Complete chloroplast genome of Cardamine hupingshanensis K.M.Liu, L.B.Chen, H.F.Bai & L.H.Liu (Brassicaceae) in Enshi, Hubei

Xiuqing Liu\(^a\) and Siying Zhang\(^b\)

\(^a\)Forestry College, Xinyang Agriculture and Forestry University, Xinyang, China; \(^b\)Tourism Management College, Xinyang Agriculture and Forestry University, Xinyang, China

**ABSTRACT**

Cardamine hupingshanensis K.M.Liu, L.B.Chen, H.F.Bai & L.H.Liu 2008, also called Cardamine enshiensis, belongs to the genus Cardamine, Brassicaceae. As a plant with selenium enrichment ability, it has high development value. Here, we analyzed the chloroplast genome of C. hupingshanensis. The complete chloroplast genome had a total size of 154,832 bp with a typical quadripartite structure, including a large single-copy region (LSC, 83,908 bp) and a small single-copy region (SSC, 17,938 bp), separated by a pair of inverted repeat regions (IRs, 26,493 bp). Genome annotation showed the chloroplast genome contained 113 unique genes, including 79 protein-coding genes, 30 tRNA genes, and four rRNA genes. A total of 143 SSRs were found in the chloroplast genome. Phylogenetic analysis showed that C. hupingshanensis was closer to the C. circaeoides and C. lyrata. This chloroplast genome resource will be useful for study of the phylogeny and evolution of Cardamine in the future.
6, 5, 5, 5, and 5 from mononucleotide to hexanucleotide, respectively. The simple sequence repeat analysis showed that 143 SSRs were identified in the chloroplast genome of *C. hupingshanensis*. Moreover, the genome size, GC content, gene number, and gene order were similar to other *Cardamine* chloroplast genomes.

In order to explore the phylogenetic relationship of *C. hupingshanensis*, the complete chloroplast genomes of 42 species from Brassicaceae and one species from Caricaceae were obtained from the GenBank database. We used the PhyloSuite v. 1.2.2 (Zhang et al. 2020) to extract 79 protein-coding genes from the chloroplast genome annotation files. Each protein-coding gene sequence was aligned by using MAFFT v. 7.4 (Katoh and Standley 2013), and then 79 aligned sequences were concatenated by using PhyloSuite v. 1.2.2 (Zhang et al. 2020). With the *Carica papaya* as the outgroup, the phylogenetic tree (Figure 1) was constructed by maximum-likelihood (ML) method with IQ-TREE v. 2.1.2 (Nguyen et al. 2015) under the optimal model of GTR + F + R4. The bootstrap value was 1000. The analysis result showed that *Cardamine* and *Nasturtium* were closer, and were monophyletic groups to each other. There were three main branches in the genus *Cardamine*. Clade A included *C. abchasica*, *C. quinquefolia*, *C. bipinnata*, *C. bulbifera*, *C. impatiens*, *C. macrophylla*, *C. hirsuta*, and *C. oligosperma*. Clade B included *C. circaeoides*, *C. hupingshanensis*, *C. lyrate*, *C. fallax*, *C. amariformis*, *C. parviflora*, *C. resedifolia*, *C. amara*, and *C. resedifolia*. Clade C included *C. kitaibelii*, *C. pentaphyllos*, and *C. heptaphylla*. In the genus *Cardamine*, *C. hupingshanensis* was closer to *C. circaeoides* and *C. lyrata*. This finding was similar to previous research results (Hu et al. 2015;...
Raman and Park 2021, 2022; Raman et al. 2021; Xu et al. 2022). Our results provide valuable data and shed light on the phylogenomic study of Cardamine and Brassicaceae.

Ethical approval
In this study, all experimental protocols relating to plant experiments were in accordance with the measures for the Wild Plant Protection Regulations of Henan Province (approved by the Henan Provincial Government in 2007) and Plant Protection Regulations of Hubei Province, China (approved by the Hubei Provincial Government in 2009). The Plant Herbarium of Xinyang Agriculture and Forestry University approved the collection and research of this material. All the research meets ethical guidelines and adheres to the legal requirements of the study country.

Author contributions
Zhang Siying conceptualized and designed research; Liu Xiqing analyzed data and wrote the manuscript. All authors read and approved the final manuscript.

Disclosure statement
No potential conflict of interest was reported by the author(s).

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Data availability statement
The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov under the accession no. ON322745. The associated ‘BioProject’, ‘BioSample’, and ‘SRA’ numbers are PRJNA830645, SAMN27735482, and SRR18884471, respectively.

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