Complete chloroplast genome sequences of the medicinal plant *Piper hancei*

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**ABSTRACT**

Chloroplast genome sequences have been used in phylogenetic and population genetics studies. Here, we assembled the chloroplast genome of *Piper hancei* Maxim. that is a traditional Chinese medicine. The genome length was 161,476 bp and included a pair of inverted repeats of 27,058 bp, a single-copy region of 89,144 bp and a small single-copy region of 18,216 bp. It contained 113 different genes, including 79 protein-coding genes, 30 transfer RNA (tRNA), and four ribosomal RNA genes. Moreover, we also identified 82 SSRs. The phylogenetic inference based on the whole chloroplast genome of 20 taxa showed *P. hancei* was sister to *P. kadsura*.

*Piper hancei* Maxim. is used as a traditional Chinese medicine within the family Piperaceae and is natively distributed in Fujian, Guangdong, Guangxi, Guizhou, Hunan, Yunnan, and Zhejiang provinces (Li and Hah). It is mainly used as a medicine to relieve pain, dispel wind and swelling, and treat rheumatic arthritis, weakness of the back and knees, and cough and asthma (Li and Hah). *Piper hancei* is also used as a gardening plant in tropical and subtropical regions of China. At present, there was less genetic information about this species, which brings difficulties to cultivation and utilization. In this study, we sequenced and analyzed the chloroplast genome of *P. hancei* based on the next-generation sequencing method (Dong, Sun, et al. 2021; Dong, Xu, et al. 2021; Wang et al. 2021). The objective of this study was to describe the chloroplast genome structure and feature for this species.

Fresh and young leaves of *P. hancei* were collected from Gannan Arboretum, Jiangxi, China (25°51’10”~114°22’25”), which was introduced from Guangdong. A specimen and DNA were deposited at the herbarium of Jiangxi Agricultural University under the voucher number of LM750014. Total genomic DNA was isolated using a mCTAB protocol (Li et al. 2013) for constructing a 350 bp insert library and sequencing on an Illumina Hiseq X ten platform. Raw data were qualified using Trimmomatic (Bolger et al. 2014) and the chloroplast genome was assembled with GetOrganelle (Jin et al. 2020) using clean data. The complete chloroplast genome was annotated with Planl using *P. auritum* (GenBank accession number: KY085906) as reference (Huang and Cronk 2015). The annotated chloroplast genome of *P. hancei* has been deposited into GenBank with the accession number of MZ046380.

The chloroplast genome of *P. hancei* was a circular DNA molecule of 161,476 bp and had a typical quadripartite structure with a pair of inverted repeats of 27,058 bp, a large single-copy region of 89,144 bp and a small single-copy region of 18,216 bp. The GC content was 38.3%, which was similar to other Piperaceae species (Cai et al. 2006). The *P. hancei* chloroplast genome encoded 113 different genes, including 79 protein-coding genes, 30 transfer RNA (tRNA), and 4 ribosomal RNA genes. Eighteen genes contain introns, 16 of which contain one intron and two (clpP and ycf3) with two introns.

Simple sequence repeats in the *P. hancei* chloroplast genomes were detected using GMAT (Wang and Wang 2016) with the minimum repeats of mono-, di-, tri-, tetra-, penta- and hexa-nucleotides being set to 10, 5, 4, 3, 3, and 3, respectively. A total of 82 perfect chloroplast genome SSRs were identified. The number of mono-, di-, tri-, tetra-, penta- and hexa-nucleotides were 49, 13, 8, 7, 4 and one, respectively.

To estimate the phylogenetic relationships of *P. hancei* with other *Piper* species. Phylogenetic analysis was performed using the whole chloroplast genome sequence from 20 Piperales species. Whole chloroplast genome sequences were aligned with MAFFT v7 (Katoh and Standley 2013) and ambiguous alignment regions were trimmed by trimAl v1.2 (Capella-Gutierrez et al. 2009). Maximum Likelihood (ML) tree was preformed using RAxML-NG (Kozlov et al. 2019). The GTR + G was chosen as the best-fit DNA substitution model according to the Akaike Information Criterion correction in ModelFinder (Kalyaanamoorthy et al. 2017). The reconstructed phylogeny revealed that *P. hancei* was sister to *P. kadsura* (Figure 1).

**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. MZ046380. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA725313, SRR14328341, and SAMN18875907, respectively.

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