The complete chloroplast genome of *Humulus lupulus* cv. ‘Fubei-1’ (Rosales: Cannabaceae)

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**ABSTRACT**

Hop (*Humulus lupulus*) is a perennial plant with commercial values. Here, we reported the complete chloroplast genome for a local hop cultivar (*Humulus lupulus* cv. ‘Fubei-1’) from Xinjiang, China. The chloroplast genome is 153,614 bp long with an A+T-biased base composition, and contains a total of 113 gene species, including 79 protein-coding, 30 tRNA, and four rRNA gene species. Nineteen gene species are duplicated, and 18 gene species harbor one or two introns. Phylogenetic analysis revealed close relatedness among the three hop cultivars (‘Saazer’, ‘Hallertauer’, and ‘Fubei-1’).

A total amount of 0.5 μg DNA was used for the DNA sequencing library preparation with TruSeq Nano DNA HT Sample Prep Kit (Illumina, San Diego, CA) following the manufacturer’s protocol. Briefly, genomic DNA sample was fragmented by sonication to a size of 350 bp. Then, DNA fragments were endpolished, A-tailed, and ligated with the full-length adapter for Illumina sequencing, followed by further PCR amplification. After that, the library was analyzed for size distribution with Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA) and quantified by real-time PCR. The clustering of the index-coded samples was performed on a cBot Cluster Generation System using HiSeq X PE Cluster Kit V2.5 (Illumina, San Diego, CA) according to the manufacturer’s instructions. After cluster generation, amplions were pooled in equal amounts, and paired-end 2–150 bp sequencing was performed using the Illumina HiSeq X Ten platform at Xuan Chen Biological Technology Co., Ltd. (Shaanxi, China).

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. PRJNA715949. The associated BioProject, SRA, and Biosample numbers are PRJN 715949, SUB9201162, and SAMN18388804, respectively.

After quality-trimming with CLC Genomics Workbench v10 (CLC Bio, Aarhus, Denmark), the raw sequencing reads were used to assemble the chloroplast genome with MITObim v1.9 (Hahn et al. 2013). The chloroplast genome of *Humulus yunnanensis* (MK423880) (Ling and Zhang 2019) was selected as the initial reference. Genome annotation was conducted in GENEIOUS R11.0.2 (Biomatters Ltd., Auckland, New Zealand) by aligning those of phylogenetically related species.
The chloroplast genome of *H. lupulus* cv. ‘Fubei-1’ was determined to be 153,614 bp long with a typical A + T-biased base composition (31.1% A, 18.8% C, 18.1% G, and 32.0% T). A set of 113 gene species were annotated, including 79 protein-coding, 30 tRNA genes, and four rRNA gene species. Gene duplication occurs in 19 of these gene species (*ndhB*, *rpl2*, *rpl23*, *rps7*, *rps12*, *ycf1*, *ycf2*, *trnA-UGC*, *trnI-CAU*, *trnI-GAU*, *trnL-CAA*, *trnN-GUU*, *trnR-ACG*, *trnV-GAC*, *rrn4.5*, *rrn5*, *rrn16*, and *rrn23*). In addition, 16 gene species (*atpF*, *ndhA*, *ndhB*, *petB*, *petD*, *rpl2*, *rpl16*, *rpoC1*, *rps12*, *rps16*, *trnA-UCC*, *trnG-UCU*, *trnL-GAU*, *trnK-UUU*, *trnL-UAA*, and *trnV-UAC*) harbored a single intron and two gene species (*clpP* and *ycf3*) harbored two introns.

To ascertain its relationship to those confamilial taxa, phylogenetic analysis was conducted based on the Bayesian analysis of chloroplast protein-coding genes for a panel of 17 taxa within the family Cannabaceae (Figure 1). Three taxa from the family Moraceae (i.e. *Broussonetia papyrifera*, *Ficus altissima*, and *Morus cathayana*) were included as outgroup taxa. DNA alignment was conducted in Geneious R11 (Biomatters, Co. Ltd., Auckland, New Zealand), and was then imported into TOPALi v2.5 (Milne et al. 2009) for the phylogenetic analysis with the implemented MrBayes v3.1.1 program (Ronquist and Huelsenbeck 2003) under the best-fit nucleotide substitution model ‘GTR + G + I’. As expected, the phylogenetic analysis indicates that the three hop cultivars (‘Saazer’, ‘Hallertauer’, and ‘Fubei-1’) are most closely related to one another than to the other congeneric or confamilial taxa.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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**Data availability statement**

The data that support the findings of this study are openly available in GenBank from NCBI at https://www.ncbi.nlm.nih.gov under the accession number MW387998.

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