The complete chloroplast genome of the subtropical species *Camellia japonica* ‘Huaheling’

Kai Yang\(^a,b\)*, Menglong Fan\(^b\)*, Yingkun Sun\(^b\), Qinghua Liu\(^b\) and Handong Gao\(^a\)

\(^a\)College of Biology and the Environment, Nanjing Forestry University, Nanjing, PR China; \(^b\)College of Landscape Architecture and Forestry, Qingdao Agricultural University, Qingdao, PR China

**ABSTRACT**

*Camellia japonica* ‘Huaheling’ is a rare subtropical *Camellia* species in China with high ornamental and medicinal value. The complete chloroplast genome of *C. japonica* ‘Huaheling’ is a 157,001-bp circular DNA molecule containing a large single-copy region (LSC, 86,704 bp), a small single-copy region (SSC, 18,393 bp), and two inverted repeat sequences (IR). Of the 131 genes identified, 86 are protein-coding genes, 8 are rRNA genes, and 37 are tRNA genes. A total of 54 simple sequence repeats (SSRs) were identified in the chloroplast genome. The phylogenetic analysis showed that *C. japonica* ‘Huaheling’ is clustered with *C. japonica*. This work provides valuable information for future study of the evolution and genetic diversity of *C. japonica* ‘Huaheling’.

---

**CONTACT** Handong Gao fannmenglong88@163.com 
College of Biology and the Environment, Nanjing Forestry University, Nanjing, Jiangsu, PR China

*These authors contributed equally to this work.

© 2021 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.
trans-splicing. A total of 54 SSR markers were detected in the chloroplast genome of C. japonica ‘Huaheling’.

To explore the phylogenetic relationships of C. japonica ‘Huaheling’ in Camellia, the phylogeny of 5 species of C. japonica and 13 Camellia L. were studied; Polyspora axillaris and Pyrenaria khasiana were used as outgroups (Figure 1). We used iQ-tree version 1.6.12 (Nguyen et al. 2015) based on the best model (TVM + F + R3) and 1000 bootstrap replicates. Eighteen plants of Camellia L. were divided into two families and C. japonica ‘Huaheling’ and C. japonica were most closely related.

Disclosure statement
The authors declare no potential conflict of interest.

Funding
This work was supported by the Science & Technology for People’s Livelihood Program of Qingdao City (No. 17-3-3-47-nsh) and the High Talents Scientific Research Fund of Qingdao Agricultural University (No. 663-1113343).

ORCID
Menglong Fan http://orcid.org/0000-0002-8243-4093

Data availability statement
The data that support the findings of this study are available in GenBank (https://www.ncbi.nlm.nih.gov/; GenBank accession number MW602996). The associated BioProject and BioSample numbers are PRJNA679998 and SAMN16869207, respectively.

References
Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, et al. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol. 19(5):455–477.
Beier S, Thiel T, Münch T, Scholz U, Mascher M. 2017. MISA-web: a web server for microsatellite prediction. Bioinformatics. 33(16):2583–2585.
Doyle JJ, Doyle JL. 1987. A rapid DNA isolation procedure from small quantities of fresh leaf tissues. Phytochem Bull. 19:11–15.
Erdal S. 2012. Androsterone-induced molecular and physiological changes in maize seedlings in response to chilling stress. Plant Physiol Biochem. 57:1–7.
Gao JY, Parks CR. 2005. Collected species of Camellia – an illustrated outline. Hangzhou (China): Zhejiang Science and Technology Press.
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.
Ueno S, Yoshimaru H, Tomaru N, Yamamoto S. 1999. Development and characterization of microsatellite markers in Camellia japonica L. Mol Ecol. 8(2):335–336.
Wu ZH, Gui ST, Quan ZW, Pan L, Wang SZ, Ke WD, Liang DQ, Ding Y. 2014. A precise chloroplast genome of Nelumbo nucifera (Nelumbonaceae) evaluated with Sanger, Illumina MiSeq, and PacBio RS II sequencing platforms: insight into the plastid evolution of basal eudicots. BMC Plant Biol. 14:289.
Zhang JY, Ding JP, Ibrahim M, Jiao XC, Song XM, Bai P, Li JM. 2021. Effects of the interaction between vapor-pressure deficit and potassium on the photosynthesis system of tomato seedlings under low temperature. Sci Hortic. 283:110089.

Figure 1. A phylogenetic analysis of the chloroplast genomes of 20 Theoideae species was constructed using maximum likelihood and with Polyspora axillaris and Pyrenaria khasiana as outgroups.