




## The complete chloroplast genome sequence of *Spiraea japonica* var. *acuminata* Franch. (Rosaceae)

Qi Wang , Min-min Chen , Xia-fang Hu, Rui-hong Wang and Qiu-Ling He 

Zhejiang Province Key Laboratory of Plant Secondary Metabolism and Regulation, College of Life Sciences and Medicine, Zhejiang Sci-Tech University, Hangzhou, China

### ABSTRACT

*Spiraea japonica* var. *acuminata* Franch. (Rosaceae) is a Chinese herbal medicine distributed in southwest and east China. The first complete chloroplast genome of *Spiraea japonica* var. *acuminata* Franch. was assembled and reported in this study. The genome is 153,822 bp in length and contained 125 encoded genes in total, including 80 protein-coding genes, eight ribosomal RNA genes, and 37 transfer RNA genes. The phylogenomic analysis showed that *Spiraea japonica* var. *acuminata* Franch. was closely related to *Spiraea blumei*, *Spiraea trilobata*, *Spiraea mongolica* and *Spiraea insularis* according to the current sampling extent.

### ARTICLE HISTORY

Received 24 October 2021  
Accepted 4 January 2022

### KEYWORDS

*Spiraea japonica*; *Spiraea japonica* var. *acuminata* Franch.; chloroplast genome; phylogeny





*Spiraea japonica* L. f. (1782) is a perennial shrubby species with pink flowers occurring in clusters at the tips of branches. It is widely dissimilar in 14 intraspecific varieties. *Spiraea japonica* var. *acuminata* Franch. is one variant of *Spiraea japonica* L. f. which is a Chinese herbal medicine classified in the Rosaceae. It is mainly distributed in southwest and east China (He et al. 2001; Zhang et al. 2006). The extracts from these plants were found to be bioactive for treating cough, anti-inflammation, headache, and analgesia (Li et al. 2002). In this study, we assembled and reported the first complete chloroplast genome of *Spiraea japonica* var. *acuminata* Franch. The cumulative data will provide potential genetic resources for evolution of Rosaceae.

The leaves of *Spiraea japonica* var. *acuminata* Franch. were collected from Hangzhou, Zhejiang, China (GPS: E120°14'14.95", N30°23'58.95"). The specimen and extracted DNA was deposited at the College of Life Sciences and Medicine, Zhejiang Sci-Tech University (Zhejiang Province Key Laboratory of Plant Secondary Metabolism and Regulation, <http://sky.zstu.edu.cn/>, Qiu-Ling He and [qlhe@zstu.edu.cn](mailto:qlhe@zstu.edu.cn)) under the voucher number ZSTULSM0001. The total genomic DNA was extracted from its fresh leaves using the CTAB method in accordance with the manufacturer's instructions. The plastome sequences were generated using the Illumina HiSeq 2500 platform (Illumina Inc., San Diego, CA). In total, ca. 20.6 million high-quality clean reads (150 bp PE read length) were generated with adaptors trimmed. These clean data were *de novo* assembled to complete chloroplast genome using GetOrganelle (Jin et al. 2020). The assembled cp genome was annotated using Geneious v11.1.5 (Drummond

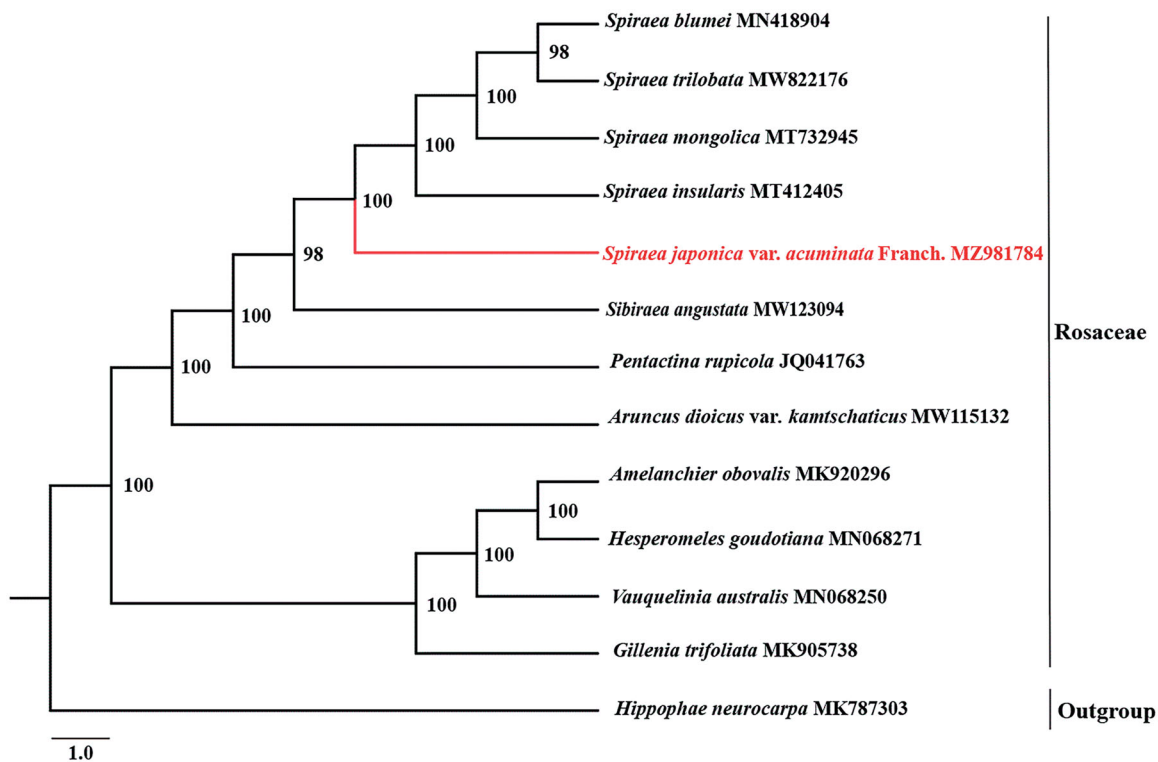
2012) with *Spiraea trilobata* plastome (GenBank: MW822176) as a reference.

The full length of *Spiraea japonica* var. *acuminata* Franch. chloroplast sequence (GenBank Accession No. MZ981784) is 153,822 bp, consisting of a large single copy region (LSC with 82,227 bp), a small single copy region (SSC with 18,907 bp), and two inverted repeat regions (IR with 26,344 bp). The overall GC content of *Spiraea japonica* var. *acuminata* Franch. chloroplast genome was 36.6% and the GC content of the LSC, SSC, and IR regions are 34.3%, 30.3%, and 42.5%. A total of 125 genes were contained in the genome (80 protein-coding genes, eight rRNA genes, and 37 tRNA genes). Sixteen genes had two copies, which were comprised of fine PCG genes (*ndhB*, *rps7*, *ycf2*, *rpl2*, *rpl23*), seven tRNA genes (*trnCAU*, *trnV-GAC*, *trnI-GAU*, *trnA-UGC*, *trnR-ACG*, *trnN-GUU*, *trnL-CAA*), and all four rRNA species (*rrn16*, *rrn23*, *rrn4.5*, *rrn5*). In the genome, nine protein-coding genes (*atpF*, *rpl2*, *ndhB*, *rps16*, *rpoC1*, *clpP*, *rpl16*, *petD*, *petB*) had one intron, *rps12* and *ycf3* gene contained two introns.

To confirm the phylogenetic position of *Spiraea japonica* var. *acuminata* Franch., we obtained 11 published complete chloroplast genomes of Rosaceae from NCBI. *Hippophae neurocarpa* was used as outgroup for constructing the phylogenetic tree. The 13 complete cp sequences were aligned using MAFFT v7.3 (Katoh and Standley 2013). The maximum-likelihood (ML) phylogenetic analyses were constructed using IQTREE v1.6.7 (Nguyen et al. 2015) with 5000 bootstraps under the TVM + F+R3 substitution model. The phylogenetic tree revealed that *Spiraea japonica* var. *acuminata* Franch. was closely related to *Spiraea blumei*, *Spiraea trilobata*, *Spiraea*

**CONTACT** Qiu-Ling He  [qlhe@zstu.edu.cn](mailto:qlhe@zstu.edu.cn)  Zhejiang Province Key Laboratory of Plant Secondary Metabolism and Regulation, College of Life Sciences and Medicine, Zhejiang Sci-Tech University, Hangzhou, China; Rui-hong Wang  [seemefly77@126.com](mailto:seemefly77@126.com)  Zhejiang Province Key Laboratory of Plant Secondary Metabolism and Regulation, College of Life Sciences and Medicine, Zhejiang Sci-Tech University, Hangzhou, China

© 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.** Phylogenetic relationship of *Spirea japonica* var. *acuminata* Franch. in Rosaceae using maximum likelihood (ML) method based on 12 species complete chloroplast genomes (accession numbers were listed behind each taxon. Statistical support values were showed on nodes).

*mongolica* and *Spirea insularis* according to the current sampling extent (Figure 1).

### Author contributions statement

Qi Wang and Min-min Chen: conception and design, analysis and interpretation of the data, the drafting of the paper. Xia-fang Hu: Data analysis. Rui-hong Wang: supervision. Qiu-ling He: review and editing, funding acquisition. All authors have agreed to be accountable for all aspects of the work..

### Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper..

### Funding

This work was supported by the Natural Science Foundation of Zhejiang Province under Grant [number LGN21H280004] and the scientific research Fund of Zhejiang Sci-Tech University under Grant [number 16042093-Y, 2019Q052].

### ORCID

Qi Wang  <http://orcid.org/0000-0002-5441-9320>  
 Min-min Chen  <http://orcid.org/0000-0002-4882-3933>  
 Qiu-Ling He  <http://orcid.org/0000-0002-9000-6726>

### Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI (<https://www.ncbi.nlm.nih.gov>) under the Accession no. MZ981784. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA759429, SRR15685682, and SAMN21168751, respectively.

### References

- Drummond A. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics*. 28:1647–1649.
- He HP, Shen YM, Zhang JX, Zuo GY, Hao XJ. 2001. New diterpene alkaloids from the roots of *Spirea japonica*. *J Nat Prod*. 64(3):379–380.
- 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.
- Li L, Shen YM, Yang XS, Zuo GY, Shen ZQ, Chen ZH, Hao XJ. 2002. Antiplatelet aggregation activity of diterpene alkaloids from *Spirea japonica*. *Eur J Pharmacol*. 449(1-2):23–28.
- Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Mol Biol Evol*. 32(1):268–274.
- Zhang Z, Fan L, Yang J, Hao X, Gu Z. 2006. Alkaloid polymorphism and ITS sequence variation in the *Spirea japonica* complex (Rosaceae) in China: traces of the biological effects of the Himalaya-Tibet Plateau uplift. *Am J Bot*. 93(5):762–769.