Characterization of the complete chloroplast genome of *Forsythia suspensa* (Oleaceae), an herb to treat antituberculous drug of artificial bone combined with drug loading to China

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**ABSTRACT**

*Forsythia suspensa* is an important medicinal plant and native to China. In this article, the complete chloroplast genome of *F. suspensa* was studied and annotated. The chloroplast genome of *F. suspensa* is 156,404 bp in length, which has a large single-copy region (LSC) of 87,150 bp, a small single-copy region (SSC) of 17,812 bp, and two of inverted-repeat regions (IRs) of 25,716 bp. The overall nucleotide composition is: 30.8% (48,103 bp) of A, 31.4% (49,193 bp) of T, 19.2% (30,066 bp) of C and 18.6% (29,042 bp) of G, and the total content of the chloroplast genome A+T content of 62.2% and G+C content of 37.8%. The chloroplast genome of *F. suspensa* contains 133 genes, including 88 protein-coding genes (PCGs), 37 transfer RNA (tRNAs), and 8 ribosome RNA (rRNAs). The phylogenetic tree result shows that *F. suspensa* is closely related to *F. intermedia* in the phylogenetic relationship by the maximum-likelihood (ML) method.

*Forsythia suspensa* belongs to the Oleaceae family and native to China. From China, it (‘Yin-Qiao’ in Chinese) has been an important medicinal plant for many years, which is traditionally used for the treatment of inflammation, pyrexia, gonorrhea, diabetes, etc. (Ha et al. 2018). But, Zhejiang integrated hospital of traditional Chinese and Western medicine used three-dimensional printing technology to prepare multi-drug slow-release drug-loaded artificial bone, combined with *Forsynthia*, which has a significant effect on sacroiliac joint tuberculosis (Ma et al. 2018). In order to further study the phylogenetic relationship of *F. suspensa* with the medicinal plant, we studied and annotated the complete chloroplast genome of *F. suspensa*, which will be useful in the clinical drug development of the herb plant and its valuable medicinal research in future.

The *F. suspensa* samples were collected from the herb market near Zhejiang Chinese Medical University located at Hangzhou, Zhejiang, China (119.89E, 30.09 N). The chloroplast genome DNA of *F. suspensa* was extracted from the fresh samples using the Plant Tissues Genomic DNA Extraction Kit (Solarbio, BJ, and CN) and stored in the Zhejiang Chinese Medical University (No. ZJCMU-002). The chloroplast genome DNA was purified and sequenced. Quality control was performed to remove low-quality reads and adapters using the FastQC (Andrews 2015). The chloroplast genome was assembled and annotated using the MitoZ software (Meng et al. 2019). The physical map of the chloroplast genome of *F. suspensa* was drawn using OGDRAW (Lohse et al. 2013).

The complete chloroplast genome of *F. suspensa* (GenBank with accession No. MK7534872) was 156,040 base pairs in length and had a typical quadripartite structure with a large single-copy region (LSC) of 87,160 bp, a small single-copy region (SSC) of 17,812 bp, and a pair of inverted-repeat regions (IRs) of 25,716 bp. The chloroplast genome of *F. suspensa* contains 133 genes, which included 88 protein-coding genes (PCGs), 37 transfer RNA genes (tRNAs), and 8 ribosomal RNA genes (rRNAs). The phylogenetic tree result (Figure 1) showed that in the phylogenetic relationship by the maximum-likelihood (ML) method was used to analyse the phylogenetic relationship of 26 herb species plants with *F. suspensa*. The phylogenetic tree was reconstructed using the MEGA X (Kumar et al. 2018) with 2000 bootstrap values replicating at each node. All of the nodes were inferred with strong support by the ML methods. The phylogenetic tree was represented using the MEGA X and edited using the iTOL 4.0 (https://itol.embl.de/)(Letunic and Bork 2016). The phylogenetic tree result (Figure 1) showed that *F. suspensa* is closely related to *F. intermedia* (GenBank No. MG255756.1). This study can be used for the

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clinical drug development of the herb and its medicinal valuable research in future.

**Disclosure statement**

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