The complete chloroplast genome sequence of *Camellia rostrata* S. X. Yang & S. F. Chai (Theaceae), a critically endangered yellow camellia from southwest China

Zhao-Yuan Zhang,a Ye-Kun Yangb, Pin-Ming Ye,c Jin-Lin Ma and Hang Yea

aGuangxi Key Laboratory of Special Non-wood Forest Cultivation and Utilization, Guangxi Forestry Research Institute, Nanning, Guangxi, China; bGolden Camellia Park, Nanning, Guangxi, China

**ABSTRACT**

*Camellia rostrata* S. X. Yang & S. F. Chai is a recently described yellow camellia species from Guangxi, China. It is a critically endangered species according to the IUCN Red List Categories and Criteria. Here, we report the complete chloroplast (cp) genome based on next-generation sequencing technology. The complete cp genome of *C. rostrata* is 156,547 bp in length and consists of a large single-copy (LSC, 86,199 bp) region, a small single-copy (SSC, 18,204 bp) region, and a pair of inverted repeats (IRs, 26,072 bp). The genome contains 135 genes including 40 tRNA, eight rRNA, and 87 protein-coding genes. Phylogenetic analysis resolved *C. rostrata* in a clade containing *C. huana* and *C. impressinervis*, both of which are classified to *Camellia* sect. *Archeacamellia*. Our findings support the placement of *C. rostrata* in C. sect. *Archeacamellia* as proposed by a previous study. The cp genome of *C. rostrata* provides valuable bioinformatic resources for the protection and utilization of this yellow camellia species.

*Camellia* contains ca. 120 species (Ming 2000; Ming and Bartholomew 2007). It is mainly distributed in East and Southeast Asia, with a diversity centered in the Southern Yangtze River of China (Ming and Zhang 1996). One of these species, *C. rostrata* S. X. Yang & S. F. Chai is a newly described yellow species of *Camellia* from Guangxi, China (Liu et al. 2020). This species is restricted in its distribution to its type locality, which reportedly has <100 individuals, and was thus proposed as a critically endangered species according to the IUCN Red List Categories and Criteria (Liu et al. 2020). In this study, we report the complete cp genome sequence of *C. rostrata*, and constructed the phylogenetic relationship between *C. rostrata* and other congeneric species. The cp genome of *C. rostrata* provides useful bioinformatics for the conservation of this wild yellow species of *Camellia*.

Young leaves of *C. rostrata* were collected from Long’an county of Guangxi in China (23°03’58"N, 107°43’49"E). The voucher specimen (S. X. Yang & F. Y. Wu 6081) was deposited in the Herbarium at Kunming Institute of Botany (KUN), Chinese Academy of Sciences (KUN 1482804, http://www.kun.ac.cn, Jing-Hua Wang, wangjh@mail.kib.ac.cn). Total genomic DNA was extracted using a modified hexadecyltrimethylammonium bromide (CTAB) approach (Doyle and Doyle 1987). Genome sequencing was performed using Illumina Hi-Seq 2500 platform. The chloroplast genome sequences were assembled using GetOrganelle (Jin et al. 2020) and annotated using PGA (Qu et al. 2019). Phylogenetic analysis of *C. rostrata* and 25 other species classified to *Camellia* as well as two outgroups was performed using RAxML version 8.2.12 (Stamatakis 2014) following a previous study (Yu et al. 2017).

The complete chloroplast genome of *C. rostrata* (GenBank accession number MW755303) was obtained with a total length of 156,547 bp and a mean sequencing depth of 155.2. The GC content of the genome is 37.3%. It consisted of a large single-copy (LSC, 86,199 bp) region, a small single-copy (SSC, 18,204 bp) region, and a pair of inverted repeats (IR, 26,072 bp). A total of 135 genes were annotated, including 87 protein-coding, 40 tRNA, and eight rRNA genes. Similar to cp genomes of other *Camellia* species from GenBank, it showed typical quadripartite structure reported in angiosperms (Shinozaki et al. 1986).

Based on morphological evidence, Liu et al. (2020) stated that *C. rostrata* was most closely related to *C. debaoensis* R. C. Hu & Y. Q. Liu. However, these phylogenetic analyses indicate that *C. rostrata*, *C. huana*, and *C. impressinervis* grouped in a strongly supported clade (BS = 94%), which is sister to another highly supported clade containing *C. debaoensis* and *C. mingii* S. X. Yang (BS = 87%) (Figure 1). *Camellia huana* and *C. impressinervis* are classified in C. sect. *Archeacamellia* (Ming and Bartholomew 2007). Thus, our findings supported the placement of *C. rostrata* in C. sect. *Archeacamellia* as proposed by Liu et al. (2020). Both *C. debaoensis* and *C. mingii* were consistently placed in C. sect. *Stereocarpus* (Hu et al., 2019; Liu et al., 2019). *Camellia sect. Archeacamellia* was not revealed as monophyletic since another one/two species...
(C. petelotii, C. nitidissima, the latter was treated as a synonym of the former according to Ming’s classification system) from this section were not nested within the C. rostrata clade. The cp genome reported here provides a reference for future study on the phylogenomics of Camellia, as well as the protection and utilization of C. rostrata.

Disclosure statement
No potential conflict of interest was reported by the authors.

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Data availability statement
The 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. MW755303. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA725164, SRR14326646, and SRS8774895, respectively.

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