

Characterization of the complete chloroplast genome of *Clerodendrum bungei* Steud. (Lamiaceae)

Yan Wang^a, Hanping Wang^b, Jinpei Wang^b, Peng Li^b, Xujiang Zhou^b, Wanqing Zhang^b, Baozhen Zhou^b, Chenxi Li^b and Zhiyong Yue^b

^aMicrobiology Institute of Shaanxi, Xi'an, Shaanxi, China; ^bCollege of Medicine, Xi'an International University, Xi'an, Shaanxi, China

ABSTRACT

Clerodendrum bungei Steud. is one kind of traditional medical herb which can be used for airway hyperreactivity treatment. In this study, the complete chloroplast genome sequence of *C. bungei* was assembled. Its complete circular chloroplast DNA length was 151,680 bp. The genome was made up of a large single-copy region of 83,189 bp, a small single-copy region of 17,311 bp, and a pair of inverted repeat regions of 25,590 bp. The genome totally encoded 130 genes, containing 85 protein-coding genes, 37 tRNA genes, and eight rRNA genes. The phylogenetic analysis indicates that *C. bungei* belongs to the Lamiaceae family.

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Clerodendrum bungei Steud. is one widely cultivated herbal species. It is used as an ornamental plant and traditional herbal medicine in many Asian countries. Current phytochemical study had identified several functional compounds from *C. bungei*, which showed positive effects to treat several diseases (Zhang et al. 2017). The effective treatment for airway hyper-responsiveness disease was confirmed using the root isolated compounds (Zeng et al. 2010). Moreover, it also had potentials in anti-complement activity (Kim et al. 2010), cancer inhibition (Shi et al. 1993) and angiotensin converting enzyme inhibitory effect (Liu et al. 2014). In this study, the chloroplast genome of *C. bungei* was assembled and its phylogenetic relationship was analyzed.



The plant sample of *C. bungei* was collected from the herb nursery of Xianyang (108.69E, 34.35 N), Shaanxi Province, China. The voucher specimen was deposited at Herbarium of the Microbiology Institute of Shaanxi, Microbiology Institute of Shaanxi (<http://sxim.xab.cas.cn/>, Yan Wang, Wangy@xab.ac.cn) under the voucher number zw2020005. The DNA from fresh leaves was extracted by CTAB method (Porebski et al. 1997). The DNA insert fragments about 400 bp in length were used for library construction. Based on the Illumina Novaseq Platform at Personal Biotechnology Co. Ltd (Shanghai, China) and 2 × 250 bp pair-end sequencing mode, total 5,021,716 reads (1.26 Gbp) were generated. The clean reads were assembled to form contig via NOVOPlasty version 4.2 (Dierckxsens et al. 2017) with *Mentha x piperita* as the reference chloroplast genome (NCBI accession number: NC_047475.1). The final chloroplast genome was annotated by CPGAVAS2 (Shi et al. 2019), and all introns/exons of genes were checked artificially.

Using the next generation sequencing technology, we assembled a circular complete chloroplast genome of *C. bungei*. The genome sequence and all gene annotations were submitted to the NCBI database with accession number of MW242824.1. The complete chloroplast genome sequence was 151,680 bp in length. The genome was consisted of a large single-copy region (LSC, 83,189 bp), a small single-copy region (SSC, 17,311 bp) and two inverted repeat regions (IR, 25,590 bp). The whole genome encoded 130 genes, including 85 protein-coding genes, 37 tRNA genes and 8 rRNA genes.

To determine the evolutionary relationship of *C. bungei*, a maximum-likelihood phylogenetic tree was constructed based on five complete chloroplast genome sequences from Lamiaceae (Figure 1). The species of *Stachys coccinea* from Lamioideae was as outgroup. All genome sequences were retrieved from the GenBank database. These sequences were aligned using MAFFT (v 7.407, Katoh and Standley 2013). Then, trimAl (v 1.4.1, Capella-Gutiérrez et al. 2009) was applied to remove poorly aligned and divergent regions with algorithm automated1. The tree was inferred using PhyML (v 20160115) ran with model and parameters: -f m -v 0 -nclases 4 -o tlr -bootstrap 100 -alpha (Guindon et al. 2010). The TVM + GTR model was chosen, and 100 bootstrap replicates were used. The result indicated that *C. bungei* belong to the subfamily of Ajugoideae.

Disclosure statement

No potential conflict of interest was reported by the author(s).

CONTACT Zhiyong Yue  yuezhiyong@nwpu.edu.cn  College of Medicine, Xi'an International University, Xi'an, Shaanxi, China

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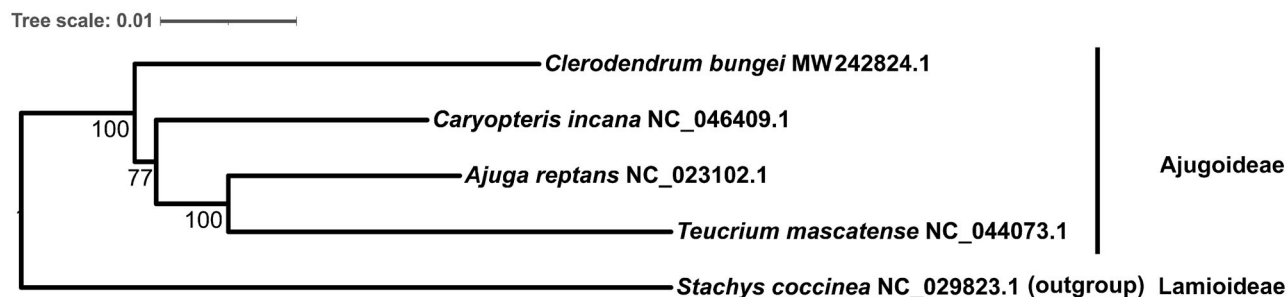


Figure 1. Phylogenetic analysis of five complete chloroplast genomes. The bootstrap support values are marked at the nodes.

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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. MW242824.1. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA682876, SRR13205877, and SAMN17013267 respectively.

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