MITOCHONDRIAL DNA PART B
2021, VOL. 6, NO. 1, 282–284
https://doi.org/10.1080/23802359.2020.1863166

Taylor & Francis
Taylor & Francis Group

MITOGENOME ANNOUNCEMENT

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

Manru Li[a,b], Yifei Zhang[a,b], Yuanjie Li[a,b] and Ling Zhang[a,b]

[a]CAS Key Laboratory of Tropical Forest Ecology, Xishuangbanna Tropical Botanical Garden, Menglun, China; [b]University of Chinese Academy of Sciences, Beijing, China

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.

ARTICLE HISTORY
Received 8 September 2020
Accepted 27 October 2020

KEYWORDS
Scurrula chingii; hemiparasite; chloroplast genome; phylogenetic analysis

Scurrula chingii (W.C. Cheng) H.S. Kiu is a stem hemiparasite distributed in southwest China (Guangxi and Yunnan provinces) and northern Vietnam at varied elevations from foothills to mountain ranges (http://www.efloras.org/). Although these plants conduct photosynthesis, they obtain a part of water and nutrients by parasitism, which is considered to be a pest as its infection intensity is high (Press and Phoenix 2005). As a generalist mistletoe, *S. chingii* can infect more than 38 host species (29 genera, 21 families) such as *Camellia oleifera* (Theaceae), *Vernicia montana* (Euphorbiaceae), and *Ficus hispida* (Moraceae) in Xishuangbanna, Southwest China (Wang and Zhang 2017). *S. chingii* can be usually found in altitudes between 490 and 1745 m a.s.l. in open forests and plantations and is less common in humid forests in Xishuangbanna, and dependent on frugivores birds for their pollination and seed dispersal (Wang and Zhang 2017). Here, we report the complete plastome of *S. chingii* based on Illumina paired-end sequencing data, reconstruct a phylogenetic tree and explore the evolutionary relationship of Loranthaceae, which will contribute to understanding the basic biological characteristics and role of mistletoe in the ecosystem further.

Fresh leaves of *S. chingii* were collected from Jinghong, Yunnan, Southwest China (Long. 101.097227 E, Lat. 22.428739 N, 860 m). The voucher specimen (accession number: LYJ-21) was deposited in the laboratory of the Research Group 'Ecology and Evolution of Plant–Animal Interaction' at Xishuangbanna Tropical Botanical Garden. Genomic DNA was extracted from the silica gel dried leaves using the modified cetyltrimethylammonium bromide (mCTAB) method (Li et al. 2013). Then, it was sheared into fragments to build Illumina libraries. The NGS (next generation sequencing) library was sequenced on Illumina HiSeq 2500 platform using 150 bp paired-end strategy. Meanwhile, the raw sequence data were uploaded on the NCBI (SRA accession number: PRJNA666529). The plastome of *S. chingii* was assembled into circular form from the raw reads using Getorganelle toolkit (Jin et al. 2020). Finally, compared to the plastome of the *Taxillus chinensis* (GenBank accession number: NC036306), it was annotated by Geneious Prime software (Kearse et al. 2012). For the fear of omitting annotations, we also manually adjusted annotations by comparing it with other plastomes of Loranthaceae that can be available on GenBank.

To confirm the phylogenetic position of the *S. chingii*, we downloaded 14 species plastomes of Loranthaceae from the GenBank and set the *Erythropalum scandens* (Olacaceae) (GenBank accession number: NC036759) as the outgroup to construct the phylogenetic tree. We used the MAFFT toolkit with default parameters to align the whole plastome sequences with one IR region (Katoh and Standley 2013). The maximum-likelihood (ML) tree was constructed using GTRCAT model with 1000 bootstrap iterations on the CIPRES portal (https://www.phylo.org) by RAxML-HPC2 toolkit (Miller et al. 2010).

The plastome of *S. chingii* (GenBank accession number: MT921832) is 122,764 bp in length, which consists of a large single-copy region (70,726 bp), a small single-copy region (6091 bp), and a pair of inverted repeat regions (22,974 bp). The

CONTACT Ling Zhang zhangl@xtbg.org.cn CAS Key Laboratory of Tropical Forest Ecology, Xishuangbanna Tropical Botanical Garden, Menglun, China

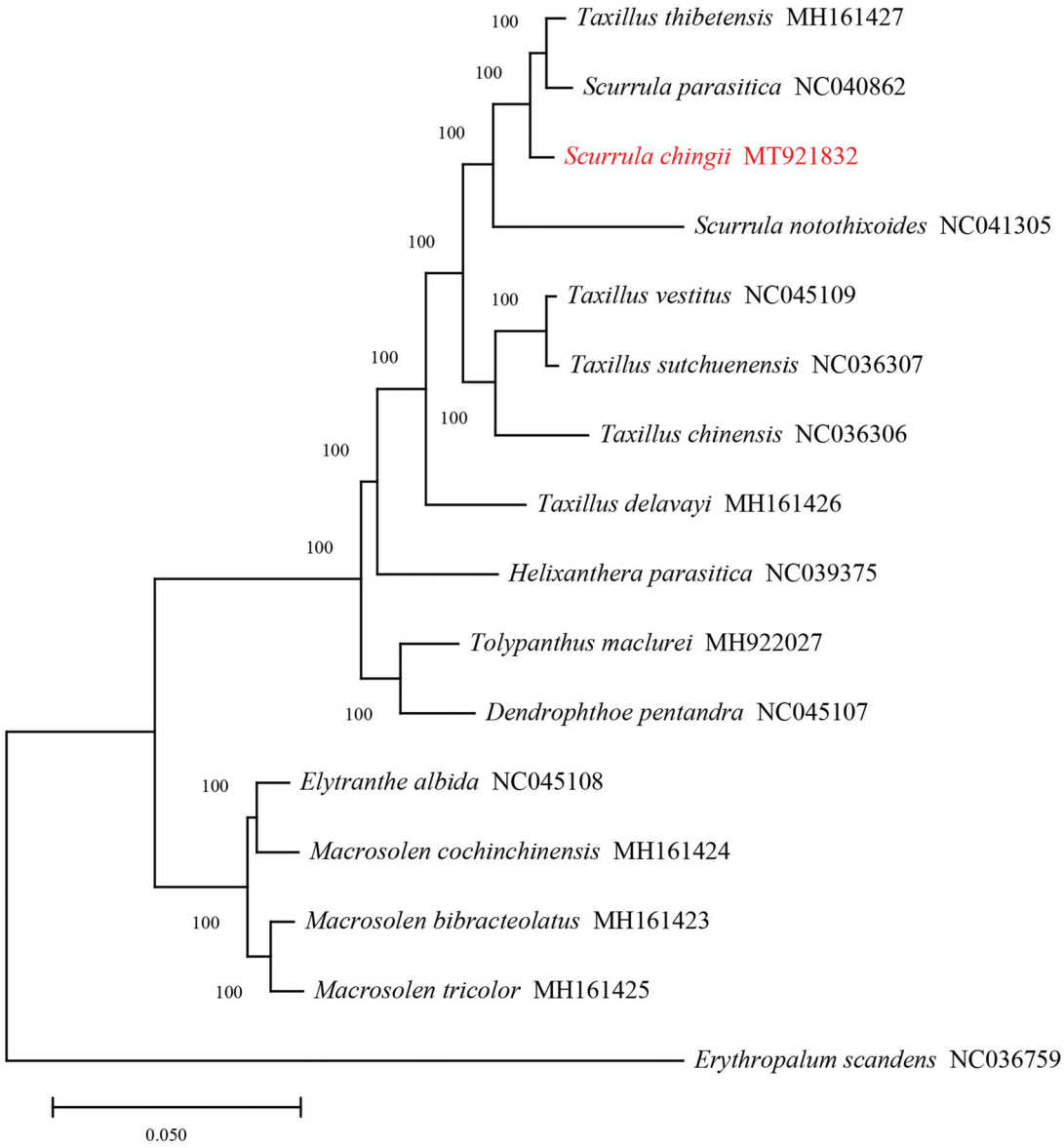

Figure 1. Maximum-likelihood phylogenetic tree based on 15 complete cp genomes ofLoranthaceae. The outgroup is Erythropalum scandens. Numbers above nodes indicate bootstrap support valueswith 1,000 replicates.

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′-*rpsl2* in IRa on the opposite strand. *rpl2* gene straddled LSC/IRa border, and *trnI*-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*, *trnI*, *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.

Acknowledgements

We would like to thank the Molecular Biology Experiment Center, Germplasm Bank of Wild Species in Southwest China, Kunming Institute of Botany, Chinese Academy of Sciences.

Disclosure statement

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

Funding

This work was supported by the National Natural Science Foundation of China under Grant [Number 31670393]. The Large-scale Scientific Facilities of the Chinese Academy of Sciences [Number 2017LSFGBOWS-02].

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.