The complete chloroplast genome sequence of rare and endangered *Camellia pubipetala* Y. Wan & S. Z. Huang (Theaceae) of South China

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**ABSTRACT**

The complete chloroplast genome sequence of rare and endangered *Camellia pubipetala* Y. Wan & S. Z. Huang (Theaceae) was mentioned in this research. By studying comparatively, we found that the *C. pubipetala* Y. Wan & S. Z. Huang chloroplast genome was 156,993 bp in length and composed of 86,590 bp LSC, 18,211 bp SSC, and two reverse repeating regions with 26,090 bp. The whole GC content was 37.33%. The genome encoded 116 functional genes, including 80 protein-coding genes, 32 tRNA genes, and 4 rRNA genes. In order to find the phylogenetic relationship of *C. pubipetala* Y. Wan & S. Z. Huang within *Camellia* genus, we reconstructed phylogenetic tree. The results indicate that *C. pubipetala* Y. Wan & S. Z. Huang was closely related to *Camellia huanua* voucher and *Camellia ptilosperma*.

*Camellia pubipetala* Y. Wan & S. Z. Huang belongs to a species in the genus *Camellia* (family Theaceae). It only distributes in several small areas of Longan and Daxin, southwestern Guangxi, China and grows in evergreen forests on limestone (Hu et al. 2019). Because of its beautiful appearance, it has ornamental value. In addition to this, it has high medicinal value and Edible value (He et al. 2016). Due to the narrow distribution area and the damage of ecological environment from human being, the survival of these species is threatened and the number of wild population decreases sharply. The species are on the verge of extinction (Qin et al. 2017). Until now, the issue of phylogenetic relationship among *Camellia* species has failed to address. The study of chloroplast genome is conducive to solve the evolutionary position and protect the germplasm resources of *Camellia* species in the genus, we reconstructed phylogenetic tree. The results indicate that *C. pubipetala* Y. Wan & S. Z. Huang was closely related to *Camellia huanua* voucher and *Camellia ptilosperma*.

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The consequence indicated that all the Camellia species formed a monophyletic branch. We found that *C. pubipetala* Y. Wan & S. Z. Huang and *Camellia huana* voucher formed a clade with high bootstrap support (100%), and then shared a sister relationship with *Camellia ptilosperma*. This result supports the suggestion that *C. sinensis* var. *assamica* was grouped with *C. grandibracteata* with 100% bootstrap support based on nrDNA ITS (Zhang et al. 2019).

**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, reference number MW186719.

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