yin H, Chen H. 2022. The complete chloroplast genome sequence of *Gynura cusimbua* (D. Don) S. Moore. *Mitochondrial DNA B Resour.* 7(1):96–97. doi:10.1080/23802359.2021.1997104.
- Shi L, Chen H, Jiang M, Wang L, Wu X, Huang L, Liu C. 2019. CPGAVAS2, an integrated plastome sequence annotator and analyzer. *Nucleic Acids Res.* 47(W1):W65–W73. doi:10.1093/nar/gkz345.
- Siu T-Y, Kong BL-H, Wong K-H, Wu H-Y, But GW-C, Shaw P-C, Lau DT-W. 2023. Characterization and phylogenetic analysis of the complete chloroplast genome of *Emilia sonchifolia* (L.) DC. *Mitochondrial DNA B Resour.* 8(1):20–22. doi:10.1080/23802359.2022.2055980.
- Tao Y, Jiang W, Cheng Y-Y, Zhang Y-F. 2012. Two new compounds from *Senecio cannabifolius*. *J Asian Nat Prod Res.* 14(9):826–830. doi:10.1080/10286020.2012.697456.
- Wang B, Li M, Yuan Y. 2018. The complete chloroplast genome of *Pericallis hybrida* (Asteridae). *Mitochondrial DNA Part B.* 4(1):233–234. doi:10.1080/23802359.2018.1542999.
- Yan MH, Wang CH, Yang L, Mian Z, Tao WZ. 2009. Chemical constituents of *Senecio cannabifolius* var. *integrilifolius*: chemical constituents of *Senecio cannabifolius* var. *integrilifolius*. *Chin J Nat Med.* 7(1):28–30.
- Yang X, Yang L, Xiong A, Li D, Wang Z. 2011. Authentication of *Senecio scandens* and *S. vulgaris* based on the comprehensive secondary metabolic patterns gained by UPLC–DAD/ESI-MS. *J Pharm Biomed Anal.* 56(2):165–172. doi:10.1016/j.jpba.2011.05.004.
- Zhang D, Gao F, Jakovlić I, Zou H, Zhang J, Li WX, Wang GT. 2019. PhyloSuite: an integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. *Mol Ecol Resour.* 20(1):348–355. doi:10.1111/1755-0998.13096.
- Zhang K, Gong S. 2023. The complete chloroplast genome and phylogenetic analysis of *Jacobaea maritima* (Asteraceae). *Mitochondrial DNA B Resour.* 8(7):771–776. doi:10.1080/23802359.2023.2238937.
- Zhong W, Du X, Wang X, Cao L, Mu Z, Zhong G. 2023. Comparative analyses of five complete chloroplast genomes from the endemic genus *Cremanthodium* (Asteraceae) in Himalayan and adjacent areas. *Physiol Mol Biol Plants.* 29(3):409–420. doi:10.1007/s12298-023-01292-x.
- Zhou Y, Li N, Choi FF-K, Qiao C-F, Song J-Z, Li S-L, Liu X, Cai Z-W, Fu PP, Lin G, et al. 2010. A new approach for simultaneous screening and quantification of toxic pyrrolizidine alkaloids in some potential pyrrolizidine alkaloid-containing plants by using ultra performance liquid chromatography–tandem quadrupole mass spectrometry. *Anal Chim Acta.* 681(1–2):33–40. doi:10.1016/j.aca.2010.09.011.