

The complete chloroplast genome of *Fuchsia standishii* J. Harrison, 1840 (Onagraceae) from Yunnan, China

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ABSTRACT

Fuchsia standishii J. Harrison, 1840, a perennial shrub, is renowned for its vividly colored and uniquely shaped blooms, which have an extended flowering season. Commonly cultivated as an ornamental potted plant, it is utilized in traditional Chinese medicine. In this study, we successfully sequenced and assembled the complete chloroplast genome of *F. standishii* using high-throughput Illumina sequencing technology. The assembled chloroplast genome displays a typical quadripartite structure, with a total length of 156,391 bp. It consists of a pair of inverted repeat regions (IRs), each measuring 25,069 bp, separated by a large single-copy region (LSC) of 87,754 bp and a small single-copy region (SSC) of 18,499 bp. The overall GC content of the genome is 37.60%. The genome includes a total of 129 genes, comprising 84 protein-coding genes, 37 tRNA genes, and eight rRNA genes. Phylogenetic analysis of 17 complete chloroplast genomes revealed that *F. standishii* forms a monophyletic group with the entire *Circaea*. This study provides a molecular foundation for future phylogenetic research on *Fuchsia*.

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Introduction


Fuchsia standishii J. Harrison, 1840 is a flowering plant species native to South America and New Zealand, belonging to the Onagraceae family (Garibaldi et al. 2012). *Fuchsia standishii* is the basionym of *Fuchsia hybrida*. Notably, it is the exclusive representative of the *Fuchsia* genus in China (Figure 1). Widely cultivated and esteemed as an ornamental potted plant, its flowers can enhance the nutritional, sensory, and functional qualities of food formulations (Castillo-Carrión et al. 2024). In studies conducted by Rios et al. (2017), *F. standishii* emerges as a crucial component in the formulation of horchata, a beverage widely integrated into the traditional practices of Southern Ecuador due to its recognized anti-inflammatory, analgesic, and diuretic properties (Rios et al. 2017). Renowned for its diverse therapeutic properties encompassing anti-inflammatory, antioxidant, antifungal, cardiotoxic, sedative, and stomachache-alleviating effects, it is a valuable botanical resource (Csepregi et al. 2016).

Despite its medicinal importance, the chloroplast genome of *F. standishii* has not been previously documented, hindering a comprehensive understanding of its genetic characteristics and evolutionary history. This study focuses on sequencing the complete chloroplast genome of *F. standishii* to lay the groundwork for further exploration and research in this field.

Materials and methods

Fresh leaves were gathered at Dali County (geospatial coordinates: 100°11'6"E, 25°84'95"N). And that is stored in the Herbarium of Dali University (<http://yxy.dali.edu.cn/yhxy/wangshuang0541@126.com>, Wang Shuang) with a voucher number WS2022111804. For whole-genome DNA sequencing, we extracted total genomic DNA using a modified CTAB method (Doyle and Doyle 1987), which was then fragmented into 150 bp for library construction and sequenced by the Illumina NovaSeq 6000 platform (Illumina, San Diego, CA, USA) (Zhang et al. 2023). This process yielded 4.64 GB of sequence data. The trimmed reads were assembled using NOVOPlasty v.4.3.1 (Dierckxsens et al. 2017). Genome annotation was performed by Geneious Prime v.2023.2.1 (Kearse et al. 2012). Manual corrections were made by comparing the sequence with the reference chloroplast genome of *Circaea cordata* (GenBank accession number: NC_060876.1). The annotated genome sequence has been submitted to GenBank (accession number: OR896387.1). We retrieved the complete chloroplast genomes of 17 Onagraceae species from GenBank. All sequences were initially aligned using MAFFT v.7.149 (Katoh and Standley, 2013). A maximum likelihood (ML) tree was constructed using IQ-TREE-1.6.8 (Nguyen et al. 2015; Wascher and Kubatko, 2021) and the TVM+F+I+R4 model, which was selected using ModelFinder (Kalyaanamoorthy et al. 2017). Using Bowtie2, the raw data is mapped back onto the assembled chloroplast

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Figure 1. *F. standishii* is a shrub with opposite leaves that are either ovate or narrow. Its flowers have a red, bell-shaped tube, with petals available in various colors, including purple, red, pink, and white. The petals are wide and obovate. The immature fruit is green and obovate oblong. A. Plant; B. Flower; C. Immature fruit. Photos of *F. standishii* were taken by Siying Li.

genome sequence (Langdon, 2015). Sorting and depth statistics are performed using samtools (Li et al. 2009). Finally, statistical plotting is conducted with a step length of one bp. CPGview was employed to generate cis-spliced and trans-spliced genes. (Liu et al. 2023).

Results

The chloroplast genome of the subject organism measures 156,391 bp and exhibits the typical quadripartite circular structure, consisting of two inverted repeat regions (IRa and IRb, each 25,069 bp), a large single-copy region (LSC, 87,754 bp), and a small single-copy region (SSC, 18,499 bp) (Figure 2). The coverage depth map of the assembly of the chloroplast genome is shown in Figure S1 and the sequencing depth at the lowest loci is 270x. This genome includes a total of 129 genes, inclusive of 84 protein-coding genes, 37 tRNA genes, and eight rRNA genes. Each of 13 protein-coding genes (*rps16*, *atpF*, *rpoC1*, *petB*, *petD*, *rpl16*, *rpl2*($\times 2$), *ndhB*($\times 2$), *ndhA*) have one intron, while two protein-coding genes (*ycf3* and *clpP*) have two introns (Figure S2), and the *rps12* gene was trans-spliced gene (Figure S3). The total GC content of the chloroplast genome is 37.60%. To unravel the phylogenetic affiliation between *F. standishii* and its relatives, we conducted a maximum likelihood (ML) analysis and constructed a phylogenetic tree (Figure 3). The resulting analysis

demonstrated that *F. standishii* forms a monophyletic group with the entire *Circaea* genus. These findings contribute significantly to the phylogenetic and evolutionary understanding of the *Fuchsia*.

Discussion and conclusions

F. standishii is highly regarded for its ornamental and medicinal properties, making it a favorite among enthusiasts. In our research, we present the complete chloroplast genome sequence of *F. standishii* for the first time, revealing a distinctive circular structure that spans 156,391 bp and contains a total of 129 genes. Phylogenetic analysis of 17 species within the Onagraceae family strongly indicates that *F. standishii* forms a monophyletic group with the entire genus *Circaea*, a finding consistent with previous molecular studies (Levin et al. 2003). Chloroplast genomes from the genus *Circaea* and *Fuchsia* are known to be maternally inherited (Corriveau and Coleman, 1988; Zhang et al. 2003). *F. standishii* forms a monophyletic group with the entire genus *Circaea* may be linked to the structural and sequence variations observed in chloroplast genomes within the Onagraceae, which differ between biparentally and maternally inherited genomes. In conclusion, our study not only enhances the genomic information available for *F. standishii* but also establishes a foundation for understanding

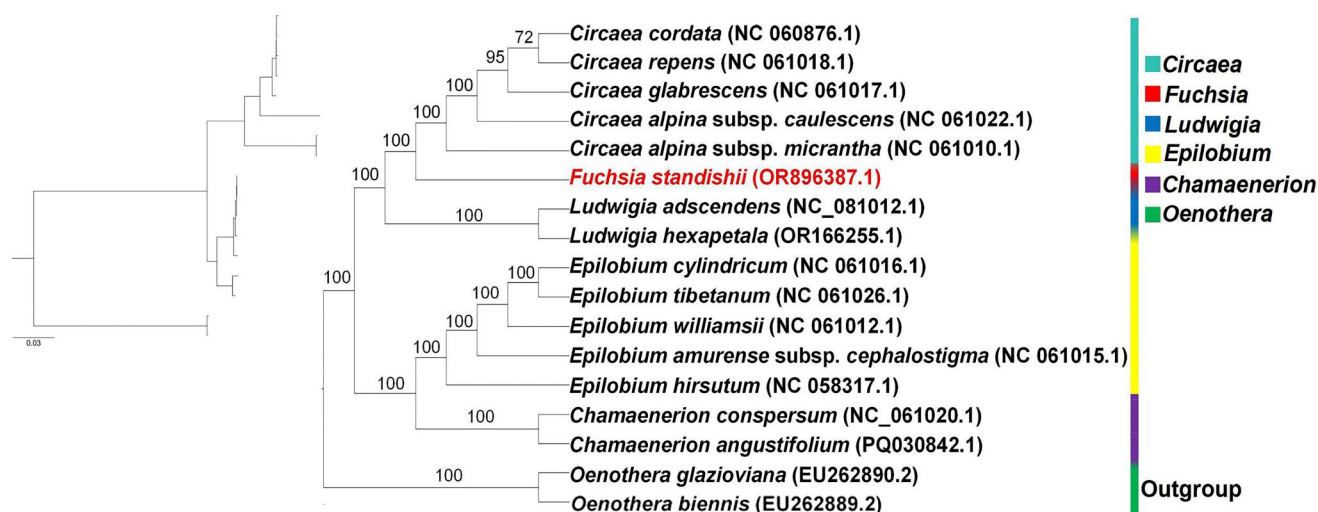


Figure 3. The phylogenetic tree was reconstructed using the maximum-likelihood (ML) optimality criterion based on 17 chloroplast genome sequences with 1,000 bootstrap replicates. The following sequences were used: *Circaea cordata* NC 060876.1 (Luo et al. 2021), *Circaea repens* NC 061018.1 (Luo et al. 2021), *Circaea glabrescens* NC 061017.1 (Luo et al. 2021), *Circaea alpina* subsp. *caulescens* NC 061022.1 (Luo et al. 2021), *Circaea alpina* subsp. *micrantha* NC 061010.1 (Luo et al. 2021), *F. standishii* OR896387.1 (This study), *Ludwigia adscendens* NC_081012.1 (No reference), *Ludwigia hexapetala* OR166255.1 (No reference), *Epilobium cylindricum* NC 061016.1 (Luo et al. 2021), *Epilobium tibetanum* NC 061026.1 (Luo et al. 2021), *Epilobium williamsii* NC 061012.1 (Luo et al. 2021), *Epilobium amurense* subsp. *cephalostigma* (NC 061015.1) (Luo et al. 2021), *Epilobium hirsutum* NC 058317.1 (No reference), *Chamaenerion conspersum* NC_061020.1 (No reference), *Chamaenerion angustifolium* PQ030842.1 (No reference), *Oenothera glazioviana* EU262890.2 (Massouh et al. 2016), *Oenothera biennis* EU262889.2 (Massouh et al. 2016).

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