**The complete chloroplast genome sequence of *Sloanea leptocarpa* (Elaeocarpaceae) from China**

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**ABSTRACT**

*Sloanea leptocarpa* Diels, 1931 of the Elaeocarpaceae is an endemic plant from China distributed in subtropical evergreen broad-leaved forests and an excellent ornamental tree. The only available chloroplast genomic resource of the genus at present is that of *S. sinensis* (Hance) Hemsl., 1900 from eastern China. Here, we report the complete chloroplast genome sequence of *S. leptocarpa* which is less common than *S. sinensis*. The complete chloroplast genome of *S. leptocarpa* is 158,077 bp in length, and shows quadripartite organization including a pair of inverted repeat regions (IRs) (24,963 bp) that is divided by a large single-copy (LSC) region (88,519 bp) and a small single-copy (SSC) region (19,632 bp). The circular chloroplast genome of *S. leptocarpa* contains 119 unique genes, composed of 74 protein-coding genes, 37 tRNA genes, and eight rRNA genes. Phylogenetic analysis involving 52 species with complete chloroplast genomes supported that *S. leptocarpa* is closely related to *S. sinensis*. This finding is in agreement with previous studies in which Elaeocarpaceae belongs to Oxalidales instead of Malvales and provides additional evidence for the monophyly of the *Sloanea*, a sister clade of the *Elaeocarpus*.

**Sloanea leptocarpa** Diels., 1931 is among seven endemic *Sloanea* spp. in China with natural habitat in the subtropical zone of broad-leaved evergreen forests and an excellent ornamental tree. The only available chloroplast genomic resource of the genus at present is that of *S. sinensis* (Hance) Hemsl., 1900 from eastern China. Here, we report the complete chloroplast genome sequence of *S. leptocarpa* which is less common than *S. sinensis*. The complete chloroplast genome of *S. leptocarpa* is 158,077 bp in length, and shows quadripartite organization including a pair of inverted repeat regions (IRs) (24,963 bp) that is divided by a large single-copy (LSC) region (88,519 bp) and a small single-copy (SSC) region (19,632 bp). The circular chloroplast genome of *S. leptocarpa* contains 119 unique genes, composed of 74 protein-coding genes, 37 tRNA genes, and eight rRNA genes. Phylogenetic analysis involving 52 species with complete chloroplast genomes supported that *S. leptocarpa* is closely related to *S. sinensis*. This finding is in agreement with previous studies in which Elaeocarpaceae belongs to Oxalidales instead of Malvales and provides additional evidence for the monophyly of the *Sloanea*, a sister clade of the *Elaeocarpus*.

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and a small single-copy (SSC 19,632 bp) region. The overall GC content of the whole genome is 37.2%, and the GC content of the LSC, SSC, and IR regions is 35.0%, 31.9%, and 43.2%, respectively. The complete chloroplast genome of *S. leptocarpa* contains 119 unique genes, including 74 protein-coding genes, 37 tRNA genes, and eight rRNA genes. The chloroplast genome length of *S. leptocarpa* is 76 bp larger than that of *S. sinensis* (Weng et al. 2021) and with similar GC content.

Phylogenetic analysis was performed to confirm the position of *S. leptocarpa*. We used the complete chloroplast genomes of 52 plant species, including *S. leptocarpa* itself and 51 additional plants from the Malvales, Oxalidales, Malpighiales, Celastrales, Fagales, Cucurbitales, and Rosales, as well as *Tropaeolum pentaphyllum*, *Cravea tapia*, *Capparis spinosa*, the member of the Brassicales, as the outgroup. The complete chloroplast genomes were aligned using Multiple Sequence Alignment based on Fast Fourier Transform – MAFFT (Nakamura et al. 2018) and a maximum-likelihood tree (Figure 1) was constructed using IQ-TREE under best-fit model GTR + G + I based on Bayesian information criterion (BIC) (Nguyen et al. 2015). The phylogenetic analysis result strongly supported that *S. leptocarpa* is closely related to *S. sinensis* in the genus *Sloanea* (Figure 1), and *S. leptocarpa* is a member of the Elaeocarpaceae family which should be placed in Oxalidales instead of Malvales. This finding is consistent with the previous studies on Elaeocarpaceae (Wang et al. 2021; Weng et al. 2021). Our work provides additional evidence for the monophyly of *Sloanea* as the sister clade of *Elaeocarpus* in the Elaeocarpaceae. In conclusion, this *S. leptocarpa* chloroplast genome will provide a genomic resource for future genetic studies and new molecular data to illuminate the Oxalidales evolution.

**Author contributions**

ZS conceptualized the research, performed data analyses, and wrote the manuscript. AP contributed to revising the manuscript. YL participated in the data analyses. JL...
participated conceptualizing the research. All authors made critical contributions to writing the manuscript.

**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 at [https://www.ncbi.nlm.nih.gov/](https://www.ncbi.nlm.nih.gov/), under the accession no. MZ359674. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA763694, SRR15909932, and SAMN21447341, respectively.

**References**

Coode MJE. 1983. A conspectus of Sloanea (Elaeocarpaceae) in the old world. Kew Bull. 38(3):894–427.

Coode MJE. 2004. Elaeocarpaceae. In: Kubitzki K, editor. The families and genera of vascular plants, Volume VI: flowering plants Dicotyledons Celastrales, Oxalidales, Rosales, Cornales, Ericales. Heidelberg: Springer; p. 135–144.

Dierckxsens N, Mardulyn P, Smits G. 2017. NOVOPlasty: de novo assembly of organelle genomes from whole genome data. Nucleic Acids Res. 45(4):e18.

Doyle JJ, Doyle JL. 1990. Isolation of plant DNA from fresh tissue. Focus. 12:13–15.

Liu C, Shi L, Zhu Y, Chen H, Zhang J, Lin X, Guan X. 2012. CpGAVAS, an integrated web server for the annotation, visualization, analysis, and GenBank submission of completely sequenced chloroplast genome sequences. BMC Genomics. 13:715.

Nakamura T, Yamada KD, Tomii K, Katoh K. 2018. Parallelization of MAFFT for large-scale multiple sequence alignments. Bioinformatics. 34(14):2490–2492.

Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol. 32(1):268–274.

Tang Y, Phengklai C. 2007. Elaeocarpaceae. In: Wu ZY, Raven PH, Hong DY, editors. Flora of China. Vol. 12 (Hippocastanaceae through Theaceae). Beijing; St. Louis: Sciences Press; Missouri Botanical Garden Press; p. 223–239.

Tillich M, Lehwark P, Pellizzer T, Ulbricht-Jones ES, Fischer A, Bock R, Greiner S. 2017. GeSeq: versatile and accurate annotation of organelle genomes. Nucleic Acids Res. 45(W1):W6–W11.

Wang H, Feng H, Zhang Y, Chen H. 2014. Contrasting regeneration strategies in climax and long-lived pioneer tree species in a subtropical forest. PLOS One. 9(11):e112385.

Wang YH, Zhang ZX, Xie YF. 2021. The complete chloroplast genome of Elaeocarpus japonicus Sieb. et Zucc. (Elaeocarpaceae). Mitochondrial DNA B Resour. 6(2):557–559.

Weng YH, Ye DQ, You YF, Chen YT, Fan FJ, Shi JS, Chen JH. 2021. The complete chloroplast genome sequence of Sloanea sinensis. Mitochondrial DNA Part B. 6(2):555–556.