The complete chloroplast genome of a solid type of *Phyllostachys nidularia* (Bambusoideae: Poaceae), a species endemic to China

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Abstract

*Phyllostachys nidularia* (Bambusoideae: Poaceae), widely distributed in the Yangtze River Basin and various provinces (regions) in southern China, is one of the most important small and medium-sized bamboo species used in both bamboo shoots and timber. In the present study, we assembled a complete chloroplast genome of the economically important bamboo form *Phyllostachys nidularia f. farcta* H.R. Zhao & A.T. Liu using whole genome sequencing data previously reported. The complete chloroplast (cp) genome is 139,706 bp in length. A total of 129 unique genes were annotated, including 82 protein-coding, 39 tRNA, and eight rRNA genes. Phylogenetic analysis results supported that *P. nidularia f. farcta* was closely related to *Phyllostachys reticulata*. This work would help us better understand the evolution of the *Phyllostachys* cp genome.

Keywords:
Chloroplast genome; *Phyllostachys nidularia f. farcta*; phylogeny; whole genome sequencing data

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the data several times and found that *Phyllostachys nidularia* and *Phyllostachys reticulata* (MNS37808.1) are more similar based on pairwise genetic distance, and do not show closer *Phyllostachys nigra* var. *henonis* of Sect. *Heteroclada* in genetic distance. Previous studies (Zhang et al. 2019) have revealed that some *Phyllostachys* species may have hybridized during their long evolutionary history, which has deepened our understanding of the phylogeny of *Phyllostachys*.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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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/](https://www.ncbi.nlm.nih.gov/) under the accession no. LC590826. The associated BioProject, SRA and Bio-Sample numbers are PRJNA642983, SRS6922745 and SAMN15402429 in NCBI.

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**Figure 1.** Phylogenetic relationships among *Phyllostachys nidularia f. farcta* and 10 complete chloroplast genomes of bamboo species. Bootstrap support values are given at the nodes.