The complete chloroplast genome sequence of *Quercus sessilifolia* Blume (Fagaceae)

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**ABSTRACT**

*Quercus sessilifolia* Blume is one of the dominant tree species in East Asian evergreen broadleaved forests. In this study, we assembled and characterized the plastome of *Q. sessilifolia* using Illumina paired-end data. The circular genome is 160,813 bp in size, consisting of two copies of inverted repeat (IR) regions of 25,862 bp, one large single-copy (LSC) region of 90,218 bp, and one small single-copy (SSC) region of 18,871 bp. It encodes a total of 113 unique genes, including 79 protein-coding genes, 30 tRNA genes, and four rRNA genes. Phylogenetic analysis based on 28 chloroplast genome sequences indicated that *Q. sessilifolia* was most closely related to *Q. myrsinifolia* with 90% bootstrap support.

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2018) was utilized to recognize locally collinear blocks among cp genomes and excavate phylogeny informative regions. Five locally collinear blocks were identified and a matrix of 99,249 bp was generated. Node support was assessed by using 1,000 fast bootstrap replicates. Our results indicated that *Q. sessilifolia* was among the members of *Quercus* section *Cyclobalanopsis*, and was most closely related to *Q. myrsinifolia* with 90% bootstrap support (Figure 1).

**Disclosure statement**

No potential conflict of interest was reported by the authors.

**Author contributions**

H.D. conceived the research; S.C. collected samples; S.C., W.Z., Y.L., X.G., X.Z., and Y.H. analyzed and interpreted data; S.C. wrote the manuscript; H.D., W.Z., and Y.L. revised the manuscript. All authors approved the final version of the article and agreed to be accountable for all aspects of the work.

**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/ under the accession no. MZ382817. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA739391, SRR14866431, and SAMN19782876, respectively.

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