Complete chloroplast genome sequence of Schima superba (Teaceae)

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ABSTRACT
Schima superba Gardn. et Champ. (Teaceae), an evergreen broad-leaved tree species, which has the characteristics of rapid growth, high yield, excellent timber and strong adaptability. It is the dominant species of subtropical evergreen broad-leaved forest in China and widely distributed in the southern of China (Yao et al. 2017). Schima superba can not only be used as an excellent wood, but also can be used for medical treatment, and landscaping. Compared with other tree species, S. superba has the advantage of ecological fire prevention function, and is listed as one of the important and high-quality tree species for afforestation in southern China (Zhang et al. 2013). In recent years, as more and more data have been uploaded to the NCBI GenBank, it has provided more information on the phylogeny of Schima superba. Here, we report the complete chloroplast genome sequences of S. superba, and reveal the phylogenetic relationships to related species in Theaceae.

The sample of S. superba was collected from Fujian Province, China (Fujian Agriculture and Forestry University, Fuzhou: 26°04′49.51″N, 119°14′23.33″E). A specimen was deposited in the Herbarium of College of Forestry, Fujian Agriculture and Forestry University (Bao Liu, liubao@fafu.edu.cn) under the specimen number: FAFU0727. The improved CTAB method (Doyle 1987) was used to extract DNA of the sample. DNA was sent to BGI (The Beijing Genomics Institute) to construct DNA library and sequenced by MGISEQ-2000RS platform, with approximately 7 GB of data generated. The chloroplast genome of S. superba was then assembled using the GetOrganelle pipe-line (https://github.com/Kinggerm/GetOrganelle), by recruiting plastid-like reads. Final reads were viewed and edited by Bandage (Wick et al. 2015). The assembled chloroplast genome annotation was based on the comparison with Schima crenata by Geneious v.11.1.5 (Kearse et al. 2012). The annotation results were drawn with the online tool OGDRAW (http://ogdraw.mpimp-golm.mpg.de/) (Marc et al. 2013). After the accomplishment by annotating, the Sequin file was output and submitted to the NCBI database to obtain the GenBank accession.

The complete chloroplast genome sequence of S. superba (GeneBank accession: MZ475301) was 157,205 bp in length with a GC content of 37.40%, including a large single-copy (LSC) region of 87,161 bp, a small single-copy (SSC) region 18,092 bp, and a pair of inverted repeats (IR) regions of 25,976 bp. The genome encoded 133 functional genes, including 88 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. The phylogenetic analysis showed that S. superba was closely related to Schima sinensis, Schima multibracteata, Schima crenata, and Schima remotisertata.

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Disclosure statement

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

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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 under the accession no.MZ475301. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA743231, SRX11369043, and SAMN20003101 respectively.

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