The complete chloroplast genome of *Scurrula chingii* (W.C. Cheng) H.S. Kiu (Loranthaceae), a hemiparasitic shrub

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**ABSTRACT**

*Scurrula chingii* (W.C. Cheng) H.S. Kiu is a stem hemiparasite of the genus *Scurrula* in the family Loranthaceae distributed in southwest China and northern Vietnam. Here, we report and characterize the complete plastid genome sequence of *S. chingii* to provide genomic resources useful for the phylogenetic studies of Santalales. The plastome of *S. chingii* is 122,764 bp in length, consisted of a large single-copy region (70,726 bp), a small single-copy region (6,091 bp), and a pair of inverted repeat regions (22,974 bp). The GC content of the whole plastome is 37.2%. It contains 109 genes, including 69 CDS (protein-coding genes), eight rRNAs, and 32 tRNAs. The alignment of 14 species complete chloroplast genomes of Loranthaceae was implemented and a phylogenetic tree was constructed using maximum-likelihood (ML) method, which revealed that *S. chingii* clustered with *Scurrula parasitica* and *Taxillus thibetensis* as a monophyletic group.
GC content of the whole plastome is 37.2%. Meanwhile, a total of 109 genes were annotated, including 69 CDS (protein-coding genes), eight rRNAs, and 32 tRNAs. Among them, seven genes (rpl16, atpF, rpoC1, trnLUAA, petB, petD, and rpl2) have the single intron and three genes (rps12, ycf3, and clpP) have two introns. The special feature of the plastome, as same as the plastome of the tobacco, is that rps12 consists of three exons and its 5' exon (5'-rps12) is located downstream from the other exons (3'-rps12) in IRb on the same strand, or downstream from the 3'-rps12 in IRa on the opposite strand. rpl2 gene straddled LSC/IRa border, and trnl-UAG gene straddled IRa/SSC and SSC/IRb border and compared to the plastome of Nicotiana tabacum (GenBank accession number: NC001879), the NADH dehydrogenase complex proteins (ndhA, ndhB, ndhC, ndhD, ndhE, ndhF, ndhG, ndhH, ndhI, ndhJ, and ndhK), four genes of ribosomal proteins (rpl2, rps15, rps16, and rpl32) and five tRNA genes (trnA, trnG, trnL, trnK, and trnV) are missing.

The topology of the phylogenetic tree shows that the S. chingii clustered with Scurrula parasitica and Taxillus thibetensis as a monophyletic group with a 100% bootstrap value (Figure 1). The study corroborated the close phylogenetic relationship between Scurrula and Taxillus. The placement of T. thibetensis, however, conflicts with the former study by Liu et al. (2018). We suspect the reason could be different DNA regions were used in the analysis and due to hemiparasitic plants do not wholly depend on their photosynthetic capacity, some genes of the plastome are lost. Similarly, the phenomenon of gene loss was also found in the other two hemiparasitic species, Taxillus chinensis and T. sutchuenensis (Li et al. 2017). Therefore, the complete chloroplast genome and phylogeny of hemiparasites from the Loranthaceae deserve further research.

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

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Data availability statement
The plastome data of *S. chingii* (accession number is MT921832) using in this manuscript are deposited in GenBank of NCBI at (https://www.ncbi.nlm.nih.gov/), which can be searched after being examined and processed. We declare that the data should only be shared when not violating the protection of human subjects, or other valid ethical, privacy, or security concerns.

References
Jin J-J, Yu W-B, Yang J-B, Song Y, dePamphilis CW, Yi T-S, Li D-Z. 2020. GetOrganelle: a fast and versatile toolkit for accurate de novo assembly of organelle genomes. Genome Biol. 21(1):241.

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 30(4):772–780.

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics. 28(12):1647–1649.

Li J-L, Wang S, Yu J, Wang L, Zhou S-L. 2013. A modified CTAB protocol for plant DNA extraction. Chin Bull Bot. 48:72–78.

Li Y, Zhou J-G, Chen X-L, Cui Y-X, Xu Z-C, Li Y-H, Song J-Y, Duan B-Z, Yao H. 2017. Gene losses and partial deletion of small single-copy regions of the chloroplast genomes of two hemiparasitic *Taxillus* species. Sci Rep. 7(1):12834.

Liu B, Le C-T, Barrett RL, Nickrent DL, Chen Z-D, Li L-M, Vidal-Russell R. 2018. Historical biogeography of Loranthaceae (Santalales): diversification agrees with emergence of tropical forests and radiation of songbirds. Mol Phylogenet Evol. 124:199–212.

Miller MA, Pfeiffer W, Schwartz T. 2010. Creating the CIPRES Science Gateway for inference of large phylogenetic trees. Proceedings of the Gateway Computing Environments Workshop (GCE); Nov 14; New Orleans, LA. p. 1–8.

Press MC, Phoenix GK. 2005. Impacts of parasitic plants on natural communities. New Phytol. 166(3):737–751.

Wang X-N, Zhang L. 2017. Species diversity and distribution of mistletoes and hosts in four different habitats in Xishuangbanna, Southwest China. J Yunnan Univ (Nat Sci). 39(4):701–711.