

Complete plastome of *Houttuynia cordata* (Saururaceae), a medicinal and edible plant

Lei Jin^{a,b}, Jin Yang^{b,c}, Changkun Liu^b, Mengling He^{a,d} and Hanjing Yan^{a,d}

^aCollege of Traditional Chinese Medicine, Guangdong Pharmaceutical University, Guangzhou, Guangdong, China; ^bKey Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, Yunnan, China; ^cSchool of Life Science, Yunnan University, Kunming, Yunnan, China; ^dKey Laboratory of State Administration of Traditional Chinese Medicine for Production & Development of Cantonese Medicinal Materials, Guangzhou, Guangdong, China

ABSTRACT

The complete plastome of *Houttuynia cordata*, an important medicinal and edible plant, was identified and sequenced in this study. The circular plastome is 160,217 bp in length and consists of a pair of inverted repeats (IRs 26,854 bp each), which is separated by a large single-copy region (LSC, 88,189 bp) and a small single-copy region (SSC, 18,320 bp). It encodes 132 genes, of which 114 are unique genes (80 protein-coding genes, 30 tRNAs, and 4 rRNAs). The phylogenetic analysis strongly reveals the sister group between *H. cordata* and the clade including *Piper kadsura*, *Piper cenocladum*, *Saruma henryi*, and *Asarum sieboldii*.

ARTICLE HISTORY

Received 10 August 2019
Accepted 16 August 2019

KEYWORDS

Houttuynia cordata;
complete plastome;
phylogenetic analysis

Houttuynia cordata Thunb., a perennial herb belonging to the family Saururaceae, grows in moist and shady places (Shingnaisui et al. 2018). The species is a medicinal plant traditionally used in China, Japan, Korea, and India for the treatment of pneumonia, severe acute respiratory syndrome, muscular sprain, as well as stomach ulcer (Lou et al. 2019). Furthermore, the species is popularly consumed as a healthy vegetable in East Asia (Toda 2005). With the increase of demand and irregular collection, wild *H. cordata* resource has greatly damaged. It is necessary to establish a strategy to conserve for this medicinally and commercially important plant as soon as possible. However, the available genomic resource of *H. cordata* is limited. Here, we report the complete plastome of *H. cordata* using high throughput Illumina sequencing technology.

Samples of *H. cordata* were collected from Tengchong, Yunnan, China (25°25'35"N, 98°39'07"E). Voucher specimen (Y. Ji 2017131) was deposited in the Herbarium of Kunming Institute of Botany, Chinese Academy of Sciences (KUN). We used the modified CTAB method (Yang et al. 2014) to extract genomic DNA from silica gel dried leaf tissues at first. Subsequently, the purified DNA was shared by sonication so that fragments of 500 bp length was obtained for constructing a paired-end library. Then the paired-end sequencing was performed using Illumina HiSeq 2000 system at BGI (Wuhan, Hubei, China). Plastome of *Asarum sieboldii* (GenBank Accession No. MG551543) was used as reference sequence

and we assembled the plastome following the method described by Jin et al (2018). Finally, the annotation of the plastome was performed in Geneious 10.2.3 (Kearse et al. 2012). The plastome was manually checked for start and stop codons and intron/exon boundaries. The validated complete plastome of *H. cordata* was deposited in the NCBI GenBank database under the accession number MN263890.

The *H. cordata* plastome is 160,217 bp in length and consists of a pair of inverted repeats (IRs, 26,854 bp each), which is separated by a large single-copy region (LSC, 88,189 bp) and a small single-copy region (SSC, 18,320 bp). It encodes 132 genes, of which 114 are unique genes (80 protein-coding genes, 30 tRNAs, and 4 rRNAs). Among unique genes, 9 protein-coding genes (*atpF*, *ndhA*, *ndhB*, *petB*, *petD*, *rpl16*, *rpl2*, *rpoC1*, and *rps12*), and 6 tRNAs (*trnA*-UGC, *trnG*-UCC, *trnI*-GAU, *trnK*-UUU, *trnL*-UAA, and *trnV*-UAC) contain one intron, while three protein-coding genes (*ycf3*, *clpP* and *rps12*) have two introns.

To identify the phylogenetic position of *H. cordata*, a maximum-likelihood (ML) (Stamatakis 2014) tree was generated using species within the order Piperales. *Drimys granadensis* was used to root the tree. The phylogenetic analysis reveals the sister group between *H. cordata* and the clade including *Piper kadsura*, *Piper cenocladum*, *Saruma henryi*, *Asarum sieboldii* (Figure 1). Our findings will provide a foundation for further investigation of genetic inheritance and evolution of *H. cordata*.

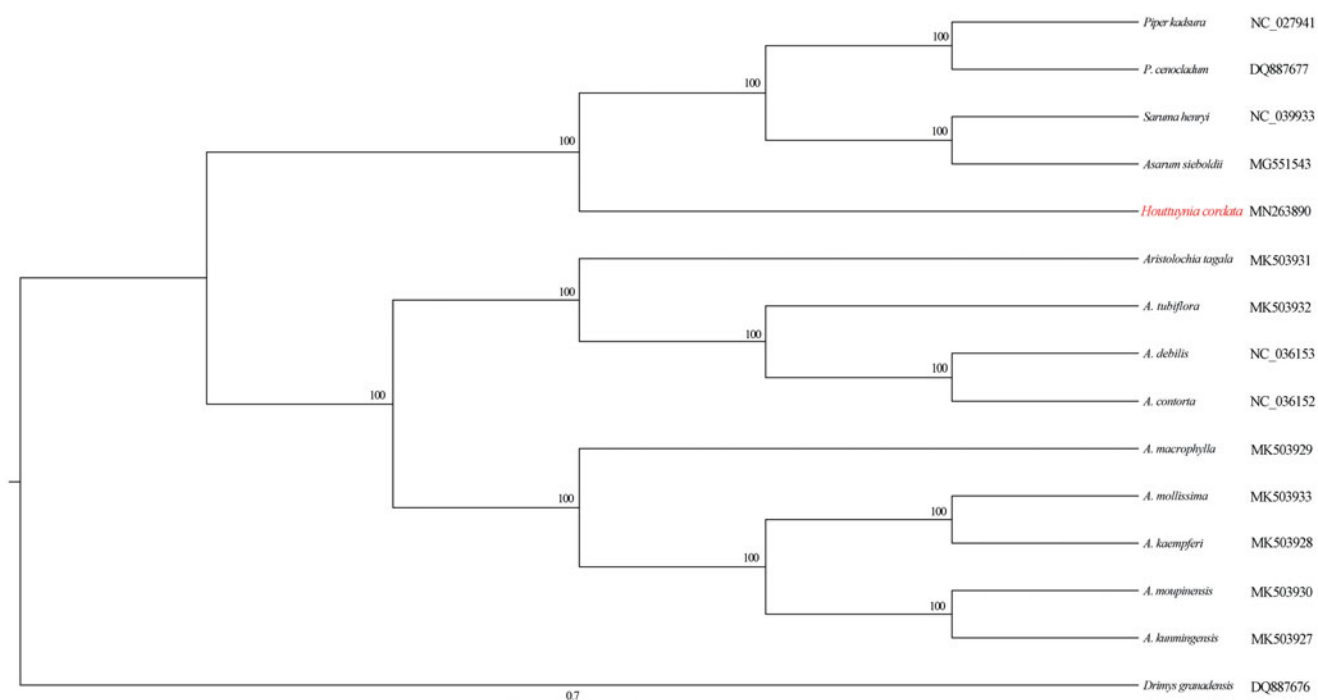


Figure 1. Phylogenetic relationships among Piperales species, based on complete plastomes.

Disclosure statement

The authors declare no potential conflict of interests.

Funding

This study was supported by Scientific and Technological Project of Guangdong Province [2017A020213023].

References

- Jin JJ, Yu WB, Yang JB, Song Y, Yi TS, Li DZ. 2018. GetOrganelle: a simple and fast pipeline for de novo assembly of a complete circular chloroplast genome using genome skimming data. bioRxiv. doi:10.1101/256479.
- 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: 1647–1649.
- Lou Y, Guo Z, Zhu Y, Kong M, Zhang R, Lu L, Wu F, Liu Z, Wu J. 2019. *Houttuynia cordata* thunb. and its bioactive compound 2-undecanone significantly suppress benzo(a)pyrene-induced lung tumorigenesis by activating the nrf2-ho-1/nqo-1 signaling pathway. *J Exp Clin Cancer Res*. 38:242.
- Shingnaisui K, Dey T, Manna P, Kalita J. 2018. Therapeutic potentials of *Houttuynia cordata* Thunb. against inflammation and oxidative stress: a review. *J Ethnopharmacol*. 220:35–43.
- Stamatakis A. 2014. Raxml version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics*. 30:1312–1313.
- Toda S. 2005. Antioxidative effects of polyphenols in leaves of *Houttuynia cordata* on protein fragmentation by copper-hydrogen peroxide in vitro. *J Med Food*. 8:266–268.
- Yang JB, Li DZ, Li HT. 2014. Highly effective sequencing whole chloroplast genomes of angiosperms by nine novel universal primer pairs. *Mol Ecol Notes*. 14:1024–1031.