The complete chloroplast genome sequence of Catalpa fargesii (Bignoniaceae), a species endemic to China

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ABSTRACT
Catalpa fargesii Bur. is endemic to China. Its complete chloroplast genome sequence was firstly reported in this study. The whole chloroplast genome of this species was 157765 bp in length including a pair of inverted repeat (IR, 30252 bp) regions separated by a small single copy (SSC, 12662 bp) and a large single copy (LSC, 84599 bp). The genome consisted of 134 genes, including 89 protein-coding genes, 8 rRNA and 37 tRNA genes. The phylogenetic analysis strongly supported that C. fargesii was closely related to C. fargesii f. duclouxii and C. bungei.

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four chains of the Markov Chain Monte Carlo (MCMC) were run for 5,000,000 generations starting with a random tree, sampling one tree every 1000 generations. Majority-rule (>50%) consensus trees were generated after removing a 25% burn-in. Phylogenetic analysis results strongly supported that *C. fargesii* was closely related to a clade including *C. fargesii* f. *duclouxii* and *C. bungei* (MP-BS = 100, BI-PP = 1.00) (Figure 1). The phylogenetic relationship of Bignoniaceae recovered from this study is congruent with that of Olmstead et al. (2009).

**Disclosure statement**

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

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**Data availability statement**

The data that support the finding of this study is available in GenBank at [https://www.ncbi.nlm.nih.gov/](https://www.ncbi.nlm.nih.gov/) with an accession number MW338733. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA715373, SANN18347870, and SRR14027477, respectively.

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